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1. Prevalensi HBsAg, anti-HBc dan anti-HBs pada subyek penelitian

Lokasi	N			HBsAg			Anti-HBc			Anti-HBs		
	n (%)	(+) (%)	n (%)	n (%)	(+) (%)	n (%)	n (%)	(+) (%)	n (%)	(+) (%)	n (%)	
RSUH	144	18 (12.5)	144 (100.0)	144 (100.0)	18 (12.5)	144 (100.0)	144 (100.0)	18 (12.5)	144 (100.0)	27 (18.8)	144 (100.0)	
RSU Palopo	140	3 (2.1)	140 (100.0)	140 (100.0)	3 (2.1)	140 (100.0)	140 (100.0)	24 (17.1)	140 (100.0)	39 (27.9)	140 (100.0)	
RSUD BANTAENG	87	7 (8.0)	87 (100.0)	87 (100.0)	7 (8.0)	87 (100.0)	84 (96.6)	26 (29.9)	84 (96.6)	27 (32.1)	84 (96.6)	
Rs. Massenrempulu	99	2 (2.0)	99 (100.0)	99 (100.0)	2 (2.0)	99 (100.0)	99 (100.0)	23 (23.2)	99 (100.0)	29 (29.3)	99 (100.0)	
Nakes RSGP	174	0 (0.0)	174 (100.0)	174 (100.0)	0 (0.0)	174 (100.0)	174 (100.0)	28 (16.1)	174 (100.0)	113 (64.9)	174 (100.0)	
Pasien RSGP	609	24 (3.9)	609 (100.0)	607 (99.7)	24 (3.9)	607 (99.7)	184 (30.3)	184 (30.3)	184 (30.2)	130 (70.7)	184 (30.2)	
	1253	54 (28.6)	1253 (100.0)	1251 (99.8)	54 (28.6)	1251 (99.8)	825 (65.8)	303 (24.2)	825 (65.8)	365 (44.2)	825 (65.8)	

LAMPIRAN

Hasil pemeriksaan anti-HCV, anti-HBV atau anti-HIV, anti-HCV dan anti-HIV

Lokasi	N	Anti-HCV			Anti-HIV			Anti-HCV atau Anti-HIV			Anti-HCV dan Anti-HIV						
		n	%	(+)	n	%	(+)	n	%	(+)	n	%	(+)	%			
RSUH	144	144	100.0	0	0.0	144	100.0	2	1.4	144	100.0	2	1.4	144	100.0	0	0.0
RSU Palopo	140	140	100.0	2	1.4	140	100.0	3	2.1	140	100.0	5	3.6	140	100.0	0	0.0
RSUD BANTAENG	87	84	96.6	0	0.0	84	96.6	1	1.2	87	96.6	1	1.2	87	96.6	0	0.0
Rs. Massenrempulu	99	0	-	-	-	0	-	-	-	99	-	-	-	99	-	0	-
Nakes RSGP	174	174	100.0	0	0.0	174	100.0	0	0.0	174	100.0	0	0.0	174	100.0	0	0.0
Pastien RSGP	609	607	99.7	15	2.5	607	99.7	9	1.5	609	99.7	22	3.6	609	99.7	2	0.3
Jumlah	1253	1149	91.7	17	1.5	1149	91.7	15	1.3	1253	91.7	30	2.6	1253	91.7	2	0.2

N : Jumlah subjek

n : jumlah diperiksa

(+): positif

Lampiran 3. Sekuens Gen S Regio determinan 'a' HBsAg dari 73 sampel OBI

	120	130	140	150	160	170	180
M54923	ATTCCAGGAT	CATCAACCAC	CAGCACCGGA	CCATGCAAAA	CCTGCACGAC	TCCTGCTCAA	GGAACCTCTA
H-0704			.G.	.G.	.t		
H-0751			.g.	.G.	.T		
H-0760				.g.	.A.		
H-0763				.g.	.a.		
H-0783			.G.	.G.	.T		
H-0784				.g.	.a.		
H-0787				.g.	.A.		
H-0831							
H-0880							
H-0896			.g.	.g.	.T		
H-1401					.A.		
H-1441							
H-1446			.g.	.g.	.g		
H-1770					.A.		.G.
H-1805							
H-1822				.g.			
HCW-032							
HCW-074			.g.	.G.	.T		
HCW-083			.G. .g	.G.			
HCW-118							
HCW-125							
HCW-164							
J-0004							
J-0023			.g.	.g.	.T		
J-0034			.g.	.g.	.T		
J-0035					.G.		
J-0039				.g.			
J-0044			.g.	.C.	.T		
J-0050							
J-0053			.g.	.g.	.T		
J-0055			.g.	.g.	.T		
J-0057			.g.	.g.	.T		
J-0059			.G.	.G.	.T		
J-0060			.G.	.G.			
J-0063							
J-0069							
J-0076			.G.	.G.	.T		
J-0077					.C.		
J-0079			.g.	.G.	.T		
J-0086			.g.	.g.	.t		
J-0095					.C.		
J-0105			.g.	.g.	.T		
J-0126				.g.			
J-0129						.T	
J-0157				.g.			
J-0159				.g.			
J-0173			.g.	.g.			
J-0182						.C.	
H-0744 (HBsAg+)			.g.	.G.	.T		
H-0745 (HBsAg+)			.G.	.G.	.T	.A.	
H-0747 (HBsAg+)			.G.	.G.	.T		
H-0843 (HBsAg+)			.G.	.G.			
H-0851 (HBsAg+)			.g.	.g.	.t		
H-1505 (HBsAg+)							
H-1605 (HBsAg+)			.G.	.G.	.T		
H-1702 (HBsAg+)							
H-1775 (HBsAg+)			.t.	.g.			
H-1812 (HBsAg+)			.G.	.G.	.T		
J-0036 (HBsAg+)				.g.			
J-0040 (HBsAg+)			.g.	.G.			
J-0043 (HBsAg+)							
J-0046 (HBsAg+)			.g.	.g.			
J-0048 (HBsAg+)			.G.	.G.	.t		
J-0066 (HBsAg+)							
			.G.	.G.			
				.g.			
					.AG.		
					.A.	.C	



M54923	TGTTTCCTC	ATGTTGCTGT	ACAAAACCTA	CGGACGGAAA	CTGCACCTGT	ATTCCCATCC	CATCATCTTG
H-0704	T	T	T	T	T	T	T
H-0751	T	T	T	T	T	T	T
H-0760							
H-0763							
H-0783	T		T		T	T	
H-0784							
H-0787							
H-0831							
H-0880	C	C					
H-0896	T		T		T	T	
H-1401							
H-1441							
H-1446	T		T		T	T	
H-1770							
H-1805							
H-1822							
HCW-032							
HCW-074	t		T		T	T	
HCW-083	t		T		T		C
HCW-118							
HCW-125							
HCW-164							
J-0004							
J-0023	T		T		t		
J-0034	T		T		T	T	
J-0035							
J-0039							
J-0044	T		T		T	T	
J-0050			T				
J-0053	T		T		T	T	
J-0055	T		T		T	T	
J-0057	T		T		T	T	
J-0059	T		T		T	T	
J-0060	T		T		T	T	
J-0063							
J-0069							
J-0076	T		T		T	T	
J-0077							
J-0079	T		t		T	A	
J-0086	T		t	T	T	T	
J-0095							
J-0105	T		t		t	T	
J-0126							
J-0129							
J-0157						T	
J-0159						T	
J-0173							
J-0182	T		T		T	T	
H-0744 (HBsAg+)	T		T		T	T	
H-0745 (HBsAg+)	T	C	T		T	T	
H-0747 (HBsAg+)	T		T		T	T	
H-0843 (HBsAg+)	T		T		T	T	
H-0851 (HBsAg+)	t		T		T	T	
H-1505 (HBsAg+)			T				
H-1605 (HBsAg+)	T		T		T	T	
H-1702 (HBsAg+)					t		
H-1775 (HBsAg+)	t		t		t	t	
H-1812 (HBsAg+)	T		T		T	T	
J-0036 (HBsAg+)							
J-0040 (HBsAg+)	T		T		T	T	
J-0043 (HBsAg+)							
J-0046 (HBsAg+)	T		T		T	T	
J-0048 (HBsAg+)	T		T		T	T	
J-0066 (HBsAg+)							
J-0068 (HBsAg+)							
	T		T		T	T	
						T	
							G
	A						



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                260       270       280       290       300       310
M54923  GGCTTTCGCA AAATACCTAT GGGAGTGGGC CTCAGTCCGT TTCCTTTGGC TCAGTTTACT AGTGCCA
H-0704  .....T.....C.....
H-0751  .....G..T.....C.....
H-0760  .....G..T.....C.....
H-0763  .....G..T.....C.....
H-0783  .....G..T.....C.....
H-0784  .....G..T.....C.....
H-0787  .....G..T.....C.....
H-0831  .....G..T.....C.....
H-0880  .....G..T.....C.....
H-0896  .....G..T.....C.....
H-1401  .....G.....A.....C.....
H-1441  .....G..T.....C.....
H-1446  .....G..T.....C.....
H-1770  .....G..T.....C.....
H-1805  .....G..T.....C.....
H-1822  .....G..T.....C.....
HCW-032 .....G..T.....C.....
HCW-074 .....G..T.....C.....
HCW-083 .....G..T.....C.....
HCW-118 .....G..T.....C.....
HCW-125 .....G..T.....C.....
HCW-164 .....G..T.....C.....
J-0004  .....G..T.....C.....
J-0023  .....G..T.....C.....
J-0034  .....G..T.....C.....
J-0035  .....G..T.....C.....
J-0039  .....G..T.....C.....
J-0044  .....G..T.....C.....
J-0050  .....G..T.....C.....
J-0053  .....G..T.....C.....
J-0055  .....G..T.....C.....
J-0057  .....G..T.....C.....
J-0059  .....G..T.....C.....
J-0060  .....G..t.....t.....c.....
J-0063  .....G..T.....C.....
J-0069  .....G..T.....C.....
J-0076  .....G..T.....C.....
J-0077  .....G..T.....C.....
J-0079  .....G..T.....C.....
J-0086  .....G..T.....C.....
J-0095  .....G..T.....C.....
J-0105  .....g..T.....C.....
J-0126  .....G..T.....A.....C.....
J-0129  .....G..T.....C.....
J-0157  .....G..T.....C.....
J-0159  .....G..T.....C.....
J-0173  .....G..T.....C.....
J-0182  .....G..T.....T.....C.....A.....
H-0744 (HBsAg+) .....G..T.....C.....
H-0745 (HBsAg+) .....G..T.....C.....
H-0747 (HBsAg+) .....G..T.....C.....
H-0843 (HBsAg+) .....G..T.....C.....
H-0851 (HBsAg+) .....G..T.....c.....T.....
H-1505 (HBsAg+) .....G..T.....C.....
H-1605 (HBsAg+) .....G..T.....C.....
H-1702 (HBsAg+) .....g..t.....c.....
H-1775 (HBsAg+) .....G..T.....C.....
H-1812 (HBsAg+) .....G..T.....C.....
J-0036 (HBsAg+) .....T..g..t.....T.....C.....
J-0040 (HBsAg+) .....T..g..t.....C.....
J-0043 (HBsAg+) .....G..T.....C.....
J-0046 (HBsAg+) .....G..T.....C.....
J-0048 (HBsAg+) .....G..T.....C.....
.....G..T.....C.....
.....G..T.....C.....
.....T.....

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Lampiran 4. Sekuens Gen S Lengkap dari 4 Sampel OBI

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      10      20      30      40      50      60      70
M54923 (2849-833)  atgggagggtt  ggtcctccaa  acctcgacaa  ggcatgggga  caaatctttc  cgtcceccaat  cctctgggat
J-0035 (OBI)      .....      .....      c.tc.....      .....      t.....      ..C.....
J-0069 (OBI)      .....      .....      .....      .....      .....      .....      .....      .....
J-0060 (OBI)      .....      .....      .....      .....      .....      .....      .....      .....
J-0063 (OBI)      .....      .....      .....      .....      .....      .....      .....      .....

      80      90      100     110     120     130     140
M54923 (2849-833)  tctttcccgga  tcaccagttg  gaccctgcat  tcaaagccaa  ctccgacaat  cccgattggg  acctcaaccc
J-0035 (OBI)      .....      .....      .....      .....      .....      A.A.....      a.....
J-0069 (OBI)      .....      .....      .....      .....      .....      .....      .....      .....
J-0060 (OBI)      .....      G.....      .....      A.G.....      GG.....      T.AA.....      A.....      T.....
J-0063 (OBI)      .....      .....      .....      .....      .....      .....      .....      .....

      150     160     170     180     190     200     210
M54923 (2849-833)  acacaaggac  aactggccgg  actccaacaa  ggtgggagt  ggagcattcg  ggccgggatt  cactccaccc
J-0035 (OBI)      C.....      .....      G.....      .....      .....      A.G.....      C.T.....
J-0069 (OBI)      .....      .....      .....      .....      .....      .....      .....      .....
J-0060 (OBI)      CA.....      t C.A.....      A.CGG.A.....      A.....      .....      A.G.....      A.....
J-0063 (OBI)      .....      .....      .....      .....      .....      .....      .....      .....

      220     230     240     250     260     270     280
M54923 (2849-833)  catgggggac  tgttggggtg  gagccctcaa  gctcagggca  tactcacaac  tgtgccaaca  gctcctctc
J-0035 (OBI)      .....      .....      .....      G.....      C.....      G.....      G.....
J-0069 (OBI)      .....      .....      .....      .....      .....      .....      .....      .....
J-0060 (OBI)      C.....      CA.T.....      T.....      G.....      G.....      A.....      G.....      G.....
J-0063 (OBI)      .....      .....      .....      .....      .....      .....      .....      .....

      290     300     310     320     330     340     350
M54923 (2849-833)  ctgcctccac  caatcggcag  ttaggaagga  agcctactcc  cctgtctcca  cctctaagag  acaactcatcc
J-0035 (OBI)      .....      .....      CG.....      C.....      G.a.....      G.....
J-0069 (OBI)      .....      A.....      G.....      .....      .....      .....      .....
J-0060 (OBI)      .....      .....      .....      .....      .....      .....      .....
J-0063 (OBI)      .....      .....      G.....      .....      .....      .....      .....

      360     370     380     390     400     410     420
M54923 (2849-833)  tcaggccatg  cagtggaact  ccaccacgtt  ccaccaaact  cttcaagatc  ccagagtcag  ggcctgttac
J-0035 (OBI)      .....      .....      T.....      T.....      .....      .....      C.C.....
J-0069 (OBI)      .....      .....      .....      .....      .....      .....      C.....      T.....
J-0060 (OBI)      .....      .....      .....      A.....      G.....      G.T.....      G.....      GC.A.G.....
J-0063 (OBI)      .....      .....      .....      .....      G.....      .....      C.....      T.....

      430     440     450     460     470     480     490
M54923 (2849-833)  tttcctgctg  gtggctccag  ttcaggaaca  gtaaaccttg  ttcagaacac  tgtctcttcc  atatcgtaa
J-0035 (OBI)      .....      .....      .....      G.G.....      C.....      T.....      G.....
J-0069 (OBI)      .....      .....      .....      G.....      .....      C.....      .....
J-0060 (OBI)      .....      .....      A.....      C.....      .....      CA.CT.....      C.....      c.....      T.....
J-0063 (OBI)      .....      .....      .....      G.....      .....      .....      C.....      .....

      500     510     520     530     540     550     560
M54923 (2849-833)  tcttatcgaa  gactggggac  cctgtgccga  acatgggagaa  catcgcatca  ggactcctag  gacccctgct
J-0035 (OBI)      C.....      .....      CA.....      .....      .....      .....      .....
J-0069 (OBI)      .....      .....      .....      .....      .....      .....      .....
J-0060 (OBI)      a...c...g.....      .....      ct.....      T.....      G.....      c.A.....      .....
J-0063 (OBI)      .....      .....      .....      .....      .....      .....      .....

      570     580     590     600     610     620     630
M54923 (2849-833)  cgtgttacag  gcggggtttt  tcttgttgac  aaaaatcctc  acaataccac  agagtctaga  ctcgtggtgg
J-0035 (OBI)      .....      .....      .....      .....      .....      .....      .....
J-0069 (OBI)      .....      .....      .....      .....      .....      .....      .....
J-0060 (OBI)      .....      .....      .....      .....      .....      .....      .....
J-0063 (OBI)      .....      .....      .....      G.....      .....      .....      .....

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        640      650      660      670      680      690      700
M54923 (2849-833) acttctetca atttctagg ggaacaccc gtgtgtcttg gccaaaattc gcagtcccaa atctccagtc
J-0035 (OBI)      ..... ..A..t... ..G..
J-0069 (OBI)      .....
J-0060 (OBI)      .....G...AC...C...T...C..C...A..
J-0063 (OBI)      .....C..

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        710      720      730      740      750      760      770
M54923 (2849-833) actcaccaac ttgttgcct cegatttgtc ctggttatcg ctggatgtgt ctgcccgttt ttatcatctt
J-0035 (OBI)      .....C.....A.....
J-0069 (OBI)      .....
J-0060 (OBI)      .....C.T.....A...A...
J-0063 (OBI)      .....

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        780      790      800      810      820      830      840
M54923 (2849-833) cctctgcatc ctgctgctat gcctcatctt cttgttggtt cttctggact atcaaggat gttgcccgtt
J-0035 (OBI)      .....
J-0069 (OBI)      .....
J-0060 (OBI)      .....T.....C.....
J-0063 (OBI)      .....

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        850      860      870      880      890      900      910
M54923 (2849-833) tgtcctctaa ttccaggatc atcaaccacc agcaccggac catgcaaaac ctgcacgact cctgctcaag
J-0035 (OBI)      .....G.....G.....
J-0069 (OBI)      .....C.....
J-0060 (OBI)      .....C...A.T...T...G...G...
J-0063 (OBI)      .....

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```

        920      930      940      950      960      970      980
M54923 (2849-833) gaacctctat gtttccctca tgttgcgtga caaaacctac ggacggaaac tgcacctgta ttcccattcc
J-0035 (OBI)      .....
J-0069 (OBI)      .....
J-0060 (OBI)      .....T.....T...T...T...
J-0063 (OBI)      .....

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```

        990      1000      1010      1020      1030      1040      1050
M54923 (2849-833) atcattcttg gctttcgcaa aatacctatg ggagtgggcc tcagtccggt tctcttggct cagtttacta
J-0035 (OBI)      .....
J-0069 (OBI)      .....
J-0060 (OBI)      .....G..t.....t...c...
J-0063 (OBI)      .....

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```

        1060      1070      1080      1090      1100      1110      1120
M54923 (2849-833) gtgccatttg ttcagtgggt cgtagggett tccccactg tctggctttc agttatatgg atgatgtggt
J-0035 (OBI)      .....
J-0069 (OBI)      .....
J-0060 (OBI)      .....T.....
J-0063 (OBI)      .....

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        1130      1140      1150      1160      1170      1180      1190
M54923 (2849-833) tttgggggcc aagtctgtac aacatcttga gtccctttat gccgctgta ccaattttct tttgtctttg
J-0035 (OBI)      .....G.....C..C.....A.....
J-0069 (OBI)      .....
J-0060 (OBI)      .....A.....G...A.....T..A..T.CA.A...C...
J-0063 (OBI)      .....

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```

        1200
M54923 (2849-833) ggtatacatt ta
J-0035 (OBI)
J-0069 (OBI)

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Lampiran 5. Karakteristik Demografi, Accession Number GenBank, Status OBI, Mutasi HBsAg, Genotipe dan Subtipe Virus Hepatitis B pada 7 Subyek dengan OBI

No	ID sampel	Umur	Kelamin	No. GenBank	OBI	Tipe_Mutasi	Subtipe	Genotipe
1	H-1401	25	P	MF947719	Ya	K160R, A166T	<i>adr</i>	B
2	H-1441	26	P	MF947720	Ya	wt	<i>adw</i>	B
3	H-1446b	30	P	-	Ya	T126S, T143S, K160R, Y161F	<i>adr</i>	C
4	H-1505	47	L	MF947722	Tidak	T143M	<i>adw</i>	B
5	H-1605	23	L	MF947723	Tidak	T126I, T143S, K160R, Y161F	<i>adr</i>	B
6	H-1702	33	P	MF947724	Tidak	wt	<i>adw</i>	B
7	H-1770	41	P	MF947725	Ya	wt	<i>adw</i>	B
8	H-1775	27	L	MF947726	Tidak	P120S, K122R, T143S, K160R, Y161F	<i>ayr</i>	B
9	H-1805	28	L	MF947727	Ya	T131A	<i>adw</i>	B
10	H-1812	32	P	MF947728	Tidak	T126I, T143S, K160R, Y161F	<i>adr</i>	C
11	H-1822	23	P	MF947729	Ya	wt	<i>adw</i>	B
12	H-0 704	30	L	MF947730	Ya	T126I, T143S, Y161F	<i>adw</i>	C
13	H-0744	29	P	MF947731	Tidak	T126I, T143S, K160R, Y161F	<i>adr</i>	C
14	H-0745	29	P	MF947732	Tidak	T126I, C139R, T143S, K160R, Y161F	<i>adr</i>	C
15	H-0747	29	P	MF947733	Tidak	T126I, T143S, K160R, Y161F	<i>adr</i>	C
16	H-0751	33	P	MF947734	Ya	T126I, T143S, K160R, Y161F	<i>adr</i>	C
17	H-0760	38	P	MF947735	Ya	K122R, P127T	<i>ayw</i>	B
18	H-0763	46	P	MF947736	Ya	K122R, P127T	<i>ayw</i>	B
19	H-0783	46	L	MF947737	Ya	T126I, T143S, K160R, Y161F	<i>adr</i>	C
20	H-0784	43	L	MF947738	Ya	K122R, P127T	<i>ayw</i>	C
21	H-0787	30	P	MF947739	Ya	K122R, P127T	<i>ayw</i>	C
22	H-0831	38	P	MF947740	Ya	wt	<i>adw</i>	B
23	H-0843	46	P	MF947741	Tidak	T143S, K160R, Y161F	<i>adr</i>	B
24	H-0851	24	P	MF947742	Tidak	T126I, T143S, K160R, Y161F, 174I	<i>adr</i>	B
25	H-0880	30	P	MF947743	Ya	F134L	<i>adw</i>	C
26	H-0896	29	P	MF947744	Ya	T126I, T143S, K160R, Y161F	<i>adr</i>	B
27	HCW- 032	61	P	MF947716	Ya	wt	<i>adw</i>	B
28	HCW- 074	37	P	MF947717	Ya	T126I, T143S, K160R, Y161F	<i>adr</i>	C
29	HCW- 083	27	P	MF947718	Ya	T143S, K160R, Y161F	<i>adr</i>	C
30	HCW- 118	25	L	MF947713	Ya	wt	<i>adw</i>	B
31	HCW- 125	46	L	MF947714	Ya	Y161F, S174I	<i>adw</i>	B
32	HCW- 164	45	P	MF947715	Ya	wt	<i>adw</i>	B
33	J-0004	37	L	-	Ya	Y161F	<i>adw</i>	B
34	J-0023	73	P	-	Ya	T126I, T143S, K160R, Y161F	<i>adr</i>	C
35	J-0034	54	P	-	Ya	T126I, T143S, K160R, Y161F	<i>adr</i>	C
		88	P	-	Ya	wt	<i>adw</i>	B
		53	L	-	Tidak	K122R	<i>ayw</i>	B
		33	L	-	Ya	K122R	<i>ayw</i>	B
		50	L	-	Tidak	T143S, A159V, K160R, Y161F, A166V	<i>adr</i>	C



No	ID sampel	Umur	Kelamin	No. GenBank	OBI	Tipe_Mutasi	Subtipe	Genotipe
40	J-0043	76	P	-	Tidak	wt	<i>adw</i>	B
41	J-0044	37	L	-	Ya	K122N, T126I, T143S, K160R, Y161F	<i>ayr</i>	C
42	J-0046	51	L	-	Tidak	T143S, K160R, Y161F	<i>adr</i>	C
43	J-0048	51	L	-	Tidak	T126I, T143S, K160R, Y161F	<i>adr</i>	C
44	J-0050	88	L	-	Ya	T140I, V168A	<i>adw</i>	B
45	J-0053	37	L	-	Ya	T126I, T143S, K160R, Y161F	<i>adr</i>	C
46	J-0055	53	P	-	Ya	T126I, T143S, K160R, Y161F	<i>adr</i>	C
47	j-0057	53	P	-	Ya	T126I, T143S, K160R, Y161F	<i>adr</i>	C
48	J-0059	71	L	-	Ya	T126I, T143S, K160R, Y161F	<i>adr</i>	C
49	J-0060	76	P	-	Ya	T143S, K160R, Y161F, R169L	<i>adr</i>	C
50	J-0063	50	L	-	Ya	wt	<i>adw</i>	B
51	J-0066	23	P	-	Tidak	wt	<i>adw</i>	B
52	J-0068	52	L	-	Tidak	wt	<i>adw</i>	B
53	J-0069	67	P	-	Ya	wt	<i>adw</i>	B
54	J-0076	44	L	-	Ya	T126I, T143S, K160R, Y161F	<i>adr</i>	C
55	J-0077	77	P	-	Ya	wt	<i>adw</i>	B
56	J-0079	50	P	-	Ya	T126I, T143S, K160R, Y161F	<i>adr</i>	C
57	J-0085	70	L	-	Tidak	wt	<i>adw</i>	B
58	J-0086	73	L	-	Ya	T126I, T143S, K160R, Y161F	<i>adr</i>	C
59	J-0093	51	L	-	Tidak	K122R, T143S, K160R, Y161F	<i>ayr</i>	C
60	J-0095	64	L	-	Ya	T125P, V168A	<i>adw</i>	B
61	J-0101	81	P	-	Tidak	Y161F	<i>adw</i>	B
62	J-0105	68	L	-	Ya	T126I, T143S, K160R, Y161F	<i>adr</i>	C
63	J-0159	50	P	-	Ya	K122R	<i>adw</i>	B
64	J-0126	54	P	-	Ya	K122R, W163*	<i>ayw</i>	B
65	J-0129	63	L	-	Ya	Q129H, Y161F	<i>adw</i>	B
66	J-0147	48	P	-	Tidak	K122R	<i>ayw</i>	B
67	J-0156	41	L	-	Tidak	T126A	<i>adw</i>	B
68	J-0157	63	L	-	Ya	K122R	<i>ayw</i>	B
69	J-0161	43	L	-	Tidak	Q129H	<i>adw</i>	B
70	J-0166	58	P	-	Tidak	K122R, P127T, F134Y	<i>ayw</i>	B
71	J-0168	48	P	-	Tidak	Y161F	<i>adw</i>	B
72	J-0173	52	P	-	Ya	Y161F	<i>adw</i>	B
73	J-0182	51	L	-	Ya	T143S, K160R, Y161F, R169L, S174N	<i>adr</i>	C

Keterangan

OBI Occult Hepatitis B

wt Wild-type



an 6. Index Antigenisitas Determinan 'a' HBsAg pada 7 Subyek OBI

Acid Position	M54923 (Ref)			H-0896			J-0055			H-0760			H-1805			H-0050			J-0095			J-0182			
	Minimum	Maximum	Mean	Minimum	Maximum	Mean	Minimum	Maximum	Mean	Minimum	Maximum	Mean	Minimum	Maximum	Mean	Minimum	Maximum	Mean	Minimum	Maximum	Mean	Residue	Index	Residue	Index
117	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	Ser	0.7	Ser	0.7
118	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	Thr	0.8	Thr	0.8
119	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	Gly	1.65	Gly	1.65
120	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	Pro	2.1	Pro	2.1
121	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	Cys	2.5	Cys	2.5
122	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	Lys	2.25	Lys	2.25
123	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	Thr	1	Thr	1
124	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	Cys	0.9	Cys	0.9
125	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	Thr	0.7	Pro	1.3
126	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	Thr	0.25	Thr	0.45
127	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	Pro	0.6	Pro	0.6
128	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	Ala	0.8	Ala	0.8
129	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	Gln	0.8	Gln	0.8
130	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	Gly	0.65	Gly	0.65
131	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	Thr	0.35	Ala	0
132	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	Ser	0.35	Ser	0.35
133	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	Met	0	Met	0
134	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	Phe	0.2	Phe	0.2
135	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	Pro	0.2	Pro	0.2
136	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	Ser	0.2	Ser	0.2
137	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	Cys	0.2	Cys	0.2
138	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	0.7	0.8	1.65	Cys	0.64	Cys	0.64





Acid Position	M54923 (Ref)			H-0896			J-0055			H-0760			H-1805			H-0050			J-0095			J-0182		
	Minimum	Maximum	Mean	Residue	Index	Residue	Index	Residue	Index	Residue	Index	Residue	Index	Residue	Index	Residue	Index	Residue	Index	Residue	Index	Residue	Index	
139				Cys	1.18	Cys	1.18	Cys	1.18	Cys	1.18	Cys	1.18	Cys	1.18	Cys	1.18	Cys	1.18	Cys	1.18	Cys	0.98	
140				Thr	1.67	Thr	1.67	Thr	1.67	Thr	1.67	Thr	1.67	Thr	1.67	Thr	1.67	Thr	1.67	Thr	1.67	Thr	1.47	
141				Lys	2.76	Lys	2.76	Lys	2.76	Lys	2.76	Lys	2.76	Lys	2.76	Lys	2.76	Lys	2.76	Lys	2.76	Lys	2.86	
142				Pro	3.4	Pro	3.4	Pro	3.4	Pro	3.4	Pro	3.4	Pro	3.4	Pro	3.4	Pro	3.4	Pro	3.4	Pro	3.4	
143				Thr	2.86	Ser	3.06	Ser	3.06	Thr	2.86	Thr	2.86	Thr	2.86	Thr	2.74	Thr	2.74	Thr	2.86	Ser	3.06	
144				Asp	2.57	Asp	2.57	Asp	2.57	Asp	2.57	Asp	2.57	Asp	2.57	Asp	3.1	Asp	3.1	Asp	2.57	Asp	2.57	
145				Gly	1.93	Gly	1.93	Gly	1.93	Gly	1.93	Gly	1.93	Gly	1.93	Gly	2.49	Gly	2.49	Gly	1.93	Gly	1.93	
146				Asn	1.59	Asn	1.59	Asn	1.59	Asn	1.59	Asn	1.59	Asn	1.59	Asn	2.18	Asn	2.18	Asn	1.59	Asn	1.19	
147				Cys	0.5	Cys	0.5	Cys	0.5	Cys	0.5	Cys	0.5	Cys	0.5	Cys	1.12	Cys	1.12	Cys	0.5	Cys	0.1	
148				Thr	-0.2	Thr	-0.2	Thr	-0.2	Thr	-0.2	Thr	-0.2	Thr	-0.2	Thr	0.11	Thr	0.11	Thr	-0.2	Thr	-0.6	
149				Cys	-0.6	Cys	-0.6	Cys	-0.6	Cys	-0.6	Cys	-0.6	Cys	-0.6	Cys	-0.6	Cys	-0.6	Cys	-0.6	Cys	-0.6	
150				Ile	-0.6	Ile	-0.6	Ile	-0.6	Ile	-0.6	Ile	-0.6	Ile	-0.6	Ile	-0.6	Ile	-0.6	Ile	-0.6	Ile	-0.6	
151				Pro	-0.6	Pro	-0.6	Pro	-0.6	Pro	-0.6	Pro	-0.6	Pro	-0.6	Pro	-0.6	Pro	-0.6	Pro	-0.6	Pro	-0.6	
152				Ile	-0.25	Ile	-0.25	Ile	-0.25	Ile	-0.25	Ile	-0.25	Ile	-0.25	Ile	-0.25	Ile	-0.25	Ile	-0.25	Ile	-0.25	
153				Pro	0.15	Pro	0.15	Pro	0.15	Pro	0.15	Pro	0.15	Pro	0.15	Pro	0.15	Pro	0.15	Pro	0.15	Pro	0.15	
154				Ser	0.35	Ser	0.35	Ser	0.35	Ser	0.35	Ser	0.35	Ser	0.35	Ser	0.35	Ser	0.35	Ser	0.35	Ser	0.35	
155				Ser	0.35	Ser	0.35	Ser	0.35	Ser	0.35	Ser	0.35	Ser	0.35	Ser	0.35	Ser	0.35	Ser	0.35	Ser	0.35	
156				Trp	0	Trp	0	Trp	0	Trp	0	Trp	0	Trp	0	Trp	0	Trp	0	Trp	0	Trp	0	
157				Ala	-0.4	Ala	-0.4	Ala	-0.4	Ala	-0.4	Ala	-0.4	Ala	-0.4	Ala	-0.4	Ala	-0.4	Ala	-0.4	Ala	-0.4	
158				Phe	-0.4	Phe	-0.4	Phe	-0.4	Phe	-0.4	Phe	-0.4	Phe	-0.4	Phe	-0.4	Phe	-0.4	Phe	-0.4	Phe	-0.4	
159				Ala	-0.4	Ala	-0.4	Ala	-0.4	Ala	-0.4	Ala	-0.4	Ala	-0.4	Ala	-0.4	Ala	-0.4	Ala	-0.4	Ala	-0.4	
160				Lys	-0.4	Arg	-0.4	Arg	-0.4	Lys	-0.4	Lys	-0.4	Lys	-0.4	Lys	-0.4	Lys	-0.4	Lys	-0.4	Arg	-0.4	
161				Tyr	-0.25	Phe	-0.4	Phe	-0.4	Tyr	-0.25	Tyr	-0.25	Tyr	-0.25	Tyr	-0.25	Tyr	-0.25	Tyr	-0.25	Phe	-0.4	

Acid Position	M54923 (Ref)		H-0896		J-0055		H-0760		H-1805		H-0050		J-0095		J-0182	
	Minimum	Maximum	Minimum	Maximum	Minimum	Maximum	Minimum	Maximum	Minimum	Maximum	Minimum	Maximum	Minimum	Maximum	Minimum	Maximum
	-0.6	3.4	-0.6	3.4	-0.6	3.4	-0.6	3.4	-0.6	3.4	-0.6	3.1	-0.6	3.4	-0.6	3.4
	0.46	0.36	0.36	0.36	0.42	0.42	0.42	0.42	0.44	0.44	0.4	0.4	0.48	0.48	0.42	0.42
	Residue	Index	Residue	Index	Residue	Index	Residue	Index	Residue	Index	Residue	Index	Residue	Index	Residue	Index
162	Leu	-0.25	Leu	-0.4	Leu	-0.25	Leu	-0.25	Leu	-0.25	Leu	-0.25	Leu	-0.25	Leu	-0.4
163	Trp	-0.4	Trp	-0.4	Trp	-0.4	Trp	-0.4	Trp	-0.4	Trp	-0.4	Trp	-0.4	Trp	-0.4
164	Glu	-0.2	Glu	-0.4	Glu	-0.4	Glu	-0.2	Glu	-0.2	Glu	-0.6	Glu	-0.6	Glu	-0.4
165	Trp	-0.2	Trp	-0.2	Trp	-0.2	Trp	-0.2	Trp	-0.2	Trp	-0.6	Trp	-0.6	Trp	-0.2
166	Ala	-0.1	Ala	-0.1	Ala	-0.1	Ala	-0.1	Ala	-0.1	Ala	0.05	Ala	0.05	Ala	-0.4
167	Ser	-0.1	Ser	-0.1	Ser	-0.1	Ser	-0.1	Ser	-0.1	Ser	-0.1	Ser	-0.1	Ser	-0.4
168	Val	-0.4	Val	-0.4	Val	-0.4	Val	-0.4	Val	-0.4	Val	-0.4	Ala	-0.4	Val	-0.4
169	Arg	-0.2	Arg	-0.2	Arg	-0.2	Arg	-0.2	Arg	-0.2	Arg	-0.2	Arg	-0.2	Arg	-0.4
170	Phe	-0.2	Phe	-0.2	Phe	-0.2	Phe	-0.2	Phe	-0.2	Phe	-0.2	Phe	-0.2	Phe	-0.2
171	Ser	-0.2	Ser	-0.2	Ser	-0.2	Ser	-0.2	Ser	-0.2	Ser	-0.2	Ser	-0.2	Ser	-0.2
172	Trp	-0.2	Trp	-0.2	Trp	-0.2	Trp	-0.2	Trp	-0.2	Trp	-0.2	Trp	-0.2	Trp	-0.2
173	Leu	-0.4	Leu	-0.4	Leu	-0.4	Leu	-0.4	Leu	-0.4	Leu	-0.4	Leu	-0.4	Leu	-0.4
174	Ser	-0.4	Ser	-0.4	Ser	-0.4	Ser	-0.4	Ser	-0.4	Ser	-0.4	Ser	-0.4	Ser	-0.4
175	Leu	-0.4	Leu	-0.4	Leu	-0.4	Leu	-0.4	Leu	-0.4	Leu	-0.4	Leu	-0.4	Leu	-0.4
176	Leu	-0.4	Leu	-0.4	Leu	-0.4	Leu	-0.4	Leu	-0.4	Leu	-0.4	Leu	-0.4	Leu	-0.4
177	Val	-0.4	Val	-0.4	Val	-0.4	Val	-0.4	Val	-0.4	Val	-0.4	Val	-0.4	Val	-0.4
178	Pro	-0.4	Pro	-0.4	Pro	-0.4	Pro	-0.4	Pro	-0.4	Pro	-0.4	Pro	-0.4	Pro	-0.4

Keterangan:

*	Berdasarkan algoritma Jameson-Wolf
	Sekuens referensi
	Asam amino penentu subdeterminan HBsAg
	Perubahan asam amino dan indeks antigenisitas

Lampiran 7. Index Antigenisitas Pretein Selubung Virus Hepatitis B pada 4 Subyek OBI

Amino Acid Position	M54923 (Ref)		J-0035		J-0069		J-0060		J-0063	
	Minimum	-0.60	Minimum	-0.60	Minimum	-0.6	Minimum	-0.60	Minimum	-0.60
	Maximum	3.40	Maximum	3.40	Maximum	3.4	Maximum	3.40	Maximum	3.40
	Mean	0.40	Mean	0.40	Mean	0.42	Mean	0.62	Mean	0.41
	Residue	Index	Residue	Index	Residue	Index	Residue	Index	Residue	Index
1	Met	-0.20	Met	-0.20	Met	-0.20	Met	-0.20	Met	-0.20
2	Gly	0.20	Gly	0.20	Gly	0.20	Gly	0.20	Gly	0.20
3	Gly	0.20	Gly	0.20	Gly	0.20	Gly	0.20	Gly	0.20
4	Trp	0.30	Trp	0.00	Trp	0.30	Trp	0.64	Trp	0.30
5	Ser	1.34	Ser	0.15	Ser	1.34	Ser	1.88	Ser	1.34
6	Ser	1.68	Ser	0.81	Ser	1.68	Ser	2.22	Ser	1.68
7	Lys	2.22	Asn	0.82	Lys	2.22	Lys	2.56	Lys	2.22
8	Pro	2.86	Leu	1.63	Pro	2.86	Pro	3.40	Pro	2.86
9	Arg	3.40	Arg	1.64	Arg	3.40	Gln	3.06	Arg	3.40
10	Gln	3.06	Gln	2.10	Gln	3.06	Gln	3.00	Gln	3.06
11	Gly	1.82	Gly	1.44	Gly	1.82	Gly	2.64	Gly	1.82
12	Met	1.33	Met	1.68	Met	1.33	Arg	2.48	Met	1.33
13	Gly	0.29	Gly	0.37	Gly	0.29	Gly	2.17	Gly	0.29
14	Thr	-0.05	Thr	0.16	Thr	-0.05	Pro	2.80	Thr	-0.05
15	Asn	-0.05	Asn	-0.20	Asn	-0.05	Asn	2.37	Asn	-0.05
16	Leu	-0.20	Leu	-0.20	Leu	-0.20	Leu	0.94	Leu	-0.20
17	Ser	-0.40	Phe	-0.60	Ser	-0.40	Ser	0.46	Ser	-0.40
18	Val	0.05	Val	-0.60	Val	0.05	Val	0.33	Val	0.05
19	Pro	-0.25	Pro	-0.45	Pro	-0.25	Pro	-0.25	Pro	-0.25
20	Asn	0.15	Asn	0.15	Asn	0.15	Asn	0.25	Asn	0.15
21	Pro	-0.05	Pro	0.15	Pro	-0.05	Pro	-0.05	Pro	-0.05
22	Leu	0.20	Leu	0.20	Leu	0.20	Leu	0.20	Leu	0.20
23	Gly	0.20	Gly	0.20	Gly	0.20	Gly	0.20	Gly	0.20
24	Phe	-0.40	Phe	-0.40	Phe	-0.40	Phe	-0.40	Phe	-0.40
25	Phe	0.03	Phe	-0.20	Phe	0.03	Phe	-0.20	Phe	0.03
26	Pro	0.71	Pro	0.25	Pro	0.71	Pro	-0.20	Pro	0.71
27	Asp	1.04	Asp	0.35	Asp	1.04	Gly	0.20	Asp	1.04
28	His	2.17	His	1.25	His	2.17	His	0.45	His	2.17
29	Gln	2.30	Gln	1.15	Gln	2.30	Gln	0.85	Gln	2.30
30	Leu	1.77	Leu	0.85	Leu	1.77	Leu	0.85	Leu	1.77
31	Asp	1.14	Asp	0.45	Asp	1.14	Asp	0.25	Asp	1.14
32	Pro	1.31	Pro	1.29	Pro	1.31	Pro	0.25	Pro	1.31
33	Ala	1.57	Ala	1.48	Ala	1.57	Ala	0.10	Ala	1.57
34	Phe	1.68	Phe	1.72	Phe	1.68	Phe	0.10	Phe	1.68
35	Lys	1.27	Lys	1.21	Lys	1.27	Gly	0.00	Lys	1.27
36	Ala	2.36	Ala	2.40	Ala	2.36	Ala	0.45	Ala	2.36
37	Asn	3.40	Asn	2.46	Asn	3.40	Asn	0.88	Asn	3.40
38	Ser	3.06	Ser	2.56	Ser	3.06	Ser	1.76	Ser	3.06
39	Asp	2.32	Glu	2.46	Asp	2.66	Asn	1.84	Asp	2.32
40	Asn	1.88	Asn	2.46	Asn	2.56	Asn	2.32	Asn	1.88
41	Pro	2.04	Pro	3.06	Pro	3.06	Pro	2.80	Pro	2.04
42	Asp	1.70	Asp	3.40	Asp	3.06	Asp	2.52	Asp	1.70
43	Trp	1.25	Trp	2.61	Trp	3.40	Trp	2.43	Trp	1.25
44	Asp	0.99	Asp	2.01	Asp	2.31	Asp	1.89	Asp	0.99
		1.33	Leu	2.01	Leu	2.16	Phe	1.95	Leu	1.33
		2.02	Asn	2.36	Lys	2.16	Asn	2.56	Asn	2.02
		2.86	Pro	2.86	Pro	2.86	Pro	3.40	Pro	2.86
		3.40	His	3.40	His	3.06	Asn	3.06	His	3.40
		2.76	Lys	2.76	Lys	3.40	Lys	2.42	Lys	2.76
		2.22	Asp	2.50	Asp	2.76	Asp	1.88	Asp	2.22
		2.18	Asn	2.74	Asn	2.72	Gln	1.54	Asn	2.18
		2.18	Trp	2.48	Trp	2.52	Trp	0.65	Trp	2.18



Amino Acid Position	M54923 (Ref)		J-0035		J-0069		J-0060		J-0063	
	Minimum	-0.60	Minimum	-0.60	Minimum	-0.6	Minimum	-0.60	Minimum	-0.60
	Maximum	3.40	Maximum	3.40	Maximum	3.4	Maximum	3.40	Maximum	3.40
	Mean	0.40	Mean	0.40	Mean	0.42	Mean	0.62	Mean	0.41
	Residue	Index	Residue	Index	Residue	Index	Residue	Index	Residue	Index
53	Pro	1.88	Pro	2.32	Pro	2.22	Pro	0.05	Pro	1.88
54	Asp	2.42	Asp	2.80	Asp	2.42	Ala	0.05	Asp	2.42
55	Ser	2.56	Ala	2.32	Ser	2.56	Ala	-0.10	Ser	2.56
56	Asn	3.40	Asn	1.99	Asn	3.40	Asn	0.70	Asn	3.40
57	Lys	2.21	Lys	1.41	Lys	2.51	Lys	0.10	Lys	2.21
58	Val	1.87	Val	0.38	Val	1.87	Val	0.10	Val	1.87
59	Gly	0.78	Gly	0.10	Gly	0.78	Gly	0.10	Gly	0.78
60	Val	-0.06	Val	-0.40	Val	-0.06	Val	-0.40	Val	-0.06
61	Gly	-0.40	Gly	-0.40	Gly	-0.40	Gly	-0.40	Gly	-0.40
62	Ala	-0.40	Ala	-0.40	Ala	-0.40	Ala	-0.40	Ala	-0.40
63	Phe	-0.40	Phe	-0.40	Phe	-0.40	Phe	-0.40	Phe	-0.40
64	Gly	0.00	Gly	0.00	Gly	0.00	Gly	0.00	Gly	0.00
65	Pro	0.35	Pro	0.35	Pro	0.35	Pro	0.35	Pro	0.35
66	Gly	0.35	Gly	0.35	Gly	0.35	Gly	0.35	Gly	0.35
67	Phe	0.30	Phe	0.30	Phe	0.30	Phe	0.30	Phe	0.30
68	Thr	-0.25	Thr	-0.25	Thr	-0.25	Thr	-0.05	Thr	-0.25
69	Pro	0.15	Pro	0.15	Pro	0.15	Pro	0.15	Pro	0.15
70	Pro	0.50	Pro	0.50	Pro	0.50	Pro	0.50	Pro	0.50
71	His	0.65	His	0.65	His	0.65	His	0.65	His	0.65
72	Gly	0.35	Gly	0.35	Gly	0.35	Gly	0.35	Gly	0.35
73	Gly	-0.05	Gly	-0.05	Gly	-0.05	Ser	-0.05	Gly	-0.05
74	Leu	-0.20	Leu	-0.20	Leu	-0.20	Leu	-0.20	Leu	-0.20
75	Leu	-0.20	Leu	-0.20	Leu	-0.20	Leu	-0.20	Leu	-0.20
76	Gly	0.00	Gly	0.00	Gly	0.00	Gly	0.00	Gly	0.00
77	Trp	-0.20	Trp	-0.40	Trp	-0.20	Trp	-0.20	Trp	-0.20
78	Ser	0.15	Ser	0.15	Ser	0.15	Ser	0.15	Ser	0.15
79	Pro	0.30	Pro	0.10	Pro	0.30	Pro	0.30	Pro	0.30
80	Gln	0.50	Gln	0.50	Gln	0.50	Gln	0.50	Gln	0.50
81	Ala	0.25	Ala	0.25	Ala	0.25	Ala	0.25	Ala	0.25
82	Gln	-0.45	Gln	-0.45	Gln	-0.45	Gln	-0.45	Gln	-0.45
83	Gly	-0.45	Gly	-0.45	Gly	-0.45	Gly	-0.45	Gly	-0.45
84	Ile	-0.60	Leu	-0.60	Ile	-0.60	Ile	-0.60	Ile	-0.60
85	Leu	-0.60	Leu	-0.60	Leu	-0.60	Leu	-0.60	Leu	-0.60
86	Thr	-0.45	Ala	-0.60	Thr	-0.60	Thr	-0.60	Thr	-0.60
87	Thr	-0.45	Thr	-0.60	Thr	-0.60	Thr	-0.60	Thr	-0.60
88	Val	-0.45	Val	-0.40	Val	-0.60	Val	-0.60	Val	-0.60
89	Pro	-0.25	Pro	-0.40	Pro	-0.60	Pro	-0.60	Pro	-0.60
90	Thr	0.05	Ala	-0.40	Ala	-0.40	Ala	-0.40	Ala	-0.40
91	Ala	0.40	Ala	0.05	Ala	0.25	Ala	0.25	Ala	-0.25
92	Pro	0.40	Pro	0.25	Pro	0.25	Pro	0.25	His	0.30
93	Pro	0.40	Pro	0.40	Pro	0.40	Pro	0.60	Pro	0.60
94	Pro	0.40	Pro	0.40	Pro	0.40	Pro	0.80	Pro	0.60
95	Ala	0.60	Ala	0.60	Ala	0.60	Ala	1.20	Ala	0.80
96	Ser	1.00	Ser	1.34	Ser	1.00	Ser	2.00	Ser	1.20
97	Thr	1.30	Thr	1.68	Thr	1.00	Thr	2.00	Thr	1.00
	Asn	1.60	Asn	2.02	Asn	1.30	Asn	1.20	Asn	1.30
	Arg	1.90	Arg	2.66	Arg	1.60	Arg	1.00	Arg	1.60
	Gln	2.30	Gln	3.40	Gln	2.00			Gln	2.00
	Leu	3.00	Ser	3.06	Val	2.30			Val	2.30
	Gly	2.70	Gly	2.72	Gly	3.00			Gly	3.00
	Arg	2.40	Arg	2.08	Arg	2.30			Arg	2.30
	Lys	1.70	Gln	1.34	Lys	2.00			Lys	2.00



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Amino Acid Position	M54923 (Ref)		J-0035		J-0069		J-0060		J-0063	
	Minimum	-0.60	Minimum	-0.60	Minimum	-0.6	Minimum	-0.60	Minimum	-0.60
	Maximum	3.40	Maximum	3.40	Maximum	3.4	Maximum	3.40	Maximum	3.40
	Mean	0.40	Mean	0.40	Mean	0.42	Mean	0.62	Mean	0.41
	Residue	Index	Residue	Index	Residue	Index	Residue	Index	Residue	Index
105	Pro	1.60	Pro	1.00	Pro	1.90			Pro	1.90
106	Thr	1.50	Thr	1.00	Thr	1.80			Thr	1.80
107	Pro	1.00	Pro	0.40	Pro	1.00			Pro	1.00
108	Leu	0.74	Val	0.54	Leu	0.74			Leu	0.74
109	Ser	0.63	Ser	0.43	Ser	0.63			Ser	0.63
110	Pro	1.27	Pro	1.87	Pro	1.27			Pro	1.27
111	Pro	2.76	Pro	2.36	Pro	2.76			Pro	2.76
112	Leu	3.40	Leu	3.40	Leu	3.40			Leu	3.40
113	Arg	2.36	Arg	2.76	Arg	2.36			Arg	2.36
114	Asp	2.42	Asp	2.42	Asp	2.42			Asp	2.42
115	Thr	2.18	Thr	2.18	Thr	2.18			Thr	1.88
116	His	1.84	His	1.84	His	1.84			His	1.84
117	Pro	1.00	Pro	1.00	Pro	1.00			Pro	1.00
118	Gln	-0.15	Gln	-0.15	Gln	-0.15			Gln	-0.15
119	Ala	-0.39	Ala	-0.39	Ala	-0.39			Ala	-0.39
120	Met	-0.33	Met	-0.33	Met	-0.33			Met	-0.33
121	Gln	-0.02	Gln	-0.02	Gln	-0.02			Gln	-0.02
122	Trp	0.19	Trp	0.19	Trp	0.19			Trp	0.19
123	Asn	0.60	Asn	0.60	Asn	0.60			Asn	0.60
124	Ser	0.39	Ser	0.39	Ser	0.39			Ser	0.39
125	Thr	0.48	Thr	0.48	Thr	0.48			Thr	0.48
126	Thr	0.42	Thr	0.42	Thr	0.42	Thr	0.40	Thr	0.42
127	Phe	0.16	Phe	0.16	Phe	0.16	Phe	0.05	Phe	0.16
128	His	-0.60	His	-0.60	His	-0.60	His	-0.30	His	-0.60
129	Gln	-0.60	Gln	-0.60	Gln	-0.60	Gln	-0.60	Gln	-0.60
130	Thr	0.26	Thr	0.26	Thr	0.26	Ala	-0.60	Thr	0.26
131	Leu	1.32	Leu	1.32	Leu	1.32	Leu	0.04	Leu	1.32
132	Gln	1.88	Gln	1.88	Gln	1.88	Leu	0.98	Gln	1.88
133	Asp	2.24	Asp	2.24	Asp	2.24	Asp	1.87	Asp	2.24
134	Pro	2.60	Pro	2.60	Pro	2.60	Pro	3.06	Pro	2.60
135	Arg	2.34	Arg	2.34	Arg	2.34	Arg	3.40	Arg	2.34
136	Val	1.78	Val	1.78	Val	1.78	Val	2.51	Val	1.78
137	Arg	0.22	Arg	0.22	Arg	0.22	Arg	1.67	Arg	0.22
138	Ala	-0.04	Ala	-0.04	Ala	-0.04	Gly	0.58	Ala	-0.04
139	Leu	-0.60	Leu	-0.60	Leu	-0.60	Leu	-0.06	Leu	-0.60
140	Tyr	-0.60	Tyr	-0.60	Tyr	-0.60	Cys	-0.10	Tyr	-0.60
141	Phe	-0.40	Phe	-0.40	Phe	-0.40	Phe	-0.40	Phe	-0.40
142	Pro	0.01	Pro	0.01	Pro	0.01	Pro	0.01	Pro	0.01
143	Ala	0.77	Ala	0.77	Ala	0.77	Ala	0.77	Ala	0.77
144	Gly	1.28	Gly	1.28	Gly	1.28	Gly	1.28	Gly	1.28
145	Gly	1.89	Gly	1.89	Gly	1.89	Gly	2.09	Gly	1.89
146	Ser	2.10	Ser	2.10	Ser	2.10	Ser	2.10	Ser	2.10
147	Ser	1.89	Ser	1.89	Ser	1.89	Ser	1.89	Ser	1.89
148	Ser	1.08	Ser	1.08	Ser	1.08	Ser	1.28	Ser	1.08
149	Gly	1.07	Gly	0.67	Gly	1.07	Gly	1.07	Gly	1.07
	Thr	0.26	Thr	0.26	Thr	0.26	Thr	0.26	Thr	0.26
	Val	-0.25	Val	0.05	Val	-0.25	Val	-0.25	Val	-0.25
	Asn	-0.05	Ser	0.25	Asn	-0.05	Asn	-0.05	Asn	-0.05
	Pro	-0.05	Pro	0.25	Pro	0.25	Pro	-0.05	Pro	-0.05
	Val	0.10	Ala	0.40	Val	0.40	Val	0.10	Val	0.10
	Gln	-0.05	Gln	0.40	Gln	0.40	Pro	0.25	Gln	0.40
	Asn	-0.15	Asn	-0.15	Asn	0.05	Thr	-0.15	Asn	0.05



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Amino Acid Position	M54923 (Ref)		J-0035		J-0069		J-0060		J-0063	
	Minimum	-0.60	Minimum	-0.60	Minimum	-0.6	Minimum	-0.60	Minimum	-0.60
	Maximum	3.40	Maximum	3.40	Maximum	3.4	Maximum	3.40	Maximum	3.40
	Mean	0.40	Mean	0.40	Mean	0.42	Mean	0.62	Mean	0.41
	Residue	Index	Residue	Index	Residue	Index	Residue	Index	Residue	Index
157	Thr	0.00	Thr	-0.15	Thr	0.40	Thr	0.00	Thr	0.40
158	Val	-0.15	Val	-0.60	Ala	0.25	Ala	-0.15	Ala	0.25
159	Ser	-0.15	Ser	-0.60	Ser	0.25	Ser	-0.15	Ser	0.25
160	Ser	-0.15	Ala	-0.60	Ser	0.25	Pro	-0.15	Ser	0.25
161	Ile	-0.45	Ile	-0.60	Ile	-0.45	Ile	-0.45	Ile	-0.45
162	Ser	-0.45	Ser	-0.60	Ser	-0.45	Ser	-0.05	Ser	-0.45
163	Ser	-0.45	Ser	-0.11	Ser	-0.45	Ser	-0.05	Ser	-0.45
164	Ile	0.04	Ile	1.28	Ile	0.04	Tyr	0.25	Ile	0.04
165	Leu	0.53	Ser	1.82	Leu	0.53	Phe	0.55	Leu	0.53
166	Ser	1.27	Ser	2.61	Ser	1.27	Ser	0.80	Ser	1.27
167	Lys	2.76	Lys	3.40	Lys	2.76	Glu	2.30	Lys	2.76
168	Thr	3.40	Thr	3.06	Thr	3.40	Thr	2.60	Thr	3.40
169	Gly	2.86	Gly	2.82	Gly	2.86	Gly	3.00	Gly	2.86
170	Asp	2.37	Asp	2.58	Asp	2.37	Asp	2.70	Asp	2.37
171	Pro	2.08	Pro	2.24	Pro	2.08	Pro	2.10	Pro	2.08
172	Val	2.14	Ala	2.40	Val	2.14	Ala	2.20	Val	2.14
173	Pro	1.80	Pro	3.00	Pro	1.80	Pro	2.40	Pro	1.80
174	Asn	2.00	Asn	2.20	Asn	2.00	Asn	2.00	Asn	2.00
175	Met	1.05	Met	1.30	Met	1.05	Met	2.00	Met	1.05
176	Glu	0.50	Glu	0.50	Glu	0.50	Glu	1.60	Glu	0.50
177	Asn	0.90	Asn	0.80	Asn	0.90	Ser	1.40	Asn	0.90
178	Ile	0.10	Ile	-0.10	Ile	0.10	Thr	1.40	Ile	0.10
179	Ala	0.10	Ala	0.10	Ala	0.10	Thr	1.05	Ala	0.10
180	Ser	-0.20	Ser	-0.20	Ser	-0.20	Ser	-0.05	Ser	-0.20
181	Gly	-0.20	Gly	-0.20	Gly	-0.20	Gly	-0.05	Gly	-0.20
182	Leu	-0.05	Leu	-0.05	Leu	-0.05	Leu	-0.05	Leu	-0.05
183	Leu	-0.25	Leu	-0.25	Leu	-0.25	Leu	-0.05	Leu	-0.25
184	Gly	-0.05	Gly	-0.05	Gly	-0.05	Gly	-0.05	Gly	-0.05
185	Pro	-0.20	Pro	-0.20	Pro	-0.20	Pro	-0.20	Pro	-0.20
186	Leu	-0.20	Leu	-0.20	Leu	-0.20	Leu	-0.20	Leu	-0.20
187	Leu	-0.20	Leu	-0.20	Leu	-0.20	Leu	-0.20	Leu	-0.20
188	Val	-0.60	Val	-0.60	Val	-0.60	Val	-0.60	Val	-0.60
189	Leu	-0.60	Leu	-0.60	Leu	-0.60	Leu	-0.60	Leu	-0.60
190	Gln	-0.60	Gln	-0.60	Gln	-0.60	Gln	-0.60	Gln	-0.60
191	Ala	-0.60	Ala	-0.60	Ala	-0.60	Ala	-0.60	Ala	-0.60
192	Gly	-0.60	Gly	-0.60	Gly	-0.60	Gly	-0.60	Gly	-0.60
193	Phe	-0.60	Phe	-0.60	Phe	-0.60	Phe	-0.60	Phe	-0.60
194	Phe	-0.60	Phe	-0.60	Phe	-0.60	Phe	-0.60	Phe	-0.60
195	Leu	-0.60	Leu	-0.60	Leu	-0.60	Leu	-0.60	Leu	-0.60
196	Leu	-0.60	Leu	-0.60	Leu	-0.60	Leu	-0.60	Leu	-0.60
197	Thr	-0.60	Thr	-0.60	Thr	-0.60	Thr	-0.60	Thr	-0.60
198	Lys	-0.60	Lys	-0.60	Lys	-0.60	Arg	-0.60	Lys	-0.60
199	Ile	-0.60	Ile	-0.60	Ile	-0.60	Ile	-0.60	Ile	-0.60
200	Leu	-0.60	Leu	-0.60	Leu	-0.60	Leu	-0.60	Leu	-0.60
201	Thr	-0.30	Thr	-0.30	Thr	-0.30	Thr	-0.30	Thr	-0.30
202	Ile	-0.33	Ile	-0.33	Ile	-0.33	Ile	-0.33	Ile	-0.33
203	Pro	0.19	Pro	0.19	Pro	0.19	Pro	0.19	Pro	0.19
204	Gln	0.61	Gln	0.61	Gln	0.61	Gln	1.01	Gln	0.61
205	Ser	1.68	Ser	1.68	Ser	1.68	Ser	1.68	Ser	1.68
	Leu	1.20	Leu	1.20	Leu	1.20	Leu	1.20	Leu	1.20
	Asp	0.83	Asp	0.83	Asp	0.83	Asp	0.83	Asp	0.83
	Ser	0.71	Ser	0.71	Ser	0.71	Ser	0.71	Ser	0.71



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Amino Acid Position	M54923 (Ref)		J-0035		J-0069		J-0060		J-0063	
	Minimum	-0.60	Minimum	-0.60	Minimum	-0.6	Minimum	-0.60	Minimum	-0.60
	Maximum	3.40	Maximum	3.40	Maximum	3.4	Maximum	3.40	Maximum	3.40
	Mean	0.40	Mean	0.40	Mean	0.42	Mean	0.62	Mean	0.41
	Residue	Index	Residue	Index	Residue	Index	Residue	Index	Residue	Index
209	Trp	0.59	Trp	0.59	Trp	0.59	Trp	0.59	Trp	0.59
210	Trp	-0.08	Trp	-0.08	Trp	-0.08	Trp	-0.08	Trp	0.62
211	Thr	-0.60	Thr	-0.60	Thr	-0.60	Thr	-0.60	Thr	0.10
212	Ser	-0.60	Ser	-0.40	Ser	-0.60	Ser	-0.60	Ser	0.30
213	Leu	-0.60	Leu	-0.40	Leu	-0.60	Leu	-0.60	Pro	0.15
214	Asn	-0.20	Asn	-0.40	Asn	-0.20	Asn	-0.20	Asn	0.35
215	Phe	-0.20	Phe	0.10	Phe	-0.20	Phe	-0.20	Phe	0.35
216	Leu	0.20	Leu	-0.40	Leu	0.20	Leu	-0.20	Leu	0.35
217	Gly	0.35	Gly	-0.20	Gly	0.35	Gly	-0.05	Gly	0.35
218	Gly	0.35	Glu	-0.60	Gly	0.35	Gly	0.15	Gly	0.35
219	Thr	0.15	Ile	-0.60	Thr	0.15	Ala	-0.05	Thr	-0.05
220	Pro	-0.45	Pro	0.30	Pro	-0.45	Pro	0.25	Pro	-0.45
221	Val	-0.60	Val	0.58	Val	-0.60	Thr	0.45	Val	-0.60
222	Cys	-0.60	Cys	0.66	Cys	-0.60	Cys	0.25	Cys	-0.60
223	Leu	-0.45	Arg	2.09	Leu	-0.45	Pro	0.25	Leu	-0.45
224	Gly	-0.05	Gly	2.37	Gly	-0.05	Gly	0.65	Gly	-0.05
225	Gln	0.80	Gln	2.80	Gln	0.80	Gln	0.40	Gln	0.80
226	Asn	0.60	Asn	2.42	Asn	0.60	Asn	0.20	Asn	0.60
227	Ser	1.20	Ser	2.04	Ser	1.20	Leu	0.20	Ser	1.20
228	Gln	0.00	Gln	0.96	Gln	0.00	Gln	0.48	Gln	0.00
229	Ser	0.00	Ser	0.68	Ser	0.00	Ser	0.96	Ser	0.00
230	Gln	0.12	Gln	0.40	Gln	0.12	Pro	1.44	Gln	0.12
231	Ile	0.09	Ile	0.05	Ile	0.09	Thr	2.52	Ile	0.09
232	Ser	0.81	Ser	0.45	Ser	0.81	Ser	2.80	Ser	0.81
233	Ser	0.93	Ser	0.45	Ser	0.93	Asn	1.72	Ser	0.93
234	His	1.20	His	0.60	His	1.20	His	1.44	His	1.20
235	Ser	0.93	Ser	0.45	Ser	0.93	Ser	1.16	Ser	0.93
236	Pro	1.01	Pro	0.65	Pro	1.01	Pro	0.63	Pro	1.01
237	Thr	0.74	Thr	0.50	Thr	0.74	Thr	0.35	Thr	0.74
238	Cys	0.62	Cys	0.50	Cys	0.62	Phe	-0.20	Cys	0.62
239	Cys	-0.20	Cys	-0.20	Cys	-0.20	Cys	-0.20	Cys	-0.20
240	Pro	-0.20	Pro	-0.20	Pro	-0.20	Pro	-0.05	Pro	-0.20
241	Pro	0.20	Pro	0.20	Pro	0.20	Pro	-0.20	Pro	0.20
242	Ile	-0.20	Ile	-0.20	Ile	-0.20	Ile	0.10	Ile	-0.20
243	Cys	-0.20	Cys	-0.20	Cys	-0.20	Ter	-0.10	Cys	-0.20
244	Pro	0.50	Pro	0.50	Pro	0.50			Pro	0.50
245	Gly	0.20	Gly	0.20	Gly	0.20			Gly	0.20
246	Tyr	0.35	Tyr	0.35	Tyr	0.35			Tyr	0.35
247	Arg	-0.60	Arg	-0.60	Arg	-0.60			Arg	-0.60
248	Trp	-0.60	Trp	-0.60	Trp	-0.60			Trp	-0.60
249	Met	-0.60	Met	-0.60	Met	-0.60			Met	-0.60
250	Cys	0.30	Cys	0.30	Cys	0.30			Cys	0.30
251	Leu	-0.60	Leu	-0.60	Leu	-0.60			Leu	-0.60
252	Arg	-0.30	Arg	-0.30	Arg	-0.30			Arg	-0.30
253	Arg	-0.60	Arg	-0.60	Arg	-0.60			Arg	-0.60
254	Phe	-0.60	Phe	-0.60	Phe	-0.60			Phe	-0.60
255	Ile	-0.60	Ile	-0.60	Ile	-0.60			Ile	-0.60
	Ile	-0.60	Ile	-0.60	Ile	-0.60			Ile	-0.60
	Phe	-0.60	Phe	-0.60	Phe	-0.60			Phe	-0.60
	Leu	-0.60	Leu	-0.60	Leu	-0.60			Leu	-0.60
	Cys	-0.60	Cys	-0.60	Cys	-0.60			Cys	-0.60
	Ile	-0.60	Ile	-0.60	Ile	-0.60			Ile	-0.60



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Amino Acid Position	M54923 (Ref)		J-0035		J-0069		J-0060		J-0063	
	Minimum	-0.60	Minimum	-0.60	Minimum	-0.6	Minimum	-0.60	Minimum	-0.60
	Maximum	3.40	Maximum	3.40	Maximum	3.4	Maximum	3.40	Maximum	3.40
	Mean	0.40	Mean	0.40	Mean	0.42	Mean	0.62	Mean	0.41
	Residue	Index	Residue	Index	Residue	Index	Residue	Index	Residue	Index
261	Leu	-0.60	Leu	-0.60	Leu	-0.60			Leu	-0.60
262	Leu	-0.60	Leu	-0.60	Leu	-0.60			Leu	-0.60
263	Leu	-0.60	Leu	-0.60	Leu	-0.60			Leu	-0.60
264	Cys	-0.60	Cys	-0.60	Cys	-0.60			Cys	-0.60
265	Leu	-0.60	Leu	-0.60	Leu	-0.60			Leu	-0.60
266	Ile	-0.60	Ile	-0.60	Ile	-0.60			Ile	-0.60
267	Phe	-0.60	Phe	-0.60	Phe	-0.60			Phe	-0.60
268	Leu	-0.60	Leu	-0.60	Leu	-0.60			Leu	-0.60
269	Leu	-0.60	Leu	-0.60	Leu	-0.60			Leu	-0.60
270	Val	-0.60	Val	-0.60	Val	-0.60			Val	-0.60
271	Leu	-0.60	Leu	-0.60	Leu	-0.60			Leu	-0.60
272	Leu	-0.60	Leu	-0.60	Leu	-0.60			Leu	-0.60
273	Asp	-0.20	Asp	-0.20	Asp	-0.20			Asp	-0.20
274	Tyr	0.20	Tyr	0.20	Tyr	0.20			Tyr	0.20
275	Gln	0.20	Gln	0.20	Gln	0.20			Gln	0.20
276	Gly	0.50	Gly	0.50	Gly	0.50			Gly	0.50
277	Met	-0.20	Met	-0.20	Met	-0.20			Met	-0.20
278	Leu	-0.60	Leu	-0.60	Leu	-0.60			Leu	-0.60
279	Pro	-0.60	Pro	-0.60	Pro	-0.60			Pro	-0.60
280	Val	-0.60	Val	-0.60	Val	-0.60			Val	-0.60
281	Cys	-0.60	Cys	-0.60	Cys	-0.60			Cys	-0.60
282	Pro	-0.60	Pro	-0.60	Pro	-0.60			Pro	-0.60
283	Leu	-0.60	Leu	-0.60	Leu	-0.60			Leu	-0.60
284	Ile	-0.20	Ile	-0.20	Ile	-0.20			Ile	-0.20
285	Pro	-0.05	Pro	-0.05	Pro	-0.05			Pro	-0.05
286	Gly	0.35	Gly	0.35	Gly	0.35			Gly	0.35
287	Ser	0.80	Ser	0.80	Ser	0.80			Ser	0.80
288	Ser	1.00	Ser	1.00	Ser	1.00			Ser	1.00
289	Thr	0.40	Thr	0.40	Thr	0.40			Thr	0.40
290	Thr	1.05	Thr	1.05	Thr	1.05			Thr	1.05
291	Ser	1.30	Ser	1.30	Ser	1.30			Ser	1.30
292	Thr	1.20	Thr	1.20	Thr	1.20			Thr	1.20
293	Gly	2.05	Gly	2.05	Gly	2.05			Gly	2.05
294	Pro	2.50	Pro	2.50	Pro	2.50			Pro	2.50
295	Cys	2.25	Cys	2.25	Cys	2.25			Cys	2.25
296	Lys	2.00	Lys	2.00	Lys	2.00			Lys	2.00
297	Thr	0.35	Thr	0.35	Thr	0.35			Thr	0.35
298	Cys	0.25	Cys	0.25	Cys	0.25			Cys	0.25
299	Thr	0.45	Thr	0.45	Thr	0.45			Thr	0.45
300	Thr	0.25	Thr	0.25	Thr	0.25			Thr	0.25
301	Pro	0.40	Pro	0.40	Pro	0.40			Pro	0.40
302	Ala	0.80	Ala	0.80	Ala	0.80			Ala	0.80
303	Gln	0.80	Gln	0.80	Gln	0.80			Gln	0.80
304	Gly	0.65	Gly	0.65	Gly	0.65			Gly	0.65
305	Thr	0.35	Thr	0.35	Thr	0.35			Thr	0.35
306	Ser	0.35	Ser	0.35	Ser	0.35			Ser	0.35
307	Met	-0.20	Met	-0.20	Met	-0.20			Met	-0.20
308	Phe	-0.20	Phe	-0.20	Phe	-0.20			Phe	-0.20
309	Pro	0.20	Pro	0.20	Pro	0.20			Pro	0.20
	Ser	0.20	Ser	0.20	Ser	0.20			Ser	0.20
	Cys	0.20	Cys	0.20	Cys	0.20			Cys	0.20
	Cys	0.64	Cys	0.64	Cys	0.64			Cys	0.64
	Cys	1.18	Cys	1.18	Cys	1.18			Cys	1.18



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Amino Acid Position	M54923 (Ref)		J-0035		J-0069		J-0060		J-0063	
	Minimum	-0.60	Minimum	-0.60	Minimum	-0.6	Minimum	-0.60	Minimum	-0.60
	Maximum	3.40	Maximum	3.40	Maximum	3.4	Maximum	3.40	Maximum	3.40
	Mean	0.40	Mean	0.40	Mean	0.42	Mean	0.62	Mean	0.41
	Residue	Index	Residue	Index	Residue	Index	Residue	Index	Residue	Index
314	Thr	1.27	Thr	1.27	Thr	1.27			Thr	1.27
315	Lys	2.36	Lys	2.36	Lys	2.36			Lys	2.36
316	Pro	3.40	Pro	3.40	Pro	3.40			Pro	3.40
317	Thr	2.86	Thr	2.86	Thr	2.86			Thr	2.86
318	Asp	2.57	Asp	2.57	Asp	2.57			Asp	2.57
319	Gly	1.93	Gly	1.93	Gly	1.93			Gly	1.93
320	Asn	1.59	Asn	1.59	Asn	1.59			Asn	1.59
321	Cys	0.10	Cys	0.10	Cys	0.10			Cys	0.10
322	Thr	-0.60	Thr	-0.60	Thr	-0.60			Thr	-0.60
323	Cys	-0.60	Cys	-0.60	Cys	-0.60			Cys	-0.60
324	Ile	-0.60	Ile	-0.60	Ile	-0.60			Ile	-0.60
325	Pro	-0.60	Pro	-0.60	Pro	-0.60			Pro	-0.60
326	Ile	-0.45	Ile	-0.45	Ile	-0.45			Ile	-0.45
327	Pro	-0.05	Pro	-0.05	Pro	-0.05			Pro	-0.05
328	Ser	0.35	Ser	0.35	Ser	0.35			Ser	0.35
329	Ser	0.35	Ser	0.35	Ser	0.35			Ser	0.35
330	Trp	-0.20	Trp	-0.20	Trp	-0.20			Trp	-0.20
331	Ala	-0.60	Ala	-0.60	Ala	-0.60			Ala	-0.60
332	Phe	-0.60	Phe	-0.60	Phe	-0.60			Phe	-0.60
333	Ala	-0.60	Ala	-0.60	Ala	-0.60			Ala	-0.60
334	Lys	-0.60	Lys	-0.60	Lys	-0.60			Lys	-0.60
335	Tyr	-0.25	Tyr	-0.25	Tyr	-0.25			Tyr	-0.25
336	Leu	-0.25	Leu	-0.25	Leu	-0.25			Leu	-0.25
337	Trp	-0.40	Trp	-0.40	Trp	-0.40			Trp	-0.40
338	Glu	-0.60	Glu	-0.60	Glu	-0.60			Glu	-0.60
339	Trp	-0.60	Trp	-0.60	Trp	-0.60			Trp	-0.60
340	Ala	-0.30	Ala	-0.30	Ala	-0.30			Ala	-0.30
341	Ser	-0.10	Ser	-0.10	Ser	-0.10			Ser	-0.10
342	Val	-0.60	Val	-0.60	Val	-0.60			Val	-0.60
343	Arg	-0.20	Arg	-0.20	Arg	-0.20			Arg	-0.20
344	Phe	-0.20	Phe	-0.20	Phe	-0.20			Phe	-0.20
345	Ser	-0.20	Ser	-0.20	Ser	-0.20			Ser	-0.20
346	Trp	-0.20	Trp	-0.20	Trp	-0.20			Trp	-0.20
347	Leu	-0.60	Leu	-0.60	Leu	-0.60			Leu	-0.60
348	Ser	-0.60	Ser	-0.60	Ser	-0.60			Ser	-0.60
349	Leu	-0.40	Leu	-0.40	Leu	-0.40			Leu	-0.40
350	Leu	-0.60	Leu	-0.60	Leu	-0.60			Leu	-0.60
351	Val	-0.60	Val	-0.60	Val	-0.60			Val	-0.60
352	Pro	-0.60	Pro	-0.60	Pro	-0.60			Pro	-0.60
353	Phe	-0.60	Phe	-0.60	Phe	-0.60			Phe	-0.60
354	Val	-0.60	Val	-0.60	Val	-0.60			Val	-0.60
355	Gln	-0.60	Gln	-0.60	Gln	-0.60			Gln	-0.60
356	Trp	-0.60	Trp	-0.60	Trp	-0.60			Trp	-0.60
357	Phe	-0.60	Phe	-0.60	Phe	-0.60			Phe	-0.60
358	Val	-0.60	Val	-0.60	Val	-0.60			Val	-0.60
359	Gly	-0.20	Gly	-0.20	Gly	-0.20			Gly	-0.20
360	Leu	-0.40	Leu	-0.40	Leu	-0.40			Leu	-0.40
361	Ser	-0.25	Ser	-0.25	Ser	-0.25			Ser	-0.25
362	Pro	-0.25	Pro	-0.25	Pro	-0.25			Pro	-0.25
	Thr	-0.20	Thr	-0.20	Thr	-0.20			Thr	-0.20
	Val	-0.60	Val	-0.60	Val	-0.60			Val	-0.60
	Trp	-0.60	Trp	-0.60	Trp	-0.60			Trp	-0.60
	Leu	-0.60	Leu	-0.60	Leu	-0.60			Leu	-0.60



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Amino Acid Position	M54923 (Ref)		J-0035		J-0069		J-0060		J-0063	
	Minimum	-0.60	Minimum	-0.60	Minimum	-0.6	Minimum	-0.60	Minimum	-0.60
	Maximum	3.40	Maximum	3.40	Maximum	3.4	Maximum	3.40	Maximum	3.40
	Mean	0.40	Mean	0.40	Mean	0.42	Mean	0.62	Mean	0.41
	Residue	Index	Residue	Index	Residue	Index	Residue	Index	Residue	Index
367	Ser	-0.60	Ser	-0.60	Ser	-0.60			Ser	-0.60
368	Val	-0.60	Val	-0.60	Val	-0.60			Val	-0.60
369	Ile	-0.60	Ile	-0.60	Ile	-0.60			Ile	-0.60
370	Trp	-0.60	Trp	-0.60	Trp	-0.60			Trp	-0.60
371	Met	-0.60	Met	-0.60	Met	-0.60			Met	-0.60
372	Met	-0.60	Met	-0.60	Met	-0.60			Met	-0.60
373	Trp	-0.60	Trp	-0.60	Trp	-0.60			Trp	-0.60
374	Phe	-0.20	Phe	-0.20	Phe	-0.20			Phe	-0.20
375	Trp	-0.40	Trp	-0.20	Trp	-0.40			Trp	-0.40
376	Gly	0.00	Gly	0.00	Gly	0.00			Gly	0.00
377	Pro	0.15	Arg	0.35	Pro	0.15			Pro	0.15
378	Ser	0.15	Ser	0.45	Ser	0.15			Ser	0.15
379	Leu	0.00	Leu	0.45	Leu	0.00			Leu	0.00
380	Tyr	0.00	Ser	0.05	Tyr	0.00			Tyr	0.00
381	Asn	0.00	Thr	-0.20	Asn	0.00			Asn	0.00
382	Ile	-0.40	Ile	-0.60	Ile	-0.40			Ile	-0.40
383	Leu	-0.40	Leu	-0.60	Leu	-0.40			Leu	-0.40
384	Ser	-0.20	Ser	-0.60	Ser	-0.20			Ser	-0.20
385	Pro	-0.20	Pro	-0.60	Pro	-0.20			Pro	-0.20
386	Phe	-0.20	Phe	-0.60	Phe	-0.20			Phe	-0.20
387	Met	-0.20	Ile	-0.60	Met	-0.20			Met	-0.20
388	Pro	-0.40	Pro	-0.60	Pro	-0.40			Pro	-0.40
389	Leu	-0.60	Leu	-0.60	Leu	-0.60			Leu	-0.60
390	Leu	-0.60	Leu	-0.60	Leu	-0.60			Leu	-0.60
391	Pro	-0.60	Pro	-0.60	Pro	-0.60			Pro	-0.60
392	Ile	-0.60	Ile	-0.60	Ile	-0.60			Ile	-0.60
393	Phe	-0.60	Phe	-0.60	Phe	-0.60			Phe	-0.60
394	Phe	-0.60	Phe	-0.60	Phe	-0.60			Phe	-0.60
395	Cys	-0.60	Cys	-0.60	Cys	-0.60			Cys	-0.60
396	Leu	-0.60	Leu	-0.60	Leu	-0.60			Leu	-0.60
397	Trp	-0.60	Trp	-0.60	Trp	-0.60			Trp	-0.60
398	Val	-0.60	Val	-0.60	Val	-0.60			Val	-0.60
399	Tyr	-0.60	Tyr	-0.60	Tyr	-0.60			Tyr	-0.60
400	Ile	-0.60	Ile	-0.60	Ile	-0.60			Ile	-0.60
401	Ter	-0.60	Ter	-0.60	Ter	-0.60			Ter	-0.60

Keterangan:

*	Berdasarkan algoritma Jameson-Wolf
	Sekuens referens
	Perubahan asam amino dan indeks antigenitas

