

1. List out where Phosphorylation happens in the position of the genome.

select POSITION.

```
FROM (C_EPIGENETICS JOIN C_CONTAINS ON C_EPIGENETICS.ALTERATIONID =
      C_CONTAINS.ALTERATIONID)
      JOIN C_GENE ON C_GENE.GENEID = C_CONTAINS.GENEID
      JOIN C_MARKERS ON C_MARKERS.MARKERID = C_GENE.MARKERID
WHERE C_EPIGENETICS.TYPE = 'Phosphorylation';
```

RESULTS:

25398

50000001

100786

2. Give the ClientID, ethnicity, Occupation, and accuracy of the client with the accuracy greater than 0.0005 for the genome.

```
SELECT C_INDIVIDUAL.CLIENTID, ETHNICITY, OCCUPATION, ACCURACY
FROM C_INDIVIDUAL, C_ETHNICITY, C_OCCUPATION, C_GENOME
WHERE C_INDIVIDUAL.CLIENTID = C_ETHNICITY.CLIENTID AND
      C_INDIVIDUAL.CLIENTID = C_OCCUPATION.CLIENTID
      AND C_INDIVIDUAL.GENOMEID = C_GENOME.GENOMEID
      AND ACCURACY > 0.0005;
```

RESULTS:

2 British Chemist 0.001

4 African Swimmer 0.1

3. List the ClientID, MutationID, and EpigeneticID for each client.

```
select CLIENTID, EPIGENETICID, MUTATIONID
from C_INDIVIDUAL, C_GENOME, C_MARKERS, C_GENE, C_CONTAINS,
      C_MUTATION, C_EPIGENETICS
WHERE C_INDIVIDUAL.GENOMEID = C_GENOME.GENOMEID and
      C_GENOME.GENOMEID = C_MARKERS.GENOMEID
      and C_MARKERS.MARKERID = C_GENE.MARKERID and C_GENE.GENEID =
      C_CONTAINS.GENEID AND C_CONTAINS.ALTERATIONID =
      C_MUTATION.ALTERATIONID
      AND C_EPIGENETICS.ALTERATIONID = C_MUTATION.ALTERATIONID;
```

RESULTS:

CLIENTID EPIGENETICID MUTATIONID

```
-----
1      1      1
2      5      5
3      4      4
4      3      3
5      2      2
```

4. Find the ClientID and PNumber of the client who have an amino acid change to 'Trp'.

```
select CLIENTID, PNUMBER
from C_INDIVIDUAL, C_GENOME, C_MARKERS, C_GENE, C_CONTAINS,
     C_MUTATION, C_CODON
WHERE C_INDIVIDUAL.GENOMEID = C_GENOME.GENOMEID and
      C_GENOME.GENOMEID = C_MARKERS.GENOMEID
and C_MARKERS.MARKERID = C_GENE.MARKERID and C_GENE.GENEID =
     C_CONTAINS.GENEID AND C_CONTAINS.ALTERATIONID =
     C_MUTATION.ALTERATIONID
AND C_MUTATION.CODONID = C_CODON.CODONID
AND AMINOACID = 'Trp';
```

RESULT:

```
3  1112324444
```

5. List out the ClientID, MarkerID, Accuracy, and Marker type in decreasing order of accuracy.

```
select CLIENTID, MARKERID, ACCURACY, TYPE
FROM (C_INDIVIDUAL JOIN C_GENOME ON C_INDIVIDUAL.GENOMEID =
      C_GENOME.GENOMEID)
JOIN C_MARKERS ON C_INDIVIDUAL.GENOMEID = C_MARKERS.GENOMEID
ORDER BY ACCURACY;
```

RESULTS:

1	1	0.00001	VNTR
3	3	0.0001	SNP
5	6	0.0001223	RFLP
5	5	0.0001223	RFLP
5	8	0.0001223	RFLP
5	7	0.0001223	RFLP
2	10	0.001	SNP
2	9	0.001	SNP
2	2	0.001	SNP
4	4	0.1	RFLP
4	11	0.1	SNP