

**LETTER OF MEDICAL NECESSITY**

**Ataxia Complete Dominant Evaluation**

**Instructions for Healthcare Provider:**

1. This letter template is being provided as a tool for clinicians to assist communication with payers.
2. Include specific patient information in the letter for this tool to be effective. The areas that must be edited/deleted are indicated in gray on the template
3. Print the template on the physician’s letterhead, **NOT** Athena letterhead. There should be no Athena branding on the letter.

[LMN: Ataxia Complete Dominant Evaluation (10.26.2021)]

<Date>

ATTN: <Medical Director/ Physician Name>, MD

 <Institution/Insurance Company>

  <Street Address>

 <City>**,** <State>  <zip code>

RE: <Patient Name>

DOB: <MM/DD/YYYY>

Member ID: <Insurance ID Number>

Group #: <Enter Group #>

Dear Doctor <Medical Director/ Physician Name>:

I am writing this letter on behalf of my patient <Patient Name> to request coverage for the Ataxia, Complete Dominant Evaluation offered by Athena Diagnostics®. This test analyzes 25 genes for pathogenic variants (16 genes) or repeat expansions (10 genes) associated with hereditary ataxias exhibiting an autosomal dominant (AD; 1 copy of a pathogenic alteration causes disease) mode of inheritance. This letter documents the medical necessity for Ataxia, Complete Dominant Evaluation, in light of my patient’s medical history. Results from the test will be used to guide appropriate medical care for my patient.

I have determined that this test is medically necessary because of the following aspects of this patient’s history:

<Patient name> is a <age>-year-old <gender> with a suspected diagnosis of hereditary ataxia. Symptoms and clinical findings are consistent with this diagnosis:

1. <Symptom #1 with ICD-10 code>

2. <Symptom #2 with ICD-10 code>

<Symptoms should support diagnosis or risk of genetic disease. Relevant information may include results of prior testing, such as an MRI scan and tests for hypothyroidism, and results of a physical examination and patient consultation.>

<Consider noting family or other personal history. Consider including information on both neurological and non-neurological problems, such as movement disorders, spasticity, peripheral neuropathy, intellectual impairment, etc.>

**Rationale for testing**

Hereditary ataxias compose a group of diseases characterized by incoordination of speech and movement.1 Obtaining a specific diagnosis is complex because genetic causes are highly heterogeneous and clinical symptoms frequently overlap among these diseases.1-3 Hereditary ataxias are broadly classified by mode of inheritance, predominantly as AD or AR ataxias, but confirming a diagnosis for a specific type of ataxia is difficult without a molecular diagnosis obtained through genetic testing.1

The presence of a family history warrants testing for specific genes (eg, genes associated with AD ataxias) to identify or confirm a pathogenic variant.4 The most common types of AD ataxia are caused by nucleotide repeat expansions, but other AD ataxias are caused by point mutations, small insertions/deletions, and other genetic variants.1,5 When an AD cerebellar ataxia is suggested based on family history, the European Federation of the Neurological Societies (EFNS) recommends testing for spinocerebellar ataxia (SCA) types 1, 2, 3, 6, 7, and 17 (and DRPLA in Asian patients), all of which are caused by repeat expansions. Further genetic testing is recommended if this initial genetic analysis is negative.6 Ataxia UK, a patient support organization that developed guidelines in consultation with >30 health professionals, does not have specific recommendations for diagnosing AD ataxias, but the recommended initial testing for the most common ataxias includes the AD SCAs 1, 2, 3, 6, and 7 (and optionally SCAs 12 and 17). Expanded testing using next generation sequencing (NGS) is recommended if initial testing is negative.7 The SCAs recommended for initial testing are the most common cerebellar ataxias, found in approximately half of dominantly inherited cases, but an estimated 40% of patients still lack a diagnosis after standard genetic testing is completed.1-3

Repeat expansions are detected using PCR-based methods that are unable to detect other conventional variants, and, conversely, sequencing methods (NGS, whole exome sequencing) cannot identify large repeat expansions. Consequently, using both PCR and sequencing methods can maximize the diagnostic yield for ataxia. This has been demonstrated in a study that tested 412 patients with AD cerebellar ataxia using a 65-gene sequencing panel. The panel provided a very likely or definite diagnosis for an additional 50 patients (12.1%) who had remained undiagnosed after testing for 6 common repeat expansions associated with ataxia.8

Thus, testing with an extended panel, such as the 25-gene Ataxia, Complete Dominant Evaluation, can increase the diagnostic yield for patients with AD ataxia and help avoid a prolonged and unsuccessful diagnostic odyssey that may result from a tiered approach. Commercially available tests differ in the genes tested and testing methods. This places the onus on the clinician to identify the most suitable test to obtain a diagnosis, which may contribute to delays in diagnosis and burden to the patient.9,10 The Ataxia, Complete Dominant Evaluation is currently the only commercially available extended panel specifically designed to detect AD ataxias. This panel increases the likelihood that a patient with AD ataxia will receive a specific diagnosis since it is able to simultaneously analyze multiple genes using both sequencing and PCR-based detection methods.

The process of obtaining a diagnosis can significantly decrease a patient’s psychological well-being and quality of life since it generally entails many visits to a succession of physicians and other health professions, during which time the patient is suffering from distressing and disabling symptoms without knowing the cause.11 A study reported a mean delay of 18.1 years (range 3-35 years) from disease onset to molecular diagnosis.9 Prompt diagnosis can provide resolution and allow for genetic counseling, life and family planning, and enrollment in support groups and research activities.4,11 Genetic diagnosis also informs patient prognosis. Similar presentations between ataxias may hide notable differences in disease characteristics and progression that impact patient management.1,2 For instance, spinocerebellar ataxia (SCA) types 1, 2, 3, and 7 are associated with shorter life spans than SCA types 5, 6, and 14.1 Furthermore, genetic diagnosis allows for the prevention or treatment of potential complications (eg, cardiac, neurologic, or ocular) that are associated with various hereditary ataxias.1

In summary, extended genetic testing with Ataxia, Complete Dominant Evaluation can improve the diagnostic yield for AD ataxia patients beyond that provided by standard testing of common genes, which provides valuable information to both the patient and clinician for appropriate clinical management and life planning. I am requesting that <Patient Name> be approved for the Ataxia, Complete Dominant Evaluation (test code 6900; see CPT codes below\*) offered by Athena Diagnostics.

I hope you will support this letter of medical necessity for <Patient Name>. Please feel free to contact me at <Physician Phone> if you have additional questions.

Sincerely,

<Physician Name>, MD

NPI #: <Physician NPI#>

Contact information:

< Address>

<City>**,** <State>, <zip code>

Contact phone no.: <phone number>

\*CPT codes: 81178, 81179, 81180, 81181, 81344, 81183, 81182, 81343, 81177, 81184, 81185, 81403, 81406(2), 81407, 81408, 81479. The CPT codes provided are based on AMA guidelines and are for informational purposes only. CPT coding is the sole responsibility of the billing party. Please direct any questions regarding coding to the payer being billed.

**References**

**1.** Jayadev S, Bird TD. Hereditary ataxias: overview. *Genet Med*. 2013;15(9):673-683. doi:10.1038/gim.2013.28

**2.** Sandford E, Burmeister M. Genes and genetic testing in hereditary ataxias. *Genes (Basel)*. 2014;5(3):586-603. doi:10.3390/genes5030586

**3.** Sailer A, Houlden H. Recent advances in the genetics of cerebellar ataxias. *Curr Neurol Neurosci Rep*. 2012;12(3):227-236. doi:10.1007/s11910-012-0267-6

**4.** Ashizawa T, Xia G. Ataxia. *Continuum (Minneap Minn)*. 2016;22(4 Movement Disorders):1208-1226. doi:10.1212/CON.0000000000000362

**5.** Kuo SH. Ataxia. *Continuum (Minneap Minn)*. 2019;25(4):1036-1054. doi:10.1212/con.0000000000000753

**6.** van de Warrenburg BP, van Gaalen J, Boesch S, et al. EFNS/ENS Consensus on the diagnosis and management of chronic ataxias in adulthood. *Eur J Neurol*. 2014;21(4):552-562. doi:10.1111/ene.12341

**7.** de Silva R, Greenfield J, Cook A, et al. Guidelines on the diagnosis and management of the progressive ataxias. *Orphanet J Rare Dis*. 2019;14(1):51. doi:10.1186/s13023-019-1013-9

**8.** Coutelier M, Coarelli G, Monin ML, et al. A panel study on patients with dominant cerebellar ataxia highlights the frequency of channelopathies. *Brain*. 2017;140(6):1579-1594. doi:10.1093/brain/awx081

**9.** Németh AH, Kwasniewska AC, Lise S, et al. Next generation sequencing for molecular diagnosis of neurological disorders using ataxias as a model. *Brain*. 2013;136(Pt 10):3106-3118. doi:10.1093/brain/awt236

**10.** Wallace SE, Bird TD. Molecular genetic testing for hereditary ataxia: what every neurologist should know. *Neurol Clin Pract*. 2018;8(1):27-32. doi:10.1212/CPJ.0000000000000421

**11.** Orengo JP, Murdock DR. Genetic testing in neuromuscular disorders. *Pract Neurol*. 2019;July/August:35-41.