Bloom Syndrome: \textit{BLM} Gene Sequencing

\textbf{Test Code: SBLM1}
\textbf{Turnaround time: 4 weeks}
\textbf{CPT Codes: 81209 x1}

\textbf{Condition Description}

Bloom syndrome should be considered in the following individuals:

- An individual with unexplained, severe intrauterine growth retardation that persists into infancy and childhood
- An unusually small, well-proportioned individual with a sun-sensitive erythematous skin lesion in a "butterfly distribution" on the face
- An unusually small individual who develops cancer

Bloom syndrome is an autosomal recessive disorder characterized by severe prenatual and postnatal growth retardation and a sun-sensitive erythematous skin lesion that occurs most commonly on the face. Recurrent infections (otitis media and pneumonia), chronic pulmonary disease, and diabetes mellitus are common. Many affected individuals have learning disabilities. Males are infertile; females enter menopause prematurely. The most common cause of death is cancer (epithelial, hematopoietic, lymphoid, connective tissue, germ cell, nervous system, and kidney), which occurs at younger-than-average ages.

The diagnosis of Bloom syndrome can be confirmed or ruled out by chromosome analysis of any cell type that can be cultured. The most commonly used cells are blood lymphocytes, but cultures of skin fibroblasts and amniocytes also can be studied. The cytogenetic features of Bloom syndrome cells in mitosis are increased numbers of chromatid gaps, breaks, and rearrangements and increased numbers of quadriradial configurations. A greatly increased frequency (e.g., greater than 50 per metaphase) of sister chromatid exchanges is demonstrable in Bloom syndrome cells exposed to bromodeoxyuridine (BrdU). \textit{BLM} (15q26.1) is the only gene known to be mutated in Bloom syndrome.

Fewer than 300 cases of Bloom syndrome have been reported. Although very rare in all populations, Bloom syndrome is less rare in Ashkenazi Jews. Approximately 25\% of persons in the Bloom Syndrome Registry have Ashkenazi Jewish ancestry. The carrier frequency in the Ashkenazi Jewish population is estimated to be approximately 1\%.

For patients with suspected Bloom syndrome, sequence analysis is recommended as the first step in mutation identification. For patients in whom mutations are not identified by full gene sequencing, deletion/duplication analysis is appropriate.

\textbf{References:}


\textbf{Genes}

\textbf{BLM}

\textbf{Indications}

This test is indicated for:

- Confirmation of a clinical diagnosis of Bloom syndrome

\textbf{Methodology}

\textbf{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.

\textbf{Detection}

Clinical Sensitivity: Unknown. Mutations in the promoter region, some mutations in the introns and other regulatory element mutations 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 biochemical phenotype.

Analytical Sensitivity: \(\sim 99\%\)

\textbf{Specimen Requirements}

Submit only 1 of the following specimen types

* Preferred specimen type: Whole Blood

\textbf{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: Refrigerate until time of shipment. Ship sample within 5 days of collection at room temperature with overnight delivery.

**Type: Saliva**

Specimen Requirements:

Oragene™ Saliva Collection kit (available through EGL) used according to manufacturer instructions.

Specimen Collection and Shipping: Store sample at room temperature. Ship sample within 5 days of collection at room temperature with overnight delivery.

**Special Instructions**

Submit copies of diagnostic biochemical test results with the sample, if appropriate. Contact the laboratory if further information is needed.

Sequence analysis is required before deletion/duplication analysis by targeted CGH array. If sequencing is performed outside of EGL Genetics, please submit a copy of the sequencing report with the test requisition.

**Related Tests**

- Deletion/duplication analysis of the *BLM* gene by CGH array is available for those individuals in whom sequence analysis is negative.
- Custom diagnostic mutation analysis (KM) is available to family members if mutations are identified by targeted mutation testing or sequencing analysis.
- Prenatal testing is available to adults who are confirmed carriers of mutations. Please contact the laboratory genetic counselor to discuss appropriate testing prior to collecting a prenatal specimen.