

The Commonwealth of Massachusetts Executive Office of Health and Human Services One Ashburton Place, 11th Floor Boston, MA 02108

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Administrative Bulletin 13-03

114.3 CMR 20.00: Coding Updates for Clinical Laboratory Services Effective January 1, 2013

Under the authority of regulation 114.3 CMR 20.01(3), "Coding Updates and Corrections," the Executive Office of Health and Human Services (EOHHS) is adding new procedure codes and deleting outdated codes as specified in the calendar year 2013 Centers for Medicare & Medicaid Services New Clinical Laboratory Fee Schedule Test Codes and Final Payment Determinations. The rates for code additions are priced at 74.67% of the prevailing Medicare fee if available, with the exception of code 81217 which directly replaces deleted code S3820. The rate for code 81217 is paid at the current rate of the deleted code S3820 contained in 114.3 CMR 20.00: Clinical Laboratory Services. The changes below are effective January 1, 2013.

All other codes in this bulletin that require pricing are reimbursed at individual consideration (I.C.). Rates listed in this informational bulletin are applicable until revised rates are issued by EOHHS. Deleted codes will no longer be available for use after 2012.

| Code | Change | Rate | Code Description |
|-------|----------|----------|--|
| 81201 | Addition | I.C. | APC (adenomatous polyposis coli) (eg, familial adenomatosis polyposis [FAP], attenuated FAP) gene analysis; full gene sequence |
| 81202 | Addition | I.C. | APC (adenomatous polyposis coli) (eg, familial adenomatosis polyposis [FAP], attenuated FAP) gene analysis; known familial variants |
| 81203 | Addition | I.C. | APC (adenomatous polyposis coli) (eg, familial adenomatosis polyposis [FAP], attenuated FAP) gene analysis; duplication/deletion variants |
| 81217 | Addition | \$385.00 | BRCA2 (breast cancer 2) (e.g. hereditary breast and ovarian cancer) gene analysis; full sequence analysis; known familial variant |
| 81235 | Addition | I.C. | EGFR (epidermal growth factor receptor) (eg, non-small cell lung cancer) gene analysis, common variants (e.g., exon 19 LREA deletion, L858R, T790M, G719A, G719S, L861Q) |
| 81252 | Addition | I.C. | GJB2 (gap junction protein, beta 2, 26kDa, connexin 30) (e.g., nonsyndromic hearing loss) gene analysis; full gene analysis |
| 81253 | Addition | I.C. | GJB2 (gap junction protein, beta 2, 26kDa, connexin 30) (e.g., nonsyndromic hearing loss) gene analysis; known familial variants |
| 81254 | Addition | I.C. | GJB6 (gap junction protein, beta 6, 30kDa, connexin 30) |

| | | | (e.g, nonsyndromic hearing loss), gene analysis, common variants (eg, 309kb [del(GJB6-D13S1830)] and 232kb |
|-------|---------------|---------|---|
| | | | [del(GJB6-D13S1854)]) |
| 81321 | Addition | I.C. | PTEN (phosphatase and tensin homolog) (e.g., Cowden syndrome, PTEN hamartoma tumor syndrome) gene |
| 21222 | | | analysis; full sequence analysis |
| 81322 | Addition | I.C. | PTEN (phosphatase and tensin homolog) (e.g., Cowden |
| | | | syndrome, PTEN hamartoma tumor syndrome) gene |
| 04222 | ۸ ماماندن میم | 1.0 | analysis; known familial variant |
| 81323 | Addition | I.C. | PTEN (phosphatase and tensin homolog) (e.g., Cowden |
| | | | syndrome, PTEN hamartoma tumor syndrome) gene analysis; duplication/ deletion analysis |
| 81324 | Addition | I.C. | PMP22 (peripheral myelin protein 22) (e.g., Charcot-Marie- |
| 01324 | Addition | 1.0. | Tooth, hereditary neuropathy with liability to pressure |
| | | | palsies) gene analysis; duplication/deletion analysis |
| 81325 | Addition | I.C. | PMP22 (peripheral myelin protein 22) (e.g., Charcot-Marie- |
| 01020 | , taaition | | Tooth, hereditary neuropathy with liability to pressure |
| | | | palsies) gene analysis; full sequence analysis |
| 81326 | Addition | I.C. | PMP22 (peripheral myelin protein 22) (e.g., Charcot-Marie- |
| | | | Tooth, hereditary neuropathy with liability to pressure |
| | | | palsies) gene analysis; known familial variant |
| 81479 | Addition | I.C. | Unlisted molecular pathology procedure |
| 81500 | Addition | I.C. | Oncology (ovarian), biochemical assays of two proteins (CA- |
| | | | 125 and HE4), utilizing serum, with menopausal status, |
| | | | algorithm reported as risk score |
| 81503 | Addition | I.C. | Oncology (ovarian), biochemical assays of five proteins (CA- |
| | | | 125, apoliproprotein A1, beta-2 microglobulin, transferring, |
| | | | pre-albumin), utilizing serum, algorithm reported as a risk |
| | | | score |
| 81506 | Addition | I.C. | Endocrinology (type 2 diabetes), biochemical assays of |
| | | | seven analytes (glucose, HbA1c, insulin, hs-CRP, |
| | | | adoponectin, ferritin, interleukin 2-receptor alpha), utilizing |
| 01500 | Addition | 1.0 | serum or plasma, algorithm reporting a risk score |
| 81508 | Addition | I.C. | Fetal congenital abnormalities, biochemical assays of two proteins (PAPP-A, hCG [any form]), utilizing maternal |
| | | | serum, algorithm reported as a risk score |
| 81509 | Addition | I.C. | Fetal congenital abnormalities, biochemical assays of three |
| 01303 | Addition | 1.0. | proteins (PAPP-A, hCG [any form], DIA), utilizing maternal |
| | | | serum, algorithm reported as a risk score |
| 81510 | Addition | I.C. | Fetal congenital abnormalities, biochemical assays of three |
| | | | analytes (AFP, uE3, hCG [any form]), utilizing maternal |
| | | | serum, algorithm reported as a risk score |
| 81511 | Addition | I.C. | Fetal congenital abnormalities, biochemical assays of four |
| | | | analytes (AFP, uE3, hCG [any form], DIA), utilizing maternal |
| | | | serum, algorithm reported as a risk score (may include |
| | | | additional results from previous biochemical testing) |
| 81512 | Addition | I.C. | Fetal congenital abnormalities, biochemical assays of five |
| | | | analytes (AFP, uE3, hCG [any form], hyperglycosylated |
| | | | hCG, DIA), utilizing maternal serum, algorithm reported as a |
| 04500 | A 1 1:4: | 1.0 | risk score |
| 81599 | Addition | I.C. | Unlisted multianalyte assay with algorithmic analysis |
| 82777 | Addition | \$13.29 | Galectin-3 Melocular diagnostical malacular isolation or outraction |
| 83890 | Deletion | | Molecular diagnostics; molecular isolation or extraction, each nucleic acid type (i.e., DNA or RNA) |
| 83891 | Deletion | | Molecular diagnostics; isolation or extraction of highly |
| | | | purified nucleic acid, each nucleic acid type (i.e., DNA or |

| | | | RNA) |
|-------|-------------|---------|--|
| 83892 | Deletion | | Molecular diagnostics; enzymatic digestion, each enzyme |
| 00002 | Deletion | | treatment |
| 83893 | Deletion | | Molecular diagnostics; dot/slot blot production, each nucleic |
| 03033 | Deletion | | acid preparation |
| 83894 | Deletion | | Molecular diagnostics; separation by gel electrophoresis |
| 03094 | Deletion | | (e.g., agarose, polyacrylamide), each nucleic acid |
| | | | |
| 83896 | Deletion | | preparation Molecular diagnostics; nucleic acid probe, each |
| | | | |
| 83897 | Deletion | | Molecular diagnostics; nucleic acid transfer (e.g., Southern, Northern), each nucleic acid preparation |
| 83898 | Deletion | | Molecular diagnostics; amplification, target, each nucleic |
| | | | acid sequence |
| 83900 | Deletion | | Molecular diagnostics; amplification, target, multiplex, first 2 |
| | | | nucleic acid sequences |
| 83901 | Deletion | | Molecular diagnostics; amplification, target, multiplex, each |
| | | | additional nucleic acid sequence beyond 2 (List separately |
| | | | in addition to code for primary procedure) |
| 83902 | Deletion | | Molecular diagnostics; reverse transcription |
| | Deletion | | Molecular diagnostics; mutation scanning, by physical |
| | | | properties (e.g., single strand conformational polymorphisms |
| | | | [SSCP] heteroduplex, denaturing gradient gel |
| | | | electrophoresis ([DGGE], RNA'ase A), single segment, each |
| 83904 | Deletion | | Molecular diagnostics; mutation identification by |
| | 20.0 | | sequencing, single segment, each segment |
| 83905 | Deletion | | Molecular diagnostics; mutation identification by allele |
| | Bolotion | | specific transcription, single segment, each segment |
| 83906 | Deletion | | Molecular diagnostics; mutation identification by allele |
| | Bolotion | | specific translation, single segment, each segment |
| 83907 | Deletion | | Molecular diagnostics; lysis of cells prior to nucleic acid |
| 00007 | Deletion | | extraction (e.g., stool specimens, paraffin, embedded |
| | | | tissue), each specimen |
| 83908 | Deletion | | Molecular diagnostics; amplification, signal, each nucleic |
| 00000 | Deletion | | acid sequence |
| 83909 | Deletion | | Molecular diagnostics; separation and identification by high |
| 03909 | Deletion | | resolution technique (e.g., capillary electrophoresis), each |
| | | | nucleic acid preparation |
| 83912 | Deletion | | Molecular diagnostics; interpretation and report |
| | Deletion | | Molecular diagnostics; RNA stabilization |
| | Deletion | | Mutation identification by enzymatic ligation or primer |
| 03914 | Deletion | | |
| | | | extension, single segment, each segment (e.g., |
| | | | oligonucleotide ligation assay [OLA], single base chain |
| 96450 | V ddition | 1.0 | extension [SBCE], or allele-specific primer extension |
| 86152 | Addition | I.C. | Cell enumeration using immunologic selection and |
| | | | identification in fluid specimen (e.g., circulation tumor cells in |
| 96450 | ۸ طط:۲: ۵:- | 1.0 | blood); |
| 86153 | Addition | I.C. | Cell enumeration using immunologic selection and |
| | | | identification in fluid specimen (e.g., circulation tumor cells in |
| 06744 | ۸ طط:۲: ۵:- | ¢44.70 | blood); physician interpretation and report |
| | Addition | \$14.78 | Antibody; JC (John Cunningham) virus |
| 86828 | Addition | \$40.62 | Antibody to human leukocyte antigens (HLA), solid phase |
| | | | assays (e.g., microspheres or beads, ELISA, flow |
| | | | cytometry); qualitative assessment of the presence or |
| | | | absence of antibody(ies) to HLA Class I and Class II HLA |
| | | 1 | antigens |

| 86829 | Addition | \$30.47 | Antibody to human leukocyte antigens (HLA), solid phase assays (e.g., microspheres or beads, ELISA, flow cytometry); qualitative assessment of the presence or |
|-------|------------|----------|--|
| | | | absence of antibody(ies) to HLA Class I or Class II HLA antigens |
| 86830 | Addition | \$82.27 | Antibody to human leukocyte antigens (HLA), solid phase |
| | | | assays (e.g., microspheres or beads, ELISA, flow |
| | | | cytometry); antibody identification by qualitative panel using |
| 06024 | A ddition | \$70.F0 | complete HLA phenotypes; HLA Class I |
| 86831 | Addition | \$70.52 | Antibody to human leukocyte antigens (HLA), solid phase assays (e.g., microspheres or beads, ELISA, flow |
| | | | cytometry); antibody identification by qualitative panel using |
| | | | complete HLA phenotypes; HLA Class II |
| 86832 | Addition | \$129.28 | Antibody to human leukocyte antigens (HLA), solid phase |
| | | | assays (e.g., microspheres or beads, ELISA, flow |
| | | | cytometry); high definition qualitative panel for identification |
| | | | of antibody specificities (e.g., individual antigen per bead methodology), HLA Class I |
| 86833 | Addition | | Antibody to human leukocyte antigens (HLA), solid phase |
| 00000 | / tadition | \$117.53 | assays (e.g., microspheres or beads, ELISA, flow |
| | | , | cytometry); high definition qualitative panel for identification |
| | | | of antibody specificities (e.g., individual antigen per bead |
| 20004 | A 1 11/1 | 000101 | methodology), HLA Class II |
| 86834 | Addition | \$364.34 | Antibody to human leukocyte antigens (HLA), solid phase |
| | | | assays (e.g., microspheres or beads, ELISA, flow cytometry); semi-qualitative panel (e.g., titer), HLA Class I |
| 86835 | Addition | \$329.09 | Antibody to human leukocyte antigens (HLA), solid phase |
| | | , | assays (e.g., microspheres or beads, ELISA, flow |
| | | | cytometry); semi-qualitative panel (e.g., titer), HLA Class II |
| 87631 | Addition | \$77.76 | Infectious agent detection by nucleic acid (DNA or RNA); |
| | | | respiratory virus (e.g., adenovirus, influenza virus, |
| | | | coronavirus, metapneumovirus, parainfluenza virus, respiratory syncytial virus, rhinovirus), multiplex reverse |
| | | | transcription and amplified probe technique, multiple types |
| | | | and subtypes, 3-5 targets |
| 87632 | Addition | \$117.90 | Infectious agent detection by nucleic acid (DNA or RNA); |
| | | | respiratory virus (e.g., adenovirus, influenza virus, |
| | | | coronavirus, metapneumovirus, parainfluenza virus, |
| | | | respiratory syncytial virus, rhinovirus), multiplex reverse transcription and amplified probe technique, multiple types |
| | | | and subtypes, 6-11 targets |
| 87633 | Addition | \$218.26 | Infectious agent detection by nucleic acid (DNA or RNA); |
| | | | respiratory virus (e.g., adenovirus, influenza virus, |
| | | | coronavirus, metapneumovirus, parainfluenza virus, |
| | | | respiratory syncytial virus, rhinovirus), multiplex reverse |
| | | | transcription and amplified probe technique, multiple types and subtypes, 12-25 targets |
| 87910 | Addition | \$84.44 | Infectious agent genotype analysis by nucleic acid (DNA or |
| | | | RNA); ctyomegalovirus |
| 87912 | Addition | \$84.44 | Infectious agent genotype analysis by nucleic acid (DNA or |
| | | | RNA); Hepitatis B virus |