# Albinism: Sequencing Panel

**Test Code:** MM135  
**Turnaround time:** 6 weeks  
**CPT Codes:** 81404 x1, 81479 x1

## Condition Description

Albinism is a general term used to describe an absence of pigment in the eyes, skin, or hair. Individuals with any of the forms of albinism may have mild to severe oculo-visual clinical manifestations. Ocular hallmarks of all types of albinism include nystagmus, iris translucency, foveal hypoplasia, reduction in visual acuity, and misrouting of the optic nerve fibers at the chiasm (detected by altered visually evoked potentials).

Pathogenic variants in the \( \text{TYR} \) gene are known to cause autosomal recessive oculocutaneous albinism type 1 (OCA1) which is characterized by the ocular changes found in all types of albinism (see introduction above) along with hypopigmentation of the skin and hair. It is divided into two general subgroups: OCA1A (loss of protein function) and OCA1B (partially active/hypomorphic protein function). Throughout life, individuals with OCA1A have white hair, white skin, blue translucent irides, retinal pigment epithelium cells without melanin, and poor vision. In comparison to OCA1A, individuals with OCA1B can have a milder phenotype with hair and iris color that may darken over time.

Pathogenic variants in the \( \text{OCA2} \) gene (previously known as the \( P \) gene) are known to cause autosomal recessive oculocutaneous albinism type 2 (OCA2) which is characterized by the ocular changes found in all types of albinism (see introduction above) along with skin and hair pigmentation that ranges from very light to almost normal for a given ethnic background. Vision is stable, usually better than found in OCA1 and may improve in adolescence.

Pathogenic variants in the \( \text{TYRP1} \) gene are known to cause autosomal recessive oculocutaneous albinism type 3 (OCA3) which is characterized by the ocular changes found in all types of albinism (see introduction above) along with an accumulation of reddish pigment in the skin and hair.

Pathogenic variants in the \( \text{SLC45A2} \) gene (previously called \( \text{MATP} \) and \( \text{AIM1} \)) are known to cause autosomal recessive oculocutaneous albinism type 4 (OCA4) which is characterized by the ocular changes found in all types of albinism (see introduction above) along with hypopigmentation of the skin and hair. The clinical presentation of OCA4 and OCA2 are very similar; however, OCA4 has a higher prevalence in the Japanese population.

Pathogenic variants in the \( \text{GPR143} \) gene are known to cause X-linked ocular albinism type 1 (OCA1, also known as Nettleship-Falls ocular albinism or XLOA) which, in males, is characterized by the ocular changes found in all types of albinism (see introduction above) along with non-progressive vision loss, strabismus, and generally minor skin findings. Carrier females may show a characteristic mosaic pigmentation pattern of the retinal pigment epithelium.

## References

- OMIM
- GeneReviews
- Emory and Rimoin's Principles and Practice of Medical Genetics, 5th Edition

## Genes

\( \text{GPR143, LRMDA, OCA2, SLC24A5, SLC45A2, TYR, TYRP1} \)

## Indications

This test is indicated for:

- Confirmation of a clinical diagnosis of albinism.
- Carrier testing in adults with a family history albinism.

## Methodology

**Next Generation Sequencing:** In-solution hybridization of all coding exons is performed on the patient's genomic DNA. Although some deep intronic regions may also be analyzed, this assay is not meant to interrogate most promoter regions, deep intronic regions, or other regulatory elements, and does not detect single or multi-exon deletions or duplications. Direct sequencing of the captured regions is performed using next generation sequencing. The patient's gene sequences are then compared to a standard reference sequence. Potentially causative variants and areas of low coverage are Sanger-sequenced. Sequence variations are classified as pathogenic, likely pathogenic, benign, likely benign, or variants of unknown significance. Variants of unknown significance may require further studies of the patient and/or family members.

## Detection

**Clinical Sensitivity:** Unknown. Pathogenic variants in the promoter region, some pathogenic variants in the introns and other regulatory element pathogenic variants cannot be detected by this analysis. Large deletions will not be detected by this analysis. Results of molecular analysis should be interpreted in the context of the patient's clinical and/or biochemical phenotype.

**Analytical Sensitivity:** ~99%.

## Specimen Requirements

Submit only 1 of the following specimen types
Type: Whole Blood

Specimen Requirements:

In EDTA (purple top) tube:
Infants (2 years): 3-5 ml
Older Children & Adults: 5-10 ml

Specimen Collection and Shipping: Ship sample at room temperature with overnight delivery.

Type: Isolated DNA

Specimen Requirements:

In microtainer: 60 ug

Isolation using the Qiagen™ Puregene kit for DNA extraction is recommended.

Specimen Collection and Shipping: Refrigerate until time of shipment in 100 ng/ul of TE buffer. Ship sample at room temperature with overnight delivery.

Special Instructions

Please include fundus photographs, electroretinogram (ERG) findings, visual field findings, and visual acuity, if available, for expert review and clinical correlation with test results.

Related Tests

- Eye Disorders: Comprehensive Sequencing and Deletion/Duplication Panels.
- Albinism: Deletion/Duplication Panel.