

International Technologist in Cytogenetics ASCP Practice Test (Sample)

Study Guide



Everything you need from our exam experts!

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Introduction

Preparing for a certification exam can feel overwhelming, but with the right tools, it becomes an opportunity to build confidence, sharpen your skills, and move one step closer to your goals. At Examzify, we believe that effective exam preparation isn't just about memorization, it's about understanding the material, identifying knowledge gaps, and building the test-taking strategies that lead to success.

This guide was designed to help you do exactly that.

Whether you're preparing for a licensing exam, professional certification, or entry-level qualification, this book offers structured practice to reinforce key concepts. You'll find a wide range of multiple-choice questions, each followed by clear explanations to help you understand not just the right answer, but why it's correct.

The content in this guide is based on real-world exam objectives and aligned with the types of questions and topics commonly found on official tests. It's ideal for learners who want to:

- Practice answering questions under realistic conditions,
- Improve accuracy and speed,
- Review explanations to strengthen weak areas, and
- Approach the exam with greater confidence.

We recommend using this book not as a stand-alone study tool, but alongside other resources like flashcards, textbooks, or hands-on training. For best results, we recommend working through each question, reflecting on the explanation provided, and revisiting the topics that challenge you most.

Remember: successful test preparation isn't about getting every question right the first time, it's about learning from your mistakes and improving over time. Stay focused, trust the process, and know that every page you turn brings you closer to success.

Let's begin.

How to Use This Guide

This guide is designed to help you study more effectively and approach your exam with confidence. Whether you're reviewing for the first time or doing a final refresh, here's how to get the most out of your Examzify study guide:

1. Start with a Diagnostic Review

Skim through the questions to get a sense of what you know and what you need to focus on. Your goal is to identify knowledge gaps early.

2. Study in Short, Focused Sessions

Break your study time into manageable blocks (e.g. 30 - 45 minutes). Review a handful of questions, reflect on the explanations.

3. Learn from the Explanations

After answering a question, always read the explanation, even if you got it right. It reinforces key points, corrects misunderstandings, and teaches subtle distinctions between similar answers.

4. Track Your Progress

Use bookmarks or notes (if reading digitally) to mark difficult questions. Revisit these regularly and track improvements over time.

5. Simulate the Real Exam

Once you're comfortable, try taking a full set of questions without pausing. Set a timer and simulate test-day conditions to build confidence and time management skills.

6. Repeat and Review

Don't just study once, repetition builds retention. Re-attempt questions after a few days and revisit explanations to reinforce learning. Pair this guide with other Examzify tools like flashcards, and digital practice tests to strengthen your preparation across formats.

There's no single right way to study, but consistent, thoughtful effort always wins. Use this guide flexibly, adapt the tips above to fit your pace and learning style. You've got this!

Questions

- 1. What should be done if high non-specific background is observed on a postwashed FISH slide?**
 - A. Decrease the dye concentration**
 - B. Increase postwash temperature**
 - C. Reduce the exposure time to the light source**
 - D. Change the type of probe used**
- 2. Which AML type is associated with the genetic change *inv(16)(p13q22)*?**
 - A. AML M4**
 - B. AML M5**
 - C. AML M6**
 - D. AML M7**
- 3. A laboratory quality assurance program typically includes what component?**
 - A. Regularly rotating laboratory staff**
 - B. Proficiency testing**
 - C. Client satisfaction surveys**
 - D. Annual cost audits**
- 4. What is the most important pretreatment for age slides in FISH analysis?**
 - A. 2x SSC at 37 degrees for 30 minutes**
 - B. Heat fixation at 75 degrees for 15 minutes**
 - C. Alcohol fixation for 10 minutes**
 - D. 0.1M PBS at room temperature for 20 minutes**
- 5. What region of the chromosome is specifically stained by quinacrine and acridine orange dyes?**
 - A. GC rich DNA**
 - B. AT rich DNA**
 - C. Telomeric DNA**
 - D. Centromeric DNA**

- 6. What should a tech consider when interpreting FISH analysis results?**
- A. The appearance of stable cells**
 - B. Interpretation of the number of signals**
 - C. Observing the morphology of nuclei**
 - D. Evaluating staining patterns**
- 7. Which chromosome is most different between C-banding and G-banding techniques?**
- A. Chromosome 16**
 - B. Chromosome 9**
 - C. Chromosome 18**
 - D. Chromosome 1**
- 8. What do the dark bands produced by routine GTG banding represent?**
- A. Gene-rich regions of the chromosome**
 - B. Euchromatin regions**
 - C. AT-rich regions of the chromosome**
 - D. Gene-poor regions of the chromosome**
- 9. For successful harvest, each new batch of hypotonic solution should be evaluated by?**
- A. Conducting a pH test**
 - B. Comparing to a lot already in use**
 - C. Checking for color change**
 - D. Assessing viscosity**
- 10. Which of the following disorders is NOT associated with a microdeletion?**
- A. Prader-Willi**
 - B. DiGeorge**
 - C. Rubinstein-Taybi**
 - D. Langer-Giedion**

Answers

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1. B
2. A
3. B
4. A
5. B
6. B
7. B
8. C
9. B
10. C

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Explanations

1. What should be done if high non-specific background is observed on a postwashed FISH slide?

- A. Decrease the dye concentration**
- B. Increase postwash temperature**
- C. Reduce the exposure time to the light source**
- D. Change the type of probe used**

When encountering high non-specific background on a post-washed FISH (Fluorescence In Situ Hybridization) slide, increasing the post-wash temperature can help enhance the specificity of the probe binding. Higher temperatures can reduce the binding of the probe to non-target regions by promoting dissociation of non-specifically bound probes, thereby decreasing background fluorescence. This enables clearer visualization of the specific hybridization signals. While other options may seem reasonable in different contexts, they do not directly address the issue of non-specific background in the same effective manner as adjusting the post-wash temperature. For instance, reducing the dye concentration might not necessarily eliminate non-specific binding, as some probes can still bind indiscriminately at lower concentrations. Changing the type of probe used may also be a solution but is more drastic and might not be required if temperature adjustments can effectively resolve the background issue. Reducing exposure time to the light source could potentially decrease the background signal, yet it risks underexposing the specific signals that are of interest, leading to a loss in overall clarity and detectability. Thus, increasing the postwash temperature is the most direct and effective approach to reducing high non-specific background in FISH analysis.

2. Which AML type is associated with the genetic change $\text{inv}(16)(\text{p13q22})$?

- A. AML M4**
- B. AML M5**
- C. AML M6**
- D. AML M7**

The genetic change $\text{inv}(16)(\text{p13q22})$ is specifically associated with Acute Myeloid Leukemia (AML) M4, which is classified as acute myelomonocytic leukemia. This chromosomal inversion leads to the formation of a fusion gene, which is often implicated in the pathology of this specific type of leukemia. The presence of $\text{inv}(16)$ typically suggests the involvement of certain myeloid cells, particularly those that are immature monocytes and granulocytes, characteristic of AML M4. In patients with this genetic alteration, there is a distinct clinical and cytogenetic profile associated with AML M4, including features such as a specific morphology and immunophenotype, which further supports the connection between the genetic change and this type of leukemia. Other types of AML, such as M5, M6, and M7, are associated with different cytogenetic abnormalities and phenotypic characteristics that do not include $\text{inv}(16)$. Therefore, recognizing the association between $\text{inv}(16)$ and AML M4 is crucial for accurate diagnosis and treatment decisions in hematological malignancies.

3. A laboratory quality assurance program typically includes what component?

- A. Regularly rotating laboratory staff**
- B. Proficiency testing**
- C. Client satisfaction surveys**
- D. Annual cost audits**

A laboratory quality assurance program is designed to ensure that the laboratory consistently produces accurate and reliable results. One critical component of such a program is proficiency testing. This involves evaluating the performance of the laboratory by comparing its results against established benchmarks or the results from other laboratories. Proficiency testing helps identify areas of improvement in testing methods, identifies potential issues with personnel or equipment, and ensures compliance with regulatory standards. Participating in proficiency testing allows laboratories to maintain high-quality standards and encourages continuous improvement in practices. It serves as an objective measure of the laboratory's reliability and competence, which is essential for gaining trust from clinicians and patients alike.

4. What is the most important pretreatment for age slides in FISH analysis?

- A. 2x SSC at 37 degrees for 30 minutes**
- B. Heat fixation at 75 degrees for 15 minutes**
- C. Alcohol fixation for 10 minutes**
- D. 0.1M PBS at room temperature for 20 minutes**

The most important pretreatment for age slides in FISH (Fluorescence In Situ Hybridization) analysis involves the use of 2x SSC (standard sodium citrate) at 37 degrees Celsius for 30 minutes. This step is crucial as it accounts for the proper hydration and denaturation of the chromosomal DNA located on the slides. When preparing slides for FISH analysis, it's essential to ensure the DNA is in a suitable condition to allow the hybridization probes to bind effectively to their target sequences. Treating the slides with 2x SSC at a specific temperature and duration promotes optimal conditions for the probes to anneal to the denatured regions of DNA, ensuring the fidelity and specificity of the FISH technique. In contrast, the other options serve different functions or do not provide the optimal environment necessary for FISH. Heat fixation, while beneficial for adhering the cells to the slides and preserving cellular structure, does not specifically prepare the DNA for hybridization in the same way that the 2x SSC does. Alcohol fixation is primarily aimed at preserving morphology, whereas using PBS works to preserve cell integrity but also lacks the specific qualities needed to prepare the DNA adequately for FISH analysis. Therefore, using 2x SSC is essential.

5. What region of the chromosome is specifically stained by quinacrine and acridine orange dyes?

- A. GC rich DNA
- B. AT rich DNA**
- C. Telomeric DNA
- D. Centromeric DNA

Quinacrine and acridine orange dyes are known for their ability to preferentially stain regions of DNA based on their base composition. These dyes specifically target AT rich regions of the DNA, as they bind more effectively to adenine-thymine pairs than to guanine-cytosine pairs. This selective staining is utilized in various cytogenetic techniques to visualize different chromosomal features. In particular, the binding mechanism of these dyes is rooted in their ability to intercalate with DNA, which is more pronounced in regions rich in AT content. This characteristic allows for enhanced contrast when visualizing chromosomes under a fluorescence microscope, aiding in the identification of specific chromosomal structures and anomalies. While GC rich DNA, telomeric DNA, and centromeric DNA have their own unique characteristics and may be highlighted using different stains or techniques, the question specifically addresses the staining properties of quinacrine and acridine orange, which predominantly target AT rich regions.

6. What should a tech consider when interpreting FISH analysis results?

- A. The appearance of stable cells
- B. Interpretation of the number of signals**
- C. Observing the morphology of nuclei
- D. Evaluating staining patterns

When interpreting FISH (Fluorescence In Situ Hybridization) analysis results, the number of signals is a critical aspect to consider because it directly relates to the presence or absence of specific genetic materials or abnormalities. FISH is utilized to detect and localize the presence or absence of specific DNA sequences on chromosomes. The results are determined by counting the fluorescent signals that correspond to the hybridized probes. For example, in normal diploid cells, one would expect to see two signals per target gene. If there are additional signals, this might indicate gene amplification, while fewer signals could suggest a deletion. Therefore, accurately interpreting the number of signals provides vital information about genetic alterations that may be relevant for diagnosis or therapeutic decisions. While the other options might provide additional context or information, they do not directly impact the interpretation of the FISH signals in the same fundamental way as counting the number of signals does. Observing the morphology of nuclei and evaluating staining patterns can be useful but are secondary to the direct analysis of signals from the probes, which is the primary function of FISH in cytogenetics.

7. Which chromosome is most different between C-banding and G-banding techniques?

- A. Chromosome 16
- B. Chromosome 9**
- C. Chromosome 18
- D. Chromosome 1

C-banding and G-banding are techniques used in cytogenetics to visualize chromosomes and identify structural features. G-banding involves staining chromosomes with a dye that preferentially binds to regions of DNA, producing a characteristic banding pattern based on the composition and organization of the chromatin. In contrast, C-banding specifically identifies heterochromatin, particularly in the centromeric regions, providing a different perspective on chromosomal structure. Chromosome 9 is known to exhibit significant differences in banding patterns between C-banding and G-banding techniques. Specifically, the centromeric heterochromatin region of chromosome 9 is prominent in C-banding and may not display the same characteristics in G-banding, where the focus is on the overall banding patterns derived from the chromosome's DNA composition. Thus, chromosome 9 serves as an ideal example of how C-banding can reveal distinct features that G-banding may not fully capture, making it the most different between the two techniques. Other chromosomes, while they have their unique banding patterns, do not show the same level of difference between C-banding and G-banding as chromosome 9 does. Hence, the emphasis on chromosome 9 is crucial in the study

8. What do the dark bands produced by routine GTG banding represent?

- A. Gene-rich regions of the chromosome
- B. Euchromatin regions
- C. AT-rich regions of the chromosome**
- D. Gene-poor regions of the chromosome

The dark bands produced by routine GTG (Giemsa-Trypsin-Giemsa) banding represent regions that are rich in adenine-thymine (AT) base pairs, which often correlate with gene-poor areas of the chromosome. During the banding process, chromosomes are treated with trypsin and then stained with Giemsa dye; the AT-rich regions absorb the dye more strongly, leading to the formation of these dark bands. These bands are important for the identification and classification of chromosomes during cytogenetic analysis, as they provide a framework for recognizing specific chromosomal abnormalities. The presence of dark bands typically indicates less transcriptionally active regions, which contributes to the assessment of gene density and overall genomic structure. In contrast, the other choices relate to regions that are not characterized by the dark bands produced by GTG banding. Gene-rich regions and euchromatin regions are usually lighter in appearance due to their composition (higher GC content or being more transcriptionally active), whereas gene-poor regions, while they may seem similar to dark bands, specifically refer to the lower density of genes rather than the AT richness that characterizes the dark bands.

9. For successful harvest, each new batch of hypotonic solution should be evaluated by?

- A. Conducting a pH test**
- B. Comparing to a lot already in use**
- C. Checking for color change**
- D. Assessing viscosity**

In the context of cytogenetic harvest procedures, the evaluation of a new batch of hypotonic solution is essential to ensure optimal conditions for cell swelling and chromosome visualization. Comparing the new batch to a lot already in use is crucial because it helps confirm that the new solution has similar characteristics to the previously validated batch. This step ensures consistency in performance and effectiveness, as variations in formulation could affect the results of chromosome analysis. The other options, while potentially relevant in different contexts, do not specifically address the primary concern of maintaining consistent and effective experimental conditions. For instance, a pH test is important for many laboratory reagents, but hypotonic solutions are generally formulated to be isotonic with specific parameters, making direct comparison a more reliable method. Checking for color change may help identify contamination, but it does not ensure the solution's functional efficacy. Lastly, assessing viscosity does not directly contribute to the assessment of the hypotonic solution's suitability for cytogenetic work, as the main focus remains on the osmotic properties rather than its physical viscosity. Thus, comparing the new hypotonic solution to a validated lot provides the best assurance of consistency and reliability in cytogenetic procedures.

10. Which of the following disorders is NOT associated with a microdeletion?

- A. Prader-Willi**
- B. DiGeorge**
- C. Rubinstein-Taybi**
- D. Langer-Giedion**

Rubinstein-Taybi syndrome is primarily caused by mutations in the CREBBP or EP300 genes rather than a microdeletion. This disorder is characterized by distinct physical features, broad thumbs and toes, and various developmental issues. In contrast, the other disorders listed are known to be associated with specific microdeletions. Prader-Willi syndrome is linked to a deletion of paternal genes on chromosome 15. DiGeorge syndrome, also connected to chromosome 22, is due to a deletion that affects the development of several body systems. Similarly, Langer-Giedion syndrome is associated with deletions in chromosome 8. Therefore, Rubinstein-Taybi stands apart because its etiology is based on point mutations rather than a microdeletion, reflecting a different genetic mechanism. This distinction clarifies why it is the correct answer in the context of disorders associated with microdeletions.

Next Steps

Congratulations on reaching the final section of this guide. You've taken a meaningful step toward passing your certification exam and advancing your career.

As you continue preparing, remember that consistent practice, review, and self-reflection are key to success. Make time to revisit difficult topics, simulate exam conditions, and track your progress along the way.

If you need help, have suggestions, or want to share feedback, we'd love to hear from you. Reach out to our team at hello@examzify.com.

Or visit your dedicated course page for more study tools and resources:

<https://internationaltechnologistcytogenicsascp.examzify.com>

We wish you the very best on your exam journey. You've got this!