Pendred Syndrome

**Contact details**
Molecular Genetics Service
Level 6, York House
37 Queen Square
London, WC1N 3BH
T +44 (0) 20 7762 6888
F +44 (0) 20 7813 8578

**Samples required**
- 5ml venous blood in plastic EDTA bottles (>1ml from neonates)
- Prenatal testing must be arranged in advance, through a Clinical Genetics department if possible.
- Amniotic fluid or CV samples should be sent to Cytogenetics for dissecting and culturing, with instructions to forward the sample to the Regional Molecular Genetics laboratory for analysis
- A completed DNA request card should accompany all samples

**Patient details**
To facilitate accurate testing and reporting please provide patient demographic details (full name, date of birth, address and ethnic origin), details of any relevant family history and full contact details for the referring clinician

**Introduction**

Pendred syndrome is an autosomal recessive form of hearing loss due to mutations in the SLC26A4 gene on chromosome 7q31 that presents with other features including goitre, enlarged vestibular aqueducts (EVA) and Mondini malformation. The estimated frequency of Pendred syndrome related hearing loss is 7%.

Mutations in SLC26A4 disrupt ion exchange activity of the polypeptide pendrin. Pendrin is expressed in non-sensory epithelia of the inner ear and in thyroid folliculocytes.

SLC26A4 has 21 exons; mutations have been reported across the gene including a small number that appear to be recurrent. p.Leu236Pro, p.Gly209Val, c.1001+1G>A, p.Glu384Gly, p.Thr410Met and p.Thr416Pro have been reported amongst Western patients (Coyle et al, Hum Mol Genet 1998, 7:7 1105-1112). c.919-2A>G, p.His723Arg, p.Ser90Leu and p.Leu676Gln have been reported to be recurrent in particular Asian populations (Park et al, J Med Genet, 2003; 40:242-248).

**Referrals**
- Patients with a clinical diagnosis / a strong likelihood of PDS
- Adult relatives of patients with SLC26A4 mutations for carrier status

**Prenatal testing**

Prenatal testing may be available for families in whom specific mutations have been identified or in whom appropriate family studies have been undertaken- please contact the laboratory to discuss.

**Service offered**
- Mutation Analysis: Direct sequencing of the 21 exons (including the non-coding exon 1).
- Detection of known mutations: In relatives of patients with confirmed SLC26A4 mutations.

**Technical**

Mutation screening is carried out by direct fluorescent sequencing.

**Target reporting time**
8 weeks for mutation screening of an index case.
2 weeks for routine testing of specific mutations (carrier testing). For urgent samples please contact the laboratory