**1.** two polymers shown;  
arranged in a double helix;  
sugar shown connected to base;  
sugar-phosphate backbone shown;  
*If only one nucleotide is drawn, award* ***[2 max]***

sugar identified as deoxyribose;  
hydrogen bonding between bases shown;  
diagram shows complementary base pairing / A bonded to T, C with G;  
*Award previous mark if bases (unlabelled) are shown in the diagram but the  
complementary base pairing is explained in the annotation.*covalent bonding between phosphate and sugar; 5 max  
*(Remember, up to TWO “quality of construction” marks per essay)*

[5]

**2.** subunits are nucleotides;  
one base, one deoxyribose and one phosphate in each nucleotide;  
description / diagram showing base linked to deoxyribose C1 and phosphate to C5;  
four different bases – adenine, cytosine, guanine and thymine;  
nucleotides linked up with sugar-phosphate bonds;  
covalent / phosphodiester bonds;  
two strands (of nucleotides) linked together;  
base to base;  
A to T and G to C;  
hydrogen bonds between bases;  
antiparallel strands;  
double helix drawn or described;  
*Accept any of the points above if clearly explained in a diagram.*

[8]

**3.**

|  |  |
| --- | --- |
| *RNA* | *DNA* |
| ribose | deoxyribose; |
| (normally) single stranded | double stranded; |
| uracil | thymine; |
| no double helix | helix; |

**NB** *Histone proteins are only in eukaryotic DNA not prokaryotic.*

[3]

**4.** D

[1]

**5.** C

[1]

**6.** helix is unwound;  
two strands are separated;  
helicase (is the enzyme that unwinds the helix separating the two strands);  
by breaking hydrogen bonds between bases;  
new strands formed on each of the two single strands;  
nucleotides added to form new strands;  
complementary base pairing;  
A to T and G to C;  
DNA polymerase forms the new complementary strands;  
replication is semi-conservative;  
each of the DNA molecules formed has one old and one new strand;

[8]

**7.** *Award* ***[1]*** *for any two of the following up to* ***[2 max]****.*

helicase;  
DNA polymerase / DNA polymerase III;  
RNA primase;  
DNA polymerase I;  
(DNA) ligase; 2 max

*Award* ***[1]*** *for one function for each of the named enzymes.*

*helicase:*splits / breaks hydrogen bonds / uncoils DNA / unwinds DNA;

*(DNA) polymerase III:*adds nucleotides (in 5' to 3' direction) / proofreads DNA;

*(RNA) primase:*synthesizes a short RNA primer (which is later removed) on DNA;

*(DNA) polymerase I:*replaces RNA primer with DNA;

*(DNA) ligase:*joins Okazaki fragments / fragments on lagging strand / makes   
sugar-phosphate bonds between fragments; 4 max

[6]

**8.** (a) *Award* ***[1]*** *if both A and B are named but no functions are given.*

|  |  |  |
| --- | --- | --- |
|  | ***Name*** | ***Function*** |
| *A* | DNA polymerase | adds complementary base pairs / links nucleotides together forms complementary strands; |
| *B* | helicase | which unwinds the DNA helix / separates the two strands; |

2

(b) nucleus 1

(c) interphase / S phase 1

(d) A (hydrogen) bonds with T and G (hydrogen) bonds with C;

complementary base pairing ensures proper base incorporated into DNA  
strand;

thus making identical copies of the DNA strand (ensuring conservation of  
the base sequence); 2 max

[6]

**9.** mutation is a change in DNA sequence;  
changes the mRNA during transcription;  
changes the amino acid sequence;  
substitution mutation / changes to one codon;  
glutamic acid is changed to valine / GAG to GTG;  
changes the shape of hemoglobin /   
hemoglobin becomes less soluble and crystallizes out;  
cannot carry oxygen as well;  
red blood cells sickle / impairs blood flow;  
causes other health problems / anemia / tiredness;  
sickle cell anemia caused by two mutated recessive alleles;

[7]

**10.** (a)  U  A  G  G  U  C  C  A  G  U  U  C  1

(b) DNA;

RNA polymerase;

(ribose) nucleotides / ribonucleotides / RNA nucleotides;

transcription factors;

nucleoside / ribonucleoside triphosphates; 3 max

Any two of the following: A / C / G / U;

[4]

**11.** consists of initiation, elongation and termination;  
mRNA translated in a 5' to 3' direction;  
binding of ribosome to mRNA;  
small sub-unit then large;  
first / initiator tRNA binds to start codon /   
to small subunit of ribosome;  
AUG is the start codon;  
second tRNA binds to ribosome;  
large subunit moves down mRNA after a second tRNA binds;  
amino acid / polypeptide on first tRNA is transferred /   
bonded to amino acid on second tRNA;  
peptide bonds between amino acids / peptidyl transferase;  
requires GTP;  
movement of ribosome /   
small subunit of ribosome down the mRNA;  
loss of tRNA and new tRNA binds;  
reach a stop codon / termination;  
polypeptide released;  
tRNA activating enzymes link correct amino acid to each tRNA;  
(activated) tRNA has an anticodon and the  
corresponding amino acid attached;

[9]

**12.** both in 5' to 3' direction;  
both require ATP;  
DNA is transcribed and mRNA is translated;  
transcription produces RNA and translation produces polypeptides / protein;  
RNA polymerase for transcription and ribosomes for translation / ribosomes  
in translation only;  
transcription in the nucleus (of eukaryotes) and translation in the cytoplasm / at ER;  
tRNA needed for translation but not transcription;

[4]

**13.** tRNA is composed of one chain of (RNA) nucleotides;  
tRNA has a position / end / site attaching an amino acid;  
*(Reject tRNA contains an amino acid.)*at the 3' terminal / consisting of CCA / ACC;  
tRNA has an anticodon;  
anticodon of three bases which are not base paired /   
single stranded / forming part of a loop;  
tRNA has double stranded sections formed by base pairing;  
double stranded sections can be helical;  
tRNA has (three) loops (sometimes with an extra small loop);  
tRNA has a distinctive three dimensional / clover leaf shape;

Accept any of the points above if clearly explained using a suitably labelled diagram.

[5]

**14.** (a) *Answers must either give DNA characteristic first or specify which is DNA*  
*and which is RNA.*

deoxyribose versus ribose;

thymine versus uracil;

two strands versus one / double helix versus single strand; 2 max

(b) *Award* ***[2]*** *for four correct and* ***[1]*** *for three or two correct.*

I. small (sub)unit (of ribosome);

II: large (sub)unit (of ribosome);

III: transfer RNA / tRNA;

IV: messenger RNA / mRNA; 2 max

(c) transfer RNA / tRNA 1

(d) codon / triplet of bases to amino acid;

nucleic acid / base sequence / (m)RNA to polypeptide / protein / amino acid  
sequence;

genetic code has to be translated; 2 max

(e) stop / terminator / nonsense codon (is reached);

polypeptide is released;

mRNA detaches from ribosome;

subunits of ribosome separate; 2 max

Ignore references to specific codons.

[9]

**15.** (a) 47–49% (*units are not needed*) 1

(b) *D. melanogaster* / *Drosophila* has few genes with one exon;  
highest percentage has 2 exons;  
most genes have 5 or fewer exons;  
a few genes have 10 or more exons / more than 8;  
maximum number of exons does not exceed 60; 2 max

(c) (i) *S. cerevisiae* / yeast has most genes with only 1 exon while mammals   
5 exons is most frequent;  
no yeast genes have more than 5 exons while some mammal genes   
have greater than 60 exons;  
mammal genes contain more exons on average;  
with a wider distribution than yeast; 2 max

(ii) *S. cerevisiae* / yeast is a unicellular organism / mammals are   
multicellular / complex;  
mammals have more transcriptional regulation;  
*S. cerevisiae* smaller in size / more compact genome; 1 max

(d) gene size – mRNA size = intron size / 25.0 – 2.1 = 22.9 kb;  
average size of intron =  = 1.6 ( 0.1) kb; (*unit required*) 2

(e) smaller genes usually have less introns / larger genes have more introns /   
relationship not clear;  
dystrophin and collagen have same number of introns but the dystrophin   
gene is larger;  
albumin has more introns but is smaller than the gene for phenylalanine  
hydroxylase; 2 max

(f) 2.4 kb (1 amino acid / 3 bases) = 800 amino acids ***or*** 799 amino acids 1

(g) epsilon and zeta (globin) 1

(h) gamma genes (mostly) expressed before birth and beta genes expressed after birth;  
beta-globin levels rise at 28(2) weeks of gestation while gamma   
levels decrease / as one rises, the other falls;  
gamma-globin expression starts at 0–2 weeks whereas   
beta-globin starts at 26 (2) weeks / gamma expression starts earlier;  
one month after birth hemoglobin has equal   
mixture of beta-globin and gamma-globin;   
gamma levels go to zero while beta becomes a regular part of hemoglobin; 3 max

(i) *10 weeks after gestation:*two alpha-globins with two gamma-globins / 49 (50)% alpha and 48 (49)% gamma;

*2 months after birth:*variety of molecules all containing alpha and two chains from the other   
three types / 6% delta, 14% gamma, 35% beta, 50% alpha; 2

[17]

**16.** (a)    1

Award the mark only if a single headed arrow is shown.

(b) Alanine / Ala 1

(c) an activating enzyme attaches amino acid to the tRNA;

specific enzyme for specific tRNA;

recognizes tRNA by its shape / chemical properties;

energy (ATP) is needed;

amino acid attached at  end;

amino acid attached at CCA; 3 max

(d) rough ER;

cytoplasm;

chloroplast (stroma of) / mitochondria (matrix of); 1 max

[6]