**Year 12 Human Biology**

**Task 9 – Extended Response**

**Evidence for Evolution and Hominid Evolutionary Trends**

**Weighting: 8.5%**

**Total Marks: 25**

**Marking Key**

***PART A Marking Criteria***

1. (a)Research component:

|  |  |
| --- | --- |
| **Description** | **Marks** |
| Research presented in a note-taking format | 1 |
| Notes are concise and do not include irrelevant information | 1 |
| Notes cover all recommended research areas | 1 |
| **Total** | **3** |

(b) Referencing Component:

|  |  |
| --- | --- |
| **Description** | **Marks** |
| Minimum of four references | **1** |
| Correct format used for selected referencing type | **1** |
| **Total** | **2** |

***PART B Marking Criteria***

2. (a)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| **DNA example ERVs**   * DNA base sequence varies between species * We can determine this base sequence using sequencing techniques. * Retroviruses are viruses that incorporate their DNA code into the cells of the infected organism. * This DNA code from the retrovirus is then passed down. * DNA of currently existing species can be analysed and compared for similarities and differences in existence and location of ERVs. | 1–4 |
| Species that are more closely related will have more similarities in ERV DNA in their genome, indicating a more recent common ancestor (or more distantly related, less similarities, less recent common ancestor) | 1 |
| **Protein** **sequence – example Ubiquitous Proteins**   * proteins made of long chains of amino acids * Amino acids coded for by triplet codons in DNA sequence. * We can determine the sequence of amino acids that form a particular protein * Ubiquitous proteins are proteins that occur in many different species. * Cytochrome C is a ubiquitous protein that can be used for comparison. * We can compare the differences in amino acids that form cytochrome c between species. | 1–4 |
| Species that are distantly related have more differences in their amino acid sequence/closely related, more similarities/more time has passed since common ancestry | 1 |
| **Total** | **10** |

2. (b)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| Ten points discussed on how bioinformatics can be used with the Human Genome Project to identify faulty genes | 1–10 |
| **Answer could include, but is not limited to:** |
| * the genome is a complete sequence of the base pairs that make up all of the DNA of an organism/including genes * the base sequences in DNA can be expressed as data that is easily read by computer software * bioinformatics is the use of computers to manage and analyse the data provided by genomics/DNA sequencing * this is significantly faster than manually comparing the data. * bioinformatics allows for the analysis and comparison of genomes * Bioinformatics can be used to identify start and stop codons and therefore loci for genes. * Bioinformatics can be used to compare the genome of healthy individuals and those with a specific genetic disease. * This comparison can allow faulty genes to be identified and then sequenced * Identification of location and sequence of faulty genes can be useful for early genetic testing and identification. * This allows treatment to begin as soon as possible * Prompt diagnosis provides better quality of life and improved life span for affected individuals * Identification of faulty genes and loci could be used for gene therapy once this technology has been fully developed. |
| **Total** | **10** |