MEDICAL POLICY – 12.04.102

Whole Exome and Whole Genome Sequencing for Diagnosis of Genetic Disorders

BCBSA Ref. Policy: 2.04.102
Effective Date: Feb. 1, 2017
Last Revised: Oct. 6, 2017
Replaces: 2.04.102

RELATED MEDICAL POLICIES:
None

Select a hyperlink below to be directed to that section.

POLICY CRITERIA | CODING | RELATED INFORMATION
EVIDENCE REVIEW | REFERENCES | HISTORY

Clicking this icon returns you to the hyperlinks menu above.

Introduction

Our DNA contains all of our genetic material, and makes us who we are. Our DNA contains about 20,000 genes which are packaged into 46 chromosomes (23 pairs). Genes are very important because they tell our cells how to make proteins. Although there are tens of thousands of genes, they make up only about 1% of our entire DNA. A large part of our DNA doesn’t code for any proteins. The protein-coding genes are also called “exomes”.

The entire collection of DNA is called the “whole genome”. If a person was only talking about the genes themselves that are contained within the whole genome, they are called the “whole exome”.

“Whole genome sequencing” is a test that looks at the entire genome, including parts of the DNA that don’t contain any genes. “Whole exome sequencing” is a test that only looks at the exomes, which is that part of the DNA that contains genes that code for proteins. As an analogy, an entire football game would be your whole genome. Only the game highlights (1% of the game) would be the exomes. Whole genome sequencing would be like watching the entire football game from start to finish, while whole exome sequencing would be like watching only the game highlights the next day.

Whole genome and whole exome sequencing tests have been used to help diagnose genetic disorders in people. Whole genome sequencing is always considered to be investigational. Not
enough good quality medical studies have been done to show that whole genome sequencing is reliable and helpful in diagnosing genetic conditions. However, whole exome sequencing may be medically necessary in some situations. This policy describes when whole exome sequencing may be medically necessary.

Note: The Introduction section is for your general knowledge and is not to be taken as policy coverage criteria. The rest of the policy uses specific words and concepts familiar to medical professionals. It is intended for providers. A provider can be a person, such as a doctor, nurse, psychologist, or dentist. A provider also can be a place where medical care is given, like a hospital, clinic, or lab. This policy informs them about when a service may be covered.

## Policy Coverage Criteria

The policy statement is intended to address the use of whole exome and whole genome sequencing for the diagnosis of genetic disorders in patients with suspected genetic disorders and for population-based screening.

This policy does not address the use of whole exome and whole genome sequencing for preimplantation genetic diagnosis or screening, prenatal (fetal) testing, or testing of cancer cells.

### Evaluation/Diagnosis of Genetic Disorders

<table>
<thead>
<tr>
<th>Service</th>
<th>Medical Necessity</th>
</tr>
</thead>
</table>
| Whole exome sequencing (WES)   | Whole exome sequencing (WES) may be considered medically necessary for the evaluation/diagnosis of unexplained congenital or neurodevelopmental disorders in individuals under the age of 18 when ALL of the following criteria are met:  
  - The patient has been evaluated by a clinician with expertise in clinical genetics and counseled about the potential risks of genetic testing.  
  **AND**  
  - The results may affect the management and clinical outcome for the individual being tested.  
  **AND**  
  - A genetic etiology is felt to be the most likely explanation for |

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Service | Medical Necessity
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- the patient’s signs and symptoms even if previous genetic testing (e.g., chromosomal microarray analysis and/or targeted single-gene testing) has not been helpful in making a diagnosis, OR the affected individual is faced with invasive procedures or testing as the next diagnostic step (e.g., muscle biopsy).

**WES is considered investigational for the diagnosis of genetic disorders in all other situations.**

Service | Investigational
--- | ---

**Whole genome sequencing (WGS)**

Whole genome sequencing (WGS) is considered investigational for the diagnosis of genetic disorders.

Screening of Genetic Disorders - Asymptomatic Individuals

Service | Investigational
--- | ---

**WES and WGS**

WES and WGS are considered investigational for screening of asymptomatic individuals for genetic disorders.

**Coding**

<table>
<thead>
<tr>
<th>Code</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>CPT</td>
<td></td>
</tr>
<tr>
<td>0012U</td>
<td>Germline disorders, gene rearrangement detection by whole genome next-generation sequencing, DNA, whole blood, report of specific gene rearrangement(s) (new code effective 8/1/17)</td>
</tr>
<tr>
<td>81415</td>
<td>Exome (eg, unexplained constitutional or heritable disorder or syndrome); sequence analysis</td>
</tr>
<tr>
<td>81416</td>
<td>Exome (eg, unexplained constitutional or heritable disorder or syndrome); sequence analysis, each comparator exome (eg, parents, siblings) (List separately in addition to code for primary procedure)</td>
</tr>
<tr>
<td>81417</td>
<td>Exome (eg, unexplained constitutional or heritable disorder or syndrome); re-</td>
</tr>
</tbody>
</table>
### Definition of Terms

**Exon:** The specific part of a gene that is involved with making a protein

**Exome:** The complete set of exons

**Gene:** A hereditary unit found within the DNA that tells the body how to make proteins

**Genome:** The entire collection of DNA

**Genotype:** The entire set of genes that a person has within their DNA; their “genetic makeup”

**Phenotype:** The observable physical characteristics of a person that are caused by their genes (eg, hair color, whether their ear lobes are attached or free, etc.).

**Variant:** a change to a gene. Also called a mutation.

**Whole Exome Sequencing:** A genetic test that looks at all of the protein-coding genes within the DNA

**Whole Genome sequencing:** A genetic test that looks at all of a person’s DNA, including the parts that don’t contain genes
Background

Clinical Context and Test Purpose

Whole exome sequencing (WES) is a genetic test that looks at the parts of the human DNA that are directly involved with making proteins (the exons), while whole genome sequencing (WGS) looks at the entire DNA molecule, including parts that are not involved in making proteins. It has been suggested that WES and WGS may be helpful in diagnosing patients who have signs and symptoms of disorders or anomalies that have not been able to be explained by standard clinical tests. Potential candidates for WES and WGS include patients who present with a broad spectrum of suspected genetic conditions. Making a definitive diagnosis may help manage the patient. For example, it can help determine appropriate follow up for a child and thus reduce his morbidity, as well as affect reproductive planning for parents and potentially the affected patient himself.

The standard diagnostic workup for patients with suspected genetic disorders may include combinations of radiographic, electrophysiologic, biochemical, biopsy, and targeted genetic evaluations. Searching for a diagnosis may thus become a time-consuming and expensive process. WES or WGS using next generation sequencing (NGS) techniques may be able to efficiently make a genetic diagnosis in patients. WES is limited to most of the protein-coding sequence of an individual (≈85%), is composed of about 20,000 genes and 180,000 exons (protein-coding segments of a gene), and constitutes approximately 1% of the genome. It is believed that the exome contains about 85% of heritable disease-causing variants. WES has the advantage of speed and efficiency relative to some other types of genetic tests. WGS uses techniques similar to WES, but includes noncoding regions. WGS has greater ability to detect large deletions or duplications in protein-coding regions compared to WES, but it requires greater data analytics. Technical aspects of WES and WGS are evolving, including databases such as the National Institutes of Health’s ClinVar database (http://www.ncbi.nlm.nih.gov/clinvar/).

In 2013, the American College of Medical Genetics and Genomics, Association for Molecular Pathology, and College of American Pathologists convened a workgroup to develop standard terminology for describing sequence variants. Guidelines that were developed by this workgroup, published in 2015, describe criteria for classifying pathogenic and benign sequence
variants based on types of data into 5 categories: pathogenic, likely pathogenic, uncertain significance, likely benign, and benign.

**Available WES/WGS Testing Services**

Several laboratories offer WES and WGS as a clinical service. Illumina offers 3 TruGenome tests: the TruGenome Undiagnosed Disease Test (indicated to find the underlying genetic cause of an undiagnosed rare genetic disease of single-gene etiology), TruGene Predisposition Screen (indicated for healthy patients interested in learning about their carrier status and genetic predisposition toward adult-onset conditions), and the TruGenome Technical Sequence Data (WGS for labs and physicians who will make their own clinical interpretations). Ambry Genetics offers 2 WGS tests, the ExomeNext and ExomeNext-Rapid, which sequence both the nuclear and the mitochondrial genomes. GeneDx offers WES with its XomeDx™ test. Medical centers may also offer WES and WGS as a clinical service.

Examples of laboratories offering WES as a clinical service and their indications for testing are summarized in **Table 1**.

**Table 1: Examples of Laboratories Offering Exome Sequencing as a Clinical Service**

<table>
<thead>
<tr>
<th>Laboratory</th>
<th>Laboratory Indications for Testing</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ambry Genetics (Aliso Viejo, CA)</td>
<td>“The patient’s clinical presentation is unclear/atypical disease and there are multiple genetic conditions in the differential diagnosis.”</td>
</tr>
<tr>
<td>GeneDx (Gaithersburg, MD)</td>
<td>“a patient with a diagnosis that suggests the involvement of one or more of many different genes, which would, if even available and sequenced individually, be prohibitively expensive”</td>
</tr>
<tr>
<td>Baylor College of Medicine (Houston, TX)</td>
<td>“used when a patient’s medical history and physical exam findings strongly suggest that there is an underlying genetic etiology. In some cases, the patient may have had an extensive evaluation consisting of multiple genetic tests, without identifying an etiology.”</td>
</tr>
<tr>
<td>Illumina (San Diego, CA)</td>
<td>The TruGenome Undiagnosed Disease Test is indicated to find the underlying genetic cause of an undiagnosed rare genetic disease of single-gene etiology.</td>
</tr>
<tr>
<td>University of California Los Angeles Health System</td>
<td>“This test is intended for use in conjunction with the clinical presentation and other markers of disease progression for the management of patients with rare genetic disorders.”</td>
</tr>
</tbody>
</table>
Laboratory | Laboratory Indications for Testing
--- | ---
EdgeBio (Gaithersburg, MD) | Recommended “In situations where there has been a diagnostic failure with no discernible path. In situations where there are currently no available tests to determine the status of a potential genetic disease. In situations with atypical findings indicative of multiple disease[s].”

Children’s Mercy Hospitals and Clinics (Kansas City, MO) | Provided as a service to families with children who have had an extensive negative workup for a genetic disease; also used to identify novel disease genes.

Emory Genetics Laboratory (Atlanta, GA) | “Indicated when there is a suspicion of a genetic etiology contributing to the proband’s manifestations.”

Note that this policy does not address the use of WES and WGS for preimplantation genetic diagnosis or screening, prenatal (fetal) testing, or for testing of cancer cells.

**Summary of Evidence**

For individuals who have unexplained multiple congenital anomalies or a neurodevelopmental disorder who receive WES, the evidence includes large case series and a within-subject comparison. Relevant outcomes are test accuracy and validity, functional outcomes, changes in reproductive decision making, and resource utilization. Patients who have multiple congenital anomalies or a developmental disorder with a suspected genetic etiology, but the specific genetic alteration is unclear or unidentified by standard clinical workup, may be left without a clinical diagnosis of their disorder, despite a lengthy diagnostic workup. Several large series and a number of smaller series report diagnostic yields of WES ranging from 25% to 60%, depending on the individual’s age, phenotype, and previous workup. One comparative study found a 44% increase in yield compared with standard testing strategies. Many of the studies also report changes in patient management including medication changes, discontinuation of or additional testing, ending the diagnostic odyssey, and family planning. However, the wide variance in diagnostic yield confers uncertainty. The evidence is insufficient to determine that the technology results in a meaningful improvement in the net health outcome.

For individuals who have a suspected genetic disorder lacking multiple congenital anomalies or a neurodevelopmental phenotype who receive WES, the evidence includes small case series. Relevant outcomes are test accuracy and validity, functional outcomes, changes in reproductive decision making, and resource utilization. There is 1 small series of patients with limb girdle muscular dystrophy (LGMD), and larger series of patients with a broad spectrum of suspected genetic disorders. The diagnostic yield for unexplained LGMD is high, but a limited number of
patients have been studied to date. The evidence is insufficient to determine the effects of the technology on health outcomes.

For individuals with a suspected genetic disorder who receive WGS, the evidence includes case series. Relevant outcomes are test accuracy and validity, functional outcomes, changes in reproductive decision making, and resource utilization. No studies were identified that directly compared WGS with alternative testing strategies in terms of the yield of testing for pathogenic variants associated with the phenotype being evaluated. One small series evaluated yield of WGS in patients with inherited retinal disorders and found a genetic cause in about half of patients. The estimated increase in diagnostic yield was 29% compared to standard workup. However, positive results were obtained in only 24 patients, and additional study is needed to evaluate WGS for other disorders. The evidence is insufficient to determine the effects of the technology on health outcomes.

Ongoing and Unpublished Clinical Trials

Some currently unpublished trials that might influence this review are listed in Table 2.

Table 2. Summary of Key Trials

<table>
<thead>
<tr>
<th>NCT No.</th>
<th>Trial Name</th>
<th>Planned Enrollment</th>
<th>Completion Date</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ongoing</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NCT02340871</td>
<td>Finding Genes With NGS Techniques in Whom Mutations Cause Neurological Diseases</td>
<td>75</td>
<td>Jul 2018</td>
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<tr>
<td>NCT02418377</td>
<td>Whole-exome Sequencing to Identify Genetic Variants Associated With Severe Childhood Obesity, and Tracking the Changing Prevalence of Obesity Related Complications</td>
<td>1200</td>
<td>Aug 2018</td>
</tr>
<tr>
<td>NCT02826694</td>
<td>North Carolina Newborn Exome Sequencing for Universal Screening</td>
<td>400</td>
<td>Aug 2018</td>
</tr>
<tr>
<td>NCT02077894</td>
<td>Whole Exome and Whole Genome Sequencing for Genotyping of Inherited and Congenital Eye Cond</td>
<td>310</td>
<td>Sep 2018</td>
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<tr>
<td>NCT01087320</td>
<td>Whole Genome Medical Sequencing for Gene Discovery</td>
<td>400</td>
<td>No date</td>
</tr>
<tr>
<td>NCT01952275</td>
<td>Assessment of the Enrichment of Rare Coding Genetic Variants in Patients Affected by Neutrophil-Mediated Inflammatory Dermatoses</td>
<td>660</td>
<td>Jan 2020</td>
</tr>
<tr>
<td>NCT No.</td>
<td>Trial Name</td>
<td>Planned Enrollment</td>
<td>Completion Date</td>
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<td>----------------------------------------------------------</td>
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</tr>
<tr>
<td>NCT02769975</td>
<td>Evaluation of Children With Endocrine and Metabolic-Related Conditions</td>
<td>15,000</td>
<td>Dec 2030</td>
</tr>
</tbody>
</table>

NCT: national clinical trial.

Practice Guidelines and Position Statements

The American College of Medical Genetics and Genomics (ACMG) states that diagnostic testing with WES (and WGS) should be considered in the clinical diagnostic assessment of a phenotypically affected individual when:

- The phenotype or family history data strongly implicate a genetic etiology, but the phenotype does not correspond with a specific disorder for which a genetic test targeting a specific gene is available on a clinical basis.
- A patient presents with a defined genetic disorder that demonstrates a high degree of genetic heterogeneity, making WES or WGS analysis of multiple genes simultaneously a more practical approach.
- A patient presents with a likely genetic disorder but specific genetic tests available for that phenotype have failed to arrive at a diagnosis.
- A fetus with a likely genetic disorder in which specific genetic tests, including targeted sequencing tests, available for that phenotype have failed to arrive at a diagnosis.

ACMG states that for screening purposes:

WGS/WES may be considered in preconception carrier screening, using a strategy to focus on genetic variants known to be associated with significant phenotypes in homozygous or hemizygous progeny.

ACMG states that WGS/WES should not be used at this time as an approach to prenatal screening or as a first-tier approach for newborn screening.

In March 2013, an ACMG board finalized its recommendations for reporting incidental findings in WGS and WES. A working group determined that reporting some incidental findings would likely have medical benefit for the patients and families of patients undergoing clinical sequencing and recommended that when a report is issued for clinically indicated exome and
genome sequencing, a minimum list of conditions, genes, and variants should be routinely evaluated and reported to the ordering clinician.

In 2014, the American Academy of Neurology and the Practices Issues review Panel of the American Association of Neuromuscular and Electrodiagnostic Medicine issued evidenced-based guidelines for the diagnosis and treatment of limb-girdle and distal dystrophies, which makes the following recommendations (see Table 3)\textsuperscript{24}.

**Table 3. AAN and AANEM Guidelines on Limb-Girdle Muscular Dystrophy**

<table>
<thead>
<tr>
<th>Recommendation</th>
<th>Level</th>
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<tbody>
<tr>
<td><strong>Diagnosis</strong></td>
<td></td>
</tr>
<tr>
<td>For patients with suspected muscular dystrophy, clinicians should use a clinical approach to guide genetic diagnosis based on the clinical phenotype, including the pattern of muscle involvement, inheritance pattern, age at onset, and associated manifestations (e.g., early contractures, cardiac or respiratory involvement).</td>
<td>B</td>
</tr>
<tr>
<td>In patients with suspected muscular dystrophy in whom initial clinically directed genetic testing does not provide a diagnosis, clinicians may obtain genetic consultation or perform parallel sequencing of targeted exomes, whole-exome sequencing, whole-genome screening, or next-generation sequencing to identify the genetic abnormality.</td>
<td>C</td>
</tr>
</tbody>
</table>

**Management of cardiac complications**

<table>
<thead>
<tr>
<th>Recommendation</th>
<th>Level</th>
</tr>
</thead>
<tbody>
<tr>
<td>Clinicians should refer newly diagnosed patients with (1) limb-girdle muscular dystrophy (LGMD1A, LGMD1B, LGMD1D, LGMD1E, LGMD2C–K, LGMD2M–P, ... or (2) muscular dystrophy without a specific genetic diagnosis for cardiology evaluation, including electrocardiogram (ECG) and structural evaluation (echocardiography or cardiac magnetic resonance imaging [MRI]), even if they are asymptomatic from a cardiac standpoint, to guide appropriate management.</td>
<td>B</td>
</tr>
<tr>
<td>If ECG or structural cardiac evaluation (e.g., echocardiography) has abnormal results, or if the patient has episodes of syncope, near-syncope, or palpitations, clinicians should order rhythm evaluation (e.g., Holter monitor or event monitor) to guide appropriate management.</td>
<td>B</td>
</tr>
<tr>
<td>Clinicians should refer muscular dystrophy patients with palpitations, symptomatic or asymptomatic tachycardia or arrhythmias, or signs and symptoms of cardiac failure for cardiology evaluation.</td>
<td>B</td>
</tr>
<tr>
<td>It is not obligatory for clinicians to refer patients with LGMD2A, LGMD2B, and LGMD2L for cardiac evaluation unless they develop overt cardiac signs or symptoms.</td>
<td>B</td>
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</table>

**Management of pulmonary complications**

<table>
<thead>
<tr>
<th>Recommendation</th>
<th>Level</th>
</tr>
</thead>
<tbody>
<tr>
<td>Clinicians should order pulmonary function testing (spirometry and maximal inspiratory/expiratory force in the upright and, if normal, supine positions) or refer for pulmonary evaluation (to identify and treat respiratory insufficiency) in muscular dystrophy patients at the time of diagnosis, or if they develop pulmonary symptoms later in their course.</td>
<td>B</td>
</tr>
<tr>
<td>Recommendation</td>
<td>Level</td>
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</tr>
<tr>
<td>In patients with a known high risk of respiratory failure (e.g., those with LGMD2I ...), clinicians should obtain periodic pulmonary function testing (spirometry and maximal inspiratory/expiratory force in the upright position and, if normal, in the supine position) or evaluation by a pulmonologist to identify and treat respiratory insufficiency.</td>
<td>B</td>
</tr>
<tr>
<td>It is not obligatory for clinicians to refer patients with LGMD2B and LGMD2L for pulmonary evaluation unless they are symptomatic.</td>
<td>C</td>
</tr>
<tr>
<td>Clinicians should refer muscular dystrophy patients with excessive daytime somnolence, nonrestorative sleep (e.g., frequent nocturnal arousals, morning headaches, excessive daytime fatigue), or respiratory insufficiency based on pulmonary function tests for pulmonary or sleep medicine consultation for consideration of noninvasive ventilation to improve quality of life.</td>
<td>B</td>
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**Medicare National Coverage**

There is no national coverage determination (NCD). In the absence of an NCD, coverage decisions are left to the discretion of local Medicare carriers.

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**Regulatory Status**

Clinical laboratories may develop and validate tests in-house and market them as a laboratory service; laboratory-developed tests (LDTs) must meet the general regulatory standards of the Clinical Laboratory Improvement Act (CLIA). Exome or genome sequencing tests as a clinical service are available under the auspices of CLIA. Laboratories that offer LDTs must be licensed by CLIA for high-complexity testing. To date, the U.S. Food and Drug Administration has chosen not to require any regulatory review of this test.

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**References**


<table>
<thead>
<tr>
<th>Date</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td>11/11/13</td>
<td>New Policy. Whole exome sequencing is considered investigational for all indications. Policy renumbered from 2.04 to 12.04 to align with genetic testing category.</td>
</tr>
<tr>
<td>11/10/14</td>
<td>Annual Review. Policy updated with literature review through August 3, 2014. References 2, 4-5, and 8-13 added. Whole genome sequencing added to policy statement; whole genome sequencing considered investigational. New CPT codes, 81415-81417, 81425 and 81426, effective 1/1/15, added to the policy.</td>
</tr>
<tr>
<td>02/01/16</td>
<td>Coding update. Removed duplicate code 81416.</td>
</tr>
<tr>
<td>12/01/16</td>
<td>Annual Review, approved November 8, 2016. Policy updated with literature review through August 22, 2016; references 9, 11, 14, 16-18, and 20-22 added. Rationale revised. No change to the policy statement.</td>
</tr>
<tr>
<td>02/01/17</td>
<td>Annual Review, approved January 10, 2017. Policy updated with literature review through August 22, 2016; references 9, 11, 14, 16-18, and 20-22 added. Rationale revised. Whole exome sequencing, previously considered investigational, may now be considered medically necessary for diagnosis of individuals under the age of 18 with multiple congenital anomalies or a neurodevelopmental disorder. All other uses of whole exome and whole genome sequencing are considered investigational. Policy statement added that whole exome and whole genome sequencing are considered investigational for screening of asymptomatic individuals. Removed appendix table.</td>
</tr>
<tr>
<td>10/01/17</td>
<td>Coding update. Added new CPT code 0012U (effective 8/1/17).</td>
</tr>
<tr>
<td>10/06/17</td>
<td>Policy moved into new format; no change to policy statements.</td>
</tr>
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</table>

**Disclaimer:** This medical policy is a guide in evaluating the medical necessity of a particular service or treatment. The Company adopts policies after careful review of published peer-reviewed scientific literature, national guidelines and local standards of practice. Since medical technology is constantly changing, the Company reserves the right to review and update policies as appropriate. Member contracts differ in their benefits. Always consult the member benefit booklet or contact a member service representative to determine coverage for a specific medical service or supply.
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  • Information written in other languages

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PO Box 91102, Seattle, WA 98111
Toll free 855-332-4535, Fax 425-918-5592, TTY 800-537-7697 (TDD)

You can file a grievance in person or by mail, fax, or email. If you need help filing a grievance, the Civil Rights Coordinator is available to help you.

You can also file a civil rights complaint with the U.S. Department of Health and Human Services, Office for Civil Rights, electronically through the Office for Civil Rights Complaint Portal, available at https://ocrportal.hhs.gov/ocr/portal/lobby.jsf, or by mail or phone at:

U.S. Department of Health and Human Services
200 Independence Avenue SW, Room 509F, HHH Building
Washington, D.C. 20201, 1-800-368-1019, 800-537-7697 (TDD)


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Call 800-722-1471 (TTY: 800-842-5357).

Oromoo (Cushite):
Lakkoofsa bilbiila 800-722-1471 (TTY: 800-842-5357) ti bilbiila.

Français (French):

Kreyòl ayisyen (Creole):
Avi sila a gen Enfòmasyon Enpòtan ladinann. Avi sila a kapab genyen enfòmasyon enpòt an konsénan aplikasyon w lan oswa konvenen kouvèti asirans lan atravè Premera Blue Cross. Kapab genyen dat ki enpòt nan avisi sila a. Ou ka gen pou pou ane aksyon avan sèten dat limit pou ka konbe kouvèti asirans sante w la oswa pou yo ka ede w akèk depans yo. Se dwa w pou resewa enfòmasyon sa a ak asisants nan lang ou pale a, san ou pa gen pou peye pou sa. Rate nan 800-722-1471 (TTY: 800-842-5357).

Deutsche (German):

Hmoob (Hmong):
Tsab ntawv tsjhay xo no muaj cov ntsiab lus tseem ceb. Tej zaum tsab ntawv tsjhay xo no muaj cov ntsiab lus tseem ceb borg xo daim ntawv thov kev pab los yog koy qhov kev pab cuam los ntawm Premera Blue Cross. Tej zaum muaj cov hnbv tseem ceb uas rau hauv daim ntawv no. Tej zaum koy kuj yuav tau uq qee yam uas pab muaj koy uas tsip hauv daim ntawm no. Tej zaum koy kuj yuav tau uq qee yam uas pab muaj koy uas tsip hauv daim ntawm no. Tej zaum koy kuj yuav tau uq qee yam uas pab muaj koy uas tsip hauv daim ntawm no. Tej zaum koy kuj yuav tau uq qee yam uas pab muaj koy uas tsip hauv daim ntawm no.

Illok (Ilocano):
Daytoy a Pakdaa ket naglaon iti Napateg nga Impormasion. Daytoy a pakdaa mabalib nga adda ket naglaon iti napateg nga impormasion maipanggep iti aplikasyonwyo yowo coverage babena iti Premera Blue Cross. Daytoy ket mabalib dagiti importante a pelsa iti daytoy a pakdaar. Mabalib nga adda rumbeng nga aramidenyo nga addang sakbay dagiti partikular a naiitdung nga aldaw tapno mapagtalaindyo ti coverage ti sulan-ayyo yowo tulong kadagit gastos. Adda karbenganyo a mangala iti daytoy nga impormasion ken tulong iti bukodoxy a pagasasao nga awan ti bayadanyo. Tumawig ti numero nga 800-722-1471 (TTY: 800-842-5357).

Italiano (Italian):