BIOL1020 Genes, Cells, and Evolution

UNIVERSITY OF QUEENSLAND · LEVEL 1 · SEMESTER 2 2026

Full guide + ask Sia about BIOL1020

SIDE 1/2 · WHAT THE FINAL REWARDS · DEFINE → LOCATE → TRACE → PREDICT · EXAM REVISION SHEET · MCQ + short answer · final 60% · exam hurdle 45%

1 · Exam Map

COURSE.JSON · BRIEF

10	15	15	FINAL 60%

TASK	WT	FORMAT / DEMAND
Practical preparation & participation	10%	Prepare; participate
Mini Test 1	15%	Short-answer and/or problem-solving
Mini Test 2	15%	Short-answer and/or problem-solving
Final exam	**60%**	MCQ + short answer; ≥45% on exam

Permitted materials: not confirmed for this offering in the course materials we hold — check the exam instructions on the LMS. *[BRIEF.md]*

The published weights total 100%. The final also carries a **45% component hurdle**, alongside at least 50% across all assessment combined. The captured materials do not state duration; use the current LMS instructions.

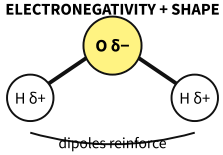
UNIVERSAL ANSWER PATH

```
name the changed part → locate it →
state the direct molecular effect →
follow intermediates → finish at
cell / phenotype / population.
```

2 · Polarity → Membrane

CH 1 · STRUCTURE PREDICTION

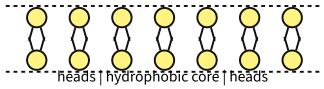
ELECTRONEGATIVITY + SHAPE



Unequal sharing creates bond dipoles; bent geometry prevents cancellation. *[Ch 1 figure]*

FEATURE	PREDICT
Charged / polar	Favourable water contacts; ions need a channel or carrier across the core
Extended hydrocarbon	Hydrophobic clustering reduces non-polar area exposed to water
Phospholipid	Heads face water; tails form internal core → bilayer
Cis-unsaturated tail	Bend disrupts packing → more fluid under comparable conditions
Weak contacts	H bonds, electrostatic and van der Waals contacts can be stable in combination yet reversible
Ion passage	Charge makes the core unfavourable; channels or carriers supply compatible routes

AMPHIPATHY BUILDS A BOUNDARY



Self-assembly hides tails while keeping polar heads in contact with water. *[Ch 1]*

3 · Cell Architecture

CH 2 · IDENTIFY + JUSTIFY

EVIDENCE	CLASSIFICATION / CONSEQUENCE
Membrane + DNA + ribosomes + ATP-linked chemistry	Shared cellular baseline; not diagnostic alone
Peptidoglycan + circular chromosome in nucleoid	Bacterium / prokaryotic organisation
Nucleus + membrane-bound organelles	Eukaryotic compartmentation
Chloroplast	Supports photosynthetic eukaryote

SECRETED PROTEIN TRAFFIC

ribosome — rough ER — Golgi → plasma membrane

target → process → sort → fuse

Trace cargo and boundary: ribosome → rough ER → Golgi → vesicle → plasma membrane. *[Ch 2]*

Scale rule: volume rises faster than surface area as diameter increases. Small cells have more membrane relative to cytoplasm; larger eukaryotes compensate partly with internal membranes, organelles and active transport.

Compartment logic: membranes concentrate enzymes and substrates, preserve different ion or chemical conditions, and separate incompatible reactions. The benefit depends on selective pores, carriers and vesicles coordinating traffic between compartments.

MICROSCOPY *Magnification enlarges; resolution separates nearby detail.*

4 · Macromolecule Logic

CH 3 · COMPARE STRUCTURE

monomer — bonding — 3D fold → function

never skip the interaction step

Exam chain: component → bond/interactions → arrangement → property → function. *[Ch 3 figure]*

COMPARE	DECISIVE MECHANISM
Glycogen vs cellulose	α linkages are digestible; β chains align into H-bonded fibres
Storage polymer branching	Many terminal sites allow rapid glucose addition/removal
Phospholipid vs triacylglycerol	Amphipathic → bilayer; mainly non-polar → storage droplet
Primary → tertiary protein	Sequence positions side chains; their contacts select fold
Dehydration vs hydrolysis	Join + release elements of water vs use water to split bond

5 · Energy Rules

CH 4 · MECHANISM + PERTURBATION

QUESTION	RULE
Favourable?	Exergonic: ΔG<0; endergonic: ΔG>0 and needs input
Fast?	Activation barrier controls rate; an enzyme lowers it
Coupled?	Shared intermediate links processes; combined ΔG must be negative
ATP hydrolysis?	Products are collectively more stable; bond breaking itself requires energy

KEEP SEPARATE

```
enzyme changes rate, not reactant-
product ΔG or equilibrium position.
```

ATP hydrolysis ΔG < 0 — shared intermediate — cell work ΔG > 0

combined ΔG < 0 → net forward

Coupling requires a mechanistic link, not two reactions merely placed together. *[Ch 4]*

CARBON → e− → H+ GRADIENT → ATP

glycolysis cytosol — pyruvate matrix — citric cycle matrix → ETC/ATP inner MB

O_2 = terminal electron acceptor
oxidised carriers must be regenerated

Respiration locations and the carrier link that lets a late block propagate backwards. *[Ch 4 figure]*

PERTURBATION DECISION RULE

1. Locate blocked transporter, enzyme, membrane or acceptor.
2. What substrate accumulates / product falls?
3. Can reduced carriers return to oxidised forms?
4. Does the H+ gradient form and remain separated?
5. Which ATP route remains?

5b · Cause → Effect Table

CH 4 FAQ

CHANGE	TRACE
No oxygen	electron flow stops → pumping stops → oxidised carriers scarce → earlier mitochondrial stages constrained
Blocked pyruvate transport	glycolysis persists; less matrix carbon → fewer reduced carriers → less oxidative ATP
Leaky inner membrane	gradient dissipates; electron transfer may continue, but ATP synthase captures less energy

Carrier logic: fuel oxidation reduces carriers; the transport chain removes their electrons; oxygen permits oxidised carrier forms to be regenerated. A late failure therefore removes acceptors needed by earlier matrix reactions even when their enzymes remain intact.

TRAP *One mitochondrial failure rarely means zero ATP: state what glycolysis can still do.*

6 · Replication Fork

CH 5 · DIRECTION EARNS MARKS



prime → extend → replace → seal

Antiparallel templates + one synthesis direction create leading and lagging asymmetry. *[Ch 5]*

ACTION	DIRECT JOB
Open / stabilise	Separate parental strands and hold them apart
Primase	Provides short RNA with a free 3′ end
DNA polymerase	Extends an existing chain 5′→3′
Primer replacement	Fills gaps with DNA
DNA ligase	Seals remaining sugar-phosphate backbone nicks

7 · Cell Cycle State

CH 5 · COUNT BEFORE NAMING

G1 — S — G2 → M

grow · copy DNA · check · separate

Replication copies in S; mitosis separates copies; cytokinesis divides cytoplasm. *[Ch 5 figure]*

PHASE / PROCESS	WHAT CHANGES
G1	Growth and normal activity; may exit to G0
S	DNA molecules copied; sister chromatids created
G2	Prepare; verify completion / integrity
Mitosis	Replicated chromosomes organised and separated
Cytokinesis	Cytoplasm divides; animal furrow vs plant cell plate

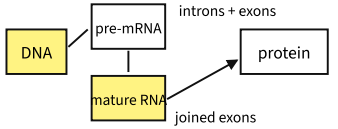
Checkpoint answer: name what should be verified, then state the abnormal material that enters the next phase if control fails.

Counting discipline: a replicated chromosome has two sister chromatids but remains an associated chromosome unit until separation. DNA amount changes in S; condensation changes visibility, not whether replication occurred. Replication must finish before segregation so each daughter receives a complete copy.

Binary fission comparison: bacteria also replicate and segregate a chromosome before cell division, but do not use the eukaryotic nuclear cycle, mitotic spindle or membrane-bound nucleus. State the shared problem and the architectural difference.

8 · Gene Expression

CH 6 · ORIENTATION FIRST



Transcribe → splice → translate; preserve every intermediate before predicting phenotype. *[Ch 6 figure]*

OBJECT	RULE
Template DNA	Read by RNA polymerase; RNA is complementary and antiparallel
Coding DNA	Same base order as RNA except DNA T ↔ RNA U
Pre-mRNA	Contains introns + exons before eukaryotic processing
Mature mRNA	Retained exons; read 5′→3′ in non-overlapping codons
tRNA anticodon	Complementary and antiparallel to mRNA codon

SEQUENCE ALGORITHM

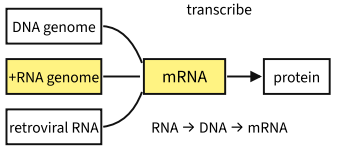
```
label 5′/3′ → identify strand → make
RNA → splice if relevant → choose
start → group codons → translate →
classify change.
```

One-base indel: downstream frameshift, many codons may change, premature stop possible. **Three-base deletion:** removes one codon but preserves downstream grouping.

Alternative splicing: different retained exon combinations can create different mature messages and protein products without changing the DNA locus.

9 · Viral Routes to mRNA

CH 7 · CLASSIFY BY MISSING STEP



Different starting genomes converge on RNA that host ribosomes can read. *[Ch 7 figure]*

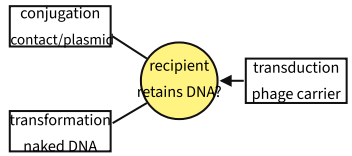
START	REQUIRED REASONING
DNA	Transcribe viral mRNA
Positive-sense RNA	Incoming genome can be translated; amplification needs complementary RNA template
Retroviral RNA	Reverse transcriptase makes DNA; proviral information can then yield RNA

Lytic = active production, assembly and release.

Lysogenic = information maintained with host before possible induction. Lifecycle timing ≠ genome chemistry.

10 · Variation & Inheritance

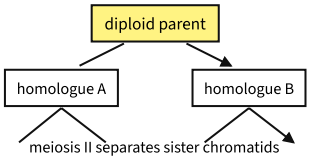
CH 8–9 · SEPARATE MECHANISMS



Carrier identifies the transfer route; stable inheritance requires replication/maintenance or recombination. *[Ch 8 figure]*

11 · Meiosis → Probability

CH 9 · CHROMOSOMES FIRST



Meiosis I separates homologues; meiosis II separates sister chromatids. *[Ch 9 figure]*

MECHANISM	MEANING
Segregation	Two alleles enter different gametes as homologues separate
Independent assortment	Different homologous pairs orient independently
Crossing over	Non-sister chromatids exchange corresponding DNA; new linked combinations
Test cross	Homozygous recessive tester exposes the unknown parent's gamete
MI nondisjunction	Homologues fail; all resulting gametes abnormal for that chromosome

Ratios are long-run probabilities, not guarantees for a small family. State independence before multiplying.

12 · Evolution & Genome Change

CH 11–12

SELECTION	DRIFT
Variation + heritability + excess offspring + unequal reproduction linked to trait	Random sampling; can raise or lower an allele regardless of effect
Repeatable direction with fitness evidence	Stronger proportional effect in small populations; replicate paths diverge

PARTITION PHENOTYPE

$V_P = V_G + V_E$; visible difference alone does not prove heritable difference.

Genome-change scale: local sequence / regulation; gene duplication; horizontal transfer; transposon movement; whole-genome duplication. Non-coding and repetitive DNA mean genome size does not rank complexity.

BIOL1020 Genes, Cells, and Evolution · Self-Test Drills

UNIVERSITY OF QUEENSLAND · ANSWER PATHS, JUDGEMENT CARDS AND CLASSIC TRAPS

Full guide + ask Sia about BIOL1020

SIDE 2/2 · FIVE WORKED DRILLS · IF X → DO Y · MCQ CONTRASTS · EXAM-MORNING RETRIEVAL

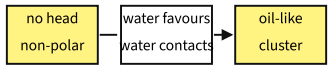
SELF-TEST BEFORE RE-READING

show the missing middle · check direction + compartment

13 · Drill A: Lost Lipid Head

CH 1 WORKED EXAMPLE

Prompt: a phospholipid loses its polar head but retains hydrocarbon tails. Predict behaviour in water.



no hydrophilic faces → no stable bilayer

Loss of amphipathy changes the stable arrangement. *[Ch 1]*

1. **Change:** main water-compatible region disappears.
2. **Interaction:** water favours its own network over exposed hydrocarbon.
3. **Arrangement:** molecules cluster, reducing exposed non-polar area.
4. **Outcome:** oil-like droplet; no hydrophilic faces for a bilayer.

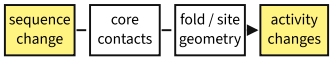
A stable bilayer needs one molecule to supply both a water-compatible face and a hidden non-polar region.

FULL-CREDIT PHRASE *Water excludes the non-polar surface; do not invent a special bond between hydrophobic groups.*

14 · Drill B: Charged Core

CH 3 WORKED EXAMPLE

Prompt: replace a buried non-polar amino acid with a charged amino acid.



Mutation → side-chain chemistry → interaction network → fold → function. *[Ch 3]*

1. Primary sequence changes.
2. Charged side chain is unfavourable in a hydrophobic core and may favour water/opposite charge.
3. Tertiary structure can rearrange or lose stability.
4. Changed active-site or binding-surface geometry can alter activity.

Never jump mutation → function. The marks sit in side-chain interactions and structural geometry.

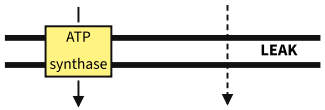
WHICH IS TRUE?	REASON
A surface substitution need not equal a core substitution	Local environment and role decide which contacts change
A substitution need not abolish activity	Fold and functional geometry may remain sufficiently intact
A non-coding change can still matter	Promoter or splice signals can alter amount or processing

15 · Drill C: Proton Leak

CH 4 WORKED EXAMPLE

Prompt: H+ crosses the inner mitochondrial membrane without ATP synthase.

INTERMEMBRANE SPACE: H+ HIGH



MATRIX: gradient collapses

A leak uncouples electron transport from efficient ATP synthesis. *[Ch 4]*

1. Gradient dissipates.
2. ATP synthase receives less proton-motive force → much less ATP.
3. Electron transport may continue and consume O_2 because the opposing gradient is relieved.
4. Glycolysis can still make direct ATP: total ATP falls, not automatically to zero.

MARKER CHECK

Did you treat electron flow, H+ pumping, gradient storage and ATP synthase as four distinct links?

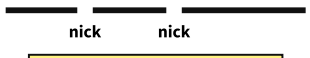
NO OXYGEN	PROTON LEAK
Terminal acceptor absent → electron transfer and pumping stop	Electrons may still flow and O_2 may still be consumed
Reduced carriers are not efficiently reoxidised	Gradient is not retained for ATP synthase
Earlier mitochondrial stages constrained	Oxidative ATP falls despite continued transport

Same low ATP, different cause: test electron flow separately from gradient capture.

16 · Drill D: No Ligase

CH 5 WORKED EXAMPLE

LAGGING-STRAND NICKS



Direct defect: covalent backbone breaks remain between fragments. *[Ch 5]*

1. Polymerase still extends primers 5′→3′.
2. Lagging strand still forms multiple Okazaki fragments.
3. After primer replacement, adjacent fragments retain nicks.
4. Without ligase, the strand stays discontinuous and vulnerable; the leading strand is less visibly affected.

17 · Drill E: 1 Base vs 3

CH 6 WORKED EXAMPLE

REGROUP THE CODONS

normal `triplet|triplet|triplet`

−1 base → new boundaries downstream

−3 bases → one codon gone; frame stays

frame shifts vs one codon removed

Grouping rule: deletion size relative to a triplet determines whether the downstream frame moves. *[Ch 6]*

1. One-base deletion changes grouping of every downstream triplet.
2. Later amino acids can change and a premature stop may appear.
3. Three-base deletion removes one codon while preserving the later frame.
4. Either may alter function; position and protein role still matter.

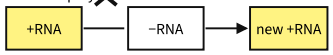
TRAP *Do not label a frameshift from intuition: write separators and regroup.*

18 · Viral Judgement Cards

CH 7 WORKED + FAQ

MUTATION JUDGEMENT	TRACE
Promoter cannot bind activator	Less initiation → less mRNA → less normal-sequence protein → dose-dependent phenotype
Four-base insertion early in exon	Frame changes downstream; many amino acids / stop may change
Silent coding substitution	Redundant code can preserve amino acid; phenotype not automatic
Somatic mutation	Genetic change in body-cell lineage; usually not passed to offspring

IF YOU SEE…	DO THIS
Incoming +RNA translated; viral RNA polymerase blocked	Early protein can form; no −RNA template → few new +RNA genomes → poor assembly
Retrovirus + inactive reverse transcriptase	Earliest block = RNA→DNA; no provirus, downstream expression fails
Virus entered but no progeny	Check readable RNA, protein production, genome copying and assembly separately
Envelope mentioned	Treat structure/entry separately from genome route
Drug target asked	Name required viral transition and why host lacks or performs it differently



Block the complementary template and genome amplification collapses after early translation. *[Ch 7]*

19 · Lab Evidence Ladder

CH 10 · CONTROLS FIRST

BUILD → DELIVER → TEST THE CLAIM



surviving colony ≠ correct insert ≠ exact sequence

Each tool supports a different claim; do not promote evidence beyond its readout. *[Ch 10 figure]*

OBSERVATION	WHAT IT SUPPORTS / DOES NOT PROVE
Growth on selective medium	Marker-bearing plasmid likely present; desired insert not established
Expected-size PCR band	Fragment of similar length amplified; complete sequence identity not proven
Negative-control band	Contamination or non-specific product; sample call invalid
Positive control absent	System failed; a negative sample cannot be trusted
Sequence result	Stronger evidence for nucleotide identity

PCR primer rule: bind different template strands; 3′ ends face into the target; polymerase extends 5′→3′. **Gel:** DNA moves toward positive electrode; smaller fragments usually travel farther.

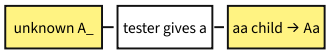
Restriction + ligation: restriction enzymes cut recognised sites and can generate compatible vector/insert ends. Base pairing aligns complementary ends, but ligase is still required to seal the covalent backbone. **PCR cycle:** separate strands → anneal primers → extend; repeating works only when primer geometry encloses the same target.

WHICH IS TRUE? *Selection finds plasmid uptake; screening tests the insert.*

20 · Inheritance Judgement

CH 8–9

DOMINANT PHENOTYPE × aa TESTER

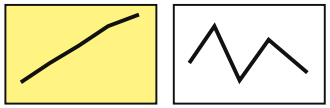


The tester's gamete is constant; offspring reveal the unknown parent's allele. *[Ch 9]*

IF YOU SEE…	CONCLUDE
Recessive offspring from dominant parent × recessive tester	Unknown parent transmitted recessive allele → heterozygous
MI nondisjunction	Homologues travel together → all gametes abnormal for that chromosome
Mutation in body-cell lineage	Copied to its cell descendants, usually not offspring

21 · Selection or Drift?

CH 11 WORKED EXAMPLE



Directional replication plus unequal descendants supports selection; wandering small populations support drift. *[Ch 11]*

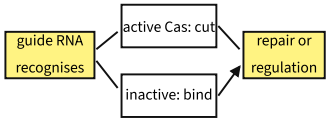
CLAIM	EVIDENCE NEEDED
Natural selection	Heritable variants differ in reproductive success; frequency changes across generations
Genetic drift	No stated fitness difference; random, divergent paths; effect proportionally stronger in small N
Adaptation	Heritable feature shaped because it improved fitness in past environment
Environmental effect	Phenotype changes without evidence that descendants inherit the difference

Bottleneck samples survivors from an existing population; **founder effect** samples a small group that starts a new one. Neither requires the sampled alleles to be advantageous.

TRAP *A frequency change alone is not proof of selection; name unequal reproductive success.*

22 · CRISPR Choice Card

CH 12 WORKED EXAMPLE



Target recognition and downstream activity are separable decisions. *[Ch 12]*

GOAL	BEST SOURCE-GROUNDED CHOICE
Permanent repair-dependent sequence change	Active nuclease cuts; cellular repair determines outcome
Temporary reduction without changing DNA sequence	Inactive Cas + repressive domain; remove system to allow recovery
Specificity concern	Test partial matches near suitable recognition motifs; do not assume perfect targeting

GENOME MECHANISM	SCALE / CONSEQUENCE
Regulatory change	Expression changes without necessarily changing protein sequence
Gene duplication	One copy can retain function while another diverges

23 · Classic MCQ Traps

FAQ + WORKED TIPS

TEMPTING FALSE CLAIM	CORRECT CONTRAST
"Polar bond = polar molecule"	Geometry adds or cancels dipoles
"Enzyme makes it favourable"	Lowers activation barrier; ΔG unchanged
"ATP bond breaking releases energy"	Breaking costs; net products are more stable
"Mitosis copies DNA"	S copies; mitosis separates
"Genetic means inherited"	Inheritance requires germline lineage
"Dominant = common / beneficial"	Dominance concerns heterozygous phenotype
"Virus entry = replication"	All later stages must work
"A band proves sequence"	Gel supports length; sequencing supports identity
"Evolution creates needs"	Variation precedes filtering
"Bigger genome = complexity"	Non-coding and repetitive DNA vary

24 · Short-Answer Frames

ALL CHAPTERS · RECITE

MECHANISM

Because [component] normally [direct job] in [location], changing it causes [first molecular effect]. Therefore [intermediate] rises/falls, leading to [cell / phenotype outcome].

COMPARE

Both A and B [shared feature]. A differs by [structure/process], causing [property]; B [contrast], so [functional consequence].

EXPERIMENTAL CLAIM

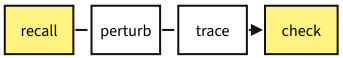
The result supports [narrow claim] because [control/readout]. It does not establish [stronger claim]; test that with [next method].

POPULATION CHANGE

Prior heritable variation + environment-specific reproductive difference → unequal descendants → allele/trait frequency changes across generations.

25 · Exam-Morning Plan

COURSE STUDY STRATEGY



strand · phase · place · link · population

Retrieval beats passive review: draw, perturb, trace, correct. *[course study strategy]*

Check your exam instructions on the LMS for what you may bring; use this sheet to revise and self-test.
UQ Semester 2 examination period, 7–21 November 2026 (check your personal exam timetable).