

A*01010101 310 320 330 340 350 360 370 380 390 400
CGTCCGGTTC GACAGCGACG CCGCGAGCCA GAAGATGGAG CCGCGGGCGC CGTGGATAGA GCAGGAGGGG CCGGAGTATT GGGACCAGGA GACACGGAAAT

A*01010101 410 420 430 440 450 460 470 480 490 500
ATGAAGGCC ACTCACAGAC TGACCGAGCG AACCTGGGA CCCTCGCGGG CTACTACAAC CAGAGCGAGG ACG|GTGAGTG ACCCGGGCCC GGGCGCAGG

A*01010101 510 520 530 540 550 560 570 580 590 600
 TCACGACCCC TCATCCCCA CGGACGGGCC AGGTCCGCCA CAGTCTCCGG GTCGAGATC CACCCGGAAG CCGCGGGACT CCGAGACCCT TGTCCCGGGA

A*01010101 610 620 630 640 650 660 670 680 690 700
 GAGGCCCAGG CGCCTTTACC CGGTTTCATT TTCAGTTTAG GCCAAAAATC CCCCCGGGT GGTCTGGGGC GGGCGGGCT CCGGGGACTG GGCTGACCCG

A*01010101 710 720 730 740 750 760 770 780 790 800
 GGGTCCGGG CAG|GTTCTC ACACCATCCA GATAATGTAT GGCTGGCAGC TGGGGCCGGA CCGGCGCTTC CTCGCGGGT ACCGGCAGGACGCCTACGAC

A*01010101 810 820 830 840 850 860 870 880 890 900
GGCAAGGATT ACATCGCCCT GAACGAGGAC CTGCGCTCTT GGACCGCGGC GGACATGGCA GCTCAGATCA CCAAGCCGAA GTGGGAGGCG GTCCATCGCG

A*01010101 910 920 930 940 950 960 970 980 990 1000
CGGAGCAGCG GAGAGTCTAC CTGGAGGGCC GGTGCTGGA CCGGCTCCCG AGATACCTGG AGAACGGGAA GGAGACGCTG CAGCGCACGG GTACCAGGGG

A*01010101 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100
 CCACGGGGCG CCTCCCTGAT CGCCTATAGA TCTCCGGGCG TGGCCTCCCA CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCAC CCTCCCTCTG

A*01010101 1110 1120 1130 1140 1150 1160 1170 1180 1190 1200
 GTCCTGAGG AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT GCTCTCTGAC ACAATTAAG GATAAAATCT

A*01010101 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
 CTGAAGGAGT GACGGGAGA CGATCCCTCG AATACTGTAT AGTGGTCCCG TTTGACACCG GCAGCAGCCT TGGGCCCGTG ACTTTTCTCT TCAGGCCTTG

A*01010101 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400
 TTCTCTGCTT CACACTCAAT GTGTGTGGG GTCTGAGTCC AGCACTTCTG AGTCTCTCAG CCTCCACTCA GGTCAAGGACC AGAAGTCGTT GTTCTCTCTT

A*01010101 1410 1420 1430 1440 1450 1460 1470 1480 1490 1500
 CAGGGAATAG AAGATTATCC CAGGTGCCTG TGTCCAGGCT GGTGTCTGGG TTCTGTGCTC TCTTCCCAT CCCGGGTGC CTGTCCATTG TCAAGATGCC

A*01010101 1510 1520 1530 1540 1550 1560 1570 1580 1590 1600
 CACATGCGTG CTGGTGGAGT GTCCCATGAC AGATGCAAAA TGCTGAATT TTCTGACTCT TCCCGTCAG|A CCCCCCAAG ACACATATGA CCACACCC

A*01010101 1610 1620 1630 1640 1650 1660 1670 1680 1690 1700
CATCTCTGAC CATGAGGCCA CCCTGAGGTG CTGGGCCCTG GGCTTCTACC CTGGGAGAT CACACTGACC TGGCAGGGG ATGGGAGGA CCAGACCCAG

A*01010101 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800
GACACGGAGC TCGTGGAGC CAGGCCTGCA GGGATGGAA CCTTCAGAA TGGGGCGGCT GTGGTGTGC CTTCTGGAGA GGAGCAGAGA TACACCTGCC

A*01010101 1810 1820 1830 1840 1850 1860 1870 1880 1890 1900
ATGTGACAGA TGAGGCTCTG CCCAAGCCCC TCACCTGAG ATGGG|GTAAG GAGGAGATG GGGGTGTCAT GTCCTTAGG GAAAGCAGGA CCTCTCTGG

A*01010101 1910 1920 1930 1940 1950 1960 1970 1980 1990 2000
 AGACCTTTAG CAGGTCAGG GCCCTCACC TTCCCTCTT TTCCAG|AGC TGTCTTCCA GCCCACCATC CCCATGCTGG GCATCATTGC GGCCCTGGTT

A*01010101 2010 2020 2030 2040 2050 2060 2070 2080 2090 2100
CTCCTTGGAG CTGTGATCAC TGGAGCTGTG GTCGCTGCCG TGATGTGGAG GAGGAAGAGC TCAG|GTGGAG AAGGGGTGAA GGGTGGGGTC GAGATTCTT

A*01010101 2110 2120 2130 2140 2150 2160 2170 2180 2190 2200
 TGTCTCACTG AGGTTTCAA GCCCCAGTA GAAATGTGCC CTGTCTCATT ACTGGGAAGC ACCTTCCACA ATCATGGGCC GACCCAGCCT GGGCCCTGTG

A*01010101 2210 2220 2230 2240 2250 2260 2270 2280 2290 2300
 TGCCAGCACT TACTCTTTG TAAAGCACCT GTTAAAATGA AGGACAGATT TATCACCTTG ATTACGGCGG TGATGGGACC TGATCCAGC AGTCACAAGT

A*01010101 2310 2320 2330 2340 2350 2360 2370 2380 2390 2400
 CACAGGGGAA GGTCCCTGAG GACAGACCTC AGGAGGGCTA TTGGTCCAGG ACCCACACCT GCTTCTTCA TGTTCCTGA TCCCGCCCTG GGTCTGCAGT

A*01010101 2410 2420 2430 2440 2450 2460 2470 2480 2490 2500
 CACACATTTG TGGAAACTTC TCTGGGTCC AAGACTAGGA GGTCTCTTA GGACCTTAAG GCCTGGGCTC CTTTCTGGTA TCTCACAGGA CATTCTCTTC

A*01010101 2510 2520 2530 2540 2550 2560 2570 2580 2590 2600
CCACAG|ATAG AAAAGGAGGG AGTTACACTC AGGCTGCAA|G TAAGTATGAA GGAGGCTGAT GCCTGAGGTC CTGGGATAT TGTGTTTGGG CCCATGGG

A*01010101 2610 2620 2630 2640 2650 2660 2670 2680 2690 2700
 GGAGCTCACC CACCCACAA TTCCTCTCT AGCCACATCT TCTGTGGGAT CTGACCAGGT TCTGTTTTG TTCTACCCA G|GGAGTGACAGTCCCAGGG

A*01010101 2710 2720 2730 2740 2750 2760 2770 2780 2790 2800
CTCTGATGTG TCTCTCACAG CTTGTAAAG|G TGAGAGCTTG GAGGGCCTGA TGTGTGTTGG GTGTTGGGTG GAACAGTGA CACAGCTGTG TATGGGGTT

```

      2810      2820      2830      2840      2850      2860      2870      2880      2890      2900
A*01010101 TCTTTGCGTT GGATGTATG AGCATGCGAT GGGCTGTTA AGGTGTGACC CCTCACTGTG ATGGATATGA ATTTGTTTCAAT GAATATTTTTTCTATAG|TG
      2910      2920      2930      2940      2950      2960      2970      2980      2990      3000
A*01010101 TGA|GACAGCT GCCTTGTGTG GGACTGAGAG GCAAGAGTTG TTCCTGCCCT TCCCTTTGTG ACTTGAAGAA CCCTGACTTT GTTTCTGCAAAGGCACCTGC
      3010      3020      3030      3040      3050      3060      3070      3080      3090      3100
A*01010101 ATGTGTCCTGT GTTCGTGTAG GCATAATGTG AGGAGGTGGG GAGAGCACCC CACCCCATG TCCACCATGA CCCTCTTCCC ACGCTGACCT GTGCTCCCTC
      3110      3120      3130      3140      3150      3160      3170      3180      3190      3200
A*01010101 CCCAATCATC TTTCCTGTTC CAGAGAGGTG GGGGTGAGGT GTCTCCATCT CTGTCTCAAC TTCATGGTGC ACTGAGCTGT AACTTCTTCC TTCCTATTA

```

Question 2:

```

      -21      -11      -1       10       20       30       40       50       60       70
A*01010101 MAVM APRLLLLLS GALALTQWA GSHSMRYFFT SVSRPGRGEP RFIANGYVDD TQFVRFSDA ASQKMEPRAP WIEQEGPEYW DQETRNKKAH
      80       90       100      110      120      130      140      150      160      170
A*01010101 SQTDRANLGT LRGYYNQSED GSHTIQIMYG CDVGPDGRFL RGYRQDAYDG KDYIALNEDL RSWTAADMAA QITKRKWEAV HAAEQRRVYL EGRCVDGLER
      180      190      200      210      220      230      240      250      260      270
A*01010101 YLENGKETLQ RTDPPKTHMT HHPISDHEAT LRCWALGFYP AEITLWQRD GEDQTQDEL VETRPAGDGT FQKWAAVVVP SGEEQRYTCH VQHEGLPKPL
      280      290      300      310      320      330      340      350
A*01010101 TLRWELSSQP TIPIVGIAG LVLLGAVITG AVVAAVMRRR KSSDRKGGSY TQAASSDSAQ GSDVSLTACK V

```

See to for codon and leader sequence.

the answer question 2 the start

Chapter 3:

Question 1:

DRA

Chapter 4:

Question 1:

No question, look up reference.

Question 2:

For example: DQB1*0501, DQB1*0201

Question 3:

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

X

DRB1*0302	DPB1*0101
∴	
DRB1*0101	DPB1*0101

DRB1*0302	DPB1*0201
-----------	-----------

Question 8:

DRB1*1304 DRB3*0201 DQA1*0201 DQB1*0201 DPA1*0104 DPB1*0401
DRB1*0402 DRB4*0101 DQA1*0201 DQB1*0201 DPA1*0104 DPB1*0401

Note the predicted association of DRB1*1304 with DRB3*0201 and DRB1*0402 with DRB4*0101.

The person is homozygous for DQ and DP.

Question 9:

See next two pages.

Question 10:

For example: Cw*0101, Cw*0201, Cw*0202, Cw*0801

Chapter 4, Question 11:

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

```

1
ConsensusATGCGGGTCA TGGCGCCCCG AACCTCCTC CTGCTGCTCT CGGGGGCCCT GGCCTGACC GAGACCTGGG CCGGCTCCA CTCCATGAGG TATTTCTACA 100
b-07021 ----t----- -----g----- -c----- -----g-----
b-0801 ----t----- -----g----- -c----- -----g-----
b-4201 ----t----- -----g----- -c----- -----g-----

101
Consensus CCGCCGTGTC CCGCCCCGGC CGCGGGGAGC CCCGCTTCAT CGCAGTGGGC TACGTGGACG ACACGCAGTT CGTGAGGTTT CACAGCGACG CCGCGAGTCC 200
b-07021 --t----- -----t----- -t----- -c-----
b-0801 ----a----- -----t----- -t----- -c-----
b-4201 --t----- -----t----- -t----- -c-----

201
Consensus GAGGATGGAG CCGCGGGCGC CGTGGATAGA GCAGGAGGGG CCGGAGTATT GGGACCGGGA GACACAGATC TTCAAGACCA ACACACAGAC TGACCGAGAG 300
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
Consensus AGCCTGCGGA ACCTGCGCGG CTACTACAAC CAGAGCGAGG CCGGTCTCA CACCCTCCAG AGGATGTATG GCTGCGACGT GGGGCCGGAC GGGCGCCTCC 400
b-07021 -----c----- -----c----- -c----- -c-----
b-0801 -----c----- -----c----- -c----- -c-----
b-4201 -----c----- -----c----- -c----- -c-----

401
Consensus TCCGCGGGTA TGACCAGTAC GCCTACGACG GCAAGGATTA CATCGCCCTG AACGAGGACC TGCCTCCTG GACCGCGGCG GACACGGCGG CTCAGATCAC 500
b-07021 -----c----- -----c----- -c----- -c-----
b-0801 -----c----- -a----- -c----- -c-----
b-4201 -----c----- -a----- -c----- -c-----

501
Consensus CCAGCGCAAG TGGGAGGCGG CCCGTGTGGC GGAGCAGCTG AGAGCCTACC TGGAGGGCAC GTGCGTGGAG TGGCTCCGCA GATACCTGGA GAACGGGAAG 600
b-07021 -----a----- -----g----- -ga-----
b-0801 -----g----- -----gac-----
b-4201 -----g----- -----gac-----

601
Consensus GAGACGCTGC AGCGCGCGGA CCCCCAAAG ACACATGTGA CCCACCACCC CATCTCTGAC CATGAGGCCA CCCTGAGGTG CTGGGCCCTG GGCTTCTACC 700
b-07021 --c-a---g----- -t----- -c----- -t-----
b-0801 --c-----g----- -c----- -c-----
b-4201 --c-----g----- -c----- -c-----

701
Consensus CTGCGGAGAT CACACTGACC TGGCAGCGGG ATGGCGAGGA CCAAACCTCAG GACACCGAGC TTGTGGAGAC CAGACCAGCA GGAGATAGAA CCTTCCAGAA 800
b-07021 -----t----- -t----- -t-----
b-0801 -----t----- -t----- -t-----
b-4201 -----t----- -t----- -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*0803, DRB1*0301 and the recipient can be DRB1*0804, DRB1*0302.

Question 4:

A) ♂
DR4/DR11

♀
DR1/DR3

children:

DR4/DR1; DR4/DR3; DR11/DR1; DR11/DR3

B) ♂

DRB1*0402/DRB1*1103

♀

DRB1*0101/DRB1*0301

children:

DRB1*0402/DRB1*0101; DRB1*0402/DRB1*0301

DRB1*1103/DRB1*0101; DRB1*1103/DRB1*0301

Question 5:

Loci: DRB1 DRB3 DRA
 DRB1*1102 DRB3*0202 DRA*0101

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*6801=A68(28), B*1301=B13, B*1804=serologic type not known, DRB1*0301=DR17(3),

DRB1*1122=serologic type not known

Question 8:

Patient exhibits serologic type A2 only; the A*2409N allele does not specify an HLA-A antigen. An A2,A24 donor would not be a good choice; a A2 donor would be better.

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 AAGCCCAATCA GCGTCTCCGC AGTCCCCTGT CTAAGTCCC CAGTCACCCA CCGGACTCA GATTCTCCCC AGACGCCGAG |ATGGGGTCA
Cw*04010101   -----G-----
Cw*050101     -----G-----
Cw*06020101   -----G-----
Cw*0802       -----G-----
Cw*12030101   -----G-----
Cw*1701       -----A-----

                20      30      40      50      60      70      80      90      100     110
Cw*010201     TGCGCCCCCG AACCCCTCATC CTGCTGCTCT CCGGAGCCCT GGCCTGACC GAGACTGGG CCT|GTGAGTG CCGGGTTGGG AGGGAACCG CCTCTGCGGA
Cw*04010101   -----G-----
Cw*050101     -----A-----
Cw*06020101   -----A-----
Cw*0802       -----A-----
Cw*12030101   -----A-----
Cw*1701       -----A-----

                120     130     140     150     160     170     180     190     200     210
Cw*010201     GAGGAACGAG GTGCCCGCCC GCGAGGGCCG CAGGACCCGG GGAGCCGCGC AGGGAGGAGG GTCGGGCGGG TCTCAGCCCC TCCTGCCCC CAG|GCTCCCA
Cw*04010101   -----G-----
Cw*050101     -----G-----
Cw*06020101   -----G-----
Cw*0802       -----G-----
Cw*12030101   -----G-----
Cw*1701       -----G-----

```

```

Cw*010201     CAGCGGAGAG CCTACTGGA GGGCACGTGC GTGGAGTGGC TCCGCAGATA CCTGGAGAAC GGGGAAGAGA CGCTGCAGCG CCGCG|GTACC AGGGCCAGTG
Cw*04010101   -----A-----
Cw*050101     -----A-----
Cw*06020101   -----A-----
Cw*0802       -----A-----
Cw*12030101   -----A-----
Cw*1701       -----GA-----

                1020    1030    1040    1050    1060    1070    1080    1090    1100    1110
Cw*010201     GGGAGCCCTTC CCCATCTCCC GTAGATCTCC CCGCATGGCC TCCCAGAGG AGGGGAGGAA AATGGGATCA GCGCTAGAAT ATCGCCCTCC CTTGAATGGA
Cw*04010101   -----G-----
Cw*050101     -----G-----
Cw*06020101   -----G-----
Cw*0802       -----G-----
Cw*12030101   -----G-----
Cw*1701       -----A-----

```


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*0411 differs in this region.

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

Question 3:

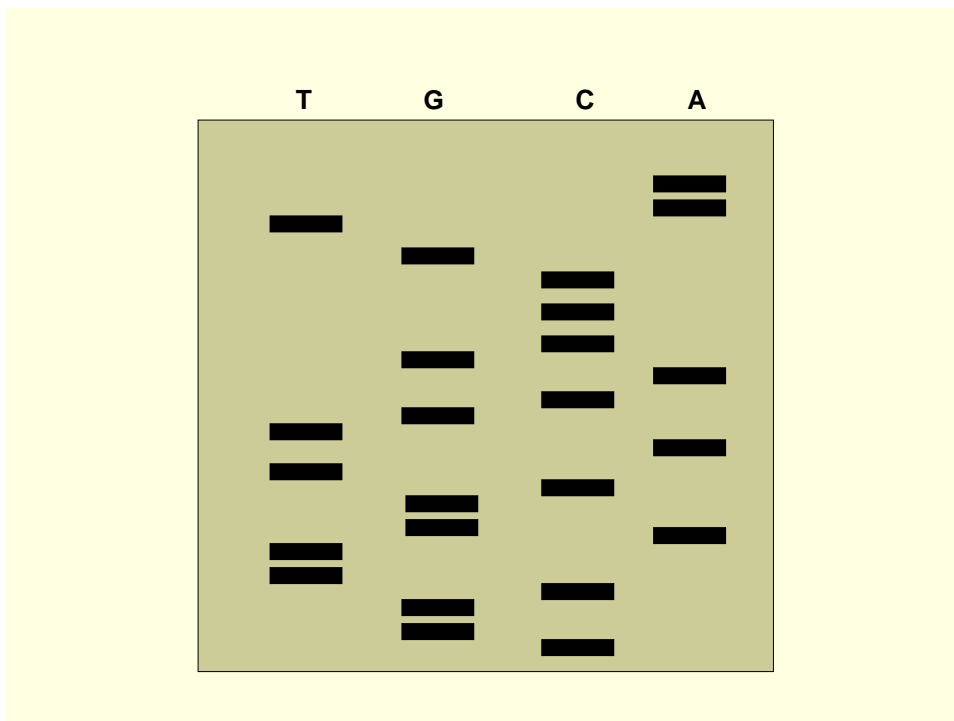
First, amplify only the DRB1*01 alleles with PCR primers designed around codons 25-31 and DRBAMPB (for example). Then use a probe to distinguish between DRB1*0101 and DRB1*0102, designed around codons 83-89. Use probe with sequence: 5' C GGG GCT GTG GAG AGC TT (for example to detect DRB1*0102 and not DRB1*0101, *0103, *0104).

Chapter 8:

Question 1:

create PCR primers that would amplify DRB1*0701

Question 2:



Chapter 9:

No questions

Chapter 10:

Question 1:

DRB1*0101, *0401

DRB1*1101, *0701

Question 2:

Sample also carries one of the DRB1*04 alleles. Since one of the DRB1*04 alleles, DRB1*0402, also carries the sequence detected by probe DR7007, it is not known if DRB1*0103 is present. As a result, the sample would be typed as [DRB1*0103 and DRB1*0401 or *0403 or *0404 or ... *0410] OR [DRB1*0101 or *0102 or *0103 and DRB1*0402]. To determine if DRB1*0103 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*030102 or DRB1*0314, is present.

Question 4:

The person could have any one of the DRB1*11 alleles (now numbering over 30) or DRB1*0308 or DRB1*0415 or DRB1*1204 or DRB1*1411. The GAG codon at 58 used to be unique for the DRB1*11 alleles but this is no longer the case.