Overview of the AMA Molecular Pathology CPT codes

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Reimbursement and CPT codes
- CPT code ≠ reimbursement
- List of services

Before January 1, 2013
- Used Molecular "stacking" CPT codes to get reimbursed
  Each step of test utilized a different CPT code to create a “stack”

CPT CODES

Creation of New AMA CPT codes for MolPath
- Tier 1
- Tier 2
- Multianalyte Assays with Algorithmic Analyses (MAAAs)

Why the new Molpath CPT codes?
- Payers wanted to know for what they were paying
- Needed clear and granular system
Relative Laboratory Testing Percentages

- Large reference laboratories
- Medium reference laboratories

New MolPath codes

- Tier 1 = analyte specific code
- Tier 2 = level of complexity code

Descriptor Caveats

- Disease state/condition is not an all inclusive list
- Common gene variant names are used
- The code includes all analytical services performed in the test (eg, cell lysis, nucleic acid stabilization, extraction, digestion, amplification, and detection)
- All analyses are qualitative unless otherwise noted

CPT Tier 1 Descriptor

- HUGO approved gene symbol (HUGO approved gene name) (eg, disease state/condition) gene analysis; analysis type

CPT Codes Tier 1 – BCR/ABL

- 81206 - BCR/ABL1 (t(9:22)) (eg, chronic myelogenous leukemia) translocation analysis; major breakpoint, qualitative or quantitative
- 81207 - Minor breakpoint, qualitative or quantitative
- 81208 - Other breakpoint, qualitative or quantitative
CPT Codes Tier 1 – CFTR

- **81220 - CFTR (cystic fibrosis transmembrane conductance regulator)** (eg, cystic fibrosis gene analysis; common variants (eg, ACOG/ACMG guidelines)
  - 81221 - Known familial variants
  - 81222 - Duplication/deletion variants
  - 81223 - Full gene sequence
  - 81224 - Intron 8 poly T analysis (eg, male infertility)

CPT Codes Tier 1 – aCGH

- **81228 - Cytogenomic constitutional (genome-wide) microarray analysis; interrogation of genomic regions for copy number variants (eg, bacterial artificial chromosome [BAC] or oligo-based comparative genomic hybridization [CGH] microarray analysis)
  - 81229 - Interrogation of genomic regions for copy number and single nucleotide polymorphism (SNP) variants for chromosomal abnormalities (Do not report 81228 in conjunction with 81229)

Tier 2

- Less common; lower volume assays
- Divided into 9 levels of complexity
- ~ 600 descriptors

81400 - Tier 2; level 1

- Identification of single germline variant [eg, SNP] by techniques such as restriction enzyme digestion or melt curve analysis

ACADM (acyl-CoA dehydrogenase, C-4 to C-12 straight chain, MCAD) (eg, medium chain acyl dehydrogenase deficiency), K304E variant

ACE (angiotensin converting enzyme) (eg, hereditary blood pressure regulation), insertion/deletion variant AGTR1 (angiotensin II receptor, type 1) (eg, essential hypertension), 1166A>C variant

BCKDHA (branched chain keto acid dehydrogenase E1, alpha polypeptide) (eg, maple syrup urine disease, type 1A), Y438N variant

CCR5 (chemokine C-C motif receptor 5) (eg, HIV resistance), 32-bp deletion mutation/794 825del32 deletion

81401 - Tier 2; level 2

- >10 SNPs, 2-10 methylated variants, or 2-10 somatic variants [typically using non-sequencing target variant analysis], immunoglobulin and T-cell receptor gene rearrangements, duplication/deletion variants of 1 exon, loss of heterozygosity [LOH], uniparental disomy [UPD]

Chromosome 18q: (eg, D18S55, D18S58, D18S61, D18S84, and D18S89) (eg, colon cancer), allelicimbalance assessment (ie, loss of heterozygosity)


ESR1/PGR (receptor 1/progesterone receptor) ratio (eg, breast cancer)

IGH@/BCL2 ([t(14;18)] (eg, follicular lymphoma) translocation analysis; major breakpoint region (MBR) and minor cluster region (mcr) breakpoints, qualitative or quantitative
### 81203 - Tier 2; level 4
- Analysis of single exon by DNA sequence analysis, analysis of >10 amplicons using multiplex PCR in 2 or more independent reactions, mutation scanning or duplication/deletion variants of 2-5 exons

- Known familial variant not otherwise specified, for gene listed in Tier 1 or Tier 2, DNA sequence analysis, each variant exon

- KRAS (Kirsten rat sarcoma viral oncogene), gene analysis, variant(s) in exon3 (eg, codon 61)
- MC4R (melanocortin 4 receptor) (eg, obesity), full gene sequence
- MICA (MHC class I polypeptide-related sequence A) (eg, solid organ transplantation), common variants (eg, *001, *002)
- MPL (myeloproliferative leukemia virus oncogene, thrombopoietin receptor, TPOR) (eg, myeloproliferative disorder), exon 10 sequence
- MT-RNR1 (mitochondrially encoded 12S RNA) (eg, nonsyndromic hearing loss), full gene sequence

### 81204 - Tier 2; level 5
- Analysis of 2-5 exons by DNA sequence analysis, mutation scanning or duplication/deletion variants of 6-10 exons, or characterization of a dynamic mutation disorder/triplet repeat by Southern blot analysis

- ACADS (acyl-CoA dehydrogenase, C-2 to C-3 short chain) (eg, short chain acyl-CoA dehydrogenase deficiency), targeted sequence analysis (eg, exons 5 and 6)
- AFR2 (AF4/FMR2 family member 2) (eg, fragile X mental retardation 2), characterization of alleles (eg, expanded size and methylation status)
- AQP2 (aquaporin 2) (eg, nephrogenic diabetes insipidus), full gene sequence
- ARX (aristaless related homeobox) (eg, X-linked lissencephaly with ambiguous genitalia, X-linked mental retardation), full gene sequence
- AVPR2 (arginine vasopressin receptor 2) (eg, nephrogenic diabetes insipidus), full gene sequence

### 81205 - Tier 2; level 6
- Analysis of 6-10 exons by DNA sequence analysis, mutation scanning or duplication/deletion variants of 11-25 exons, regionally targeted cytogenomic array

- CYP17A1 (cytochrome P450, family 17, subfamily A, polypeptide 1) (eg, congenital adrenarcheal hyperplasia), full gene sequence
- CYP21A2 (cytochrome P450, family 21, subfamily A, polypeptide2) (eg, steroid 21-hydroxylase isofrom, congenital adrenal hyperplasia), full gene sequence
- Cytogenomic constitutional targeted microarray analysis of chromosome 22q13 by interrogation of genomic regions for copy number and single nucleotide polymorphism (SNP) variants for chromosomal abnormalities
- Cytogenomic constitutional targeted microarray analysis of the X chromosome by interrogation of genomic regions for copy number and single nucleotide polymorphism (SNP) variants for chromosomal abnormalities
- DBT (dihydropyrimidinase branched chain transacylase E2) (eg, maple syrup urine disease, type 2), duplication/deletion analysis

### 81206 - Tier 2; level 7
- Analysis of 11-25 exons by DNA sequence analysis, mutation scanning or duplication/deletion variants of 26-50 exons, cytogenomic array analysis for neoplasia

- CRB1 (crumbs homolog 1) (eg, Leber congenital amaurosis), full gene sequence
- CREBBP (CREB binding protein) (eg, Rubinstein-Taybi syndrome), duplication/deletion analysis
- Cytogenomic microarray analysis, neoplasia (eg, interrogation of copy number, and loss-of-heterozygosity via single nucleotide polymorphism [SNP]-based comparative genomic hybridization [CGH] microarray analysis)
- DBT (dihydropyrimidinase branched chain transacylase E2) (eg, maple syrup urine disease, type 2), full gene sequence

### 81207 - Tier 2; level 8
- Analysis of 26-50 exons by DNA sequence analysis, mutation scanning or duplication/deletion variants of >50 exons, sequence analysis of multiple genes on one platform

- ABCC8 (ATP-binding cassette, sub-family C [CFTR/MRP], member 8) (eg, familial hyperinsulinism), full gene sequence
- AGL (amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase) (eg, glycogen storage disease typeIII), full gene sequence
- AH1 (Abelson helper integration site 1) (eg, Joubert syndrome), full gene sequence
- CACNA1A (calcium channel, voltage-dependent, P/Q type, alpha 1A subunit) (eg, familial hemiplegic migraine), full gene sequence
- CHD7 (chromodomain helicase DNA binding protein 7) (eg, CHARGE syndrome), full gene sequence
- COL4A4 (collagen, type IV, alpha 4) (eg, Alport syndrome), full gene sequence

### 81208 - Tier 2; level 9
- Analysis of >50 exons in a single gene by DNA sequence analysis

- COL4A5 (collagen, type IV, alpha 5) (eg, Alport syndrome), full gene sequence
- DMD (dystrophin) (eg, Duchenne/Becker muscular dystrophy), full gene sequence
- DYSF (dystrophin, limp girdle muscular dystrophy 2B [autosomal recessive]) (eg, limb-girdle muscular dystrophy), full gene sequence
- FB1N (fibulin 1) (eg, Marfan syndrome), full gene sequence
What do you do if your genes/analytes are not listed?

- 81479
- You cannot self assign
- You cannot use multiples of 81479
- Submit a coding change proposal (CCP)

Coding Change Proposal (CCP)

- Form available on AMA website
- References to document clinical validity
- Clinical vignette
- Description of service

Clinical vignette and description of service

Example: BRAF (eg, colorectal carcinoma) gene analysis, V600E variant

Clinical Vignette
- A 54-year-old man with metastatic colorectal carcinoma is being considered for targeted therapy with anti-epidermal growth factor receptor (EGFR) monoclonal antibodies. Initial molecular studies indicate the tumor does not contain any of 12 common KRAS mutations at codons 12 or 13. A tumor-rich tissue sample is submitted for BRAF gene mutation testing.

Description of Service
- Paraffin is removed, and high quality DNA is isolated from the patient’s tumor tissue. DNA is subjected to PCR amplification for exon 15 of the BRAF gene. The PCR products undergo bidirectional dideoxynucleotide chain termination sequencing on a capillary electrophoresis instrument. The pathologist or other qualified healthcare professional evaluates the electropherograms to identify nucleotide sequence variants. The pathologist or other qualified healthcare professional composes a report which specifies the patient’s mutation status. The report is edited, signed and the results are communicated to appropriate caregivers.

Parameters for Analyte Assignment

- In the case of Mendelian and somatic disorders, there is a demonstrated relationship between biomarker and phenotype (ie, clinical validity)
- Biomarkers (eg, SNPs) that have an association but not a proven causative effect to a known clinical phenotype(s) should have demonstrated clinical usefulness (eg, high positive predictive value, high negative predictive value, directing therapy/management).
- At least two U.S. laboratories are performing the analysis, unless proprietary (eg, intellectual property) issues exist
- The analysis involves ≥ 10 variants identified in unrelated families. Multiple reports of the same variant may be included.
- For dup/del assessment for Tier 2 code assignment the following guidelines will be used: Search GeneTests database. If ≥ 10% of disease alleles are associated with dup/del and ≥ 2 dup/dels are documented, place dup/del for analyte on Tier 2 list.
  If BIOBASE HGMD® Professional database search identifies ≥ 10% of variants that are associated with dup/del (gross deletion or insertion variants/total number of BIOBASE® variants reported), place dup/del for analyte on Tier 2 list.

From CCP

Where does NGS/Multi-Gene panels fit?

- AMP submitted a Coding Change Proposal (CCP) Multi-gene panels
  - Quantitative genomic sequence analysis
  - Exome genomic sequence analysis
  - Genome genomic sequence analysis
  - Separates report and interpretation from analytes
  - Provides mechanism for re-analysis
  - AMA convened an open meeting for all to discuss
  - AMA developed new CPT codes for 2015

NGS/Multi-gene Panels

- 81410: Aortic Dysfunction
- 81430: Nonsyndromic Hearing Loss
- 81470: X-Linked Intellectual Disability
- 81435: Inherited Colon Cancer
- 81420: Fetal Chromosomal Aneuploidy
- 81445: Targeted Neoplastic Genomic Sequence
- 81460: Whole Mitochondrial
- 81415: Whole Exome
- 81425: Whole Genome

www.ama-assn.org
MAAAs

- CMS announced that MAAA codes will be gapfilled if the Medicare contractor determines that the code is payable under the CLFS.


Questions

- Why didn’t each gene get its own code? Not enough available CPT codes
- Can a code be moved from Tier 2 to Tier 1? Yes; has to be requested by a Coding Change Proposal and approved by the AMA

Physician fee schedule (PFS) vs. Clinical lab fee schedule (CLFS)

- Background
  - Molecular "stacking" codes were on CLFS
  - The RUC recommended PFS
    - Specialty Society Relative Value Update Committee (RUC) = AMA multi-specialty committee tasked with making relative value recommendations to CMS for new and revised codes, as well as annually updating relative value units (RVUs) to reflect changes in medical practice
  - Federal laws related to physician practice
    - MD vs PhD
    - Copays
    - Anti kickback rules
    - Physician signature requirements
  - CMS placed all new Tier 1 and Tier 2 codes on CLFS

PFS vs. CLFS – Physician practice

- 42 CFR 415.130 Physician pathology services. The carrier pays for pathology services furnished by a physician to an individual beneficiary on a fee schedule basis only if the services meet the conditions for payment in § 415.102(a)* and are one of the following services:
  1. Surgical pathology services.
  2. Specific cytopathology, hematology, and blood banking services that have been identified to require performance by a physician and are listed in program operating instructions.
  3. Clinical consultation services that meet the requirements in paragraph (c) of this section.
  4. Clinical laboratory interpretative services that meet the requirements of paragraphs (C)(1), (c)(3), and (c)(4) of this section and that are specifically listed in program operating instructions.

* § 415.102(a) requires the services be ordinarily performed by a physician and directly contribute to the diagnosis of an individual patient.

PFS vs. CLFS – other requirements

- Placement of MolPath CPT codes on PFS: Labs would have to collect 20% copays
- Special signature rules not required of clinical laboratory tests, and Medicare policies regarding physician kickbacks and purchased test rules different than those for clinical laboratory tests, and Pathology tests are paid on a different, and much lower fee schedule, in the Medicare Hospital Outpatient setting, whereas clinical laboratory tests are paid on the same clinical laboratory fee schedule in this setting.
- Indirect costs would be assigned on the basis of all pathologist indirect costs, including hospital-based pathologists and the mean indirect costs of pathology tests, dominated by the routine preparation of paraffin blocks and slides. These indirect costs likely far below the indirect expense of a molecular diagnostics center, with far more expensive staff, development, and QC costs.
Coding for Physician Interpretation and Reporting

- CMS created Healthcare Common Procedure Coding System (HCPCS) code G0452 (Molecular pathology procedure: physician interpretation and report) effective Jan 1, 2013
- This code allows physicians (MDs) to bill for interpretation and reporting services that go beyond the technical reporting of test results
- The code CANNOT be billed by non-physician geneticists or other lab personnel
- The rates established for the Tier 1 and Tier 2 codes are meant to account for work performed by non-physician personnel, including PhD-certified geneticists
- In 2013, this code is reimbursed at $18.71 under the Medicare Physician Fee Schedule (MPFS)

Crosswalking

- If test is comparable to an existing test
- CMS sets reimbursement of new test to existing test
- Assigned a local fee and corresponding National Limitation Amount (NLA)

<table>
<thead>
<tr>
<th>HCPCS</th>
<th>Description</th>
<th>Local</th>
<th>Mid</th>
</tr>
</thead>
<tbody>
<tr>
<td>81227</td>
<td>CYP2C9 (cytochrome P450, family 2, subfamily C, polypeptide 9) (eg, drug metabolism), common variants (eg, *2, *3, *4, *8, *17) familial variant</td>
<td>$199.00</td>
<td>$199.00</td>
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<tr>
<td>81225</td>
<td>CYP2C19 (cytochrome P450, family 2, subfamily C, polypeptide 19) (eg, drug metabolism), common variants (eg, *2XN, *4XN)</td>
<td>$227.00</td>
<td>$227.00</td>
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<tr>
<td>81217</td>
<td>BRCA2 (breast cancer 2) (eg, hereditary breast and ovarian cancer) gene analysis, uncommon duplication/deletion variants (eg, 13 del 3.835kb, exon 13 dup 6kb, exon 14-20 del 26kb, exon 22 del 510bp, exon 8-9 del 7.1kb)</td>
<td>$358.47</td>
<td>$358.47</td>
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<tr>
<td>81213</td>
<td>BRCA1, BRCA2 (breast cancer 1 and 2) (eg, hereditary breast and ovarian cancer) gene analysis, full sequence analysis and common duplication/deletion variants in BRCA1 (ie, exon 12 del 13.8kb, exon 13 dup 6kb, exon 16 del 26kb, exon 22 del 510bp, exon 8-9 del 7.1kb)</td>
<td>$178.64</td>
<td>$178.64</td>
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<tr>
<td>81210</td>
<td>BRAF (v-raf murine sarcoma viral oncogene homolog B1) (eg, colon cancer), gene analysis, qualitative or quantitative breakpoint, full sequence analysis and common duplication/deletion variants in BRCA1 (ie, exon 12 del 13.8kb, exon 13 dup 6kb, exon 16 del 26kb, exon 22 del 510bp, exon 8-9 del 7.1kb)</td>
<td>$178.64</td>
<td>$178.64</td>
</tr>
</tbody>
</table>

2 methods for CMS to determine reimbursement

- Crosswalk
- Gapfill

Gapfilling

- CMS determines no adequate comparable
- Medicare carriers are instructed to Gapfill
  - Empirical process based on local pricing patterns
  - Medical Directors may meet and share information regarding the new test, though cannot reach a formal consensus.
  - Approximate Timeline
    - April 30 - CMS posted interim contractor-specific amounts online
    - 60-day comment period on interim amounts (May-June)
  - CMS posts final contractor-specific amounts and National Limitation Amounts (NLA) online
  - CMS sets the NLA for each CPT code at the median of the contractor specific amounts
  - Reconsideration requests accepted for 30 days
  - Final NLAs made effective January 1 for the entire country

CMS posted Gapfill rates Tier1

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<tr>
<td>81275</td>
<td>KRAS (v-Ki-ras2 Kirsten rat sarcoma viral oncogene) (eg, carcinoma) gene analysis, variants in codons 12 and 13</td>
<td>$198.97</td>
<td>$198.97</td>
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<tr>
<td>81270</td>
<td>JAK2 (Janus kinase 2) (eg, myeloproliferative disorder) gene analysis, p.Val617Phe (V617F) variant</td>
<td>$126.00</td>
<td>$126.00</td>
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<tr>
<td>81268</td>
<td>Chimerism (engraftment) analysis, post hematopoietic stem cell transplantation specimen, includes comparison to previously performed baseline analysis, critical ill recipient and donor germline testing, post-transplant non-hematopoietic recipient germline testing, or donor testing, twin zygosity testing, or maternal cell contamination of hematopoietic tissue</td>
<td>$285.17</td>
<td>$285.17</td>
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<tr>
<td>81267</td>
<td>Chimerism (engraftment) analysis, post hematopoietic stem cell transplantation specimen, includes comparison to previously performed baseline analysis, critical ill recipient and donor germline testing, post-transplant non-hematopoietic recipient germline testing, or donor testing, twin zygosity testing, or maternal cell contamination of hematopoietic tissue</td>
<td>$285.17</td>
<td>$285.17</td>
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<tr>
<td>81264</td>
<td>IGK@ (Immunoglobulin kappa light chain locus) (eg, leukemia and lymphoma), gene rearrangement analysis to detect abnormal clonal population(s); amplified methodology (eg, polymerase chain reaction)</td>
<td>$455.00</td>
<td>$455.00</td>
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Gapfill rates, con't

<table>
<thead>
<tr>
<th>HCPCS</th>
<th>Description</th>
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<tbody>
<tr>
<td>81256</td>
<td>HFE (hemochromatosis) (eg, hereditary hemochromatosis) gene analysis; common variants (eg, C282Y, H63D)</td>
<td>$294.00</td>
<td>$294.00</td>
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<tr>
<td>81245</td>
<td>FLT3 (fms-related tyrosine kinase 3) (eg, acute myeloid leukemia), gene analysis, internal tandem duplication (ITD) variants (ex, exon 13, 14)</td>
<td>$93.94</td>
<td>$93.94</td>
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<td>81235</td>
<td>EGFR (epidermal growth factor receptor) (eg, non-small cell lung cancer) gene analysis; common variants (eg, L858R, T790M, G719A, G719S, L861Q)</td>
<td>$176.40</td>
<td>$176.40</td>
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<tr>
<td>81231</td>
<td>ESR1 (estrogen receptor 1) (eg, breast adenocarcinoma), gene rearrangement analysis to detect abnormal clonal population(s), critical ill recipient and donor germline testing, post-transplant non-hematopoietic recipient germline testing, or donor testing, twin zygosity testing, or maternal cell contamination of hematopoietic tissue</td>
<td>$180.60</td>
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<td>81221</td>
<td>ETV6 (v-ets erythroleukemia viral related) (eg, leukemia and lymphoma), gene rearrangement analysis to detect abnormal clonal population(s), critical ill recipient and donor germline testing, post-transplant non-hematopoietic recipient germline testing, or donor testing, twin zygosity testing, or maternal cell contamination of hematopoietic tissue</td>
<td>$199.08</td>
<td>$199.08</td>
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<tr>
<td>81220</td>
<td>ETV6 (v-ets erythroleukemia viral related) (eg, leukemia and lymphoma), gene rearrangement analysis to detect abnormal clonal population(s), critical ill recipient and donor germline testing, post-transplant non-hematopoietic recipient germline testing, or donor testing, twin zygosity testing, or maternal cell contamination of hematopoietic tissue</td>
<td>$225.38</td>
<td>$225.38</td>
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Crosswalking

- If test is comparable to an existing test
- CMS sets reimbursement of new test to existing test
- Assigned a local fee and corresponding National Limitation Amount (NLA)
**Gapfill rates, con’t**

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<thead>
<tr>
<th>HCPCS</th>
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<th>National</th>
<th>Local</th>
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<th>NFL</th>
<th>RFL</th>
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<tbody>
<tr>
<td>81377</td>
<td>HLA Class II typing, low resolution (eg, antigen equivalents); one antigen equivalent, each</td>
<td>$126.20</td>
<td>$126.20</td>
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<tr>
<td>81376</td>
<td>HLA Class II typing, low resolution (eg, antigen equivalents); one locus(eg, HLA-DRB1, -DRB3/4/5, -DQB1, -DQA1, -DPB1, or -DPA1)</td>
<td>$290.01</td>
<td>$290.01</td>
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<td>81375</td>
<td>HLA Class II typing, low resolution (eg, antigen equivalents); HLA-DRB1/3/4/5 and -DQB1</td>
<td>$303.43</td>
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<td>81373</td>
<td>HLA Class I typing, low resolution (eg, antigen equivalents); one locus (eg, HLA-A, -B, or -C), each</td>
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<td>HLA Class I typing, low resolution (eg, antigen equivalents); complete (ie, HLA-A, -B, and -C)</td>
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<td>81371</td>
<td>HLA Class I and II typing, low resolution (eg, antigen equivalents); HLA-A, -B, and -DRB1</td>
<td>$475.00</td>
<td>$475.00</td>
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<td>81317</td>
<td>Microsatellite instability analysis (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; full sequence analysis</td>
<td>$398.03</td>
<td>$398.03</td>
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<td>81299</td>
<td>MSH6 (mutS homolog 6 [E. coli]) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; duplication/deletion variants</td>
<td>$168.00</td>
<td>$168.00</td>
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<td>81293</td>
<td>MLH1 (mutL homolog 1, colon cancer, nonpolyposis type 2) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; duplication/deletion variants</td>
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<td>$100.00</td>
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<td>MTHFR (5,10-methylenetetrahydrofolate reductase) (eg, hereditary hypercoagulability) gene analysis; known familial variants</td>
<td>$60.00</td>
<td>$60.00</td>
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<tr>
<td>81291</td>
<td>MTHFR (5,10-methylenetetrahydrofolate reductase) (eg, hereditary hypercoagulability) gene analysis; duplication/deletion variants</td>
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<td>$651.12</td>
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<td>81282</td>
<td>TRB@ (T cell antigen receptor, beta) (eg, leukemia and lymphoma), gene rearrangement analysis to detect abnormal clonal population(s); using direct probe methodology (eg, polymerase chain reaction) translocation analysis; single breakpoint (eg, intron 3, intron 6 or exon 6), qualitative or quantitative</td>
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<td>$787.19</td>
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<td>81332</td>
<td>SERPINA1 (serpin peptidase inhibitor, clade A, alpha-1 antiproteinase, antitrypsin, member 1) (eg, alpha-1-antitrypsin deficiency), gene analysis, common variants (eg, *S and *Z)</td>
<td>$68.16</td>
<td>$68.16</td>
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<tr>
<td>81342</td>
<td>TRG@ (T cell antigen receptor, gamma) (eg, leukemia and lymphoma), gene rearrangement analysis to detect abnormal clonal population(s)</td>
<td>$284.97</td>
<td>$284.97</td>
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<tr>
<td>81318</td>
<td>PMS2 (postmeiotic segregation increased 2 [S. cerevisiae]) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; full sequence analysis</td>
<td>$100.00</td>
<td>$100.00</td>
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</tbody>
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**Genomic sequencing procedure (GSPs) codes**

- CMS to Gap-fill
- Similar process to MolPath
- Final reimbursement expected in late summer 2015

[http://www.cms.gov/Medicare/Medicare-Fee-for-Service-Payment/ClinicalLabFeeSched/Laboratory_Public_Meetings.html](http://www.cms.gov/Medicare/Medicare-Fee-for-Service-Payment/ClinicalLabFeeSched/Laboratory_Public_Meetings.html)

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**Medicare Administrative Contractors (MACs)**

**Proposed MAC Gapfill Rates**

- Many of the MACs appear to have coordinated on their proposed gap-fill rates for MolPath
- Although some MACs (such as Palmetto) established payment rates for individual analyses assigned to each Tier 2 code, CMS did not include them in their release
- CMS has finalized reimbursement levels for any Tier 2 codes MACs will continue to establish prices for tests that fall in this coding category.
Summary

- The complete revision of the MolPath CPTs has had a huge impact on reimbursement for molecular pathology assays