



A\*01010101 CCTCTGCGGG GAGAAGCAAG GGGCCCTCCT GCGGGGGGCG CAGGACCGGG GGAGCCGCGC CGGGAGGAGG GTCGGGGCAGG TCTCACGCCAC TGCTCGCCCC

A\*01010101 CAG|GCTTCCA CTCATGAGG TATTCTTCA CATCCGTGC CCGGCCCGG CCGGGGGAGC CCGCTTCAT CGCCGTGGGC TAGCTGGAGC CACCGAGTT

A\*01010101 CGTCCGGTTC GACAGCGACG CCGCGAGCCA GAAGATGGAG CCGCGGGCGC CGTGGATAGA GCAGGAGGGG CCGGAGTATT GGGACCAGGA GACACCGAAT

A\*01010101 ATGAAGGCC ACTCACGAC TGACCGAGCG AACCTGGGGA CCCTGCGCGG CTACTAGAAC CAGAGCGAGG ACG|GTGAGTG ACCCCGGGCC GGGCGCAGG

A\*01010101 TCACGACCCC TCATCCCCA CGGACGGGCC AGGTCCGCCA CAGTCTCCGG GTCCGAGATC CACCCCGAAG CCGGGGGACT CCGAGACCCT TGTCGCCGGA

A\*01010101 GAGGCCCAGG CGCCTTACC CGGTTTATT TTCAGTTAG GCCAAAATC CCCCAGGGTT GGTCCGGGGC GGGGGGGGCT CCGGGGACTG GGCTGACCGC

A\*01010101 GGGTCCGGGG CCAG|GTTCTC ACACCATCCA GATAATGAT GGCTGCGAGC TGGGGCCGGA CCGGCGGGTT CTCGCGGGT ACCCGGAGGACGCCTACGAC

A\*01010101 GGCAGGATT ACATCGCCT GAACGAGGAC CTGCGCTCTT GGACCGCGG GGACATGGCA GCTCAGATCA CCAAGCGCAA GTGGGAGGGC GTCCATGCGG

A\*01010101 CGGAGCAGG GAGAGTCTAC CTGGAGGGCC GGTCTGGGA CCGGCTCCGC AGATACCTGG AGAACGGGA GGAGCGGCT CAGCGCAGGT GTACCAGGGG

A\*01010101 CCACGGGGGG CCTCCCTGAT CGCCTATAGA TCTCCCGGGC TGGCCTCCCA CAAGGAGGGG AGACAATTGG GACCAACT AGAATATCAC CCTCCCTCTG

A\*01010101 GTCTCGAGG AGAGGAATC TCCTGGGTTT CCAGTCTCG TACCAGAGAG TGAGTCTGAG GTTCCGCTCT GCTCTCTGAC ACAATTAAGG GATAAAATCT

A\*01010101 CTGAAGGAGT GACGGGAAGA CGATCCCTCG AATACTGATG AGTGTTCC CTTGACACCG GCAGCAGCCT TGGGCCCGT ACTTTTCTC TCAGCCCTTG

A\*01010101 TTCTCTGCTT CACACTCAAT GTGTGTGGGG GTCTGAGTCC AGCACTTCTG AGTCTCTCAG CCTCACTCA GGTGAGGACC AGAAGTAAAGT GTTCCCTTCT

A\*01010101 CAGGGAATAG AAGATTATCC CAGGTGCCTG TGTCCAGGCT GGTGTCTGGG TTCTGTGCTC TCTTCCCAT CCCGGGTGC CTGTCCATTC TCAAGATGCC

A\*01010101 CACATGCGTG CTGGTGGAGT GTCCCATGAC AGATGCAAAA TGCCTGAATT TTCTGACTCT TCCCGTCAG|A CCCCCCAAG ACACATATGA CCACCACCC

A\*01010101 CATCTCTGAC CATGAGGCA CCCTGAGGTG CTGGCCCTG GGCTTCTACC CTGGGAGAT CACACTGACC TGGCAGCGG ATGGGGAGGA CCAGCCGAG

A\*01010101 GACACGGAGC TCGTGGAGC CAGGCCTGCA GGGGATGAA CCTTCCGAA GTGGGCGGCT GTGGTGGTG CTTCTGAGA GGAGCAGGA TACACCTGGC

A\*01010101 ATGTGCAGCA TGAGGGTCTG CCCAAGCCCC TCACCCTGAG ATGGG|GTAAG GAGGAGATG GGGGTGTCAT GTCTCTTAGG GAAAGCAGGA CCTCTCTGG

A\*01010101 AGACCTTATG CAGGGTCAGG GCCCTCACC TTCCCTCTT TTCCAG|AGC TGTCTTCCA GCCCACCATC CCCATCGTGG GCATCATTC GGCCTGGTT

A\*01010101 CTCCTGGAG CTGTGATCAC TGGAGCTGTG GTCGCTGCCG TGATGTGGAG GAGGAAGAGC TCAG|GTGGAG AAGGGGTGAA GGGTGGGGTC GAGATTTCT

A\*01010101 TGTCTCACTG AGGGTTCAA GCCCCAGCTA GAAATGTGCC CTGTCTATT AGTGGGAAGC ACCTTCCACA ATCATGGGCC GACCCAGCCT GGGCCCTGTG

A\*01010101 TGCCAGCACT TACTCTTTTG TAAAGCACCT GTTAAAATGA AGGACAGATT TATCACCTTG ATTACGGCGG TGATGGGACC TGATCCAGC AGTCACAAGT

A\*01010101 CACAGGGGAA GGTCCCTGAG GACAGACCTC AGGAGGGCTA TTGGTCCAG ACCCACACCT GCTTCTTCA TGTTCCTGA TCCCGCCCTG GGTCTGCAGT

A\*01010101 CACACATTC TGAAACTTC TCTGGGTCC AAGACTAGGA GGTCTCTA GGACCTAAG GCCTGGCTC CTTTCTGTA TCTCACAGGA CATTCTCTC

A\*01010101 CCACAG|ATAG AAAAGGAGG AGTTACACTC AGGCTGCAA|G TAAGTATGAA GGAGGCTGAT GCCTGAGGTC CTGGGATAT TGTGTTGGG CCCATGGG

A\*01010101 GGAGCTCAC CACCCACAA TTCTCTCTT AGCCACATCT TCTGTGGGAT CTGACCAGGT TCTGTTTTG TTACACCCA G|GCAGTGACAGTCCCAGGG

A\*01010101 CTCTGATGTG TCTCTCAGC CTTGTAAAG|G TGAGAGCTTG GAGGGCTGA TGTGTGTTG GTGTGGGTG GAACAGTGA CACAGCTGTG TATGGGTT

```

A*01010101      2810      2820      2830      2840      2850      2860      2870      2880      2890      2900
TCTTTGCGTT GGATGTATTG AGCATGCGAT GGGCTGTTTA AGGTGTGACC CCTCACGTG ATGGATATGA ATTTGTTTCAAT GAATATTTTTTCTATAG|TG

A*01010101      2910      2920      2930      2940      2950      2960      2970      2980      2990      3000
TGA|GACAGCT GCCTGTGTG GACTGAGAG GCAAGAGTTG TTCCTGCCCT TCCCTTTGTG ACTTGAAGAA CCTGACTTT GTTCTGCAAAGGCACCTGC

A*01010101      3010      3020      3030      3040      3050      3060      3070      3080      3090      3100
ATGTGTCTGT GTTCGTGTAG GCATAATGTG AGGAGGTGGG GAGAGCACCC CACCCCATG TCCACCATGA CCCTCTTCCC ACGCTGACCT GTGCTCCCTC

A*01010101      3110      3120      3130      3140      3150      3160      3170      3180      3190      3200
CCCAATCATC TTTCTGTTC CAGAGAGGTG GGGCTGAGGT GTCTCCATCT CTGTCTCAAC TTCATGGTGC ACTGAGCTGT AACTTCTTCC TTCCCTATTA

```

Question 2:

```

A*01010101      -21      -11      -1       10       20       30       40       50       60       70
MAVM APRILLLLLS GALALITQWA GSHSMRYFFT SVSRPGRGEP RFIAGYVDD TQFVRFSDA ASQKMEPRAP WIEQEGPEYW DQETRNMKAH

A*01010101      80       90       100      110      120      130      140      150      160      170
SQTRANLGT LRGYYNQSED GSHTIQIMYG CDVGPDGRPL RGYRQDAYDG KDYIALNEDL RSWTAADMAA QITKRKWEAV HAAEQRRVYL EGRCVDGLRR

A*01010101      180      190      200      210      220      230      240      250      260      270
YLENGKETLQ RTDPPKTHMT HHPISDHEAT LRCNALGFYP ABITLTWQRD GEDQTQDEL VETRPAGDGT FQKWAAVVVP SGBEQRYTCH VQHEGLPKEL

A*01010101      280      290      300      310      320      330      340      350
TLRWELSSQP TIPIVGIAG LVLLGAVITG AVVAAVMRRR KSSDRKGSY TQAASSDSAQ GSDVSLTACK V

```

See the answer to question 2 for the start codon and signal sequence.

**Chapter 3:**

**Question 1:**

DRA

**Chapter 4:**

**Question 1:**

No question, look up reference.

**Question 2:**

For example: DQB1\*05:01, DQB1\*02:01

Question 3:

$$(1.9/100) \times (7/100) = 13.3/10,000 = 0.133/100 = 0.133\%$$

Question 4:

DRB1\*01:01:

GGG GAC ACC CGA CCA CGT TTC TTG TGG CAG CTT AAG TTT GAA  
Gly Asp Thr Arg Pro Arg Phe Leu Trp Gln Leu Lys Phe Glu  
TGT CAT TTC TTC AAT GGG  
Cys His Phe Phe Asn Gly

DRB1\*13:02:

GGG GAC ACC AGA CCA CGT TTC TTG GAG TAC TCT ACG TCT GAG  
Gly Asp Thr Arg Pro Arg Phe Leu Glu Tyr Ser Thr Ser Glu  
TGT CAT TTC TTC AAT GGG  
Cys His Phe Phe Asn Gly

Question 5:

Example:

ACC GGA TAT TTT GAA  
Thr Gly Tyr Phe Glu

Question 6:

♂ DRB1\*04:01, DRB1\*11:03

♀ DRB1\*01:01, DRB1\*03:01

Possible DRB1 combinations of children:

DRB1\*04:02, \*03:01

DRB1\*04:02, \*01:01

DRB1\*11:03, \*03:01

DRB1\*11:03, \*01:01

Yes, it is possible for two children to be DR identical. No children are homozygous; all are heterozygous (i.e., carry 2 different alleles).

Question 7:

♂  
\_\_\_\_\_  
DRB1\*04:03, DPB1\*02:01  
DRB1\*11:01, DPB1\*02:01

♀  
\_\_\_\_\_  
DRB1\*01:01, DPB1\*02:01  
DRB1\*03:02, DPB1\*01:01

Possible DR, DP combinations of children:

DRB1\*04:03, DPB1\*02:01; DRB1\*01:01, DPB1\*02:01

DRB1\*04:03, DPB1\*02:01; DRB1\*03:02, DPB1\*01:01

DRB1\*11:01, DPB1\*02:01; DRB1\*01:01, DPB1\*02:01

DRB1\*11:01, DPB1\*02:01; DRB1\*03:02, DPB1\*01:01

and many more possibilities by recombination, for example:  
DRB1\*04:03, DPB1\*02:01; DRB1\*03:02, DPB1\*0:201

Yes, DRB1\*04:03, DPB1\*02:01; DRB1\*01:01, DPB1\*01:01 is possible by recombination.

DRB1*01:01	DPB1*02:01
X	
DRB1*03:02	DPB1*01:01
∴	
DRB1*01:01	DPB1*01:01
DRB1*03:02	DPB1*02:01

Question 8:

DRB1\*13:04 DRB3\*02:01 DQA1\*02:01 DQB1\*02:01 DPA1\*01:04 DPB1\*04:01  
DRB1\*04:02 DRB4\*01:01 DQA1\*02:01 DQB1\*02:01 DPA1\*01:04 DPB1\*04:01

Note the predicted association of DRB1\*13:04 with DRB3\*02:01 and DRB1\*04:02 with DRB4\*01:01.

The person is homozygous for DQ and DP.

Question 9:

See next two pages.

Question 10:

For example: C\*01:01, C\*02:01, C\*02:02:01, C\*08:01

## Chapter 4-Question 9:

Part One:

```

DRB1*0101      1                               10                               20                               30
GGG GAC ACC CGA CCA CGT TTC TTG TGG CAG CTT AAG TTT GAA TGT CAT TTC TTC AAT GGG ACG GAG CGG GTG CGG TTG CTG GAA AGA TGC ATC TAT AAC CAA
DRB1*0102      --- --- --- --- --- T-- --- --- CA- --- GA- --- -A- -G --- --- --- -C --- --- --- C-C --- G-- --- --- ---
DRB5*0202      --- --- --- --- --- T-- --- --- CA- --- GA- --- -A- -G --- --- --- -C --- --- --- C-C --- G-- --- --- ---

DRB1*0101      40                               50                               60
GAG GAG TCC GTG CGC TTC GAC AGC GAC GTG GGG GAG TAC CGG GCG GTG ACG GAG CTG GGG CGG CCT GAT GCC GAG TAC TGG AAC AGC CAG AAG GAC CTC CTG
DRB1*0102      --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
DRB5*0202      --- --- AA- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- A-- ---

DRB1*0101      70                               80                               90                               100
GAG CAG AGG CGG GCC GCG GTG GAC ACC TAC TGC AGA CAC AAC TAC GGG GTT GGT GAG AGC TTC ACA GTG CAG CGG CGA GTT GAG CCT AAG GTG ACT GTG TAT
DRB1*0102      --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
DRB5*0202      --- --- GC- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

DRB1*0101      110                              120                              130
CCT TCA AAG ACC CAG CCC CTG CAG CAC CAC AAC CTC CTG GTC TGC TCT GTG AGT GGT TTC TAT CCA GGC AGC ATT GAA GTC AGG TGG TTC CGG AAC GGC CAG
DRB1*0102      --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
DRB5*0202      --- G-- -G- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- A-

DRB1*0101      140                              150                              160                              170
GAA GAG AAG GCT GGG GTG GTG TCC ACA GGC CTG ATC CAG AAT GGA GAT TGG ACC TTC CAG ACC CTG GTG ATG CTG GAA ACA GTT CCT CGG AGT GGA GAG GTT
DRB1*0102      --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
DRB5*0202      --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -TT

DRB1*0101      180                              190                              200
TAC ACC TGC CAA GTG GAG CAC CCA AGT GTG ACG AGC CCT CTC ACA GTG GAA TGG AGA GCA CGG TCT GAA TCT GCA CAG AGC AAG ATG CTG AGT GGA GTC GGC
DRB1*0102      --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
DRB5*0202      --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -A- --- A--

DRB1*0101      210                              220                              230
GGC TTC GTG CTG GGC CTG CTC TTC CTT GGG GCC GGG CTG TTC ATC TAC TTC AGG AAT CAG AAA GGA CAC TCT GGA CTT CAG CCA ACA GGA TTC CTG AGC TGA
DRB1*0102      --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
DRB5*0202      --- --- T-- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- C-- G--

```



**Chapter 4, Question 11:**

Shared sequences are those marked by dashes compared to top line.

	1										100
Consensus	ATGCGGGTCA	TGGCGCCCCG	AACCCTCCTC	CTGCTGCTCT	CGGGGGCCCT	GGCCCTGACC	GAGACCTGGG	CCGGCTCCCA	CTCCATGAGG	TATTTCTACA	
b-07021	----t-----	-----	----g-----	-----	---c-----	-----	-----	-----	-----	-----	
b-0801	----t-----	-----	----g-----	-----	---c-----	-----	-----	-----	-----	-----g---	
b-4201	----t-----	-----	----g-----	-----	---c-----	-----	-----	-----	-----	-----	
	101										200
Consensus	CCGCCGTGTC	CCGGCCCCGC	CGCGGGGAGC	CCCCTTCAT	CGCAGTGGGC	TACGTGGACG	ACACGCAGTT	CGTGAGGTTT	GACAGCGACG	CCGCGAGTCC	
b-07021	--t-----	-----	-----	-----	-t-----	-----	---c-----	-----	-----	-----	
b-0801	----a-----	-----	-----	-----	-t-----	-----	---c-----	-----	-----	-----	
b-4201	--t-----	-----	-----	-----	-t-----	-----	---c-----	-----	-----	-----	
	201										300
Consensus	GAGGATGGAG	CCGCGGGCGC	CGTGGATAGA	GCAGGAGGGG	CCGGAGTATT	GGGACCGGGA	GACACAGATC	TTCAAGACCA	ACACACAGAC	TGACCGAGAG	
b-07021	---aga-----	-----	-----	-----	-----	-----a-	c-----	-a---g--c	-gg-----	-----	
b-0801	---aga-----	-----	-----	-----	-----	-----a-	c-----	-a---g--c	-gg-----	-----	
b-4201	---aga-----	-----	-----	-----	-----	-----a-	c-----	-a---g--c	-gg-----	-----	
	301										400
Consensus	AGCCTGCGGA	ACCTGCGCGG	CTACTACAAC	CAGAGCGAGG	CCGGGTCTCA	CACCCTCCAG	AGGATGTATG	GCTGCGACGT	GGGGCCGGAC	GGGCGCCTCC	
b-07021	-----	-----	-----	-----	-----	-----	---c---c-	-----	-----	-----	
b-0801	-----	-----	-----	-----	-----	-----	---c---c-	-----	-----	-----	
b-4201	-----	-----	-----	-----	-----	-----	---c---c-	-----	-----	-----	
	401										500
Consensus	TCCGCGGGTA	TGACCAGTAC	GCCTACGACG	GCAAGGATTA	CATCGCCCTG	AACGAGGACC	TGCGCTCCTG	GACCGCGGCG	GACACGGCGG	CTCAGATCAC	
b-07021	-----c-	-----	-----	-----	-----	-----	-----	-----c--	-----	-----	
b-0801	-----c-	-a-----	-----	-----	-----	-----	-----	-----	-----c--	-----	
b-4201	-----c-	-a-----	-----	-----	-----	-----	-----	-----	-----c--	-----	
	501										600
Consensus	CCAGCGCAAG	TGGGAGGCGG	CCCCTGTGGC	GGAGCAGCTG	AGAGCCTACC	TGGAGGGCAC	GTGCGTGGAG	TGGCTCCGCA	GATACCTGGA	GAACGGGAAG	
b-07021	-----	-----	-----a--	-----g-	-----	-----ga	-----	-----	-----	-----	
b-0801	-----	-----	-----	-----gac	-----	-----	-----	-----	-----	-----	
b-4201	-----	-----	-----	-----gac	-----	-----	-----	-----	-----	-----	
	601										700
Consensus	GAGACGCTGC	AGCGCGCGGA	CCCCCAAAG	ACACATGTGA	CCCACCACCC	CATCTCTGAC	CATGAGGCCA	CCCTGAGGTG	CTGGGCCCTG	GGCTTCTACC	
b-07021	--c-a---g	-----t--	-----	-----c--	-----	-----	-----	-----	-----	-----t--	
b-0801	--c-----g	-----	-----	-----c--	-----	-----	-----	-----	-----	-----	
b-4201	--c-----g	-----	-----	-----c--	-----	-----	-----	-----	-----	-----	
	701										800

ANSWERS TO THE MANUAL QUESTIONS

Consensus	CTGCGGAGAT	CACACTGACC	TGGCAGCGGG	ATGGCGAGGA	CCAAACTCAG	GACACCGAGC	TTGTGGAGAC	CAGACCAGCA	GGAGATAGAA	CCTTCCAGAA
b-07021	-----	-----	-----	-----	-----	-----t---	-----	-----	-----	-----
b-0801	-----	-----	-----	-----	-----	-----t---	-----	-----	-----	-----
b-4201	-----	-----	-----	-----	-----	-----t---	-----	-----	-----	-----
	801									900
Consensus	GTGGGCAGCT	GTGGTGGTGC	CTTCTGGAGA	AGAGCAGAGA	TACACATGCC	ATGTACAGCA	TGAGGGGCTG	CCGAAGCCCC	TCACCCTGAG	ATGGGAGCCA
b-07021	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----g
b-0801	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----g
b-4201	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----g
	901									1000
Consensus	TCTTCCCAGT	CCACCATCCC	CATCGTGGGC	ATTGTTGCTG	GCCTGGCTGT	CCTAGCAGTT	CTAGTGGTCA	TCGGAGCTGT	GGTCGCTGCT	GTGATGTGTA
b-07021	-----	-----g	-----	-----	-----	-----	-----	-----	-----	-----
b-0801	-----	-----g	-----	-----	-----	-----	-----	-----	-----	-----
b-4201	-----	-----g	-----	-----	-----	-----	-----	-----	-----	-----
	1001									1100
Consensus	GGAGGAAGAG	CTCAGGTGGA	AAAGGAGGGA	GCTACTCTCA	GGCTGCGTCC	AGCGACAGTG	CCCAGGGCTC	TGATGTGTCT	CTCACAGCTT	GAAAAGTGTG
b-07021	-----	t-----	-----	-----	-----g-	-----	-----	-----	-----	-----
b-0801	-----	-----	-----	-----	-----g-	-----	-----	-----	-----	-----
b-4201	-----	-----	-----	-----	-----g-	-----	-----	-----	-----	-----

## Chapter 5

Question 1: No question.

Question 2: No question.

Question 3:

Not necessarily. There are many alleles of DR3 and DR8. Serologic testing cannot distinguish between the alleles. For example, the donor can be DRB1\*08:03, DRB1\*03:01 and the recipient can be DRB1\*08:04, DRB1\*03:02.

Question 4:

A) ♂  
DR4/DR11

♀  
DR1/DR3

children:  
DR4/DR1; DR4/DR3; DR11/DR1; DR11/DR3

B) ♂  
DRB1\*04:02/DRB1\*11:03

♀  
DRB1\*01:01/DRB1\*03:01

children:  
DRB1\*04:02/DRB1\*01:01; DRB1\*04:02/DRB1\*03:01  
DRB1\*11:03/DRB1\*01:01; DRB1\*11:03/DRB1\*03:01

Question 5:

Loci: DRB1            DRB3            DRA  
          DRB1\*11:02 DRB3\*02:02 DRA\*01:01

Question 6:

♂  
A2,A3,B27,B53

♀  
A2,A11,B51,B71

Children:

A2,B27;A2,B51 -or- A2,B53;A2,B51 -or- A3,B27;A2,B51 -or- A3,B53;A2,B51  
A2,B27;A2,B71 -or- A2,B53;A2,B71 -or- A3,B27;A2,B71 -or- A3,B53;A2,B71  
A2,B27;A11,B71 -or- A2,B53;A11,B71 -or- A3,B27;A11,B71 -or- A3,B53;A11,B71  
A2,B27;A11,B51 -or- A2,B53;A11,B51 -or- A3,B27;A11,B51 -or- A3,B53;A11,B51

parent one: A2,B27 and A3,B53

parent two: A2,B71 and A11,B51

Question 7:

A\*68:01=A68(28), B\*13:01=B13, B\*18:17=serologic type not known,  
DRB1\*03:01=DR17(3), DRB1\*11:22=serologic type not known

Question 8:

Patient exhibits serologic type A2 only; the A\*24:09N allele does not specify an HLA-A antigen. An A2,A24 donor would not be a good choice; a A2 donor would be better.



The polymerase copies the DNA until the temperature is changed (e.g., 72°C → 94°C). In the initial cycles of the PCR, the original DNA strands yield long pieces of DNA when copied by Taq. As the cycles proceed, a major DNA product appears that is a fixed size, bounded by the primers.

After 3rd cycle:  
8 dsDNA molecules

There are 26 bp in the amplified fragment.  
after 3 cycles =  $2^3 = 8$  copies  
after 10 cycles =  $2^{10} = 1024$  copies

Question 3:

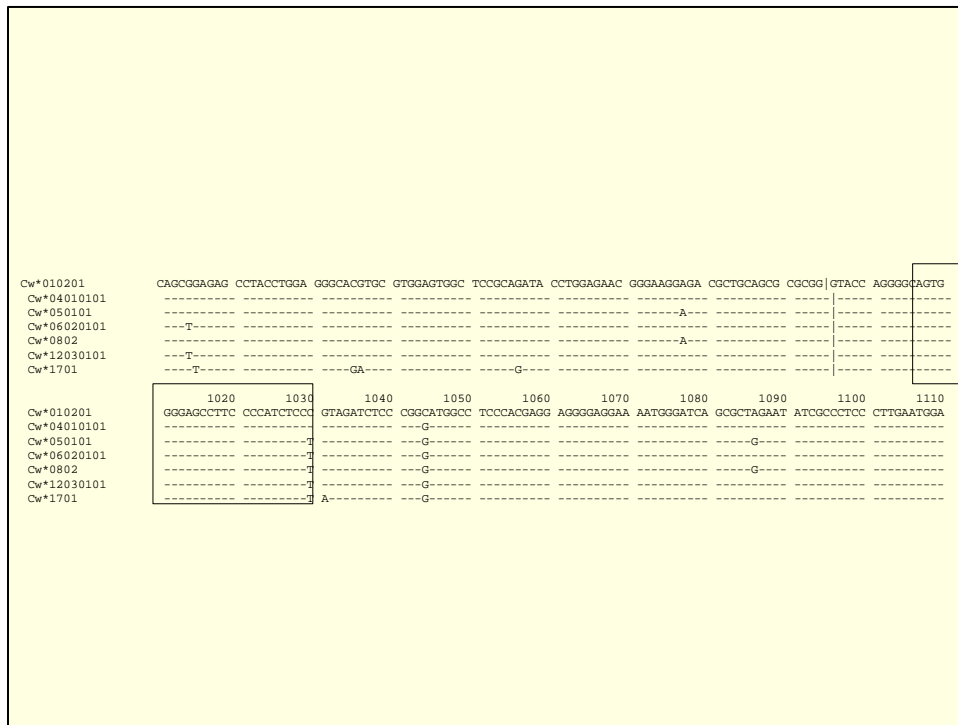
Find the answer in the answer for Chapter 2 question 1, the primer annealing sites are underlined. The primer sequences cannot be found entirely in the cDNA sequence because the primers are partially (forward) or completely positioned in the introns.

Question 4:

```

Cw*010201      GGTTCCTAGAG AAGCCAATCA GCGTCTCCGC AGTCCCGGTT CTAAGTCCC CAGTCACCCA CCCGGACTCA GATTCTCCCC AGACGCCGAG |ATGCGGGTCA
Cw*04010101    -----
Cw*050101      -----
Cw*06020101    -----
Cw*0802        -----
Cw*12030101    -----
Cw*1701        -----
                20      30      40      50      60      70      80      90      100     110
Cw*010201      TGGCGCCCGG AACCCATCATC CTGCTGCTCT CGGGAGCCCT GGCCTGACC GAGACCTGGG CCT|GTGAGTG CGGGGTGGG AGGGAACGG CCTCTGCGGA
Cw*04010101    -----
Cw*050101      -----
Cw*06020101    -----
Cw*0802        -----
Cw*12030101    -----
Cw*1701        -----
                -A -G - - -C - - - - -T - -G |
                120     130     140     150     160     170     180     190     200     210
Cw*010201      GAGGAACGAG GTGCCC GCCGAGGGCG CAGGACCCGG GGAGCCGCGC AGGGAGGAGG GTCGGGCGGG TCTCAGCCCC TCCTCGCCCC CAG|GCTCCCA
Cw*04010101    -----
Cw*050101      -----
Cw*06020101    -----
Cw*0802        -----
Cw*12030101    -----
Cw*1701        -----

```



**Question 5:**

For example:

Forward:

5' GGT GTA AAC TTG TAC CAG 3'

Reverse:

5' CAA CTC TAC CGC TGC TAC 3'

**Question 6:**

270,000 copies

**Question 7:**

Part one: 5' CTT GGA GCA GGT TAA ACA 3' for example (codon 7-13). Place the mismatch on the 3' end of a PCR primer.

Part two: Can't do this. The best choice is: 5' CTG GGG CGG CCT GAT GAG 3' (codon 52-58) which will amplify all DRB1\*11 alleles plus a few other alleles like DRB1\*14:15.

Part three: No, it can not be done!!

**Chapter 7:**

**Question 1:**

3' GATGCGGATT 5'. If the DNA is double stranded, the complementary sequence of 5' CTACGCCTAA 3' can also be used.

50% G+C. Approximate melting temperature is  $30E([4X5]+[2x5]=30)$ . No hybridization will occur at 50E, because it is above the melting temperature. If the probe is positioned so the variation between the alleles is at the 3' or 5' end of the probe, it will be very difficult to achieve specific hybridization; the probe will likely bind well to both alleles.

Question 2:

Part one: For example: 5' CGG CCT GAT GAG GAG TAC (codon 55-60). Place the mismatch in the center of the oligo for a probe.

Part two: For example: 5' TGG AAC AGC CAG AAG GAC (codon 61-66) although DRB1\*04:11 differs in this region.

Part three: 5' GAG GAG GTT AAG TTT GAG (codon 9 -14).

Question 3:

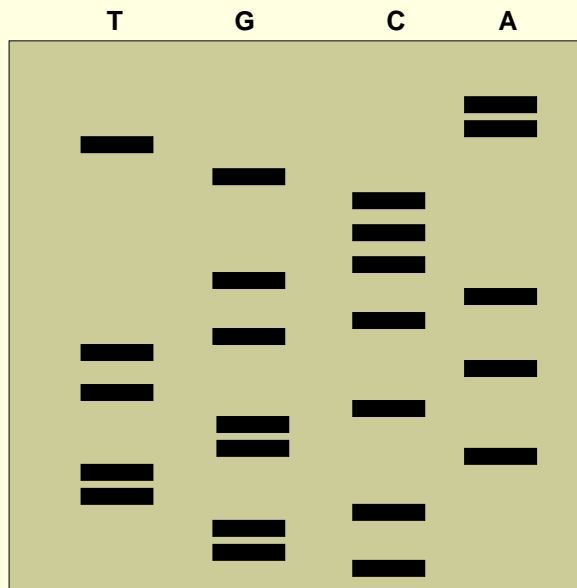
First, amplify only the DRB1\*01 alleles with PCR primers designed around codons 25-31 and DRBAMPB (for example). Then use a probe to distinguish between DRB1\*01:01 and DRB1\*01:02, designed around codons 83-89. Use probe with sequence: 5' C GGG GCT GTG GAG AGC TT (for example to detect DRB1\*01:02 and not DRB1\*01:01, \*01:03, \*01:04).

**Chapter 8:**

Question 1:

create PCR primers that would amplify DRB1\*07:01

Question 2:



**Chapter 9:**

No questions

**Chapter 10:**

**Question 1:**

DRB1\*01:01, \*04:01

DRB1\*11:01, \*07:01

**Question 2:**

Sample also carries one of the DRB1\*04 alleles. Since one of the DRB1\*04 alleles, DRB1\*04:02, also carries the sequence detected by probe DR7007, it is not known if DRB1\*01:03 is present. As a result, the sample would be typed as [DRB1\*01:03 and DRB1\*04:01 or \*04:03 or \*04:04 or ... \*04:10] OR [DRB1\*01:01 or \*01:02 or \*01:03 and DRB1\*04:02]. To determine if DRB1\*01:03 is present, you would need to amplify DRB1\*01 using a group-specific amplification.

Question 3: These two allele combinations would have exactly the same sequence. Positions of mixed bases (i.e., two bases, a polymorphic residue) are the same. One must isolate individual alleles to identify which combination is present. Look at the sequence of the two alternative DRB1\*03 alleles and see how knowing whether the DRB1\*03 specific sequence at codons 9-14 is on the same strand of DNA (i.e., in the same allele) as the sequence at codons 77 and 86 will identify which allele, DRB1\*03:01:02 or DRB1\*03:14, is present.

Question 4: A\*74:02 can't be distinguished from A\*74:01 by just sequencing exons 2 and 3 of these alleles. The genotype A\*01:17, A\*01:28 cannot be distinguished from A\*01:01:01G, A\*01:13 if you sequence both HLA-A alleles simultaneously and only examine exons 2 and 3.

Question 5: The person could have any one of the DRB1\*11 alleles (now numbering almost 100) or DRB1\*03:08 or DRB1\*04:15 or DRB1\*12:04 or DRB1\*14:11. The GAG codon at 58 used to be unique for the DRB1\*11 alleles but this is no longer the case.