INTERNATIONAL BIOLOGY OLYMPIAD e. V. IBO



General Instructions

The Animal Anatomy and Electrophysiology practical exam consists of two parts:

- **Part A:** Sheep Eyeball Dissection (65 points)
- **Part B:** Cellular Electrophysiology (22 points)

Keep in mind:

- For **part A**, you will be given one eye sample, it will not be replaced in case you mechanically damage it by dropping or smashing it.
- It is recommended (not mandatory, though) to start with sheep eye **dissection**.
- For **part B**, there is no need for any materials or equipment
- An answer sheet will be provided. **Only the answers provided in the answer sheet will be scored.** Make sure you transfer all your answers to the answer sheet.
- **START** the exam only after you hear a whistle.
- **STOP** answering and put down the pen immediately when you will hear a whistle again at the end of the exam.
- Check the equipment and materials provided according to the table below. If anything from the table is absent, please raise your "Other Queries **(Red)**" card.
- If you need water, please raise the "Drinking Water **(Blue)**" card.
- If you need to use the washroom, please raise the "Washroom **(Yellow)**" card.
- If you have any other questions, please raise the "Other Queries **(Red)**" card.
- Materials, papers, or equipment should not be taken out of the examination room.
- If you have color vision deficiency let assistants know by raising a question card.
- Please be **accurate and calm** during the dissection because you are working with sharp objects; do not rush as you have enough time.

Drinking water	Washroom	Task completed	Other queries
			

Equipment and Materials

General:

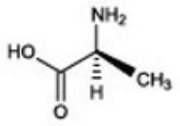
Item name	Quantity
Nitrile gloves	1 pair
Paper towels	6 pieces
Pen	1 piece
Ruler	1 piece
Calculator	1 piece
Clock	1 piece
Bottle with 70% ethanol	1 piece
Waste bin	1 piece
Other queries card	1 piece
Drinking water card	1 piece
Washroom card	1 piece
"Task completed" card	1 piece

For Part I:

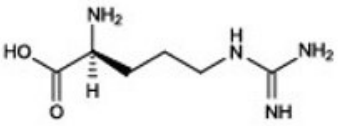
Item name	Quantity
Sheep eye	1 piece
Disposable scalpel	1 piece
Forceps	1 piece
Magnifying glass	1 piece
Protecting apron	1 piece
Needles of 7 different colors	1 set
Dissecting tray	1 piece
Foam pan with your ID number	1 piece
Goggles	1 piece

Appendix 1

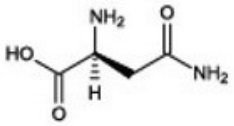
Amino acid structures with abbreviations: **G**-glycine, **A**-alanine, **S**-Serine, **T**-Threonine, **C-** Cysteine, **V** -Valine, **L**-Leucine, **I-** Isoleucine, **M**- Methionine, **P**- Proline, **F-** Phenylalanine, **Y**- Tyrosine, **W**- Tryptophan, **D-** Aspartic acid, **E-** Glutamic acid, **N**- Asparagine, **Q-**Glutamine, **H-** Histidine, **K**- Lysine, **R-** Arginine



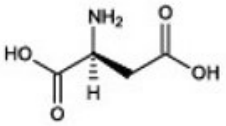
(Ala, A)



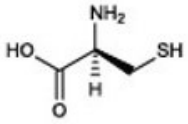
(Arg, R)



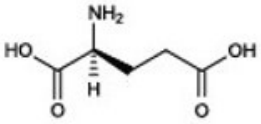
(Asn, N)



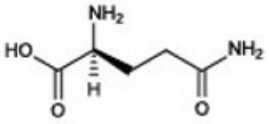
(Asp, D)



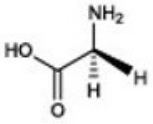
(Cys, C)



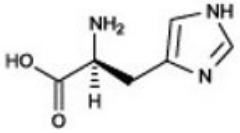
(Glu, E)



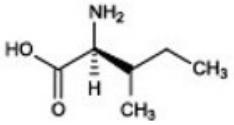
(Gln, Q)



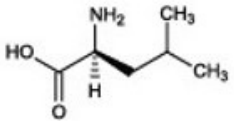
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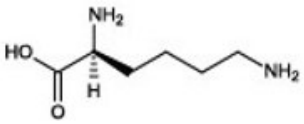
(His, H)



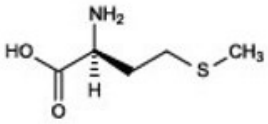
(Ile, I)



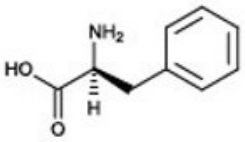
(Leu, L)



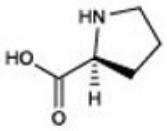
(Lys, K)



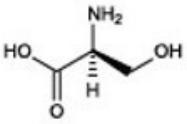
(Met, M)



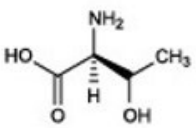
(Phe, F)



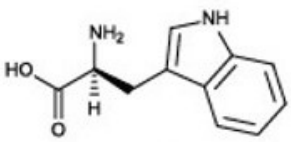
(Pro, P)



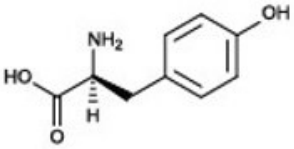
(Ser, S)



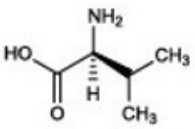
(Thr, T)



(Trp, W)



(Tyr, Y)



(Val, V)

35th International Biology Olympiad

Introduction

The eye is crucial for sensing environmental changes and detecting possible prey or predators. Different animals have developed different eye types as shown in Figure 1. Some animals have created a structure called tapetum to enhance night vision.

In Kazakhstan's steppe, the main predators of sheep are wolves. Therefore, developing sheep's escape and wolf detection mechanisms is crucial. Recently, an interesting theory concerning predator detection systems was described.

In **Part A,** you will first dissect the sheep's eye and correctly identify its internal structures. Next, you are going to learn how different metabolites derived from the eye can be used in post-mortem interval estimation. Then, you will predict how the activity or distribution of different proteins changes in response to predator presence according to the proposed theory. The rest of **Part A** includes additional theoretical questions.

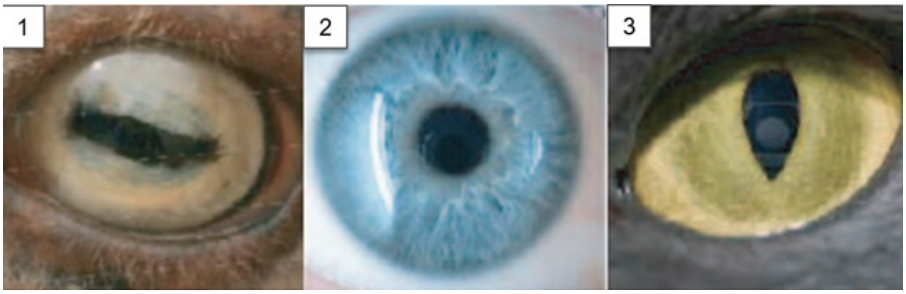


Figure 1. Different types of mammal eyes. Needed for **question 1.3.4.**

Part A: Sheep eyeball Dissection

Protocol

A. Wear the provided gloves, apron, and goggles. Take the eye and examine it.

B. You should perform dissection **only** on the dissecting tray. Start with removing the eyelid, muscle, and excessive fatty tissue using a scalpel and forceps until you reach the sclera layer. This layer is usually tough and not easily detached.

C. Place your specimen on the dissecting tray and gently cut it into two halves through the sclera along the **cutting line** as indicated in Figure 1.1. Inside the eye, there is a *structure T* which is mainly situated towards the posterior direction.

Some amount of substance from *structure T* might leak out when cut. There is no need to keep s*tructure T.* Imagine, that a quantity of a substance from structure T has been sent for analysis as sample 3 along with the other three samples provided in question 1.4.

If the sample is getting dry you can use 70% ethanol to rinse it. Note, that the sample usually starts to dry 45-50 minutes after opening the eye.

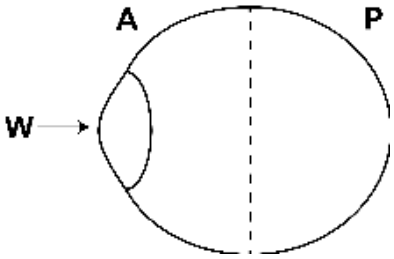


Figure 1.1. Schematic view of sheep eye. W - Cover X, A - Anterior, P - Posterior, ----- Cutting line

From steps **D, E,** and **F** you should obtain a total of **4 different anatomical parts** (labeled as **I, II, III,** and **IV**). Also, you need to identify **7 structures** labeled by the bold text (in **D, E,** and **F** steps) by using colored needles as referenced in table 1.1.

D. By now you should have obtained two hemispheres: with anterior (A) pole and a posterior (P) pole. From the posterior hemisphere gently peel away the **first layer** which you observe on the inside surface. You are expected to peel away only half-way, no need to extract the whole first layer. Now you should be able to expose the **second layer** on the peeled part. These 2 layers are the structures that should be identified later.

E. Now take the anterior hemisphere and gently remove the jelly-like structure. You will not need this jelly-like structure. Then slowly remove the **ball-like structure** along with **its attachment.** Save these structures since you will need to identify them and show them to a volunteer later.

F. Now gently cut out the **cover X** from the anterior hemisphere, shown in Figure 1.1. After this you should reveal some structures below the cover X, you should name the **opening** and **structure surrounding** that opening and show it to a volunteer later.

Internal Structure Identification

From the *posterior hemisphere* **(I)** you should identify the 1st and 2nd layers as described in **D**.

From the *anterior hemisphere*, you should get **3** distinct structures: **cover X (II)**, the **ball-like structure with its attachment (IV)** and **the remaining anatomical part (III)** after removing structures II and IV**.**

Transfer eye parts on the provided foam **pan** in order **I, II, III, IV**, from left to right, and then identify structures using colored needles and make sure that they are visible for assessment from above.

Remember, that **I** refers to the posterior hemisphere with 2 layers (**purple** and **green** needles), **II** refers to cover X of the anterior hemisphere (**pink** needle), **III** represents the remaining anatomical part (**yellow** and **white** needles), **IV** refers to the ball-like structure with its attachment (**blue** and **black** needles).

	Correctness of order will be assessed in an all-or-none manner, structures (I, II, III, IV) should be in order and presented separately. Only structures transferred onto the foam pan will be assessed.	2.0pt

Anatomy and Physiology of Animals and Humans

Q1-3

English (Official)

Question 1.1: Please use the below labels of differently colored needles for your reference to identify different structures obtained from steps **D, E,** and **F** . 21pt

Table 1.1. Reference needle colors and structure labels **(1-7).**

Needle Color	Needle Color	Structure name designated by numbers
Purple		Tapetum **(1)**
Pink		Cornea **(2)**
Yellow		Iris **(3)**
White		Pupil **(4)**
Blue		Lens **(5)**
Black		Suspensory ligaments **(6)**
Green		Retina **(7)**

Once you have separated these 4 parts (7 structures) and identified them by appropriate color needle, put a "task completed" card on a binder clip located on the side partition of your table. It is advised to submit your work without delay because dissected eye parts will dry with time. After showing this card, you are not allowed to make any changes to the needles' position. A volunteer will take a picture and it will be assessed later.

Once you have completed dissection and structure identification you can take off gloves, apron, and goggles, since the rest of the exam will be paper-based.

Question 1.2. Fill the table provided in your answer sheet by using the structure labels from **1 to 7** provided in Table 1.1, to match with the correct function or characteristic. Use only **one** for each function/characteristic from **1-7**, put **X** if nothing from 1-7 correctly corresponds. 4.0pt

Question #	Structure label (1-7 or X)	Function or Characteristic
1.2.1		Actively regulates the amount of light passing to the eye
1.2.2		By changing its shape, it aids in focusing
1.2.3		Photoreceptors are evenly distributed over the entire area of the structure
1.2.4		Transparent structure - continuation of the sclera on the front

Question 1.3. 4.0pt

Question 1.3. Put √ to mark statements as True(T) or False(F). For numbered structures use labels from Table 1.1	**T**	**F**
1.3.1. *Structure T* (from protocol **step C**) is aqueous humor that aids in intraocular pressure maintenance		
1.3.2. *Structure 6* plays **NO** role in sheep eye accommodation (focusing)		
1.3.3. Within the eye, the *choroid* is the first damaged by hypoxia		
1.3.4. In most cases type 1 eye belongs to a prey (see Figure 1).		

PMI estimations

In forensic science, determining the time of death (post-mortem interval, PMI) is crucial. Eye metabolomics analysis offers a promising method for this purpose. Studies have shown a correlation between the concentration of extracted potassium ions and PMI.

Selectivity ratio (SR) plots are a helpful tool to visualize how a specific substance (in this case, potassium) relates to various metabolites. These plots depict the strength and direction (positive or negative) of this correlation on the y-axis (SR value), while the x-axis displays the different metabolites (as seen in Figure 1.4B). Table 1.4 provides information about samples 1-4, with the letter **"N"** referring to data that is not provided.

Figure 1.4 visually represents two key points: **A)** the relationship between potassium concentration and estimated PMI, and **B)** the SR plot of potassium concentration against various metabolites. Additionally, PMI can be estimated using choline concentration instead of potassium, as demonstrated by **Equation 1.4**.

The golden standard method is the best available one used as a reference when comparing other methods.

Equation 1.4: $PMI(h) = 37 + 1.2 * [Choline, mM]$

Table 1.4. Data regarding samples 1-4.

Sample	K^+(mM)	Measured PMI (h) by Choline (Cho), Potassium (K^+) or (G) golden standard method
1	N	55 **(Cho)**
2	75	47 **(Cho)**
3	N	>70 **(K^+)**
4	?	<20 **(G)**

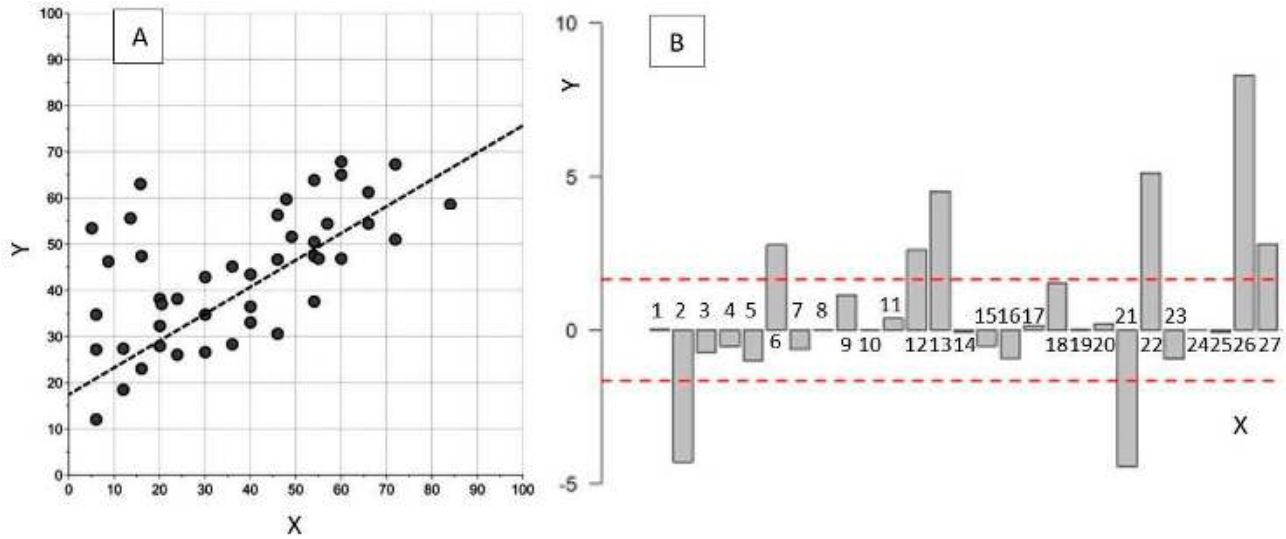


Figure 1.4. A) Potassium concentration and estimated PMI. X-PMI (h), Y- [K+] (mM). **B)** SR value plot (Y-axis) for potassium concentration vs metabolites (X-axis) (labeled by numbers,1-27), where dashed red lines illustrate SR thresholds at the significance level of α=0.05.

Question 1.4	8.0pt

Question 1.4: Based on the data above put ✓ to mark statements as True (T) or False (F).	**T**	**F**
1.4.1. Sample 3 most likely contains metabolite 26		
1.4.2. The concentration of choline in sample 1 is 15 mM		
1.4.3. In most cases samples with real PMIs within the range 0 - 20 hours will be more severely overestimated by the model from Figure 1.4A than samples with real PMIs within the range 20 - 40 hours.		
1.4.4. Time of death estimates based on potassium and choline methods are nearly identical		

A predator detection theory

This theory is based on the interplay of 3 different proteins. The first protein, *RUN*, activates signaling pathways that eventually inform a prey that a predator is nearby. In a safe situation when a prey does not see the predator, protein *RUN* is successfully degraded by another protein, *BeCalm,* both are synthesized throughout the prey eye's liquid. However, a third protein, *NoWay*, can inhibit *BeCalm*. In case of a predator threat, the release of *NoWay* occurs. *NoWay* is released from the anterior to the posterior side when a prey sees a predator. Figure 1.5A shows this relationship. The methodology of measuring *NoWay* protein concentrations does not depend on the activity of the proteins. *NoWay* covalently binds to *BeCalm* during inhibition.

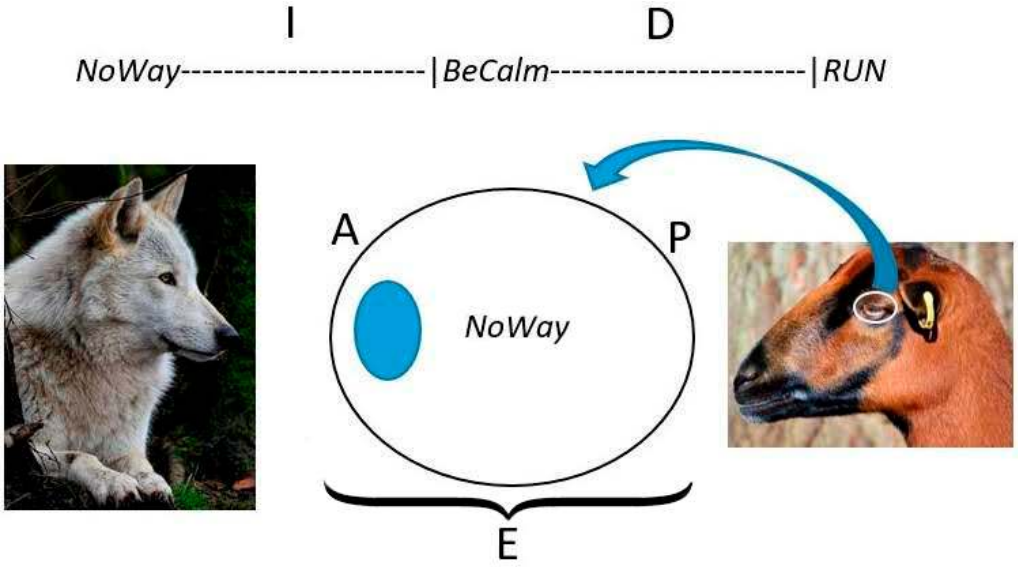


Figure 1.5A. Relationship between three proteins. I - inhibition, D - degradation. A - anterior, P - posterior, E - simplified prey eye's scheme.

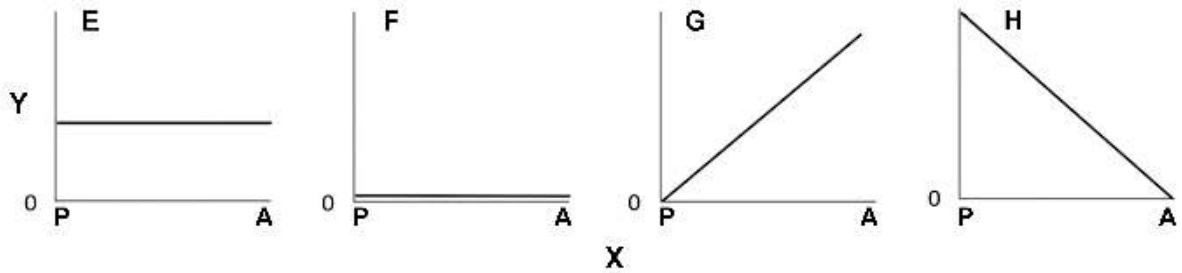


Figure 1.5B. Different graphs (E, F, G, H) show the relationship between a protein Activity or Distribution (Y) and distance from the posterior eye side (X). Axis (X, Y) are the same everywhere.

Question 1.5. Fill the table below with appropriate graph letters (E, F, G, H) from Figure 1.5B, so that a chosen graph gives the best approximation of either activity or distribution of protein in different scenarios. **N**- no need to fill in. 16pt

Activity or Distribution	**Before seeing a predator**	**After seeing a predator**
1.5.1. The distribution of *RUN*		
1.5.2. The distribution of unbound *BeCalm*		
1.5.3. The activity of *RUN*		
1.5.4. The distribution of unbound *NoWay*	**N**	
1.5.5. The activity of *BeCalm*	**N**	

Protein RUN kinetics

Scientists studied the kinetics of the protein RUN degradation (Figure 1.6A). An enzyme, called *Enzyme N*, breaks down RUN and has a single active site. However, the scientists introduced a mutation by deleting an amino acid, resulting in a new enzyme named *Enzyme M.* The investigation into the enzymes' kinetic properties is presented in Figure 1.6B. **Equation 1.6.3** describes the reaction rate, which is a second-order bimolecular reaction. **Kcat**, the *turnover number*, refers to the number of substrate molecules converted into products by a single active site per unit of time.

Equation 1.6.1: $\mathrm{E} + \mathrm{S} \underset{k_{-1}}{\overset{k_1}{\rightleftarrows}} \mathrm{ES} \xrightarrow{kcat} \mathrm{P} + \mathrm{E}$

E- enzyme, S- substrate, ES- enzyme-substrate complex, P-product

Equation 1.6.2: $Km = \frac{(k_{-1}+k_{cat})}{k_1}$

Equation 1.6.3: $Vo = \frac{[Et]\cdot[S]\cdot kcat}{Km}$ **,** where [Et]- total enzyme concentration.

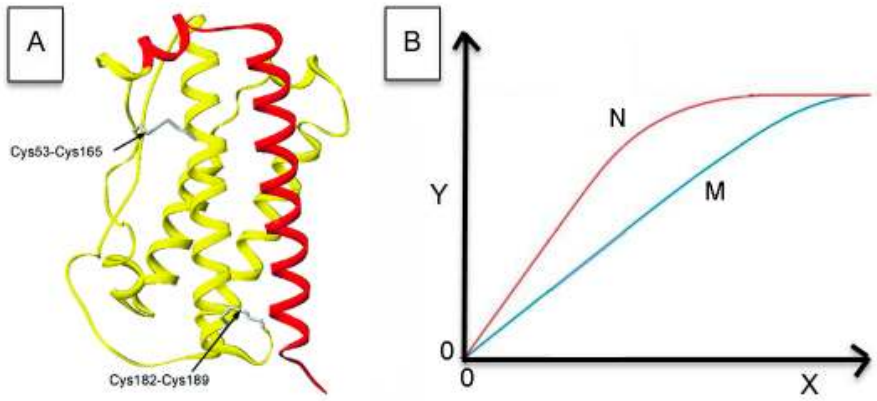


Figure 1.6. A) The ribbon representation of the RUN; cysteine residues are shown in grey. Different coloring was applied in order to make visual perception easier; other than that, it serves no purpose. **B)** X- substrate concentration, Y- rate of reaction, N - *Enzyme N*, M - *Enzyme M*.

Question 1.6: Based on the data above, enter a tick (√) in the table below to mark statements as True (T) or False (F)." 4.0pt

Question 1.6	**T**	**F**
1.6.1. The formation of the ES complex is slower in *Enzyme M* than in *Enzyme N*.		
1.6.2. An SDS-PAGE analysis of RUN under excessive reducing conditions will display three distinct bands.		
1.6.3.Equation 1.6.3 was derived by assuming that the concentration of RUN is far less than its Km.		
1.6.4. The maximum reaction rate (Vmax) is attained by **equation 1.6.3** when the $\frac{kcat}{Km}$ value is very close to the k_1 value		

Question 1.6.5: Which protein structure(s) might be affected in *Enzyme M*? Put a tick (√) everywhere you think it applies. There might be several correct answers. **No partial credits are given**. 1.0pt

i) Primary structure	**ii)** Secondary structure	**iii)** Tertiary structure

Hormonal response to stress

Sheep might employ a wolf detection system, to avoid stressful situations. Humans also have a complex physiological response to stress managed by the hypothalamic-pituitary-adrenal (HPA) axis, illustrated in Figure 1.7. The HPA axis is negatively regulated by cortisol. Some tests aid physicians in identifying the problematic site or organ that causes hormonal impairment.

Some abnormal tissue overgrowth might start producing hormones at sites where these hormones are normally not produced.

Below are 5 different patients (A, B, C, D, and E) with various impairments. Some of them have received hormonal interventions and results are provided in table 1.7.

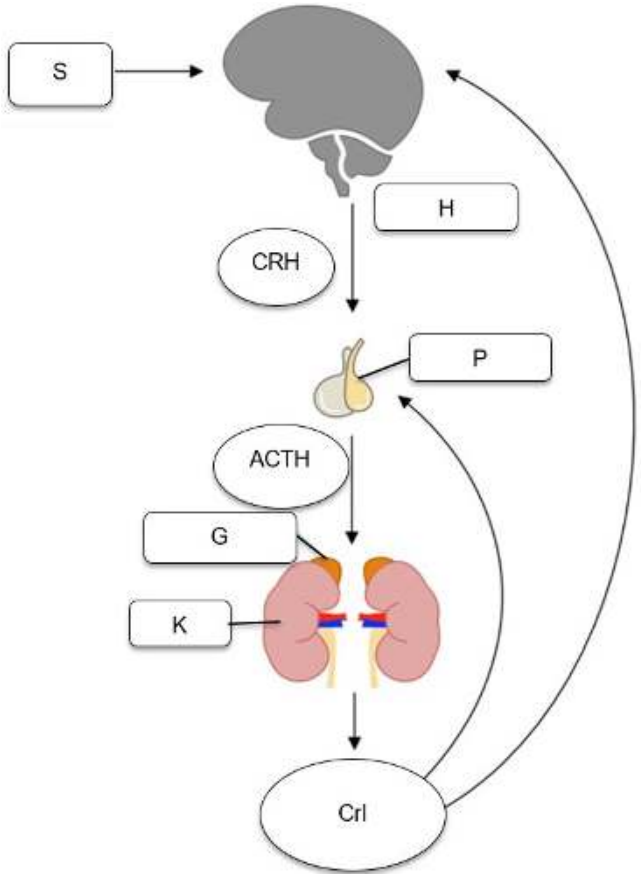


Figure 1.7. HPA axis. CRH - corticotropin-releasing hormone, ACTH - adrenocorticotropic hormone, Crl - cortisol, S - stress, H - hypothalamus, P - pituitary, G - adrenal gland, K - kidney.

Table 1.7. Patients with different interventions. Dexamethasone is a synthetic analogue of cortisol. Hd dex - high dose dexamethasone, CRH - corticotropin-releasing hormone, ACTH - adrenocorticotropic hormone, L - Low, H - High. (+) means administration

Patient	Intervention type	Before			After		
		CRH	ACTH	Crl	CRH	ACTH	Crl
A	+ Hd dex	L	H	H	L	H	H
B	+ Hd dex	L	L	H	L	L	H
C	+ CRH	H	H	L	H	H	L
D	+ CRH	H	L	L	H	L	L
E	+ ACTH	L	L	L	L	H	L

Question 1.7. Put √ to mark statements as True (T) or False (F) 5.0pt

Question 1.7	T	F
1.7.1. Administration of ACTH instead of CRH to patient C will restore cortisol level		
1.7.2. Patient B has an adrenal tumor that secretes cortisol		
1.7.3. Patient A has a tumor that is secreting ACTH		
1.7.4. Patient D has impairment in the adrenal gland itself		
1.7.5. Administration of CRH to patient E, will restore the cortisol level		

Part B: Cellular Electrophysiology

Predator detection and fast reaction are crucial for a prey's survival. The latter is achieved by fast nerve impulse propagation and relay of the signals, based on action potential generation.

In **Part B,** you will be given some background information about voltage-gated channels and their electrophysiology. Then you will answer questions based on the provided experimental data.

Background information

The generation of action potential plays a vital role in many physiological processes related to nerves and skeletal muscles. Electrochemical gradient across the membranes drives and modulates the opening and closing of channels. Two types of currents are involved in channel kinetics: *ionic* and *gating.*

Gating currents:

- Definition: Small, transient currents generated by the movement of charged residues within the channel protein during conformational changes.
- Purpose: These changes open (**gating activation**) or close (**gating deactivation**) the channel pore, controlling the flow of ions through the pore itself. Gating current doesn't involve actual ion flow through the pore.

Ionic currents:

- Definition: The main current generated by the flow of ions (like sodium, potassium, and calcium) through the open channel pore.
- Purpose: Let specific ions across the cell membrane, contributing to electrical signalling and various cellular functions like muscle contraction, nerve impulse transmission, and neurotransmitter release.
- **Ionic activation** refers to the opening of the channel and subsequent flow of ions due to gating activation
- **Ionic Deactivation** refers to the closing of the channel and cessation of ion flow due to gating deactivation

Voltage-gated channel states: Three states characterize these channels: *open, closed,* and *inactivated.* Depending on membrane potential, these states interchange with different rate constants. Figure 2.1 shows these states at different voltages.

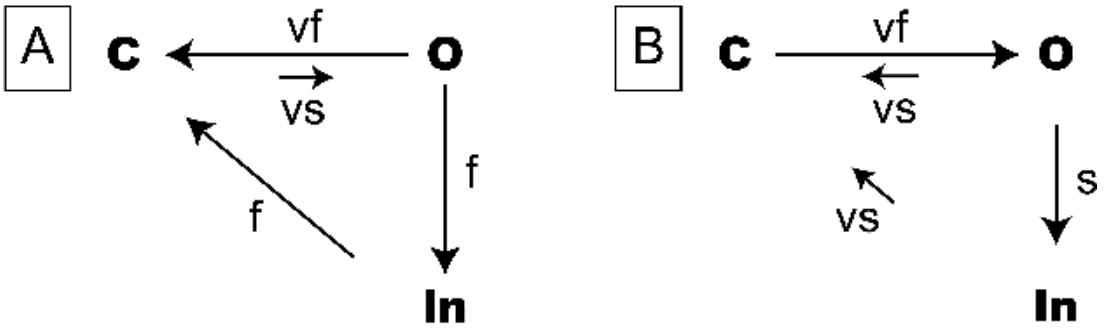


Figure 2.1. A) Channel states at membrane voltage = -80mV. **B)** Channel states at membrane voltage = +10mV. The longer the arrow length the higher the rate constant value. C - closed, O - open, In - inactivated, vf - very fast, f - fast, vs - very slow, s - slow.

Voltage sensors:

Voltage sensors are crucial components of voltage-gated ion channels, playing a key role in translating changes in membrane potential (voltage) into the opening and closing of the channel pore.

The time course of activation and deactivation in ion channels can be measured as the **time constant (τ)** using appropriate experimental techniques. More specifically, the time constant characterizes the speed of activation/deactivation of ionic and gating currents. It can be calculated using the following equation: $\tau = r_m \times c_m$,

where $\mathbf{r_m}$ is the resistance across the membrane and $\mathbf{c_m}$ is the capacitance of the membrane.

Investigators **hypothesized** that a protein TrT can physically interact with voltage sensors and thus might affect time constant. They studied two voltage-gated channels (*ChW* and *ChZ*) in *Xenopus* oocytes, both with and without protein TrT co-expressed. Additionally, they examined other channels (*ChN* and *ChM*) without protein TrT. In their experimental set-up membrane capacitance was kept constant. The figures 2.2A, and 2.2B summarize the results.

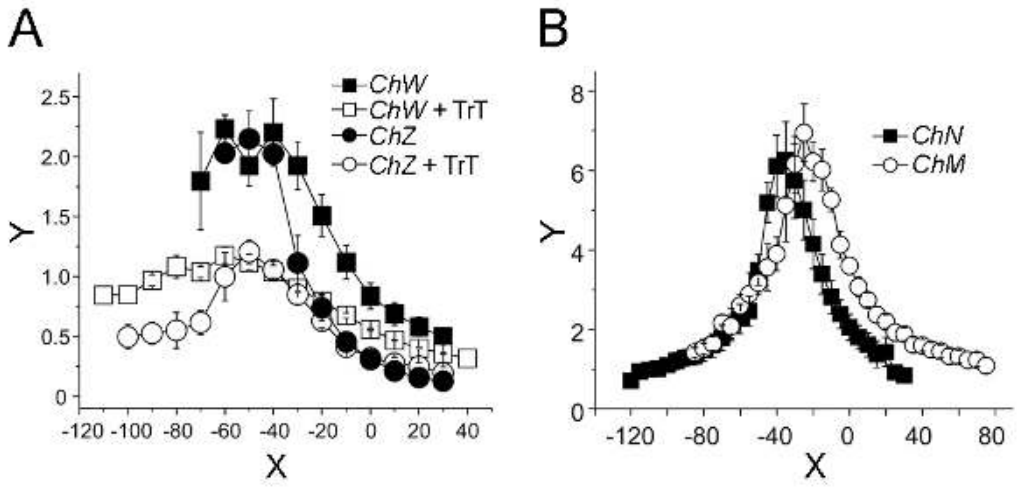


Figure 2.2. For both graphs: X - Voltage(mV), Y - gating activation time constant (ms). **A)** Gating activation time constant changes in response to various voltages upon *ChW* and *ChZ* channels with and without protein TrT. **B)** Gating activation time constant for *ChN* and *ChM.* Error bars show ±SEM.

Question 2.1: Based on the data above put √ to mark statements as True (T) or False (F) 8.0pt

Question 2.1	**T**	**F**
2.1.1. Protein TrT delays the opening of both *ChW* and *ChZ* channel pores for approximately 2-fold.		
2.1.2. The best way to test their hypothesis is to measure ionic currents.		
2.1.3. Gating currents develop faster in ChW channels compared to ChN channels at -40 mV, regardless of the presence of the protein TrT		
2.1.4. Voltage change from -40 mV to -20mV will cause less current flow within *ChN* compared to *ChW*		

It is widely recognized that the activation process of the four voltage sensors (VSr) within the subunits of ChW channels operates asynchronously. Some voltage sensors out of **DI–DIV** (Figure 2.3A) undergo *rapid* rearrangement, leading to the opening of the channel pore, and other(s) VSr undergo(es) *slow* rearrangement. Figure 2.3A illustrates the S2 and S4 amino acid sequence portions of different wild-type voltage sensors of *ChW, ChN, ChM, ChO* and *ChS*. Whereas Figure 2.3B shows portion segments where some mutations were introduced. *Mut 1, Mut 2, Mut 3, Mut 5* are mutants of *ChW,* whereas *Mut 4* is a mutant channel of ChN. Mutations were introduced on 5^{th}, 13^{th}, 16^{th} aminoacid residues which were considered as "speed-control residues". Mutant functionings were investigated, and results are provided in Figures 2.3C-E.

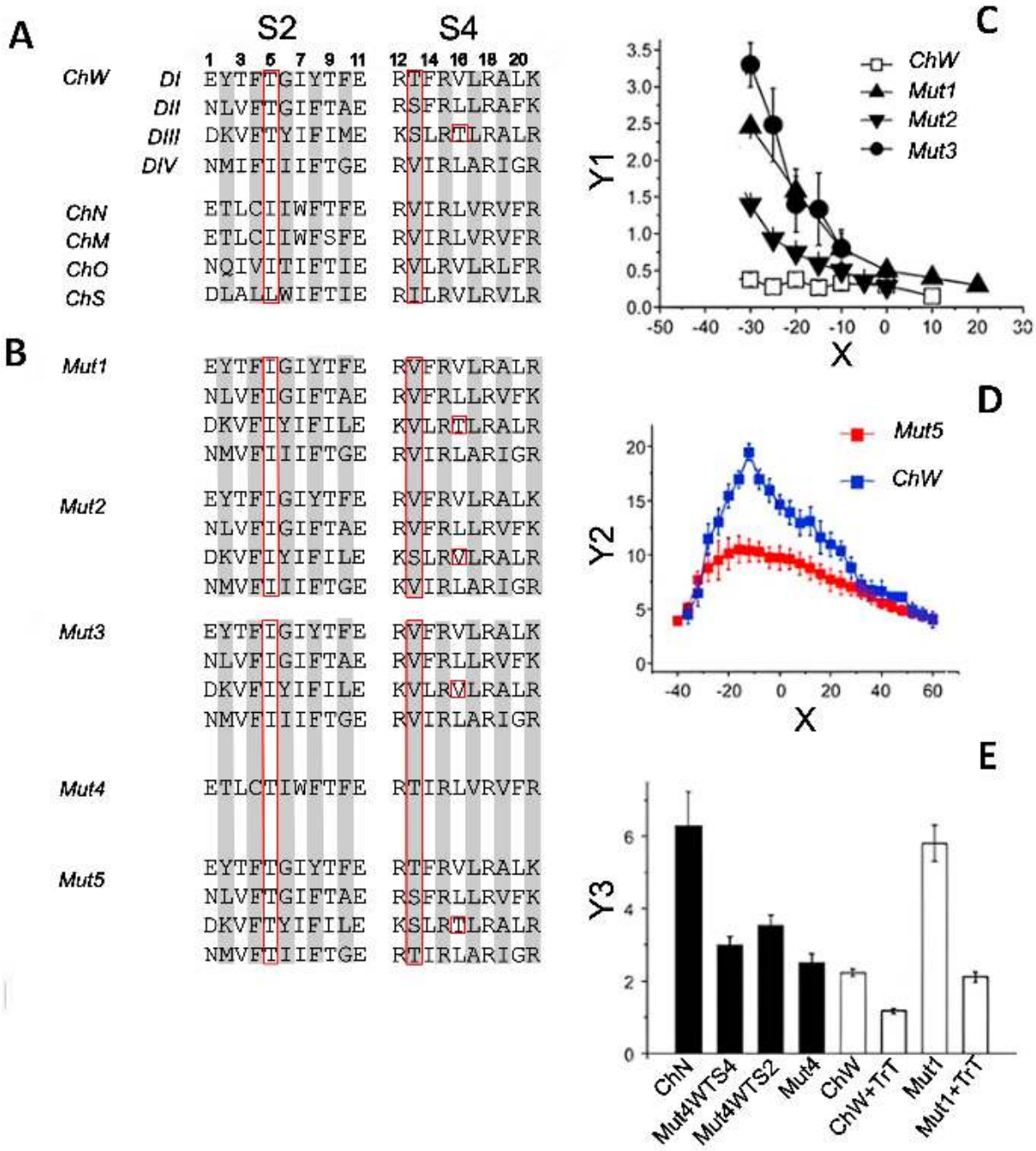


Figure 2.3. **A)** Different voltage sensor's amino acid sequence. **B)** Different mutations of *ChW* or *ChN* channels. **C)** Activation time constant (τ) for ionic current plotted as a function of voltage for wild-type and mutant channels. Y1 – ionic activation time constant (τ) (ms), X1 –voltage (mV). **D)** Time constant comparisons of *ChW* and Mut 5. X2 – voltage (mV). Y2 – ionic inactivation time constant (ms). **E)** Mean τ_{max} values change upon addition of TrT to *ChW* and *Mut1*. Y3 – Gating activation τ_{max} (ms). Mut4WTS4- mut4, but with wild type S4, Mut4WTS2-Mut4, but with wild type S2.

Question 2.2: Based on the data above put √ to mark statements as True (T) or False (F). ***** Corresponding amino acids on the *13th* and *16th* positions. 14pt

Question 2.2	**T**	**F**
2.2.1. Hydrophilic amino acids on "speed-control residues" increase the velocity of voltage sensor rearrangements.		
2.2.2. Amino acid *****S^{13} in S4 of DIII of *ChW* channel is less functionally important than *****T^{16}.		
2.2.3. From figure 2.3C at -30mV, the average channel opening time across all mutant channels is around 5-6 fold longer compared to *ChW.*		
2.2.4. Alterations to the "speed-control" residues impair functionality of the protein TrT.		
2.2.5. Mut 4 possesses a slower velocity of voltage sensor rearrangement than ChN		
2.2.6. Based on graph 2.3D, in *Mut5* channels absolute refractory period starts earlier than in *ChW* channels.		
2.2.7. *ChN, ChM,* and *ChO* voltage sensors exhibit a *slow* voltage sensor rearrangement pace compared to ChW		

35th International Biology Olympiad

Part A: Sheep Eyeball Dissection

Internal Structure Identification

1.0 (2.0 pt)
Correctness of order will be assessed in an all-or-none manner, structures (**I, II, III, IV**) should be in order and presented separately. Only structures transferred onto the foam pan will be assessed.

1.1 (21 pt)
Question 1.1 Structure identifications will be assessed

1.2 (4.0 pt)
Question 1.2

Question 1.2	Structure label (1-7 or X)
1.2.1	
1.2.2	
1.2.3	
1.2.4	

1.3 (4.0 pt)

Question 1.3	T	F
1.3.1		
1.3.2		
1.3.3		
1.3.4		

1.4 (8.0 pt)

Question 1.4:	T	F
1.4.1		
1.4.2		
1.4.3		
1.4.4		

1.5 (16.0 pt)
Question 1.5. N- no need to fill**.**

Activity or Distribution	Before seeing a predator	After seeing a predator
1.5.1		
1.5.2		
1.5.3		
1.5.4	**N**	
1.5.5	**N**	

1.6 (4.0 pt)

Question 1.6	T	F
1.6.1		
1.6.2		
1.6.3		
1.6.4		

1.6.5 (1.0 pt)

Question 1.6.5. Put a tick (√) everywhere you think it applies. There might be several correct answers. **No partial credits are given**.

i	ii	iii

1.7 (5.0 pt)

Question 1.7	T	F
1.7.1		
1.7.2		
1.7.3		
1.7.4		
1.7.5		

Part B: Cellular Electrophysiology

2.1 (8.0 pt)

Question 2.1	T	F
2.1.1		
2.1.2		
2.1.3		
2.1.4		

2.2 (14.0 pt)

Question 2.2	T	F
2.2.1		
2.2.2		
2.2.3		
2.2.4		
2.2.5		
2.2.6		
2.2.7		

Student code: .	Student name: .

35th International Biology Olympiad

7th-14th July 2024 Astana, Kazakhstan

Practical Exam: Animal Anatomy and Physiology

Answer key

Total points: 87
Duration: 90 min

Part A: Sheep Eyeball Dissection (65 points)

Internal structure identification

Correctness of order is assessed----- 2 points

Question 1.1 (21 points) Structure identifications will be assessed

Question 1.2 (4 points)

Question	Structure label (1-7 or X)
1.2.1	3
1.2.2	5
1.2.3	X
1.2.4	2

Question 1.3 (4 points)

Question	T	F
1.3.1		√
1.3.2		√
1.3.3		√

1.3.4	√	

Question 1.4 (8 points):

Question	**T**	**F**
1.4.1	√	
1.4.2	√	
1.4.3	√	
1.4.4		√

Question 1.5 (16 points)

Activity/ Distribution	**Before seeing a wolf**	**After seeing a wolf**
1.5.1	F	G
1.5.2	E	H
1.5.3	F	G
1.5.4	**N**	G
1.5.5	**N**	H

Question 1.6 (4 points)

Question	T	F
1.6.1	√	
1.6.2		√
1.6.3	√	
1.6.4	√	

Question 1.6.5 (1 point)

i	ii	iii
√	√	√

Question 1.7 (5 points)

Question	T	F
1.7.1		√
1.7.2	√	
1.7.3	√	

1.7.4		√
1.7.5		√

Part B: Cellular Electrophysiology

Question 2.1 (8 points)

Statements	T	F
2.1.1		√
2.1.2		√
2.1.3	√	
2.1.4	√	

Question 2.2 (14 points)

Statements	T	F
2.2.1	√	
2.2.2		√
2.2.3	√	
2.2.4		√
2.2.5		√
2.2.6	√	
2.2.7	√	

Part B: Cellular Electrophysiology

2.1.1. False.

Protein TrT actually fasten the gating activation, since the lower tau the faster is activation. It is inferred from equation: tau= r_m xC_m.

2.1.2. False.

Instead gating currents should be measured, because they can be measured when there is a physical voltage sensor rearrangements.

2.1.3. True

This is directly seen from figure 2.2, by inspection of garting activation constant time at -40 mV

2.1.4. True.

Since tau is higher for *ChN* compared to *ChW* during mentioned voltage change, the resistence in ChN is also higher (from formula) meaning less current flows within the channel.

2.2.1. True.

Indeed it is seen on figure 2.3D, where changing an aminoacid on 5th position of ChW in S2 of DIV from hydrophobic to hydrophilic, fastens voltage sensor rearrangements. Inversely, changing aminoacids on 5th position of ChW in S2 of DI-DIII from hydrophilic to hydrophobic slows voltage sensoe movements (evidenced from 2.4C).

2.2.2. False.

Serine on 13 position is important to maintain rapid voltage sensor rearrangement in ChW. It is evidenced from 2.3C, and a conclusion about incorrectness of the statement is reached by carefully comparing three mutation channels(mut1, mut2, mut3) and noting how particular aminoacid changes in the 13th and 16th positions affect the velocity of voltage sensor movements.

2.2.3. True.

Need to find an ariphmetic mean of the tau of Mut1, mut2 and mut3 and then calculate how many times tau of ChW is faster.

2.2.4. False

As it is seen from 2.3E protein TrT can accelerate mut 1, which means, alterations in speed control residues do not affect proper functioning of Protein TrT

2.2.5. False

The mutation actually accelerates the ChN's voltage sensor rearrangements

2.2.6. true.

Since it is evident that a mut5 channel closes faster than ChW, it means it enters absolute refractory period earlier than ChW.

2.2.7. true.

We see from fig2.3C that changing hydrophilic aminoacid to hydrophobic at 5^{th} position of S2 in ChW slows voltage sensor rearengements, thus channels (ChN, ChM, ChO) that have hydrophobic residues at 5^{th} position of S2 should display a slow rearengement pace as well.