Clinical Features and Molecular Genetics:

Early infantile epileptic encephalopathy (EIEE), also known as Ohtahara syndrome, is a severe form of epilepsy characterized by frequent tonic spasms with onset in the first months of life. EEG reveals suppression-burst patterns, characterized by high-voltage bursts alternating with almost flat suppression phases. Seizures are medically intractable with evolution to West syndrome at 3-6 months of age and then Lennox-Gastaut syndrome at 1-3 years of age. EIEE represents approximately 1% of all epilepsies occurring in children less than 15 years of age (1). Patients have severe developmental delay and poor prognosis. The diagnostic workup of EIEEs remains challenging because of frequent difficulties in defining etiologies.

Acquired structural abnormalities like hypoxic-ischemic insults and isolated cortical malformations, which represent the most common causes of epileptic encelphalopathy in infancy should be excluded first (2).

Our EIEE Panel includes analysis of all 60 genes listed below

<table>
<thead>
<tr>
<th>Gene</th>
<th>Inheritance</th>
<th>Clinical Features and Molecular Pathology</th>
</tr>
</thead>
<tbody>
<tr>
<td>AARS</td>
<td>AR</td>
<td>Biallelic mutations in AARS have been reported in two siblings and one unrelated individual with EIEE. In-vitro studies showed that both mutations identified resulted in loss of AARS function (3).</td>
</tr>
<tr>
<td>ALDH7A1</td>
<td>AR</td>
<td>Mutations in ALDH7A1 are associated with pyridoxine-dependent epilepsy (PDE), which is characterized by EIEE that is resistant to antiepileptic drugs but responsive to large doses of pyridoxine (vitamin B6) (6).</td>
</tr>
<tr>
<td>ALG13</td>
<td>XL</td>
<td>A hemizygous de novo mutation in ALG13 was identified by Timal et al. (2012) in a male patient with a congenital disorder of glycosylation, microcephaly, seizures, and death at one year of age (4). The Epi4K Consortium identified a de novo mutation in ALG13 in two female patients with infantile spasms and developmental delays (5). Both patients exhibited hypsarrhythmia on EEG.</td>
</tr>
<tr>
<td>ARFGEF2</td>
<td>AR</td>
<td>Homozygous splice-site mutations in the ubiquitously expressed ARFGEF2 gene were identified in a consanguineous Pakistani kindred with multiple children who presented with West syndrome, evolving to Lennox–Gastaut syndrome with severe intellectual disability, microcephaly and associated with diffuse periventricular heterotopia (7).</td>
</tr>
<tr>
<td>ARHGEF9</td>
<td>xl</td>
<td>Shimojima et al. (2011) identified a nonsense mutation in ARHGEF9 in one out of 23 males with severe intellectual disability and epilepsy (8). A missense mutation in ARHGEF9 in a male with severe intellectual disability, hyperekplexia (excessive startle) and refractory infantile-onset epilepsy has also previously been described (9).</td>
</tr>
</tbody>
</table>
| ARV1       | AR          | Homozygous splice site and missense mutations in ARV1 have been identified in two consanguineous families with children affected by EIEE. Transfection of the mutations into
<table>
<thead>
<tr>
<th>Gene</th>
<th>OMIM#</th>
<th>Mutation Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ARX</td>
<td>OMIM#300382</td>
<td>XL</td>
<td>Up to 10% of males with a clinical diagnosis of EIEE or West syndrome/cryptogenic infantile spasms may have mutations in the ARX gene (1, 14). Carrier females of ARX mutations can be asymptomatic (15).</td>
</tr>
<tr>
<td>BRAT1</td>
<td>OMIM#614506</td>
<td>AR</td>
<td>Several studies have identified homozygous or compound heterozygous mutations in the BRAT1 gene in patients with a neonatal lethal form of rigidity and multifocal seizure syndrome, including a founder mutation in the Amish population (16-18). Horn, et al, described two brothers who were compound heterozygotes for BRAT1 mutations, with EIEE and a milder phenotype and survival into childhood (19).</td>
</tr>
<tr>
<td>CACNA1A</td>
<td>OMIM#601011</td>
<td>AD</td>
<td>Pathogenic mutations in CACNA1A were identified in five probands and one sibling with early-onset epileptic encephalopathy (5, 20). Of the 6 infants with CACNA1A mutations, five began having seizures on the first day of life, with the affected siblings additionally showing seizure-like movements in utero. Multiple seizure types were present in all affected individuals, as well as developmental delay.</td>
</tr>
<tr>
<td>CACNA2D2</td>
<td>OMIM#607082</td>
<td>AR</td>
<td>Edvardson et al. (2013) identified a homozygous missense mutation in CACNA2D2 in three affected siblings from a consanguineous family (21). An unaffected sibling was a carrier of the mutation. Seizures onset in the affected individuals was at 20-60 days of age. Seizures were refractory to treatment and included atonic, clonic, and tonic seizures. Functional studies demonstrated dysfunction of the α2 omega2 subunit of high voltage gated calcium channels, resulting in reduced current density and slow inactivation in neuronal calcium channels (21).</td>
</tr>
<tr>
<td>CASK</td>
<td>OMIM#300172</td>
<td>XL</td>
<td>Hemizygous loss of function mutations in the CASK gene were identified by Saito et al. (2012) in two males with Ohtahara syndrome. One patient had a de novo nonsense mutation and the other had a deletion involving exon 2 that was maternally inherited from a carrier with somatic mosaicism for the deletion (22).</td>
</tr>
<tr>
<td>CDKL5</td>
<td>OMIM#300203</td>
<td>XL</td>
<td>Archer et al. (2006) identified CDKL5 mutations in 7/42 (17%) of females with severe mental retardation and seizures in the first 6 months of life (23). The most common feature found in patients reported to date with CDKL5 mutations is the early onset of seizures. CDKL5 mutations have been reported in more female than male patients, however, Elia, et al (2008) reported CDKL5 mutations in 3/8 boys with severe mental retardation and early-onset seizures (24).</td>
</tr>
<tr>
<td>CHD2</td>
<td>OMIM#602119</td>
<td>AD</td>
<td>In a cohort of 500 patients with epileptic encephalopathy, 1.2% were found to have de novo mutations in CHD2 (25). Reported features include: Dravet syndrome (26), myoclonic seizures, absence seizures, photosensitivity, and moderate to severe intellectual disability (25). Mutations leading to protein truncation, as well as missense mutations have been reported.</td>
</tr>
<tr>
<td>CLCN4</td>
<td>OMIM#302910</td>
<td>XL</td>
<td>In a group of children with difficult to control epilepsy and developmental delay, Veeramah et al (2013) found a single patient with a hemizygous de novo missense mutation in CLCN4 (10). In addition to epilepsy, this child had microcephaly, hypotonia, myotonia, and intellectual disability.</td>
</tr>
<tr>
<td>DNM1</td>
<td>OMIM#602377</td>
<td>AD</td>
<td>Heterozygous mutations in DNM1 are associated with EIEE-31. The EuroEPINOMICS-RES Consortium et al. (2014) reported 5 unrelated patients with EIEE who were found to have de novo heterozygous mutations in DNM1 (27). All patients were reportedly normal at birth and developed treatment-resistant seizures between 2 and 13 months of age. Three of the five patients had developmental delays prior to seizure onset, and all patients exhibited severe to profound intellectual disabilities at the time of evaluation (27).</td>
</tr>
<tr>
<td>DOCK7</td>
<td>OMIM#615730</td>
<td>AR</td>
<td>Perrault, et al. (2014) identified compound heterozygous nonsense mutations in DOCK7 in two siblings with early-onset intractable epilepsy, global developmental delays and intellectual disabilities, and cortical blindness (28). The patients exhibited dysmorphic features including low anterior hairline, telecanthus, and broad nasal tip with anteverted nares. An unrelated patient with seizures starting at 5 months of age, profound developmental delays, and cortical blindness was subsequently found to also be a compound heterozygote for two nonsense mutations in DOCK7 (28).</td>
</tr>
<tr>
<td>EEF1A2</td>
<td>OMIM#602959</td>
<td>AD</td>
<td>In 2012, de Ligt et al. identified a de novo missense mutation in a patient with a history of neonatal hypotonia and seizures at 4 months with intellectual disability, autistic features, and aggressive behavior (29). Subsequently, in a group of children with difficult to control epilepsy and developmental delay, Veeramah et al (2013) found a single patient with a de novo missense mutation in EEF1A2 (10).</td>
</tr>
<tr>
<td>EFHC1</td>
<td>OMIM#608815</td>
<td>AD/AR</td>
<td>Berger et al. (2012) described a family with primary intractable epilepsy in infancy with a homozygous missense mutation in EFHC1 (30). The affected children died at 18-36 months of age. Heterozygous mutations in EFHC1 have been associated with increased susceptibility to juvenile myoclonic epilepsy (31).</td>
</tr>
<tr>
<td>Gene</td>
<td>OMIM#</td>
<td>Allele</td>
<td>Clinical Features</td>
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<tr>
<td><strong>ETHE1</strong></td>
<td>[OMIM#608451]</td>
<td>AR</td>
<td>Homozygous or compound heterozygous mutations in ETHE1 are associated with ethylmalonic encephalopathy, a rare metabolic disorder characterized by neurodevelopmental regression and progressive pyramidal findings, seizures, petechiae, and death typically occurring in the first decade of life. Papetti et al. (2015) reported a patient who presented with epileptic encephalopathy at 3 months of life. By 5 months of age the patient’s EEG findings had progressed to West syndrome (32). The patient later developed petechiae, developmental regression, and pyramidal signs. This patient was found to have a truncating variant in ETHE1 on the paternal allele and two missense variants on the maternal ETHE1 allele. ETHE1 protein was absent on Western blot analysis. This is the first report of a patient with ETHE1 mutations and an early pure epileptic onset (32).</td>
</tr>
<tr>
<td><strong>FHF1 (FGF12)</strong></td>
<td>[OMIM#601513]</td>
<td>AD</td>
<td>Siekierska et al. (2016) reported a de novo heterozygous missense mutation in the FHF1 gene in two siblings affected by a lethal disorder consisting of EIEE and progressive cerebellar atrophy. Further functional studies support a gain of function phenotype, and studies in zebrafish enhanced epileptiform discharges in larval-stage animals (33).</td>
</tr>
<tr>
<td><strong>FRRS1L</strong></td>
<td>[OMIM#604574]</td>
<td>AR</td>
<td>Four different homozygous mutations in the FRRS1L gene were identified in eight patients from four unrelated families with EIEE. Functional studies in fibroblasts showed reduced FRRS1L protein levels, and mouse models indicated that FRRS1L is expressed throughout the brain (34). Affected members of another consanguineous family with EIEE were also found to have a homozygous mutation in the FRRS1L gene (35).</td>
</tr>
<tr>
<td><strong>GABRA1</strong></td>
<td>[OMIM#137160]</td>
<td>AD</td>
<td>Carvill, et al. (2014) identified heterozygous, de novo missense mutations in four SCN1A-negative patients with Dravet syndrome (36). Patients had onset of seizures between 8 and 11 months of age. Multiple seizure types were observed, including absence, focal dyscognitive, hemiclonic, myoclonic, tonic-clonic, and status epilepticus. All patients had mild to moderate developmental delays (36). Heterozygous mutations in GABRA1 have previously been associated with susceptibility to familial juvenile myoclonic epilepsy and generalized epilepsy (37, 38).</td>
</tr>
<tr>
<td><strong>GABRB3</strong></td>
<td>[OMIM#137192]</td>
<td>AD</td>
<td>The Epi4K Consortium identified heterozygous de novo GABRB3 mutations in four unrelated patients with epileptic encephalopathy. Three of the reported patients had a Lennox-Gastaut syndrome phenotype; the fourth had infantile spasms (5).</td>
</tr>
<tr>
<td><strong>GNAO1</strong></td>
<td>[OMIM#139311]</td>
<td>AD</td>
<td>Nakamura et al. (2013) identified de novo mutations in four individuals with EIEE, three of whom were described as having Ohtahara syndrome, and two of whom had involuntary movements (39). One of the patients had somatic mosaicism, with only one third to half of various cell types harboring the mutation. Missense mutations and a small in-frame deletion were reported.</td>
</tr>
<tr>
<td><strong>GRIN2A</strong></td>
<td>[OMIM#613971]</td>
<td>AD</td>
<td>Endele et al. (2010) found heterozygous GRIN2A mutations in two out of 127 individuals with a history of idiopathic epilepsy and/or abnormal EEG findings and a variable degree of intellectual disability (40). The most consistent clinical feature seen in individuals with GRIN2A mutations is epilepsy, which varies in severity between individuals. The most severe cases are associated with EIEE (40).</td>
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<tr>
<td><strong>GRIN2B</strong></td>
<td>[OMIM#138252]</td>
<td>AD</td>
<td>Lemke et al. (2014) identified de novo heterozygous missense mutations in GRIN2B in three unrelated individuals with early epileptic encephalopathy/West syndrome (41). The affected individuals had severe developmental delays and onset of focal epilepsy in early infancy. GRIN2B encodes the beta subunit of the glutamate-activated N-methyl-D-aspartate (NMDA) receptor. Two of the GRIN2B mutations were introduced into <em>Xenopus laevis</em> oocytes and functional studies revealed dramatically increased Ca** permeability, consistent with a gain of function effect of these mutations (41).</td>
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<tr>
<td><strong>HCN1</strong></td>
<td>[OMIM#602780]</td>
<td>AD</td>
<td>Nava et al. (2014) identified heterozygous mutations in HCN1 in six unrelated patients with EIEE (42). The mutation was confirmed to be de novo in five of the six patients. Seizure onset ranged from 4 to 13 months. Seizures seen in affected individuals included febrile, tonic-clonic, clonic, absence, focal, and myoclonic. Patients exhibited mild to severe intellectual disabilities and the majority of patients also had behavioral concerns. Two of the patients also exhibited ataxia. Functional studies of the confirmed de novo mutations in Chinese hamster ovary cells indicated gain-of-function in three of the five mutations and a possible dominant negative effect in the remaining two de novo cases (42).</td>
</tr>
<tr>
<td><strong>ITPA</strong></td>
<td>[OMIM#616647]</td>
<td>AR</td>
<td>Kevelam et al. (2015) identified biallelic loss of function mutations in ITPA in seven patients from four families. The patients presented with EIEE and brain abnormalities noted on MRI, microcephaly, variable cardiac defects and early death. ITPase activity in erythrocytes and fibroblasts was severely reduced in patient cell lines when compared to controls (43).</td>
</tr>
<tr>
<td><strong>KCNA2</strong></td>
<td>[OMIM#176262]</td>
<td>AD</td>
<td>Syrbe et al. (2015) identified de novo heterozygous mutations in KCNA2 in 7 unrelated patients with severe early onset epilepsy. Onset of seizures occurred between 5 and 17 months of age, and remission of seizures occurred in childhood or adolescence for 4 patients. All patients exhibited normal development prior to onset of seizures but had...</td>
</tr>
</tbody>
</table>
Onset of epilepsy (44). In vitro functional assays in Xenopus laevis revealed that some mutations had dominant negative effect and other mutations led to gain of function (44).

**KCNB1**
[OMIM#600397]
**AD**
Torkamani et al. (2014) identified de novo heterozygous missense mutations in 3 unrelated patients with early onset epileptic encephalopathy and difficult to control seizures. All patients exhibited developmental delays (45).

**KCNH5**
[OMIM#605716]
**AD**
In a group of children with difficult to control epilepsy and developmental delay, Veeraramah et al. (2013) found a single patient, whose presentation was consistent with West syndrome, with a de novo heterozygous mutation in KCNH5 (10).

**KCNQ2**
[OMIM#602235]
**AD**
Weckhuysen et al. (2012) identified heterozygous KCNQ2 mutations in 8 out of 80 patients with EIEE, 6 of which were confirmed to be de novo. Mutations in KCNQ2 can also be associated with other phenotypes including benign familial neonatal seizures (BFNS), which is an autosomal dominant seizure disorder typically associated with a good prognosis (46). Parental mosaicism has been described in one family with a mutation in KCNQ2 (46, 47).

**KCNT1**
[OMIM#608167]
**AD**
Barcia et al. (2012) identified de novo heterozygous gain-of-function mutations in KCNT1 in 6 patients with a subtype of EIEE known as malignant migrating partial seizures of infancy (48). Missense mutations in KCNT1 have also been reported in families with autosomal dominant nocturnal frontal lobe epilepsy-5 (49).

**NECAP1**
[OMIM#611623]
**AR**
A homozygous nonsense mutation in NECAP1 was identified by Alazami et al. (2014) in multiple individuals with EIEE from a consanguineous family (50). The affected individuals exhibited decreased fetal movement, hypotonia and poor feeding. Severe intractable seizures developed in affected individuals in early infancy. Two of the affected individuals underwent brain MRI and were found to have generalized brain atrophy (50).

**PCDH19**
[OMIM#300088]
**XL**
Mutations in the PCDH19 gene have been associated with EIEE. Marini et al. (2010) identified 13 different mutations in the PCDH19 gene in 13 (11%) of 117 female patients with febrile seizures and a wide spectrum of epilepsy phenotypes (51). PCDH19 mutations are X-linked, with the phenotype being restricted to females. Males with hemizygous mutations are apparently unaffected with normal cognitive functions. This unusual mode of inheritance is likely to be due to cellular interference, a mechanism assuming that only the co-existence of PCDH19 positive and negative cells, as a result of random X inactivation in females, is pathogenic (23).

**PLCB1**
[OMIM#607120]
**AR**
Kurian et al. (2010) identified a homozygous deletion of the promoter element and exons 1-3 of the PLCB1 gene in a child with EIEE from a consanguineous family of Bangladeshi descent.

**PNKP**
[OMIM#613402]
**AR**
Mutations in the PNKP gene are associated with early-onset intractable epilepsy, microcephaly, developmental delay and behavioral abnormalities (52). Missense and frameshift mutations identified in PNKP have been associated with severe encephalopathy, whereas an intronic deletion identified in one individual, that was predicted to disrupt proper mRNA splicing, was associated with a milder phenotype (52, 53). The PNKP protein is involved in DNA repair of both double and single-stranded breaks, however at this time no features typically associated with DNA repair defects, such as cancer predisposition or immunological abnormalities have been reported in affected individuals (52).

**PNPO**
[OMIM#603287]
**AR**
Mills et al (2005) found homozygous mutations in PNPO in 3 individuals with early infantile epileptic encephalopathy and biochemical changes in the CSF, indicative of reduced activity of aromatic L-amino acid decarboxylase (AADC) (54). This was found to be due to deficiency of pyridoxal phosphate (PLP), which is a co-factor of AADC and is synthesized by the enzyme encoded for by the PNPO gene. Of the 3 affected children, only one was treated with PLP and survived the neonatal period, however he continued to have symptoms such as seizures, severe developmental delays and dystonic spasms (54).

**POLG**
[OMIM#174763]
**AR**
In a study of 213 children with early or juvenile onset nonsyndromic intractable epilepsy, Uusimaa et al. (2013) identified 5 (2.3%) with compound heterozygous or homozygous mutations in the POLG gene (55). The majority of patients had elevated cerebrospinal fluid lactate. A proportion of affected individuals may develop liver failure, particularly if their seizures are being treated with sodium valproate (55).

**SCN1A**
[OMIM#607208]
**AD**
Mutations in the SCN1A gene can cause EIEE6, which is more commonly known as Dravet syndrome. EIEE6 is characterized by onset of seizures in the first year of life, often triggered by fever, photostimulation, or modest hyperthermia, which usually evolve to include myoclonic seizures over time (56). Mutations in SCN1A associated with EIEE6 are typically de novo (1). Of those with a clinical diagnosis of EIEE6, 85% have a mutation in SCN1A (56).

**SCN2A**
[OMIM#182390]
**AD**
Ogiwara et al. (2009) identified 2 de novo mutations in the SCN2A gene in a cohort of 116 patients with intractable childhood epilepsies (57). Mutations in the SCN2A gene can also...
cause benign familial neonatal seizures (BFNS).

<table>
<thead>
<tr>
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<tbody>
<tr>
<td>SIK1 [OMIM#616341]</td>
<td>AD</td>
<td>Hansen et al. (2015) identified different de novo heterozygous mutations in SIK1 in 6 unrelated children with early-onset epilepsy. Seizures began shortly after birth in all patients, along with severely delayed psychomotor development. Two patients died in infancy, while the remaining four had significant cognitive impairment and EEG abnormalities (59)</td>
</tr>
<tr>
<td>SLC1A2 [OMIM#600300]</td>
<td>AD</td>
<td>De novo mutations in SLC1A2 have been reported in three female patients with early-onset epileptic encephalopathies (5, 20). These infants had a severe epilepsy phenotype characterized by seizure onset in the first week of life and profound developmental impairment. All three individuals had multiple seizure types with prominent myoclonic and tonic seizures as well as spasms.</td>
</tr>
<tr>
<td>SLC1A4 [OMIM#600229]</td>
<td>AR</td>
<td>Homozygous and compound heterozygous mutations in SLC1A4 have been associated with a condition predominantly found in the Ashkenazi Jewish population, consisting of microcephaly, severe developmental delay, neuroimaging abnormalities, and seizures. The majority of reported patients have been found to be homozygous for a founder mutation, p.Glu256Lys. A report by Conroy et al. (2016) described a patient of European descent born to consanguineous parents, who presented with an early-onset seizure disorder with infantile spasms, focal motor, and focal dyssynergic seizures. The patient was found to be heterozygous for a nonsense mutation in the SLC1A4 gene. This finding suggests that truncating mutations may cause a more severe seizure and developmental phenotype than the previously described Ashkenazi Jewish patients (60).</td>
</tr>
<tr>
<td>SLC12A5 [OMIM#616645]</td>
<td>AR</td>
<td>Biallelic mutations in SLC12A5 were identified in four children from two families with EIEE. The children presented with infantile-onset focal migrating seizures, neurological regression and developmental delay. In vitro studies showed that the mutations negatively impact expression and glycosylation of the potassium chloride co-transporter KCC2, which resulting in impaired synaptic inhibition (61).</td>
</tr>
<tr>
<td>SLC13A5 [OMIM#608305]</td>
<td>AR</td>
<td>Homozygous or compound heterozygous mutations in SLC13A5 are associated with EIIEE25 (62, 63). Affected individuals develop seizures in the first week of life. Other features seen in affected individuals include ataxia, choreoathetosis, spasticity, and microcephaly. Some affected individuals also were found to have tooth hypoplasia or hypodontia (63).</td>
</tr>
<tr>
<td>SLC25A22 [OMIM#609302]</td>
<td>AR</td>
<td>Homozygous mutations in SLC25A22 have been described in case reports of consanguineous families with EIEE (57, 64).</td>
</tr>
<tr>
<td>SLC2A1 [OMIM#606777]</td>
<td>AD</td>
<td>Glucose transporter-1 (GLUT1) deficiency syndrome is caused by heterozygous mutations in the SLC2A1 gene, which lead to impaired glucose transport in the brain. The classic GLUT-1 deficiency syndrome presentation is drug-resistant infantile-onset seizures, developmental delay, acquired microcephaly, hypotonia, spasticity, ataxia and dystonia (64). Seizures are typically refractory and worsen during periods of fasting (65). The majority of reported cases are due to de novo mutations (66).</td>
</tr>
<tr>
<td>ST3GAL3 [OMIM#606494]</td>
<td>AR</td>
<td>A homozygous mutation in ST3GAL3 was identified in a consanguineous Palestinian family with four individuals affected by severe early infantile epileptic encephalopathy (68). Mutations in ST3GAL3 have also been described in patients with mild to moderate non-syndromic intellectual disability (68).</td>
</tr>
<tr>
<td>ST3GAL5 [OMIM#604402]</td>
<td>AR</td>
<td>Mutations in ST3GAL5 are associated with infantile onset of refractory and recurrent seizures, associated with profoundly delayed psychomotor development, abnormal movements, and vision loss (69). A founder mutation is present in the Amish community (69). A homozygous mutation was also found in an affected child of French ancestry.</td>
</tr>
<tr>
<td>STXBP1 [OMIM#602926]</td>
<td>AD</td>
<td>Sequencing of STXBP1 detected mutations in 4 out of 106 patients with EIEE (70). Earlier reports identified 4 heterozygous nonsense mutations in 13 patients with EIEE (71). Parental mosaicism has been described in one family with a mutation in STXBP1 (46, 47).</td>
</tr>
<tr>
<td>SYNGAP1 [OMIM#603384]</td>
<td>AD</td>
<td>Carvill et al. (2013) identified heterozygous de novo nonsense mutations in two unrelated individuals with epileptic encephalopathy with seizure onset in infancy. Three additional patients were found to have truncating mutations in SYNGAP1 but parents were not available in these cases to confirm the de novo nature of the variants (25). All patients exhibited developmental delays prior to seizure onset. Multiple seizure types were observed, including absence, atypical absence, focal dyscognitive, tonic-clonic, and myoclonic seizures (25).</td>
</tr>
</tbody>
</table>
| SZT2       | AR          | In 2 unrelated patients with EIEE, Basel-Vanagaite et al. (2013) identified biallelic
truncating mutations in the SZT2 gene (72). The phenotype was characterized by lack of psychomotor development apparent from birth, dysmorphic facial features, early onset of refractory seizures, and thick corpus callosum and persistent cavum septum pellucidum on brain imaging.

**Test methods:**
Comprehensive sequence coverage of the coding regions and splice junctions of all genes in this panel is performed. Targets of interests are enriched and prepared for sequencing using the Agilent SureSelect system. Sequencing is performed using Illumina technology and reads are aligned to the reference sequence. Variants are identified and evaluated using a custom collection of bioinformatic tools and comprehensively interpreted by our team of directors and genetic counselors. All pathogenic and likely pathogenic variants are confirmed by Sanger sequencing. The technical sensitivity of this test is estimated to be >99% for single nucleotide changes and insertions and deletions of less than 20 bp. Comprehensive sequence coverage of the coding regions and splice junctions of all genes in this panel is performed. Targets of interests are enriched and prepared for sequencing using the Agilent SureSelect system. Sequencing is performed using Illumina technology and reads are aligned to the reference sequence. Variants are identified and evaluated using a custom collection of bioinformatic tools and comprehensively interpreted by our team of directors and genetic counselors. All pathogenic and likely pathogenic variants are confirmed by Sanger sequencing. The technical sensitivity of this test is estimated to be >99% for single nucleotide changes and insertions and deletions of less than 20 bp.

Our CNV detection algorithm was developed and its performance determined for the sole purpose of identifying deletions and duplications within the coding region of the gene(s) tested. Partial exonic copy number changes and rearrangements of less than 400 bp may not be detected by this methodology. Regions of high homology and repetitive regions may not be analyzed.

Our Epilepsy Exome Panel is also available (see website). In addition, mutation analysis of individual genes is offered separately for several of the genes on the EIEE panel, including ARX, CDKL5, PCDH19, PNKP, STXBP1, SLC25A22 and SPTAN1. Please see our website for more details regarding these other test options.

<table>
<thead>
<tr>
<th><strong>EIEE Panel (59 genes)</strong></th>
<th>Sample specifications: 3 to 10 cc of blood in a purple top (EDTA) tube</th>
<th>Cost: $3000</th>
<th>CPT codes: 81406, 81407</th>
<th>Turn-around time: 8 weeks</th>
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</table>

*Note: We cannot bill insurance for the EIEE panel*

**Results:**
Results, along with an interpretive report, are faxed to the referring physician as soon as they are completed. One report will be issued for the entire EIEE panel. All abnormal results are reported by telephone or email.

*For more information about our testing options, please visit our website at dnatesting.uchicago.edu or contact us at 773-834-0555.*
References:

20. epi4k@columbia.edu EKCEa, Consortium EK. De Novo Mutations in SLCL1A2 and CACNA1A Are Important Causes of Epileptic Encephalopathies. Am J Hum Genet 2016: 99: 775.

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