# **Bloom Syndrome**

Maeve Flanagan, BA and Christopher M Cunniff, MD, FACMG.

## Author Information

Initial Posting: March 22, 2006; Last Update: February 14, 2019.

Estimated reading time: 24 minutes

## <u>Go to:</u>

## Summary

### Clinical characteristics.

Bloom syndrome (BSyn) is characterized by severe pre- and postnatal growth deficiency, immune abnormalities, sensitivity to sunlight, insulin resistance, and a high risk for many cancers that occur at an early age. Despite their very small head circumference, most <u>affected</u> individuals have normal intellectual ability. Women may be fertile but often have early menopause, and men tend to be infertile, with only one confirmed case of paternity. Serious medical complications that are more common than in the general population and that also appear at unusually early ages include chronic obstructive pulmonary disease, diabetes mellitus as a result of insulin resistance, and cancer of a wide variety of types and anatomic sites.

#### Diagnosis/testing.

The diagnosis of BSyn is established in a <u>proband</u> with characteristic clinical features and/or <u>biallelic</u> pathogenic variants in *BLM* identified on <u>molecular genetic testing</u>. Identification of increased frequency of sister-chromatid exchanges on specialized <u>cytogenetic</u> studies and exclusion of *RMI1*, *RMI2*, and *TOP3A*-related disorders may be helpful in establishing the diagnosis in those with characteristic clinical features who do not have biallelic pathogenic variants in *BLM*.

## Management.

*Treatment of manifestations:* Skin protection, including coverage of exposed skin and use of broad-spectrum sunscreen with SPF of at least 30 to reduce the sun-sensitive rash. Increased-calorie-density formulas and foods may promote weight gain. Although growth hormone treatment may improve linear growth, many clinicians caution against its use because of reports of early onset of cancer in some treated children. Developmental services and therapies as needed. Hyperglycemia from insulin resistance is treated as in type 2 diabetes. In persons with BSyn who have cancer, reduced chemotherapy dosage and duration to reduce risks of severe complications; caution should be exercised with use of ionizing radiation or alkylating agents, particularly busulfan, cyclophosphamide, or melphalan. Individuals with recurrent infections and defects in humoral immunity may be treated with gamma globulin infusions to decrease frequency and severity of infections.

*Surveillance*: Abdominal ultrasound examination every three months until age eight years for Wilms tumor. Screening and family education regarding signs/symptoms of leukemia and lymphoma at every health visit. Whole-body MRI every one to two years beginning at age 12-13 years for risk of lymphoma. Annual colonoscopy beginning at age 10-12 years. Fecal immunochemical testing every six months beginning at age 10-12 years. Annual breast MRI in women beginning at age 18 years. Annual fasting blood glucose and hemoglobin A1C beginning at age ten years. Annual serum TSH with reflex to T4 beginning at age ten years. Annual lipid profile beginning at age ten years.

*Agents/circumstances to avoid:* Sun exposure may provoke an erythematous rash, especially on the face. Exposure to ionizing radiation should be minimized.

#### Genetic counseling.

BSyn is inherited in an <u>autosomal recessive</u> manner. Identification of both pathogenic *BLM* variants in the <u>proband</u> is required for <u>carrier (heterozygote)</u> testing in at-risk families. *BLM* is included in expanded carrier screening panels, and most pathogenic variants can be identified through sequencing. Preimplantation and <u>prenatal diagnosis</u> are possible if the *BLM* pathogenic variants have been identified in the at-risk couple.

### Go to:

## Diagnosis

### **Suggestive Findings**

Bloom syndrome (BSyn) **should be suspected** in an individual with any of the following clinical or <u>cytogenetic</u> findings.

#### **Clinical findings**

- Prenatal-onset growth deficiency that usually includes linear growth, weight gain, and head circumference and that persists into infancy, childhood, and adulthood
- Moderate-to-severe growth deficiency and a sun-sensitive, erythematous rash that commonly involves the face and appears in a butterfly distribution
- Moderate-to-severe growth deficiency and a diagnosis of cancer, usually occurring at an earlier age than in the general population

#### **Cytogenetic findings**

- Increased numbers of sister-chromatid exchanges
- Increased quadriradial configurations (Qrs) in cultured blood lymphocytes (a mean of 1%-2% Qrs are observed in cultured blood lymphocytes from a person with BSyn vs none in controls)
- Chromatid gaps, breaks, and rearrangements

## **Establishing the Diagnosis**

The diagnosis of BSyn **is established** in a <u>proband</u> by identification of <u>biallelic</u> pathogenic variants in *BLM* on <u>molecular genetic testing</u> (see <u>Table 1</u>).

Note: An increased frequency of sister-chromatid exchanges (SCEs) on specialized <u>cytogenetic</u> studies may be helpful in circumstances where *BLM* variant analysis is inconclusive. SCE analysis alone is not sufficient to confirm a diagnosis of BSyn because increased SCEs are also observed in persons with <u>biallelic</u> pathogenic variants in *RMI1*, *RMI2*, and *TOP3A* [Hudson et al 2016, Martin et al 2018].

Molecular genetic testing approaches can include a combination of <u>gene-targeted testing</u> (single-gene testing, <u>multigene panel</u>) and **comprehensive <u>genomic</u> testing** (<u>exome</u> <u>sequencing</u>, <u>genome sequencing</u>) depending on the <u>phenotype</u>.

Gene-targeted testing requires that the clinician determine which <u>gene(s)</u> are likely involved, whereas <u>genomic</u> testing does not. Because the <u>phenotype</u> of BSyn is broad, individuals with the distinctive findings described in <u>Suggestive Findings</u> are likely to be diagnosed using gene-targeted testing (see <u>Option 1</u>), whereas those with a phenotype indistinguishable from many other inherited disorders with growth deficiency are more likely to be diagnosed using genomic testing (see <u>Option 2</u>).

#### **Option 1**

When the phenotypic and laboratory findings suggest the diagnosis of Bloom syndrome <u>molecular genetic testing</u> approaches can include **single-<u>gene</u> testing** or use of a <u>multigene</u> <u>panel</u>:

- Single-<u>gene</u> testing. Sequence analysis of *BLM* detects small intragenic deletions/insertions and <u>missense</u>, <u>nonsense</u>, and <u>splice site</u> variants; typically, <u>exon</u> or whole-gene deletions/duplications are not detected. Perform <u>sequence analysis</u> first. If only one or no <u>pathogenic variant</u> is found, perform gene-targeted <u>deletion/duplication</u> <u>analysis</u> to detect intragenic deletions or duplications.
- A <u>multigene panel</u> that includes *BLM* and other genes of interest (see <u>Differential</u> <u>Diagnosis</u>) is most likely to identify the genetic cause of the condition at the most reasonable cost while limiting identification of variants of <u>uncertain significance</u> and pathogenic variants in genes that do not explain the underlying <u>phenotype</u>. Note: (1) The genes included in the panel and the diagnostic <u>sensitivity</u> of the testing used for each <u>gene</u> vary by laboratory and are likely to change over time. (2) Some multigene panels may include genes not associated with the condition discussed in this *GeneReview*. (3) In some laboratories, panel options may include a custom laboratorydesigned panel and/or custom phenotype-focused <u>exome</u> analysis that includes genes specified by the clinician. (4) Methods used in a panel may include <u>sequence analysis</u>, <u>deletion/duplication analysis</u>, and/or other non-sequencing-based tests.

For an introduction to multigene panels click <u>here</u>. More detailed information for clinicians ordering genetic tests can be found <u>here</u>.

#### **Option 2**

When the <u>phenotype</u> is indistinguishable from many other inherited disorders characterized by growth deficiency, **comprehensive** <u>genomic</u> testing (which does not require the clinician to

determine which <u>gene[s]</u> are likely involved) is the best option. **Exome sequencing** is most commonly used; <u>genome sequencing</u> is also possible.

For an introduction to comprehensive <u>genomic</u> testing click <u>here</u>. More detailed information for clinicians ordering genomic testing can be found <u>here</u>.

.

### Table 1.

Molecular Genetic Testing Used in Bloom Syndrome

Gene <sup>1</sup>	Took Mathad	% of Pathogenic Variants <sup>2</sup> Detectable by This Method		
	Test Method	<u>Ashkenazi Jewish</u> Ancestry	Non-Jewish Ancestry	
	Targeted analysis for c.2207_2212delinsTAGTTC	93% <sup>3</sup>	6% <sup>4</sup>	
BLM	Sequence analysis <sup>5</sup>	~99% <sup>3</sup>	87% <sup>4</sup>	
	Gene-targeted <u>deletion/duplication</u> analysis <sup>6</sup>	1% <sup>4</sup>	4% <sup>4</sup>	
<b>TT 1</b>	7			

Unknown <sup>7</sup> NA

### 1.

See <u>Table A. Genes and Databases</u> for <u>chromosome locus</u> and protein.

#### 2.

See Molecular Genetics for information on allelic variants detected in this gene.

#### 3.

German et al [2007]

#### 4.

Bloom Syndrome Registry

#### 5.

Sequence analysis detects variants that are benign, likely benign, of <u>uncertain</u> <u>significance</u>, likely pathogenic, or pathogenic. Pathogenic variants may include small intragenic deletions/insertions and <u>missense</u>, <u>nonsense</u>, and <u>splice site</u> variants; typically, <u>exon</u> or whole-<u>gene</u> deletions/duplications are not detected. For issues to consider in interpretation of <u>sequence analysis</u> results, click <u>here</u>.

#### 6.

Gene-targeted <u>deletion/duplication analysis</u> detects intragenic deletions or duplications. Methods used may include: <u>quantitative PCR</u>, long-range PCR,

multiplex ligation-dependent probe amplification (MLPA), and a <u>gene</u>-targeted microarray designed to detect single-<u>exon</u> deletions or duplications.

7.

In nine individuals with BSyn, pathogenic variants in *BLM* were not detected, suggesting the possibility of <u>locus</u> heterogeneity [<u>German et al 2007</u>].

**Sister-chromatid exchanges (SCEs).** Individuals with BSyn have a mean of 40-100 SCEs per metaphase (normal SCEs: <10 per metaphase). Increased frequency of SCEs is demonstrable in BSyn cultured cells (including lymphocytes, fibroblasts, and amniocytes) allowed to proliferate in a medium containing 5'bromo-2'-deoxyuridine (BrdU). Increased SCEs are not unique to BSyn. Three additional <u>autosomal recessive</u> disorders (*RMI1-, RMI2-,* and *TOP3A*-related disorders) are associated with increased SCEs and similar clinical findings to individuals with BSyn. SCE analysis may be a useful adjunct for diagnosis of BSyn, in the circumstance where only one *BLM* pathogenic variant is identified, and <u>molecular genetic testing</u> finds no pathogenic variants in *RMI1, RMI2,* or *TOP3A*. The presence of increased SCEs alone, however, is not sufficient to confirm the diagnosis of BSyn.

Go to:

## **Clinical Characteristics**

## **Clinical Description**

The range of clinical features in persons with Bloom syndrome (BSyn) has been tracked through the <u>Bloom Syndrome Registry</u>. The clinical and genetic histories have been obtained from registered persons diagnosed between 1954 and 2018 and their clinical courses have been followed [German & Passarge 1989, German 1993, German & Ellis 2002].

The main clinical features of BSyn are the following:

• Size and appearance. The most consistent clinical feature of BSyn seen throughout all stages of life is growth deficiency affecting height, weight, and head circumference. Body proportions are normal. Subcutaneous adipose tissue is sparse throughout childhood and adolescence, but adults may develop central obesity. Providing increased calories in childhood and adolescence does not usually result in substantial changes in growth parameters, particularly linear growth. Plasma growth hormone concentration is normal.

The <u>affected</u> fetus is smaller than normal for gestational age. The mean birth weight of affected males is 1,760 g (range 900-3,189 g) and of affected females, 1,754 g (range 700-2,892 g). The average adult height of men is 149 cm (range 128-164 cm) and of women, 138 cm (range 115-160 cm).

The facial appearance of people with BSyn is variable and may be indistinguishable from unaffected persons of similar age and size. More commonly, the face appears narrow, with underdeveloped malar and mandibular prominences and retrognathia or

micrognathia. A paucity of subcutaneous fat may cause the nose and/or ears to appear prominent.

- Feeding problems. Most parents report that feeding is an issue for their newborns, infants, and young children. The child with BSyn characteristically feeds slowly, has a decreased appetite, and eats a limited variety of foods. In a minority of infants with BSyn, nursing and eating are normal. Because of their slow growth and weight gain, many children are prescribed formula with increased caloric density and later are prescribed nutritional supplements that provide extra calories. Many infants have had gastrostomy tubes placed. Despite these maneuvers, weight gain continues to be modest, and children are rarely in the normal range for growth. Gastroesophageal reflux is common and may contribute to the feeding issues.
- Skin lesions. The skin at birth and during early infancy appears normal; however, typically following sun exposure during the first or second year of life, a red, sunsensitive rash appears on the nose and cheeks and sometimes also on the dorsa of the hands and forearms. This rash varies in severity and extent among <u>affected</u> individuals; in some, it is minimal. It is usually characterized by telangiectasia but in others is described as poikiloderma. In severely affected individuals, the lesion can be bright red and can extend onto adjacent areas. Additional dermatologic manifestations include cheilitis, blistering and fissuring of the lips, eyebrow and eyelash hair loss, alopecia areata, and vesicular and bullous lesions with excessive or intense sun exposure. Café au lait macules and areas of hypopigmented skin are more numerous and larger than in those without BSyn.
- **Immunodeficiency.** In children and adults who have had laboratory evaluation of their immune system, the concentration of one or more of the plasma immunoglobulins is usually abnormally low. IgM and IgA levels are most commonly affected. Although the numbers of T and B cells are usually normal, variable abnormalities of the adaptive immune system suggest a possible role in the frequent infections reported in <u>affected</u> individuals.
- **Infections.** Parents of children with BSyn report that their <u>affected</u> children have more childhood infections than their sibs and peers; none, however, has had an opportunistic infection, and few persons with BSyn have had bacterial sepsis, meningitis, or pneumonia.
- Fertility. Most men with BSyn appropriately examined have had azoospermia or severe oligospermia. There is, however, one confirmed case of paternity [Ben Salah et al 2014]. Women with BSyn, although often fertile, may enter menopause prematurely. Eleven women with BSyn followed in the Registry have become pregnant at least once; seven of them have delivered a total of 11 healthy babies of normal size.
- **Intelligence.** There are no systematic studies of academic achievement or cognitive performance in persons with BSyn. The great majority appear to perform within the normal range of intellectual development. Some have required academic support for attention-related issues and task orientation, but it is not clear that the prevalence of these problems is different from that seen in the general population. Many others have excelled in school, with some earning graduate degrees.
- Other clinical features. Major anatomic defects are not increased in frequency. In the 281 persons in the Registry as of 2018, only single examples of the following have occurred: tracheoesophageal fistula, cardiac malformation, absent thumbs, and absence of a toe and malformation of a thumb.

**Medical complications** of BSyn, all serious, in order of increasing frequency are the following:

- Chronic obstructive pulmonary disease. Chronic bronchitis and bronchiectasis are common, and pulmonary failure has been the cause of death in six persons.
- **Myelodysplasia** has been diagnosed in 23 persons in the Registry at a median age of 22.1 years (range 3-47), and it has progressed to acute myelogenous leukemia in at least seven. In all but three, the myelodysplasia was preceded by some form of cancer for which chemotherapy and/or radiotherapy had been administered.
- Diabetes mellitus. Abnormalities in insulin release and glucose tolerance have been detected in the eight healthy children (ages 9 months to 13 years) and the three healthy young adults with BSyn (ages 22, 28, and 28 years) appropriately studied [Diaz et al 2006]. Because of insulin resistance, the diabetes mellitus of BSyn resembles type 2 diabetes but has a much earlier age of onset than in the general population. Paradoxically, diabetes in persons with BSyn commonly occurs in the setting of low body mass index (BMI), rather than high BMI. Diabetes has been diagnosed in 47 of 281 persons in the Registry (16.7%) at a mean age of 26.6 years (range 4-45 years). Although most individuals do not have severe complications, 16 have required insulin, and retinopathy has developed in two. Lipid profile abnormalities were also identified by Diaz et al [2006] in five of the ten subjects tested.
- **Cancer** is the most frequent medical complication in BSyn and the most common cause of death. Although the wide distribution of cell types and anatomic sites of cancer resemble that in the general population, it occurs more frequently and at much earlier ages in BSyn. Development of multiple cancers in a single individual is also much more common. <u>Table 2</u> summarizes the cancers diagnosed in individuals followed in the Registry.

## Table 2.

The 226 Malignant Neoplasms Diagnosed in 145 Persons in the Bloom Syndrome Registry (1954-2018)

Malignancy Type / Tissue	Subtype	Frequency	Age at Diagnosis (years)		
1 15800			Median	Mean	Range
	Acute myeloid	17	21	19	6-32
Leukemia	Acute lymphoblastic	11	14	17	4-40
	Other/biphenotypic/undefined	12	18	19	2-40
Lymphoma		37	20	21	4-49
	Tongue	9	37	37	30-48
Quanhawingaal	Pharynx	6	32	34.8	31-45
Oropharyngeal	Tonsil	4	40	38	25-46
	Other	5	NA	NA	NA
	Esophageal	5	39	37	25-48
Upper GI	Gastric	5	31	29	24-33
	Other	4	NA	NA	NA
Colorectal		28	37	35	16-49

Malignancy Type / Tissue	Subtype	Frequency	Age at D (years) Median	0	
<b>C : :</b>	Cervical	5	22	21	19-23
Genitourinary	Other	9	NA	NA	NA
Breast		24	33	33	21-52
	Basal cell	13	29	28	18-38
Skin	Squamous cell (uncategorized)	5	35	35	35-36
	Other/undefined	4	NA	NA	NA
Wilms tumor		8	3	3	1-8
Lung		4	37	36	32-40
All other		12	NA	NA	NA

GI = gastrointestinal

Adapted from Cunniff et al [2018]

### **Genotype-Phenotype Correlations**

**Homozygotes and compound heterozygotes.** A similar <u>phenotype</u> is produced by either homozygosity or compound heterozygosity for any of the more than 60 pathogenic variants in *BLM* identified to date.

## Prevalence

Few individuals with BSyn have been reported in the medical literature since its description half a century ago [Bloom 1954], and fewer than 300 are known to the Bloom Syndrome Registry.

Although rare in all populations, BSyn is relatively less rare among Ashkenazi Jews. Sixtyseven of the 281 persons in the Registry are of <u>Ashkenazi Jewish</u> ancestry. The predominant *BLM* pathogenic variant identified in Ashkenazi Jews is <u>c.2207\_2212delinsTAGATTC</u>, a 6bp <u>deletion</u>/7-bp <u>insertion</u> in <u>exon</u> 10 of *BLM*, often (for brevity) designated blm<sup>Ash</sup>; the second most common pathogenic variant is <u>c.2407dupT</u>.

The approximate <u>carrier</u> frequency of the blm<sup>Ash</sup> <u>allele</u>:

- One in 100 Ashkenazi Jews dwelling both in New York City [Li et al 1998] and in Israel [Peleg et al 2002]
- One in 37 Ashkenazi Jews dwelling in Israel, all four of whose grandparents were from Poland [Shahrabani-Gargir et al 1998]

#### Go to:

## **Genetically Related (Allelic) Disorders**

No phenotypes other than those discussed in this *GeneReview* are known to be associated with <u>germline</u> pathogenic variants in *BLM*.

Go to:

## **Differential Diagnosis**

## Table 3.

Other Genetic Etiologies of Interest in the Differential Diagnosis of Bloom Syndrome (BSyn)

Gene(s) /		MOI	Clinical Features of Differential Diagnosis Disorder		
Genetic Mechanism	Disorder		Overlapping w/BSyn	Distinguishing from BSyn	
RMI1 <sup>1</sup>	RECQ- mediated genome instability 1 (OMIM <u>610404</u> )	AR		• Cancer not observed, but reported persons are all relatively	
RMI2 <sup>1</sup>	RECQ- mediated genome instability 2 (OMIM <u>612426</u> )	AR	<ul> <li>↑ SCE</li> <li>Small size</li> <li>Multiple café au lait macules in persons w/TOP3A &amp; RMI2</li> </ul>	<ul> <li>young: cancer predisposition may be identified in future.</li> <li>No abnormal skin findings in persons w/<i>RMI1</i></li> </ul>	
TOP3A <sup>1</sup>	Microcephaly , growth restriction, & increased sister- chromatid exchange 2 (OMIM <u>618097</u> )	AR	pathogenic variants	<ul> <li>pathogenic variants</li> <li>No malar rash in persons w/TOP3A pathogenic variants</li> </ul>	
Chromosome 11p15 hypomethylatio n or matUPD7	<u>Russell-Silver</u> syndrome	See footnot e 2	Growth deficiency	<ul> <li>Not associated w/↑ SCE</li> <li>Ophthalmalogic abnormalities</li> </ul>	
ATM	<u>Ataxia-</u> telangiectasia	AR	<ul> <li>Small stature</li> <li>Evidence of excessive <u>genomic</u> instability</li> <li>Telangiectasis</li> </ul>	<ul> <li>Progressive cerebellar ataxia from early childhood</li> <li>↑ alpha- fetoprotein levels</li> </ul>	

Gene(s) /	Disorder	MOI	Clinical Features of Differential Diagnosis Disorder		
Genetic Mechanism			Overlapping w/BSyn	Distinguishing from BSyn	
BRCA2 BRIP1 FANCA FANCB FANCC FANCD2 FANCE FANCF FANCG FANCI <sup>3</sup>	<u>Fanconi</u> anemia	AR (AD XL)	<ul> <li>Sinopulmonary infection</li> <li>Immunodeficienc y</li> <li>Small stature</li> <li>Evidence of excessive <u>genomic</u> instability</li> <li>↑ cancer susceptibility</li> <li>Cutaneous abnormalities (café au lait macules, hyper- or hypopigmentation )</li> <li>↓ fertility</li> <li>Endocrinopothy</li> </ul>	<ul> <li>Skeletal malformations</li> <li>Bone marrow failure</li> </ul>	
MRE11	Ataxia- telangiectasia -like disorder (OMIM <u>604391</u> )		<ul> <li>Small stature</li> <li>Evidence of excessive genomic instability</li> </ul>	<ul> <li>Progressive cerebellar degeneration</li> <li>No telangiectasias or immunodeficienc y</li> </ul>	
NBN	<u>Nijmegen</u> <u>breakage</u> syndrome	AR	<ul> <li>Small stature</li> <li>Evidence of excessive genomic instability</li> <li>Immunodeficienc y</li> <li>Café au lait macules</li> <li>Predisposition to lymphoid malignancy</li> </ul>	<ul> <li>Decline in intellectual performance</li> <li>No telangiectasias</li> </ul>	
WRN	<u>Werner</u> syndrome	AR	• Small stature	• Premature artherosclerosis	

Gene(s) /	Disorder	MOI	Clinical Features of Differential Diagnosis Disorder			
Genetic Mechanism	Disorder	WIOI	Overlapping w/BSyn	Distinguishing from BSyn		
			<ul> <li>Evidence of excessive genomic instability</li> <li>↑ incidence of diabetes</li> </ul>	Prematurely aged     appearance		

AD = autosomal dominant; AR = autosomal recessive; matUPD7 = maternaluniparental disomy for chromosome 7; MOI = mode of inheritance; SCE = sisterchromatid exchange; <math>XL = X-linked

#### 1.

*RMI1*, *RMI2*, and *TOP3A* encode proteins that make up the BTRR complex. The **B**LM protein forms the BTRR complex with topoisomerase III alpha (TopIIIa) and RecQ-mediated genome instability proteins 1 and 2 (**R**MI1 and **R**MI2, respectively). Together, these proteins process double Holliday junctions that arise as a result of homologous-recombination-mediated repair of double-stranded DNA breaks during DNA synthesis.

#### 2.

Russell-Silver syndrome has multiple etiologies including: epigenetic changes that modify expression of genes in the <u>imprinted</u> region of <u>chromosome</u> 11p15.5, maternal UPD7, and (infrequently) <u>autosomal dominant</u> or <u>autosomal recessive</u> inheritance.

#### 3.

Listed genes represent the most common genetic causes of Fanconi anemia. For other genes associated with this <u>phenotype</u> (20 genes have been identified), see <u>Fanconi</u> anemia.

#### Go to:

## Management

#### **Evaluations Following Initial Diagnosis**

To establish the extent of disease and needs in an individual diagnosed with Bloom syndrome (BSyn), in addition to the routine medical history, family history, and physical examination, the evaluations summarized in <u>Table 4</u> (if not performed as part of the evaluation that led to the diagnosis) are recommended.

#### Table 4.

Recommended Evaluations Following Initial Diagnosis in Individuals with Bloom Syndrome (BSyn)

System/Concern	Evaluation	Comment
Gastrointestinal	Consultation w/gastroenterologist &/or feeding specialist	Evaluation for gastroesophageal reflux & problem feeding behaviors
	Colonoscopy & fecal immunochemical testing Careful history & skin examination for sun-	In probands age $\geq 10$ yrs
Dermatologic	sensitive skin rash & for moles or nevi suspicious for basal cell or squamous cell carcinoma	
Immune	<ul> <li>Immunodeficiency screening incl immunoglobulin level, antibody responses to vaccines, &amp; number of B &amp; T lymphocytes</li> <li>Referral to immunologist as needed</li> </ul>	If patient has experienced severe &/or recurrent infections
Endocrine	Fasting blood glucose & hemoglobin A1C concentration	In probands age $\geq 10$ yrs to evaluate for evidence of diabetes mellitus
	Thyroid function testing: TSH w/reflex to T4 Lipid profile	At any age Beginning at age 10 yrs
Renal	Abdominal ultrasound examination for Wilms tumor	In probands age $\leq 8$ yrs
Lymphoreticular Whole-body MRI scan for lymphoma		In probands age $\geq 12$ yrs
Breast	Breast MRI scan	In female probands age ≥18 yrs
Developmental	Developmental assessment	If indicated based on developmental history
Other	Consultation w/clinical geneticist &/or genetic counselor	

#### **Treatment of Manifestations**

Health supervision recommendations that address diagnosis, treatment, and surveillance for complications in persons with BSyn have been published [Cunniff et al 2018].

**Skin.** Reduce excessive exposure to sunlight by seeking shade, particularly between 10 am and 4 pm. Cover exposed skin with clothing, including a broad-brimmed hat and UV-blocking sunglasses. Apply a broad-spectrum sunscreen with SPF of 30 twice daily, or every two to three hours if outdoors.

**Psychosocial.** Family and teachers are encouraged to relate to persons with BSyn appropriately for their chronologic age rather than the younger age suggested by their unusually small size.

**Growth.** Growth hormone administration to children with BSyn has not consistently increased growth rate in most persons, but some have experienced improved linear growth. Use of growth hormone has been approached cautiously in this population because of concerns regarding an increased risk of developing tumors as a result of their treatment. If growth hormone is prescribed, the growth response and serum IGF-1 and IGFBP-3 levels should be closely monitored, and unless there is an increase in growth velocity while under treatment, it should be discontinued.

**Nutrition.** Until additional information is available regarding treatment of problematic feeding behaviors and gastrointestinal symptoms, standard treatment for these concerns is recommended. This may include consultation with a gastroenterologist or feeding specialist, use of high-calorie diets, institution of reflux precautions, and use of anti-reflux medications. Studies of small cohorts of individuals with BSyn have shown that supplemental feeding may result in increased fat deposition but not in improved linear growth. Because abnormalities have been identified in the lipid profile of persons with BSyn, caution should be exercised in the use of high-fat and/or high-cholesterol diets.

**Cognitive.** Infants, toddlers, and preschool-age children with BSyn should have close developmental monitoring and referral for early intervention services. If developmental delays are present, physical, occupational, and speech therapy can help. School performance should be assessed regularly and parents made aware of available educational support.

Diabetes mellitus. Treatment of diabetes mellitus in BSyn is the same as in other persons.

**Hypothyroidism.** Thyroid hormone replacement therapy is recommended according to standard protocols.

Dyslipidemia. Dietary treatment according to standard protocols is recommended.

**Cancer.** The hypersensitivity of persons with BSyn to both DNA-damaging chemicals and ionizing radiation ordinarily necessitates modification of standard cancer treatment regimens, which usually includes a reduction of both dosage and duration. Individuals with BSyn have usually tolerated doses at or below 50% of the standard chemotherapy dosage, with no clear evidence that this has resulted in poorer outcomes. However, full weight-based dosing may be appropriate for some chemotherapeutic drugs such as steroids and tyrosine kinase inhibitors. Absence of information as to the ideal dosages makes such treatment particularly challenging to the physician; nevertheless, the fact that the cancers themselves often appear unusually responsive to the treatment justifies the special effort.

**Bone marrow transplantation (BMT).** Hematopoietic stem cell transplantation (HSCT) has been performed in three persons in the Bloom Syndrome Registry. One person had more than five years of disease-free survival before succumbing to another cancer, and the other two persons died in the immediate post-transplant period. If HSCT is being contemplated, nonmyeloablative transplantation is likely to be tolerated more readily than other regimens. Additionally, the required ablative therapy prior to BMT often may require modification of standard protocols because of the hypersensitivity of persons with BSyn to DNA-damaging agents.

**Immune.** Defects in humoral immunity can be managed with weekly subcutaneous or monthly intravenous infusions of gamma globulin. Cough assist devices, vibration vests, and

daily nasal lavage can be used for mucociliary clearance for bronchiectasis. If an individual with BSyn experiences recurrent, severe, or opportunistic infection, immunodeficiency screening (including immunoglobulin level, antibody responses to vaccines, and quantitative B- and T-lymphocyte measurements) is recommended.

#### Fertility

- Men with BSyn can undergo semen analysis to reveal azoospermia, oligospermia, or asthenospermia. Those who wish to conceive should consider consulting a fertility specialist. It is unclear if assisted reproductive technology (ART) may be helpful in persons with oligospermia or other abnormalities.
- Women with BSyn should be aware of signs of early menopause. Oocyte cryopreservation can be considered. Additionally, ART may be beneficial if natural conception is not possible; the authors are not aware of any prior use of ART in this population.

#### Surveillance

Health supervision recommendations for surveillance in persons with BSyn have been published [Cunniff et al 2018]. It should be recognized, however, that these recommendations are based on limited data from the Bloom Syndrome Registry and on expert opinion. There are currently no clinical trials or case-control studies that address outcomes in people with BSyn. Because of the unusually high risk for early development of cancer, much of the health supervision effort is directed to early detection and treatment.

#### Table 5.

Recommended Surveillance for Individuals with Bloom Syndrome (BSyn)

Manifestation	Evaluation	Frequency
Wilms tumor	<ul> <li>Abdominal ultrasound</li> <li>Screen for signs/symptoms incl hematuria &amp; a painless abdominal mass</li> </ul>	Every 3 mos from time of diagnosis to age 8 yrs
Leukemia	Screening & family education on signs/symptoms incl pallor, abnormal bleeding, petechiae, fatigue, unintentional weight loss	Every health visit
Lymphoma	Screening & family education on signs/symptoms incl enlarged lymph nodes, unexplained fevers, drenching night sweats, fatigue, unintentional weight loss	Every health visit
	Whole-body MRI	Every 1-2 yrs from age 12-13 yrs
Colorectal	Colonoscopy	Annually from age 10-12 yrs
cancer	Fecal immunochemical testing	Every 6 mos from age 10-12 yrs

Manifestation	Evaluation	Frequency
Breast cancer	Breast MRI in females	Annually from age 18 yrs
Skin cancer	Skin examination w/dermatologist for any suspicious skin lesions	On recognition of suspicious lesions & annually thereafter
Diabetes mellitus	<ul> <li>Fasting blood glucose &amp; hemoglobin A1C</li> <li>Screening &amp; family education on signs/symptoms of polyuria, polydipsia, weight loss</li> </ul>	Annually from age 10 yrs
Hypothyroidism	<ul> <li>Serum TSH w/reflex to T4</li> <li>Screening &amp; family education on signs/symptoms incl fatigue, constipation, cold sensitivity, weight gain</li> </ul>	Annually from age 10 yrs
Dyslipidemia	Lipid profile	Annually from age 10 yrs

## **Agents/Circumstances to Avoid**

Sun exposure to the face and other exposed areas, particularly in infancy and early childhood, should be avoided.

Exposure to ionizing radiation should be minimized.

#### **Evaluation of Relatives at Risk**

It is appropriate to evaluate sibs of a <u>proband</u> in order to identify as early as possible those who would benefit from avoidance of sun exposure to the face and early surveillance for cancer (see <u>Surveillance</u>).

- Molecular genetic testing can be used to evaluate sibs if the *BLM* pathogenic variants in the family are known.
- An unusually low birth weight followed by short stature throughout childhood is typically present in <u>affected</u> sibs; sibs of normal stature are likely unaffected and may not need further testing.

See <u>Genetic Counseling</u> for issues related to the testing of at-risk relatives for <u>genetic</u> <u>counseling</u> purposes.

#### **Pregnancy Management**

Eleven women with BSyn followed in the Registry have become pregnant at least once; seven of them have delivered a total of 11 healthy babies of normal size.

See <u>MotherToBaby</u> for more information on medication use during pregnancy.

## **Therapies Under Investigation**

Search <u>ClinicalTrials.gov</u> in the US and <u>EU Clinical Trials Register</u> in Europe for information on clinical studies for a wide range of diseases and conditions. Note: There may not be clinical trials for this disorder.

## Go to:

## **Genetic Counseling**

Genetic counseling is the process of providing individuals and families with information on the nature, inheritance, and implications of genetic disorders to help them make informed medical and personal decisions. The following section deals with genetic risk assessment and the use of family history and genetic testing to clarify genetic status for family members. This section is not meant to address all personal, cultural, or ethical issues that individuals may face or to substitute for consultation with a genetics professional. —ED.

## **Mode of Inheritance**

Bloom syndrome (BSyn) is inherited in an autosomal recessive manner.

## **Risk to Family Members**

#### Parents of a proband

- Both parents of an individual with BSyn may be assumed to be <u>heterozygous</u> for a <u>pathogenic variant</u> in *BLM*. However, a single example of <u>uniparental disomy</u> has been reported [Woodage et al 1994], suggesting that molecular testing of parents may be warranted to confirm their genetic status.
- Heterozygotes (carriers) are asymptomatic and are not at risk of developing BSyn.
- The cancer risk of heterozygotes as a group has been examined in association studies but is yet to be determined [Antczak et al 2013, Prokofyeva et al 2013].

#### Sibs of a proband

- At conception, each sib of an individual with BSyn has a 25% chance of being <u>affected</u>, a 50% chance of being an asymptomatic <u>carrier</u> of a *BLM* <u>pathogenic variant</u>, and a 25% chance of being unaffected and not a carrier.
- The cancer risk of heterozygotes as a group has been examined in association studies but is yet to be determined [Antczak et al 2013, Prokofyeva et al 2013].

#### Offspring of a female proband

• Children born to a woman with BSyn are usually <u>heterozygous</u> for a *BLM* <u>pathogenic</u> <u>variant</u>. However, because approximately 1% of individuals of <u>Ashkenazi Jewish</u> descent carry a *BLM* pathogenic variant, the risk for BSyn in the children of a union between a woman with BSyn and an Ashkenazi Jewish man whose BSyn <u>carrier</u> status has not been determined is 1/200.

• Children born to a woman with BSyn and a reproductive partner who is a <u>carrier</u> of a <u>pathogenic variant</u> have a 50% chance of having BSyn and a 50% chance of being carriers.

**Other family members.** Each sib of the <u>proband</u>'s parents is at a 50% risk of being a <u>carrier</u> of a *BLM* <u>pathogenic variant</u>.

## **Carrier (Heterozygote) Detection**

**Carrier testing for at-risk** relatives requires prior identification of the *BLM* pathogenic variants in the family.

## **Population Screening**

**Individuals of <u>Ashkenazi Jewish</u> heritage.** Because of the relatively increased <u>carrier rate</u> of the blm<sup>Ash</sup> <u>allele</u> in Ashkenazi Jews, individuals of Ashkenazi heritage should be aware of their carrier risk, and practitioners should consider screening in this population [<u>ACOG</u> <u>Committee on Genetics 2017</u>].

**Expanded** <u>carrier</u> screening. Bloom syndrome is included on most expanded carrier screening panels.

## **Related Genetic Counseling Issues**

See Management, <u>Evaluation of Relatives at Risk</u> for information on evaluating at-risk relatives for the purpose of early diagnosis and treatment.

#### Family planning

- The optimal time for determination of genetic risk, clarification of <u>carrier</u> status, and discussion of the availability of prenatal testing is before pregnancy.
- It is appropriate to offer <u>genetic counseling</u> (including discussion of potential risks to offspring and reproductive options) to young adults who are <u>affected</u>, are carriers, or are at risk of being carriers.

**DNA banking** is the storage of DNA (typically extracted from white blood cells) for possible future use. Because it is likely that testing methodology and our understanding of genes, allelic variants, and diseases will improve in the future, consideration should be given to banking DNA of <u>affected</u> individuals.

## **Prenatal Testing and Preimplantation Genetic Diagnosis**

**Molecular genetic testing.** Once the *BLM* pathogenic variants have been identified in an <u>affected</u> family member, <u>prenatal diagnosis</u> (by amniocentesis or chorionic villus sampling [CVS]) and <u>preimplantation genetic diagnosis</u> are possible. Preimplantation genetic diagnosis has been successfully utilized in a single family [Bloom Syndrome Registry, unpublished data].

Note: Ultrasound measurements are not reliable for estimating gestation age if <u>prenatal</u> <u>diagnosis</u> confirms the diagnosis of BSyn in the fetus.

#### Go to:

## Resources

GeneReviews staff has selected the following disease-specific and/or umbrella support organizations and/or registries for the benefit of individuals with this disorder and their families. GeneReviews is not responsible for the information provided by other organizations. For information on selection criteria, click <u>here</u>.

• Bloom's Syndrome Association (BSA)

P.O. Box 727

Hanover NH 03755-0727

Phone: 603-643-2850

Email: info@bloomssyndromeassociation.org

www.bloomssyndromeassociation.org

#### • Bloom's Syndrome Foundation (BSF)

7095 Hollywood Boulevard

#583

Los Angeles CA 90028

Email: info@bloomssyndrome.org

www.bloomssyndrome.org

#### • National Library of Medicine Genetics Home Reference

Bloom syndrome

#### • Center for Jewish Genetics

Ben Gurion Way

30 South Wells Street

Chicago IL 60606

**Phone:** 312-357-4718

Email: jewishgeneticsctr@juf.org

#### www.jewishgenetics.org

#### • Xeroderma Pigmentosum Society, Inc (XP Society)

XP Society has material on their site related to UV protection/avoidance.

437 Syndertown Road

Craryville NY 12521

Phone: 877-XPS-CURE (877-977-2873); 518-851-2612

Email: xps@xps.org

www.xps.org

#### • Bloom Syndrome Registry

Weill Cornell Medicine

505 East 70th Street

3rd floor, Box 128

New York NY 10021

Phone: 646-962-2205

Bloom Syndrome Registry

#### Go to:

## **Molecular Genetics**

Information in the Molecular Genetics and OMIM tables may differ from that elsewhere in the GeneReview: tables may contain more recent information. —ED.

#### Table A.

Bloom Syndrome: Genes and Databases

Gene Chromosome Locus	Protein	Locus-Specific Databases	HGMI	) ClinVar
<u>BLM</u> <u>15q26.1</u>	Bloom syndrome protein	BLM database BLMbase: Mutation registry	<u>BLM</u>	<u>BLM</u>
	<u>+</u>	for Bloom Syndrome		

Data are compiled from the following standard references: <u>gene</u> from <u>HGNC</u>; <u>chromosome locus</u> from <u>OMIM</u>; protein from <u>UniProt</u>. For a description of databases (Locus Specific, HGMD, ClinVar) to which links are provided, click <u>here</u>.

## Table B.

OMIM Entries for Bloom Syndrome (View All in OMIM)

210900 BLOOM SYNDROME; BLM 604610 RECQ PROTEIN-LIKE 3; RECQL3

## **Molecular Pathogenesis**

Bloom syndrome (BSyn) is the prototype of the class of human diseases sometimes referred to as the <u>chromosome</u> breakage syndromes [German 1969]. These include BSyn, <u>Fanconi</u> anemia, <u>ataxia-telangiectasia</u>, ataxia-telangiectasia-like disorder (OMIM <u>604391</u>), <u>Nijmegen</u> <u>breakage syndrome</u>, and <u>Werner syndrome</u>. These clinically disparate disorders are caused by pathogenic variants in genes encoding enzymes comprising pathways of DNA replication and repair that are responsible for the maintenance of <u>genomic</u> stability. In all of these disorders, the diagnostic <u>cytogenetic</u> abnormalities are accompanied by an increased rate of spontaneous reversion (mutation) to the normal state in somatic cells. This hypermutability explains the cancer predisposition shared by these disorders.

**Gene structure.** A 4,528-bp <u>cDNA</u> sequence defines *BLM*, which contains a long <u>open</u> reading frame encoding a 1,417-amino-acid protein, BLM. *BLM* comprises 22 exons and is located at <u>chromosome</u> band 15q26.1. For a detailed summary of <u>gene</u> and protein information, see <u>Table A</u>, **Gene**.

**Pathogenic variants.** Most individuals of <u>Ashkenazi Jewish</u> heritage with BSyn have the <u>pathogenic variant c.2207\_2212delinsTAGATTC</u> [Ellis et al 1998]. A second, rarer pathogenic variant segregating in the Ashkenazi Jewish population, <u>c.2407dupT</u>, has been identified [Ellis et al 1998, German et al 2007].

Pathogenic variants identified in several studies of individuals with BSyn fall into the following four broad classes [German et al 2007, Amor-Guéret et al 2008, Shastri & Schmidt 2015]:

- Nucleotide insertions and deletions that result in frameshifts and elimination of the C terminus of the protein where the nuclear localization signals of BLM are located; BLM is therefore absent from the nucleus (~1/3 of all pathogenic variants)
- Nonsense variants that convert sense codons to <u>nonsense</u> or chain-terminating codons that predict translation of a truncated BLM protein (~1/3 of all pathogenic variants)
- Intron variants that cause <u>splicing</u> defects (~1/6 of all pathogenic variants)
- Missense variants that result in the production of nonfunctional BLM protein (~1/6 of all pathogenic variants)

## Table 6.

BLM Pathogenic Variants Discussed in This GeneReview

DNA Nucleotide Change (Alias <sup>1</sup> )	Predicted Protein Change Reference Sequences		
c.2207_2212delinsTAGATTC (2281del6/ins7) (blm <sup>Ash</sup> )	<sup>2</sup> p.Tyr736LeufsTer5 <sup>2</sup>	<u>NM_000057.2</u>	
c.2407dupT (insT2407)	p.Trp803LeufsTer4	<u>NP_000048.1</u>	

Variants listed in the table have been provided by the authors. *GeneReviews* staff have not independently verified the classification of variants.

*GeneReviews* follows the standard naming conventions of the Human Genome Variation Society (varnomen.hgvs.org). See <u>Quick Reference</u> for an explanation of nomenclature.

1.

Variant designation that does not conform to current naming conventions

2.

Also known as the blm<sup>Ash</sup> <u>allele</u>

See <u>Table 7</u> (pdf) for pathogenic variants identified in registered persons of various nationalities and ethnic groups.

**Normal <u>gene product</u>.** The 1,417-amino acid protein named BLM contains an amino acid <u>domain</u> consisting of seven motifs characteristic of DNA and RNA helicases. The helicase domain of BLM is 40%-45% identical to the helicase domain in the RecQ subfamily of DNA helicases and is known to be important in other species for the maintenance of <u>genomic</u> integrity. Molecular and genetic evidence implicates BLM in the cellular mechanisms that maintain genomic stability [<u>Hickson et al 2001</u>, <u>Monnat 2010</u>, <u>Larsen & Hickson 2013</u>, <u>Suhasini & Brosh 2013</u>, <u>Cunniff et al 2017</u>].

BLM is a cell cycle-regulated protein that is distributed diffusely throughout the nucleus but also is concentrated in nuclear foci, many of which have been identified as PML (promyelocytic leukemia protein) bodies [Sanz et al 2000]. DNA-dependent ATPase and DNA duplex-unwinding activities have been demonstrated for BLM; the nucleic acid substrates that it acts on in the cell remain to be identified.

**Abnormal** <u>gene product</u>. The major consequence of loss of BLM function for a somatic cell is an abnormally high rate of <u>recombination</u> and mutation. The pathogenic variants that arise in the cells of a person with BSyn are of several types and affect many regions of the genome. Thus, although the cancer predisposition in BSyn is attributable to the cellular hyper-recombinability and hypermutability, the proportional small size – the constant feature of BSyn – remains unexplained, as do the important medical complications of BSyn other than cancer.

#### Go to:

## References

## Literature Cited

- ACOG Committee on Genetics. ACOG Committee Opinion No. 691: Carrier screening for genetic conditions. Obstet Gynecol. 2017;129:e41–55. [PubMed]
- Amor-Guéret M, Dubois-d'Enghien C, Laugé A, Onclercq-Delic R, Barakat A, Chadli E, Bousfiha AA, Benjelloun M, Flori E, Doray B, Laugel V, Lourenço MT, Gonçalves R, Sousa S, Couturier J, Stoppa-Lyonnet D. Three new BLM gene mutations associated with Bloom syndrome. Genet Test. 2008;12:257–61. [PubMed]
- Antczak A, Kluźniak W, Wokołorczyk D, Kashyap A, Jakubowska A, Gronwald J, Huzarski T, Byrski T, Dębniak T, Masojć B, Górski B, Gromowski T, Nagorna A, Gołąb A, Sikorski A, Słojewski M, Gliniewicz B, Borkowski T, Borkowski A, Przybyła J, Sosnowski M, Małkiewicz B, Zdrojowy R, Sikorska-Radek P, Matych J, Wilkosz J, Różański W, Kiś J, Bar K, Domagała P, Stawicka M, Milecki P, Akbari MR, Narod SA, Lubiński J, Cybulski C, Bryniarski P, Paradysz A, Jersak K, Niemirowicz J, Słupski P, Jarzemski P, Skrzypczyk M, Dobruch J, Domagała W, Chosia M, van de Wetering T, Serrano-Fernández P, Puszyński M, Soczawa M, Switała J, Archimowicz S, Kordowski M, Zyczkowski M, Borówka A, Bagińska J, Krajka K, Szwiec M, Haus O, Janiszewska H, Stembalska A, Sąsiadek MM, et al. A common nonsense mutation of the BLM gene and prostate cancer risk and survival. Gene. 2013;532:173–6. [PubMed]
- Ben Salah G, Salem IH, Masmoudi A, Kallabi F, Turki H, Fakhfakh F, Ayadi H, Kamoun H. A novel frameshift mutation in BLM gene associated with high sister chromatid exchanges (SCE) in heterozygous family members. Mol Biol Rep. 2014;41:7373–80. [PubMed]
- Bloom D. Congenital telangiectatic erythema resembling lupus erythematosus in dwarfs; probably a syndrome entity. AMA Am J Dis Child. 1954;88:754–8. [PubMed]
- Cunniff C, Bassetti JA, Ellis NA. Bloom's syndrome: clinical spectrum, molecular pathogenesis, and cancer predisposition. Mol Syndromol. 2017;8:4–23. [PMC free article] [PubMed]
- Cunniff C, Djavid AR, Carrubba S, Cohen B, Ellis NA, Fein Levy C, Jeong S, Lederman HM, Vogiatzi M, Walsh MF, Zauber AG. Health supervision for people with Bloom syndrome. Am J Med Genet. 2018;176:1872–81. [PubMed]
- Diaz A, Vogiatzi MG, Sanz MM, German J. Evaluation of short stature, carbohydrate metabolism and other endocrinopathies in Bloom's syndrome. Horm Res. 2006;66:111–7. [PubMed]
- Ellis NA, Ciocci S, Proytcheva M, Lennon D, Groden J, German J. The Ashkenazic Jewish Bloom syndrome mutation blmAsh is present in non-Jewish Americans of Spanish ancestry. Am J Hum Genet. 1998;63:1685–93. [PMC free article] [PubMed]
- German J. Bloom's syndrome. I. Genetical and clinical observations in the first twenty-seven patients. Am J Hum Genet. 1969;21:196–227. [PMC free article] [PubMed]
- German J. Bloom syndrome: a Mendelian prototype of somatic mutational disease. Medicine (Baltimore). 1993;72:393–406. [PubMed]
- German J, Ellis N. Bloom syndrome. In: Vogelstein B, Kingler RW, eds. *The Genetic Basis of Human Cancer*. 2 ed. New York, NY: McGraw-Hill; 2002:267-88.
- German J, Passarge E. Bloom's syndrome. XII. Report from the Registry for 1987. Clin Genet. 1989;35:57–69. [PubMed]

- German J, Sanz MM, Ciocci S, Ye TZ, Ellis NA. Syndrome-causing mutations of the BLM gene in persons in the Bloom's Syndrome Registry. Hum Mutat. 2007;28:743– 53. [PubMed]
- Hickson ID, Davies SL, Li JL, Levitt NC, Mohaghegh P, North PS, Wu L. Role of the Bloom's syndrome helicase in maintenance of genome stability. Biochem Soc Trans. 2001;29:201–4. [PubMed]
- Hudson DF, Amor DJ, Boys A, Butler K, Williams L, Zhang T, Kalitsis P. Loss of RMI2 increases genome instability and causes a Bloom-like syndrome. PLOS Genetics. 2016;12:e1006483. [PMC free article] [PubMed]
- Larsen NB, Hickson ID. RecQ helicases: conserved guardians of genomic integrity. In: Spies M, ed. *DNA Helicases and DNA Motor Proteins, Advances in Experimental Medicine and Biology*. New York, NY: Springer Science; 2013:161-84. [PubMed]
- Li L, Eng C, Desnick RJ, German J, Ellis NA. Carrier frequency of the Bloom syndrome blmAsh mutation in the Ashkenazi Jewish population. Mol Genet Metab. 1998;64:286–90. [PubMed]
- Martin CA, Sarlós K, Logan CV, Thakur RS, Parry DA, Bizard AH, Leitch A, Cleal L, Ali NS, Al-Owain MA, Allen W, Altmüller J, Aza-Carmona M, Barakat BAY, Barraza-García J, Begtrup A, Bogliolo M, Cho MT, Cruz-Rojo J, Dhahrabi HAM, Elcioglu NH, Gorman GS, Jobling R, Kesterton I, Kishita Y, Kohda M, Le Quesne Stabej P, Malallah AJ, Nürnberg P, Ohtake A, Okazaki Y, Pujol R, Ramirez MJ, Revah-Politi A, Shimura M, Stevens P, Taylor RW, Turner L, Williams H, Wilson C, Yigit G, Zahavich L, Alkuraya FS, Surralles J, Iglesais A, Murayama K, Wollnik B, Dattani M, Heath KE, Hickson ID, Jackson AP. Mutations in TOP3A cause a Bloom syndrome-like disorder. Am J Hum Genet. 2018;103:221–31. [PMC free article] [PubMed]
- Monnat RJ. Human RECQ helicases: roles in DNA metabolism, mutagenesis and cancer biology. Semin Cancer Biol. 2010;20:329–39. [PMC free article] [PubMed]
- Peleg L, Pesso R, Goldman B, Dotan K, Omer M, Friedman E, Berkenstadt M, Reznik-Wolf H, Barkai G. Bloom syndrome and Fanconi's anemia: rate and ethnic origin of mutation carriers in Israel. Isr Med Assoc J. 2002;4:95–7. [PubMed]
- Prokofyeva D, Bogdanova N, Dubrowinskaja N, Bermisheva M, Takhirova Z, Antonenkova N, Turmanov N, Datsyuk I, Gantsev S, Christiansen H, Park-Simon TW, Hillemanns P, Khusnutdinova E, Dörk T. Nonsense mutation p.Q548X in BLM, the gene mutated in Bloom's syndrome, is associated with breast cancer in Slavic populations. Breast Cancer Res Treat. 2013;137:533–9. [PubMed]
- Sanz MM, Proytcheva M, Ellis NA, Holloman WK, German J. BLM, the Bloom's syndrome protein, varies during the cell cycle in its amount, distribution, and colocalization with other nuclear proteins. Cytogenet Cell Genet. 2000;91:217–23.
   [PubMed]
- Shahrabani-Gargir L, Shomrat R, Yaron Y, Orr-Urtreger A, Groden J, Legum C. High frequency of a common Bloom syndrome Ashkenazi mutation among Jews of Polish origin. Genet Test. 1998;2:293–6. [PubMed]
- Shastri VM, Schmidt KH. Cellular defects caused by hypomorphic variants of the Bloom syndrome helicase gene BLM. Mol Genet Genomic Med. 2015;4:106–19.
   [PMC free article] [PubMed]
- Suhasini AN, Brosh Jr RM. DNA helicases associated with genetic instability, cancer, and aging. In: Spies M, ed. *DNA Helicases and DNA Motor Proteins, Advances in Experimental Medicine and Biology*. New York, NY: Springer Science; 2013:123-44.
- Woodage T, Prasad M, Dixon JW, Selby RE, Romain DR, Columbano-Green LM, Graham D, Rogan PK, Seip JR, Smith A, Trent RJ. Bloom syndrome and maternal

uniparental disomy for chromosome 15. Am J Hum Genet. 1994;55:74–80. [PMC free article] [PubMed]