

---

**Lab Dept:**                    **Anatomic Pathology**

**Test Name:**                **OTOGENOME TEST FOR HEARING LOSS**

---

***General Information***

**Lab Order Codes:**        OTOG

**Synonyms:**                Hearing Loss Genes

**CPT Codes:**              81430 x1 – Hearing loss (eg, nonsyndromic hearing loss, Usher syndrome, Pendred syndrome); genomic sequence analysis panel, must include at least 60 genes  
81431 X1 – Hearing loss; deletion/duplication panel

**Test Includes:**            Sequence testing for 70 genes known to cause nonsyndromic hearing loss and syndromes that can present as nonsyndromic.

---

***Logistics***

**Test Indications:**        Evaluation of undiagnosed hearing loss.

**Lab Testing Section:**    Anatomic Pathology - Sendouts

**Referred to:**              Harvard Medical School Laboratory for Molecular Genetics

**Phone Numbers:**        MIN Lab: 612-813-6280

STP Lab: 651-220-6550

**Test Availability:**        Daily, 24 hours

**Turnaround Time:**        8 - 12 weeks

**Special Instructions:**    Please send completed [Harvard requisition and consent](#) with the patient or specimen to the laboratory. The consent portion of the form is required. Please note that incomplete or missing paperwork may delay the start of testing.

---

***Specimen***

**Specimen Type:**            Whole blood

**Container:**                 Lavender top (EDTA) tube

**Draw Volume:**             7 mL (Minimum 3-5 mL for an infant) blood

<b>Processed Volume:</b>	Same as Draw Volume
<b>Collection:</b>	Routine venipuncture
<b>Special Processing:</b>	Lab Staff: Send lavender tubes labeled with a minimum of Name, Date of Birth, and Age. The reference laboratory accepts samples Monday through Friday from 9am to 5pm. Labeled specimens and requisitions/consents should be sent overnight at room temperature.  **Notice: Samples are NOT accepted on Saturdays, Sundays or holidays. Please keep blood samples collected on these days at refrigerated temperatures until the next business day.
<b>Patient Preparation:</b>	None
<b>Sample Rejection:</b>	Mislabeled or unlabeled specimens

---

### ***Interpretive***

<b>Reference Range:</b>	Benign for familial variants
<b>Methodology:</b>	Next generation sequencing using oligonucleotide-based target capture (Agilent SureSelect) followed by Illumina HiSeq sequencing of the coding regions and splice sites. Sanger sequencing is used to confirm all clinically significant variants and fill in regions with insufficient coverage.
<b>References:</b>	<a href="#">Harvard Medical School, Laboratory for Molecular Genetics, Partners Health Care Center for Personalized Genetic Medicine</a> Phone: 617-768-8500 Fax: 617-768-8513 Email: <a href="mailto:Imm@partners.org">Imm@partners.org</a>
<b>Updates:</b>	1/21/2014: CPT update 3/5/2015: CPT update 6/9/2016: CPT update