Medical Policy

Proteogenomic Testing for Patients with Cancer (GPS Cancer Test)

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Policy Number: 838
BCBSA Reference Number: 2.04.140
NCD/LCD: N/A

Related Policies
None

Policy
Commercial Members: Managed Care (HMO and POS), PPO, and Indemnity Medicare HMO BlueSM and Medicare PPO BlueSM Members

Proteogenomic testing of patients with cancer (including, but not limited to GPS Cancer test) is considered INVESTIGATIONAL for all indications.

Prior Authorization Information
Pre-service approval is required for all inpatient services for all products.
See below for situations where prior authorization may be required or may not be required for outpatient services.
Yes indicates that prior authorization is required.
No indicates that prior authorization is not required.
N/A indicates that this service is primarily performed in an inpatient setting.

<table>
<thead>
<tr>
<th>Outpatient</th>
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<tbody>
<tr>
<td>Commercial Managed Care (HMO and POS)</td>
<td>This is not a covered service.</td>
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<tr>
<td>Commercial PPO and Indemnity</td>
<td>This is not a covered service.</td>
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<tr>
<td>Medicare HMO BlueSM</td>
<td>This is not a covered service.</td>
</tr>
<tr>
<td>Medicare PPO BlueSM</td>
<td>This is not a covered service.</td>
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CPT Codes / HCPCS Codes / ICD Codes

Inclusion or exclusion of a code does not constitute or imply member coverage or provider reimbursement. Please refer to the member’s contract benefits in effect at the time of service to determine coverage or non-coverage as it applies to an individual member.
Providers should report all services using the most up-to-date industry-standard procedure, revenue, and diagnosis codes, including modifiers where applicable.

The following codes are included below for informational purposes only; this is not an all-inclusive list.

**CPT Codes**
There is no specific CPT code for this test.

**Description**
This evidence review provides an overview of the emerging field of proteogenomics, with an emphasis on the currently available proteogenomic test, GPS Cancer test. In addition to focusing on the GPS Cancer test, this review describes and outlines types of proteogenomic research currently reported in the literature and that have potential clinical applications.

**PROTEOGENOMICS**
The term *proteome* refers to the entire complement of proteins produced by an organism or cellular system, and *proteomics* refers to the large-scale comprehensive study of a specific proteome. Similarly, the term *transcriptome* refers to the entire complement of transcription products (messenger RNAs [mRNAs]), and *transcriptomics* refers to the study of a specific transcriptome. Proteogenomics refers to the integration of genomic information with proteomic and transcriptomic information to provide a more complete picture of the function of the genome.

A system’s proteome is related to its genome and genomic alterations. However, while the genome is relatively static over time, the proteome is more dynamic and may vary over time and/or in response to selected stressors.1,2

Proteins undergo a number of modifications as part of normal physiologic processes. Following protein translation, modifications occur by splicing events, alternative folding mechanisms, and incorporation into larger complexes and signaling networks. These modifications are linked to protein function and result in functional differences that occur by location and over time.2 Some of the main potential applications of proteogenomics in medicine include:

- Identifying biomarkers for diagnostic, prognostic, and predictive purposes
- Detecting cancer by proteomic profiles or “signatures”
- Quantitating levels of proteins and monitoring levels over time for:
  - Cancer activity
  - Early identification of resistance to targeted tumor therapy
- Correlating protein profiles with disease states

Proteogenomics is an extremely complex field due to the intricacies of protein architecture and function, the many potential proteomic targets that can be measured, and the numerous testing methods used. We discuss the types of targets currently being investigated and the testing methods used and under development next.

**Proteomic Targets**
A proteomic target can be any altered protein that results from a genetic variant.3 Protein alterations can result from both germline and somatic genetic variants. Altered protein products include mutated proteins, fusion proteins, alternative splice variants, noncoding mRNAs, and posttranslational modifications (PTMs).

**Sequence Alterations (Mutated Protein)**
A mutated protein has an altered amino acid sequence that arises from a genetic variant. A single amino acid may be replaced in a protein or multiple amino acids in sequence may be affected.3 Mutated proteins can arise from either germline or somatic genetic variants. Somatic variants can be differentiated from germline variants by comparison with normal and diseased tissue.
Fusion Proteins
Fusion proteins are the product of one or more genes that fuse together. Most fusion genes discovered to date have been oncogenic, and fusion genes have been shown to have clinical relevance in a variety of cancers.

Alternative Splice Events
Posttranslational enzymatic splicing of proteins results in numerous protein isoforms. Alternative splicing events can lead to abnormal protein isoforms with altered function. Some alternative splicing events have been associated with tumor-specific variants.

Noncoding RNAs
Noncoding portions of the genome serve as the template for noncoding RNA (ncRNA), which plays various roles in the regulation of gene expression. There are 2 classes of ncRNA: shorter ncRNAs, which include microRNAs and related transcript products, and longer ncRNAs, which are thought to be involved in cancer progression.

Posttranslational Modifications
PTMs of histone proteins occur in normal cells and are genetically regulated. Histone proteins are found in the nuclei and play a role in gene regulation by structuring the DNA into nucleosomes. A nucleosome is composed of a histone protein core surrounded by DNA. Nucleosomes are assembled into chromatin fibers composed of multiple nucleosomes assembled in a specific pattern. PTMs of histone proteins include a variety of mechanisms, including methylation, acetylation, phosphorylation, glycosylation, and related modifications.

Proteogenomic Testing Methods
Proteogenomic testing involves isolating, separating, and characterizing proteins from biologic samples, followed by correlation with genomic and transcriptomic data. Isolation of proteins is accomplished by trypsin digestion and solubilization. The soluble mix of protein isolates is then separated into individual proteins. This is generally done in multiple stages using high-performance liquid chromatography ionexchange chromatography, 2-dimensional gel electrophoresis, and related methods. Once individual proteins are obtained, they may be characterized using various methods and parameters, some of which we describe below.

Immunohistochemistry/Fluorescence in situ Hybridization
Immunohistochemistry (IHC) and fluorescence in situ hybridization are standard techniques for isolating and characterizing proteins. IHC identifies proteins by using specific antibodies that bind to the protein. Therefore, this technique can only be used for known proteins and protein variants because it relies on the availability of a specific antibody. This technique also can only test a relatively small number of samples at once.

There are a number of reasons why IHC and fluorescence in situ hybridization are not well-suited for large-scale proteomic research. They are semiquantitative techniques and involve subjective interpretation. They are considered low-throughput assays that are time-consuming and expensive and require a relatively large tissue sample. Some advances in IHC and fluorescence in situ hybridization have addressed these limitations, including tissue microarray and reverse phase protein array.

- Tissue microarrays can be constructed that enable simultaneous analysis of up to 1000 tissue samples.
- Reverse phase protein array, a variation on tissue microarrays, allows for a large number of proteins to be quantitated simultaneously.

Mass Spectrometry
Mass spectrometry (MS) separates molecules by their mass to charge ratio and has been used as a research tool for studying proteins for many years. Development of technology that led to the application
of MS to biologic samples has advanced the field of proteogenomics rapidly. However, the application of MS to clinical medicine is in its formative stages. There are currently several types of mass spectrometers and a lack of standardization in the testing methods. Additionally, MS equipment is expensive and currently largely restricted to tertiary research centers.

The potential utility of MS lies in its ability to provide a wide range of proteomic information in an efficient manner, including:

- Identification of altered proteins;
- Delineation of protein or peptide profiles for a given tissue sample;
- Amino acid sequencing of proteins or peptides;
- Quantitation of protein levels;
- 3-dimensional protein structure and architecture; and
- Identification of PTMs.

“Top-down” MS refers to identification and characterization of all proteins in a sample without prior knowledge of which proteins are present. This method provides a profile of all proteins in a system, including documentation of PTMs and other protein isoforms. This method, therefore, provides a protein “profile” or “map” of a specific system. Following initial analysis, intact proteins can be isolated and further analyzed to determine amino acid sequences and related information.

“Bottom-up” MS refers to the identification of known proteins in a sample. This method identifies peptide fragments that indicate the presence of a specific protein. This method depends on having peptide fragments that can reliably identify a specific protein. Selective reaction monitoring-MS is a bottom-up modification of MS that allows for direct quantification and specific identification of low-abundance proteins without the need for specific antibodies. This method requires the selection of a peptide fragment or “signature” that is used to target the specific protein. Multiplex assays have also been developed to quantitate the epidermal growth factor receptor, human epidermal growth factor receptors 2 and 3, and insulin-like growth factor-1 receptor.

Bioinformatics
Due to the complexity of proteomic information, the multiple tests used, and the need to integrate this information with other genomic data, a bioinformatics approach is necessary to interpret proteogenomic data. Software programs are available that integrate and assist in the interpretation of the vast amounts of data generated by proteogenomics research. One software platform that integrates genomic and proteomic information is PARADIGM, which is used by The Cancer Genome Atlas (TCGA) project for data analysis. Other software tools currently available include:

- The Genome Peptide Finder matches the amino acid sequence of peptides predicted de novo with the genome sequence.
- The Proteogenomic Mapping Tool is an academic software for mapping peptides to the genome.
- Peppy is an automated search tool that generates proteogenomic data from translated databases and integrates this information for analysis.
- VESPA is a software tool that integrates data from various platforms and provides a visual display of integrated data.

Ongoing Proteogenomic Database Projects
Numerous ongoing databases are being constructed for proteogenomic research. Some are shown in Table 1.

There are also networks of researchers coordinating their activities in this field. The Clinical Proteomic Tumor Analysis Consortium is a coordinated project among 8 analysis sites sponsored by the National Cancer Institute. This project seeks to characterize the genomic and transcriptomic profiles of common cancers systematically. As of 2014, this consortium had cataloged proteomic information for breast,
colon, and ovarian cancers. All data from this project are freely available.

Many existing genomic databases have begun to incorporate proteomic information. TCGA intends to profile changes in the genomes of 20 different cancers. As part of its analysis, mRNA expression is used to help define signaling pathways that are either upregulated or deregulated in conjunction with genetic variations. Currently, TCGA has published comprehensive molecular characterizations of breast, colorectal, lung, gliomas, renal, and endometrial cancers.

Table 1. Proteogenomic Databases

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<tr>
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<tr>
<td>Human Protein Reference Database17,18</td>
<td>Centralized platform integrating information related to protein structure alterations, posttranslational modifications, interaction networks, and disease association. The intent is to catalog this information for each protein in the human proteome. Data compiled from published literature and publicly available databases.</td>
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<tr>
<td>Human Cancer Proteome Variation Database (CanProVar)19,20</td>
<td>Protein sequence database that integrates information from various publicly available datasets into 1 platform. Contains germline and somatic variants with an emphasis on cancer-related variants.</td>
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<tr>
<td>Cancer Mutant Proteome Database (CMPD)21,22</td>
<td>Protein sequence database compiled from the exome sequencing results of the NCI-60 cell lines, CCLE, and 5600 cases from TCGA network genomics studies. Contains germline and somatic variants with an emphasis on cancer-related variants.</td>
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<tr>
<td>ChimerDB 2.023</td>
<td>A comprehensive database of fusion proteins, including transcript products, compiled from various publicly available datasets.</td>
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<tr>
<td>The Synthetic Alternative Splicing Database (SASD)24</td>
<td>A comprehensive database of alternative splicing peptides and transcript products constructed from the Integrated Pathway Analysis Database.</td>
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<tr>
<td>NONCODE25</td>
<td>Database of noncoding RNAs integrating data from literature mining, specialized databases, and GenBank.</td>
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<tr>
<td>IncRNAtor26</td>
<td>Database of long noncoding RNA integrating data from multiple datasets including TCGA and ENCODE.</td>
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<td>CPTAC Data Portal27,28</td>
<td>Centralized data repository for proteomic data collected by Proteome Characterization Centers in the CPTAC. The portal currently hosts 6.3 TB of data and includes proteomics, transcriptomics, and genomics data of breast, colorectal, and ovarian tumor tissues from TCGA.</td>
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GPS CANCER TEST
The GPS Cancer test is a commercially available proteogenomic test intended for patients with cancer. The test includes whole-genome sequencing (20,000 genes, 3 billion base pairs), whole transcriptome (RNA) sequencing, and quantitative proteomics by mass spectrometry. The test is intended to inform personalized treatment decisions for cancer, and treatment options are listed when available, although treatment recommendations are not made. Treatment options may include U.S. Food and Drug Administration-approved targeted drugs with potential for clinical benefit, active clinical trials of drugs with potential for clinical benefit, and/or available drugs to which the cancer may be resistant.

Summary
Proteogenomics refers to the integration of genomic data with proteomic and transcriptomic data to provide a more complete picture of the function of the genome. The current focus of proteogenomics is primarily on the diagnostic, prognostic, and predictive potential of proteogenomics in various cancers. There is one commercially available proteogenomic test, the GPS Cancer test.
For individuals who have cancer and indications for genetic testing who receive proteogenomic testing (GPS Cancer test), the evidence includes cross-sectional studies that correlate results with standard testing and that report comprehensive molecular characterization of various cancers, and cohort studies that use proteogenomic markers to predict outcomes and that follow quantitative levels over time. Relevant outcomes are overall survival, disease-specific survival, test accuracy and validity, and treatment-related mortality and morbidity. There is no published evidence on the analytic validity or clinical utility of the GPS Cancer test. For proteogenomic testing in general, the research is at an early stage. There is a lack of standardization of testing methods and uncertain accuracy for most proteogenomic technologies. A few studies have described assay development and validation for proteogenomic targets and correlation of proteogenomic testing results with standard testing methods. Other studies have used proteogenomic in conjunction with genomic testing to provide a more comprehensive molecular characterization of various cancers. Very few studies have used proteogenomic tumor markers for diagnosis or prognosis, and at least 1 study has reported following quantitative protein levels for surveillance purposes. Further research is needed to standardize and validate proteogenomic testing methods. When standardized and validated testing methods are available, the analytic validity and clinical utility of proteogenomic testing can be adequately evaluated. The evidence is insufficient to determine the effect of the technology on health outcomes.

### Policy History

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### Information Pertaining to All Blue Cross Blue Shield Medical Policies

Click on any of the following terms to access the relevant information:
- Medical Policy Terms of Use
- Managed Care Guidelines
- Indemnity/PPO Guidelines
- Clinical Exception Process
- Medical Technology Assessment Guidelines

### References