

Article - Billing and Coding: MolDX: Repeat Germline Testing (A57332)

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Contractor Information

CONTRACTOR NAME	CONTRACT TYPE	CONTRACT NUMBER	JURISDICTION	STATES
Noridian Healthcare Solutions, LLC	A and B MAC	02101 - MAC A	J - F	Alaska
Noridian Healthcare Solutions, LLC	A and B MAC	02102 - MAC B	J - F	Alaska
Noridian Healthcare Solutions, LLC	A and B MAC	02201 - MAC A	J - F	Idaho
Noridian Healthcare Solutions, LLC	A and B MAC	02202 - MAC B	J - F	Idaho
Noridian Healthcare Solutions, LLC	A and B MAC	02301 - MAC A	J - F	Oregon
Noridian Healthcare Solutions, LLC	A and B MAC	02302 - MAC B	J - F	Oregon
Noridian Healthcare Solutions, LLC	A and B MAC	02401 - MAC A	J - F	Washington
Noridian Healthcare Solutions, LLC	A and B MAC	02402 - MAC B	J - F	Washington
Noridian Healthcare Solutions, LLC	A and B MAC	03101 - MAC A	J - F	Arizona
Noridian Healthcare Solutions, LLC	A and B MAC	03102 - MAC B	J - F	Arizona
Noridian Healthcare Solutions, LLC	A and B MAC	03201 - MAC A	J - F	Montana
Noridian Healthcare Solutions, LLC	A and B MAC	03202 - MAC B	J - F	Montana
Noridian Healthcare Solutions, LLC	A and B MAC	03301 - MAC A	J - F	North Dakota
Noridian Healthcare Solutions, LLC	A and B MAC	03302 - MAC B	J - F	North Dakota
Noridian Healthcare Solutions, LLC	A and B MAC	03401 - MAC A	J - F	South Dakota
Noridian Healthcare Solutions, LLC	A and B MAC	03402 - MAC B	J - F	South Dakota
Noridian Healthcare Solutions, LLC	A and B MAC	03501 - MAC A	J - F	Utah
Noridian Healthcare Solutions, LLC	A and B MAC	03502 - MAC B	J - F	Utah
Noridian Healthcare Solutions, LLC	A and B MAC	03601 - MAC A	J - F	Wyoming
Noridian Healthcare Solutions, LLC	A and B MAC	03602 - MAC B	J - F	Wyoming

Article Information

General Information

Article ID
A57332

Article Title

AMA CPT / ADA CDT / AHA NUBC Copyright Statement

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Article Type

Billing and Coding

Original Effective Date

08/03/2020

Revision Effective Date

01/01/2021

Revision Ending Date

N/A

Retirement Date

N/A

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CMS National Coverage Policy

Title XVIII of the Social Security Act, §1833(e). Prohibits Medicare payment for any claim which lacks the necessary information to process the claim.

CMS Internet-Only Manuals, Publication 100-04, Medicare Claims Processing Manual, Chapter 23, §10. Reporting ICD Diagnosis and Procedure Codes.

Article Guidance

Article Text

The following coding and billing guidance is to be used with its associated Local coverage determination.

Coding Information

CPT/HCPCS Codes

Group 1 Paragraph:

For the following CPT® codes associated with germline testing, a beneficiary may only be covered for one test per lifetime. This list does not imply coverage for any of the below codes; it identifies codes within scope of the Repeat Germline Testing Policy.

If non-duplicative testing is considered medically reasonable and necessary but utilizes the same billing codes as prior testing, please use a -77 modifier to trigger a medical review for coverage. This includes testing to identify

different genetic content or information, such as different variant types or classes, or leveraging newer and more sensitive methodologies. Providers will be expected to provide a rationale for additional testing.

Group 1 Codes:

CODE	DESCRIPTION
81105	HUMAN PLATELET ANTIGEN 1 GENOTYPING (HPA-1), ITGB3 (INTEGRIN, BETA 3 [PLATELET GLYCOPROTEIN IIIA], ANTIGEN CD61 [GPIIIA]) (EG, NEONATAL ALLOIMMUNE THROMBOCYTOPENIA [NAIT], POST-TRANSFUSION PURPURA), GENE ANALYSIS, COMMON VARIANT, HPA-1A/B (L33P)
81106	HUMAN PLATELET ANTIGEN 2 GENOTYPING (HPA-2), GP1BA (GLYCOPROTEIN IB [PLATELET], ALPHA POLYPEPTIDE [GPIBA]) (EG, NEONATAL ALLOIMMUNE THROMBOCYTOPENIA [NAIT], POST-TRANSFUSION PURPURA), GENE ANALYSIS, COMMON VARIANT, HPA-2A/B (T145M)
81107	HUMAN PLATELET ANTIGEN 3 GENOTYPING (HPA-3), ITGA2B (INTEGRIN, ALPHA 2B [PLATELET GLYCOPROTEIN IIB OF IIB/IIIA COMPLEX], ANTIGEN CD41 [GPIIB]) (EG, NEONATAL ALLOIMMUNE THROMBOCYTOPENIA [NAIT], POST-TRANSFUSION PURPURA), GENE ANALYSIS, COMMON VARIANT, HPA-3A/B (I843S)
81108	HUMAN PLATELET ANTIGEN 4 GENOTYPING (HPA-4), ITGB3 (INTEGRIN, BETA 3 [PLATELET GLYCOPROTEIN IIIA], ANTIGEN CD61 [GPIIIA]) (EG, NEONATAL ALLOIMMUNE THROMBOCYTOPENIA [NAIT], POST-TRANSFUSION PURPURA), GENE ANALYSIS, COMMON VARIANT, HPA-4A/B (R143Q)
81109	HUMAN PLATELET ANTIGEN 5 GENOTYPING (HPA-5), ITGA2 (INTEGRIN, ALPHA 2 [CD49B, ALPHA 2 SUBUNIT OF VLA-2 RECEPTOR] [GPIA]) (EG, NEONATAL ALLOIMMUNE THROMBOCYTOPENIA [NAIT], POST-TRANSFUSION PURPURA), GENE ANALYSIS, COMMON VARIANT (EG, HPA-5A/B [K505E])
81110	HUMAN PLATELET ANTIGEN 6 GENOTYPING (HPA-6W), ITGB3 (INTEGRIN, BETA 3 [PLATELET GLYCOPROTEIN IIIA, ANTIGEN CD61] [GPIIIA]) (EG, NEONATAL ALLOIMMUNE THROMBOCYTOPENIA [NAIT], POST-TRANSFUSION PURPURA), GENE ANALYSIS, COMMON VARIANT, HPA-6A/B (R489Q)
81111	HUMAN PLATELET ANTIGEN 9 GENOTYPING (HPA-9W), ITGA2B (INTEGRIN, ALPHA 2B [PLATELET GLYCOPROTEIN IIB OF IIB/IIIA COMPLEX, ANTIGEN CD41] [GPIIB]) (EG, NEONATAL ALLOIMMUNE THROMBOCYTOPENIA [NAIT], POST-TRANSFUSION PURPURA), GENE ANALYSIS, COMMON VARIANT, HPA-9A/B (V837M)
81112	HUMAN PLATELET ANTIGEN 15 GENOTYPING (HPA-15), CD109 (CD109 MOLECULE) (EG, NEONATAL ALLOIMMUNE THROMBOCYTOPENIA [NAIT], POST-TRANSFUSION PURPURA), GENE ANALYSIS, COMMON VARIANT, HPA-15A/B (S682Y)
81161	DMD (DYSTROPHIN) (EG, DUCHENNE/BECKER MUSCULAR DYSTROPHY) DELETION ANALYSIS, AND DUPLICATION ANALYSIS, IF PERFORMED
81162	BRCA1 (BRCA1, DNA REPAIR ASSOCIATED), BRCA2 (BRCA2, DNA REPAIR ASSOCIATED) (EG, HEREDITARY BREAST AND OVARIAN CANCER) GENE ANALYSIS; FULL SEQUENCE ANALYSIS AND FULL DUPLICATION/DELETION ANALYSIS (IE,

CODE	DESCRIPTION
	DETECTION OF LARGE GENE REARRANGEMENTS)
81163	BRCA1 (BRCA1, DNA REPAIR ASSOCIATED), BRCA2 (BRCA2, DNA REPAIR ASSOCIATED) (EG, HEREDITARY BREAST AND OVARIAN CANCER) GENE ANALYSIS; FULL SEQUENCE ANALYSIS
81164	BRCA1 (BRCA1, DNA REPAIR ASSOCIATED), BRCA2 (BRCA2, DNA REPAIR ASSOCIATED) (EG, HEREDITARY BREAST AND OVARIAN CANCER) GENE ANALYSIS; FULL DUPLICATION/DELETION ANALYSIS (IE, DETECTION OF LARGE GENE REARRANGEMENTS)
81165	BRCA1 (BRCA1, DNA REPAIR ASSOCIATED) (EG, HEREDITARY BREAST AND OVARIAN CANCER) GENE ANALYSIS; FULL SEQUENCE ANALYSIS
81166	BRCA1 (BRCA1, DNA REPAIR ASSOCIATED) (EG, HEREDITARY BREAST AND OVARIAN CANCER) GENE ANALYSIS; FULL DUPLICATION/DELETION ANALYSIS (IE, DETECTION OF LARGE GENE REARRANGEMENTS)
81167	BRCA2 (BRCA2, DNA REPAIR ASSOCIATED) (EG, HEREDITARY BREAST AND OVARIAN CANCER) GENE ANALYSIS; FULL DUPLICATION/DELETION ANALYSIS (IE, DETECTION OF LARGE GENE REARRANGEMENTS)
81168	CCND1/IGH (T(11;14)) (EG, MANTLE CELL LYMPHOMA) TRANSLOCATION ANALYSIS, MAJOR BREAKPOINT, QUALITATIVE AND QUANTITATIVE, IF PERFORMED
81171	AFF2 (AF4/FMR2 FAMILY, MEMBER 2 [FMR2]) (EG, FRAGILE X MENTAL RETARDATION 2 [FRAXE]) GENE ANALYSIS; EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81172	AFF2 (AF4/FMR2 FAMILY, MEMBER 2 [FMR2]) (EG, FRAGILE X MENTAL RETARDATION 2 [FRAXE]) GENE ANALYSIS; CHARACTERIZATION OF ALLELES (EG, EXPANDED SIZE AND METHYLATION STATUS)
81173	AR (ANDROGEN RECEPTOR) (EG, SPINAL AND BULBAR MUSCULAR ATROPHY, KENNEDY DISEASE, X CHROMOSOME INACTIVATION) GENE ANALYSIS; FULL GENE SEQUENCE
81174	AR (ANDROGEN RECEPTOR) (EG, SPINAL AND BULBAR MUSCULAR ATROPHY, KENNEDY DISEASE, X CHROMOSOME INACTIVATION) GENE ANALYSIS; KNOWN FAMILIAL VARIANT
81177	ATN1 (ATROPHIN 1) (EG, DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY) GENE ANALYSIS, EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81178	ATXN1 (ATAXIN 1) (EG, SPINOCEREBELLAR ATAXIA) GENE ANALYSIS, EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81179	ATXN2 (ATAXIN 2) (EG, SPINOCEREBELLAR ATAXIA) GENE ANALYSIS, EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81180	ATXN3 (ATAXIN 3) (EG, SPINOCEREBELLAR ATAXIA, MACHADO-JOSEPH DISEASE) GENE ANALYSIS, EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES

CODE	DESCRIPTION
81181	ATXN7 (ATAXIN 7) (EG, SPINOCEREBELLAR ATAXIA) GENE ANALYSIS, EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81182	ATXN8OS (ATXN8 OPPOSITE STRAND [NON-PROTEIN CODING]) (EG, SPINOCEREBELLAR ATAXIA) GENE ANALYSIS, EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81183	ATXN10 (ATAXIN 10) (EG, SPINOCEREBELLAR ATAXIA) GENE ANALYSIS, EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81184	CACNA1A (CALCIUM VOLTAGE-GATED CHANNEL SUBUNIT ALPHA1 A) (EG, SPINOCEREBELLAR ATAXIA) GENE ANALYSIS; EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81185	CACNA1A (CALCIUM VOLTAGE-GATED CHANNEL SUBUNIT ALPHA1 A) (EG, SPINOCEREBELLAR ATAXIA) GENE ANALYSIS; FULL GENE SEQUENCE
81186	CACNA1A (CALCIUM VOLTAGE-GATED CHANNEL SUBUNIT ALPHA1 A) (EG, SPINOCEREBELLAR ATAXIA) GENE ANALYSIS; KNOWN FAMILIAL VARIANT
81187	CNBP (CCHC-TYPE ZINC FINGER NUCLEIC ACID BINDING PROTEIN) (EG, MYOTONIC DYSTROPHY TYPE 2) GENE ANALYSIS, EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81188	CSTB (CYSTATIN B) (EG, UNVERRICHT-LUNDBORG DISEASE) GENE ANALYSIS; EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81189	CSTB (CYSTATIN B) (EG, UNVERRICHT-LUNDBORG DISEASE) GENE ANALYSIS; FULL GENE SEQUENCE
81190	CSTB (CYSTATIN B) (EG, UNVERRICHT-LUNDBORG DISEASE) GENE ANALYSIS; KNOWN FAMILIAL VARIANT(S)
81191	NTRK1 (NEUROTROPHIC RECEPTOR TYROSINE KINASE 1) (EG, SOLID TUMORS) TRANSLOCATION ANALYSIS
81192	NTRK2 (NEUROTROPHIC RECEPTOR TYROSINE KINASE 2) (EG, SOLID TUMORS) TRANSLOCATION ANALYSIS
81193	NTRK3 (NEUROTROPHIC RECEPTOR TYROSINE KINASE 3) (EG, SOLID TUMORS) TRANSLOCATION ANALYSIS
81194	NTRK (NEUROTROPHIC-TROPOMYOSIN RECEPTOR TYROSINE KINASE 1, 2, AND 3) (EG, SOLID TUMORS) TRANSLOCATION ANALYSIS
81200	ASPA (ASPARTOACYLASE) (EG, CANAVAN DISEASE) GENE ANALYSIS, COMMON VARIANTS (EG, E285A, Y231X)
81201	APC (ADENOMATOUS POLYPOSIS COLI) (EG, FAMILIAL ADENOMATOSIS POLYPOSIS [FAP], ATTENUATED FAP) GENE ANALYSIS; FULL GENE SEQUENCE
81202	APC (ADENOMATOUS POLYPOSIS COLI) (EG, FAMILIAL ADENOMATOSIS POLYPOSIS [FAP], ATTENUATED FAP) GENE ANALYSIS; KNOWN FAMILIAL VARIANTS
81203	APC (ADENOMATOUS POLYPOSIS COLI) (EG, FAMILIAL ADENOMATOSIS POLYPOSIS

CODE	DESCRIPTION
	[FAP], ATTENUATED FAP) GENE ANALYSIS; DUPLICATION/DELETION VARIANTS
81204	AR (ANDROGEN RECEPTOR) (EG, SPINAL AND BULBAR MUSCULAR ATROPHY, KENNEDY DISEASE, X CHROMOSOME INACTIVATION) GENE ANALYSIS; CHARACTERIZATION OF ALLELES (EG, EXPANDED SIZE OR METHYLATION STATUS)
81205	BCKDHB (BRANCHED-CHAIN KETO ACID DEHYDROGENASE E1, BETA POLYPEPTIDE) (EG, MAPLE SYRUP URINE DISEASE) GENE ANALYSIS, COMMON VARIANTS (EG, R183P, G278S, E422X)
81209	BLM (BLOOM SYNDROME, RECQ HELICASE-LIKE) (EG, BLOOM SYNDROME) GENE ANALYSIS, 2281DEL6INS7 VARIANT
81212	BRCA1 (BRCA1, DNA REPAIR ASSOCIATED), BRCA2 (BRCA2, DNA REPAIR ASSOCIATED) (EG, HEREDITARY BREAST AND OVARIAN CANCER) GENE ANALYSIS; 185DELAG, 5385INSC, 6174DELT VARIANTS
81215	BRCA1 (BRCA1, DNA REPAIR ASSOCIATED) (EG, HEREDITARY BREAST AND OVARIAN CANCER) GENE ANALYSIS; KNOWN FAMILIAL VARIANT
81216	BRCA2 (BRCA2, DNA REPAIR ASSOCIATED) (EG, HEREDITARY BREAST AND OVARIAN CANCER) GENE ANALYSIS; FULL SEQUENCE ANALYSIS
81217	BRCA2 (BRCA2, DNA REPAIR ASSOCIATED) (EG, HEREDITARY BREAST AND OVARIAN CANCER) GENE ANALYSIS; KNOWN FAMILIAL VARIANT
81225	CYP2C19 (CYTOCHROME P450, FAMILY 2, SUBFAMILY C, POLYPEPTIDE 19) (EG, DRUG METABOLISM), GENE ANALYSIS, COMMON VARIANTS (EG, *2, *3, *4, *8, *17)
81226	CYP2D6 (CYTOCHROME P450, FAMILY 2, SUBFAMILY D, POLYPEPTIDE 6) (EG, DRUG METABOLISM), GENE ANALYSIS, COMMON VARIANTS (EG, *2, *3, *4, *5, *6, *9, *10, *17, *19, *29, *35, *41, *1XN, *2XN, *4XN)
81227	CYP2C9 (CYTOCHROME P450, FAMILY 2, SUBFAMILY C, POLYPEPTIDE 9) (EG, DRUG METABOLISM), GENE ANALYSIS, COMMON VARIANTS (EG, *2, *3, *5, *6)
81228	CYTOGENOMIC CONSTITUTIONAL (GENOME-WIDE) MICROARRAY ANALYSIS; INTERROGATION OF GENOMIC REGIONS FOR COPY NUMBER VARIANTS (EG, BACTERIAL ARTIFICIAL CHROMOSOME [BAC] OR OLIGO-BASED COMPARATIVE GENOMIC HYBRIDIZATION [CGH] MICROARRAY ANALYSIS)
81229	CYTOGENOMIC CONSTITUTIONAL (GENOME-WIDE) MICROARRAY ANALYSIS; INTERROGATION OF GENOMIC REGIONS FOR COPY NUMBER AND SINGLE NUCLEOTIDE POLYMORPHISM (SNP) VARIANTS FOR CHROMOSOMAL ABNORMALITIES
81230	CYP3A4 (CYTOCHROME P450 FAMILY 3 SUBFAMILY A MEMBER 4) (EG, DRUG METABOLISM), GENE ANALYSIS, COMMON VARIANT(S) (EG, *2, *22)
81231	CYP3A5 (CYTOCHROME P450 FAMILY 3 SUBFAMILY A MEMBER 5) (EG, DRUG METABOLISM), GENE ANALYSIS, COMMON VARIANTS (EG, *2, *3, *4, *5, *6, *7)

CODE	DESCRIPTION
81232	DPYD (DIHYDROPYRIMIDINE DEHYDROGENASE) (EG, 5-FLUOROURACIL/5-FU AND CAPECITABINE DRUG METABOLISM), GENE ANALYSIS, COMMON VARIANT(S) (EG, *2A, *4, *5, *6)
81233	BTK (BRUTON'S TYROSINE KINASE) (EG, CHRONIC LYMPHOCYTIC LEUKEMIA) GENE ANALYSIS, COMMON VARIANTS (EG, C481S, C481R, C481F)
81234	DMPK (DM1 PROTEIN KINASE) (EG, MYOTONIC DYSTROPHY TYPE 1) GENE ANALYSIS; EVALUATION TO DETECT ABNORMAL (EXPANDED) ALLELES
81238	F9 (COAGULATION FACTOR IX) (EG, HEMOPHILIA B), FULL GENE SEQUENCE
81239	DMPK (DM1 PROTEIN KINASE) (EG, MYOTONIC DYSTROPHY TYPE 1) GENE ANALYSIS; CHARACTERIZATION OF ALLELES (EG, EXPANDED SIZE)
81240	F2 (PROTHROMBIN, COAGULATION FACTOR II) (EG, HEREDITARY HYPERCOAGULABILITY) GENE ANALYSIS, 20210G>A VARIANT
81241	F5 (COAGULATION FACTOR V) (EG, HEREDITARY HYPERCOAGULABILITY) GENE ANALYSIS, LEIDEN VARIANT
81242	FANCC (FANCONI ANEMIA, COMPLEMENTATION GROUP C) (EG, FANCONI ANEMIA, TYPE C) GENE ANALYSIS, COMMON VARIANT (EG, IVS4+4A>T)
81243	FMR1 (FRAGILE X MENTAL RETARDATION 1) (EG, FRAGILE X MENTAL RETARDATION) GENE ANALYSIS; EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81244	FMR1 (FRAGILE X MENTAL RETARDATION 1) (EG, FRAGILE X MENTAL RETARDATION) GENE ANALYSIS; CHARACTERIZATION OF ALLELES (EG, EXPANDED SIZE AND PROMOTER METHYLATION STATUS)
81247	G6PD (GLUCOSE-6-PHOSPHATE DEHYDROGENASE) (EG, HEMOLYTIC ANEMIA, JAUNDICE), GENE ANALYSIS; COMMON VARIANT(S) (EG, A, A-)
81248	G6PD (GLUCOSE-6-PHOSPHATE DEHYDROGENASE) (EG, HEMOLYTIC ANEMIA, JAUNDICE), GENE ANALYSIS; KNOWN FAMILIAL VARIANT(S)
81249	G6PD (GLUCOSE-6-PHOSPHATE DEHYDROGENASE) (EG, HEMOLYTIC ANEMIA, JAUNDICE), GENE ANALYSIS; FULL GENE SEQUENCE
81250	G6PC (GLUCOSE-6-PHOSPHATASE, CATALYTIC SUBUNIT) (EG, GLYCOGEN STORAGE DISEASE, TYPE 1A, VON GIERKE DISEASE) GENE ANALYSIS, COMMON VARIANTS (EG, R83C, Q347X)
81251	GBA (GLUCOSIDASE, BETA, ACID) (EG, GAUCHER DISEASE) GENE ANALYSIS, COMMON VARIANTS (EG, N370S, 84GG, L444P, IVS2+1G>A)
81252	GJB2 (GAP JUNCTION PROTEIN, BETA 2, 26KDA, CONNEXIN 26) (EG, NONSYNDROMIC HEARING LOSS) GENE ANALYSIS; FULL GENE SEQUENCE
81253	GJB2 (GAP JUNCTION PROTEIN, BETA 2, 26KDA, CONNEXIN 26) (EG, NONSYNDROMIC HEARING LOSS) GENE ANALYSIS; KNOWN FAMILIAL VARIANTS
81254	GJB6 (GAP JUNCTION PROTEIN, BETA 6, 30KDA, CONNEXIN 30) (EG,

CODE	DESCRIPTION
	NONSYNDROMIC HEARING LOSS) GENE ANALYSIS, COMMON VARIANTS (EG, 309KB [DEL(GJB6-D13S1830)] AND 232KB [DEL(GJB6-D13S1854)])
81255	HEXA (HEXOSAMINIDASE A [ALPHA POLYPEPTIDE]) (EG, TAY-SACHS DISEASE) GENE ANALYSIS, COMMON VARIANTS (EG, 1278INSTATC, 1421+1G>C, G269S)
81256	HFE (HEMOCHROMATOSIS) (EG, HEREDITARY HEMOCHROMATOSIS) GENE ANALYSIS, COMMON VARIANTS (EG, C282Y, H63D)
81257	HBA1/HBA2 (ALPHA GLOBIN 1 AND ALPHA GLOBIN 2) (EG, ALPHA THALASSEMIA, HB BART HYDROPS FETALIS SYNDROME, HBH DISEASE), GENE ANALYSIS; COMMON DELETIONS OR VARIANT (EG, SOUTHEAST ASIAN, THAI, FILIPINO, MEDITERRANEAN, ALPHA3.7, ALPHA4.2, ALPHA20.5, CONSTANT SPRING)
81258	HBA1/HBA2 (ALPHA GLOBIN 1 AND ALPHA GLOBIN 2) (EG, ALPHA THALASSEMIA, HB BART HYDROPS FETALIS SYNDROME, HBH DISEASE), GENE ANALYSIS; KNOWN FAMILIAL VARIANT
81259	HBA1/HBA2 (ALPHA GLOBIN 1 AND ALPHA GLOBIN 2) (EG, ALPHA THALASSEMIA, HB BART HYDROPS FETALIS SYNDROME, HBH DISEASE), GENE ANALYSIS; FULL GENE SEQUENCE
81260	IKBKAP (INHIBITOR OF KAPPA LIGHT POLYPEPTIDE GENE ENHANCER IN B-CELLS, KINASE COMPLEX-ASSOCIATED PROTEIN) (EG, FAMILIAL DYSAUTONOMIA) GENE ANALYSIS, COMMON VARIANTS (EG, 2507+6T>C, R696P)
81269	HBA1/HBA2 (ALPHA GLOBIN 1 AND ALPHA GLOBIN 2) (EG, ALPHA THALASSEMIA, HB BART HYDROPS FETALIS SYNDROME, HBH DISEASE), GENE ANALYSIS; DUPLICATION/DELETION VARIANTS
81271	HTT (HUNTINGTIN) (EG, HUNTINGTON DISEASE) GENE ANALYSIS; EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81274	HTT (HUNTINGTIN) (EG, HUNTINGTON DISEASE) GENE ANALYSIS; CHARACTERIZATION OF ALLELES (EG, EXPANDED SIZE)
81278	IGH@/BCL2 (T(14;18)) (EG, FOLLICULAR LYMPHOMA) TRANSLOCATION ANALYSIS, MAJOR BREAKPOINT REGION (MBR) AND MINOR CLUSTER REGION (MCR) BREAKPOINTS, QUALITATIVE OR QUANTITATIVE
81279	JAK2 (JANUS KINASE 2) (EG, MYELOPROLIFERATIVE DISORDER) TARGETED SEQUENCE ANALYSIS (EG, EXONS 12 AND 13)
81283	IFNL3 (INTERFERON, LAMBDA 3) (EG, DRUG RESPONSE), GENE ANALYSIS, RS12979860 VARIANT
81284	FXN (FRATAXIN) (EG, FRIEDREICH ATAXIA) GENE ANALYSIS; EVALUATION TO DETECT ABNORMAL (EXPANDED) ALLELES
81285	FXN (FRATAXIN) (EG, FRIEDREICH ATAXIA) GENE ANALYSIS; CHARACTERIZATION OF ALLELES (EG, EXPANDED SIZE)
81286	FXN (FRATAXIN) (EG, FRIEDREICH ATAXIA) GENE ANALYSIS; FULL GENE

CODE	DESCRIPTION
	SEQUENCE
81288	MLH1 (MUTL HOMOLOG 1, COLON CANCER, NONPOLYPOSIS TYPE 2) (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) GENE ANALYSIS; PROMOTER METHYLATION ANALYSIS
81289	FXN (FRATAXIN) (EG, FRIEDREICH ATAXIA) GENE ANALYSIS; KNOWN FAMILIAL VARIANT(S)
81290	MCOLN1 (MUCOLIPIN 1) (EG, MUCOLIPIDOSIS, TYPE IV) GENE ANALYSIS, COMMON VARIANTS (EG, IVS3-2A>G, DEL6.4KB)
81291	MTHFR (5,10-METHYLENETETRAHYDROFOLATE REDUCTASE) (EG, HEREDITARY HYPERCOAGULABILITY) GENE ANALYSIS, COMMON VARIANTS (EG, 677T, 1298C)
81292	MLH1 (MUTL HOMOLOG 1, COLON CANCER, NONPOLYPOSIS TYPE 2) (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) GENE ANALYSIS; FULL SEQUENCE ANALYSIS
81293	MLH1 (MUTL HOMOLOG 1, COLON CANCER, NONPOLYPOSIS TYPE 2) (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) GENE ANALYSIS; KNOWN FAMILIAL VARIANTS
81294	MLH1 (MUTL HOMOLOG 1, COLON CANCER, NONPOLYPOSIS TYPE 2) (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) GENE ANALYSIS; DUPLICATION/DELETION VARIANTS
81295	MSH2 (MUTS HOMOLOG 2, COLON CANCER, NONPOLYPOSIS TYPE 1) (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) GENE ANALYSIS; FULL SEQUENCE ANALYSIS
81296	MSH2 (MUTS HOMOLOG 2, COLON CANCER, NONPOLYPOSIS TYPE 1) (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) GENE ANALYSIS; KNOWN FAMILIAL VARIANTS
81297	MSH2 (MUTS HOMOLOG 2, COLON CANCER, NONPOLYPOSIS TYPE 1) (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) GENE ANALYSIS; DUPLICATION/DELETION VARIANTS
81298	MSH6 (MUTS HOMOLOG 6 [E. COLI]) (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) GENE ANALYSIS; FULL SEQUENCE ANALYSIS
81299	MSH6 (MUTS HOMOLOG 6 [E. COLI]) (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) GENE ANALYSIS; KNOWN FAMILIAL VARIANTS
CODE	DESCRIPTION
81300	MSH6 (MUTS HOMOLOG 6 [E. COLI]) (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) GENE ANALYSIS; DUPLICATION/DELETION VARIANTS

CODE	DESCRIPTION
81302	MECP2 (METHYL CPG BINDING PROTEIN 2) (EG, RETT SYNDROME) GENE ANALYSIS; FULL SEQUENCE ANALYSIS
81303	MECP2 (METHYL CPG BINDING PROTEIN 2) (EG, RETT SYNDROME) GENE ANALYSIS; KNOWN FAMILIAL VARIANT
81304	MECP2 (METHYL CPG BINDING PROTEIN 2) (EG, RETT SYNDROME) GENE ANALYSIS; DUPLICATION/DELETION VARIANTS
81306	NUDT15 (NUDIX HYDROLASE 15) (EG, DRUG METABOLISM) GENE ANALYSIS, COMMON VARIANT(S) (EG, *2, *3, *4, *5, *6)
81312	PABPN1 (POLY[A] BINDING PROTEIN NUCLEAR 1) (EG, OCULOPHARYNGEAL MUSCULAR DYSTROPHY) GENE ANALYSIS, EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81317	PMS2 (POSTMEIOTIC SEGREGATION INCREASED 2 [S. CEREVISIAE]) (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) GENE ANALYSIS; FULL SEQUENCE ANALYSIS
81318	PMS2 (POSTMEIOTIC SEGREGATION INCREASED 2 [S. CEREVISIAE]) (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) GENE ANALYSIS; KNOWN FAMILIAL VARIANTS
81319	PMS2 (POSTMEIOTIC SEGREGATION INCREASED 2 [S. CEREVISIAE]) (EG, HEREDITARY NON-POLYPOSIS COLORECTAL CANCER, LYNCH SYNDROME) GENE ANALYSIS; DUPLICATION/DELETION VARIANTS
81321	PTEN (PHOSPHATASE AND TENSIN HOMOLOG) (EG, COWDEN SYNDROME, PTEN HAMARTOMA TUMOR SYNDROME) GENE ANALYSIS; FULL SEQUENCE ANALYSIS
81322	PTEN (PHOSPHATASE AND TENSIN HOMOLOG) (EG, COWDEN SYNDROME, PTEN HAMARTOMA TUMOR SYNDROME) GENE ANALYSIS; KNOWN FAMILIAL VARIANT
81323	PTEN (PHOSPHATASE AND TENSIN HOMOLOG) (EG, COWDEN SYNDROME, PTEN HAMARTOMA TUMOR SYNDROME) GENE ANALYSIS; DUPLICATION/DELETION VARIANT
81324	PMP22 (PERIPHERAL MYELIN PROTEIN 22) (EG, CHARCOT-MARIE-TOOTH, HEREDITARY NEUROPATHY WITH LIABILITY TO PRESSURE PALSIES) GENE ANALYSIS; DUPLICATION/DELETION ANALYSIS
81325	PMP22 (PERIPHERAL MYELIN PROTEIN 22) (EG, CHARCOT-MARIE-TOOTH, HEREDITARY NEUROPATHY WITH LIABILITY TO PRESSURE PALSIES) GENE ANALYSIS; FULL SEQUENCE ANALYSIS
81326	PMP22 (PERIPHERAL MYELIN PROTEIN 22) (EG, CHARCOT-MARIE-TOOTH, HEREDITARY NEUROPATHY WITH LIABILITY TO PRESSURE PALSIES) GENE ANALYSIS; KNOWN FAMILIAL VARIANT
81328	SLCO1B1 (SOLUTE CARRIER ORGANIC ANION TRANSPORTER FAMILY, MEMBER 1B1) (EG, ADVERSE DRUG REACTION), GENE ANALYSIS, COMMON VARIANT(S) (EG, *5)

CODE	DESCRIPTION
81329	SMN1 (SURVIVAL OF MOTOR NEURON 1, TELOMERIC) (EG, SPINAL MUSCULAR ATROPHY) GENE ANALYSIS; DOSAGE/DELETION ANALYSIS (EG, CARRIER TESTING), INCLUDES SMN2 (SURVIVAL OF MOTOR NEURON 2, CENTROMERIC) ANALYSIS, IF PERFORMED
81330	SMPD1(SPHINGOMYELIN PHOSPHODIESTERASE 1, ACID LYSOSOMAL) (EG, NIEMANN-PICK DISEASE, TYPE A) GENE ANALYSIS, COMMON VARIANTS (EG, R496L, L302P, FSP330)
81331	SNRPN/UBE3A (SMALL NUCLEAR RIBONUCLEOPROTEIN POLYPEPTIDE N AND UBIQUITIN PROTEIN LIGASE E3A) (EG, PRADER-WILLI SYNDROME AND/OR ANGELMAN SYNDROME), METHYLATION ANALYSIS
81332	SERPINA1 (SERPIN PEPTIDASE INHIBITOR, CLADE A, ALPHA-1 ANTIPROTEINASE, ANTITRYPSIN, MEMBER 1) (EG, ALPHA-1-ANTITRYPSIN DEFICIENCY), GENE ANALYSIS, COMMON VARIANTS (EG, *S AND *Z)
81333	TGFBI (TRANSFORMING GROWTH FACTOR BETA-INDUCED) (EG, CORNEAL DYSTROPHY) GENE ANALYSIS, COMMON VARIANTS (EG, R124H, R124C, R124L, R555W, R555Q)
81335	TPMT (THIOPURINE S-METHYLTRANSFERASE) (EG, DRUG METABOLISM), GENE ANALYSIS, COMMON VARIANTS (EG, *2, *3)
81336	SMN1 (SURVIVAL OF MOTOR NEURON 1, TELOMERIC) (EG, SPINAL MUSCULAR ATROPHY) GENE ANALYSIS; FULL GENE SEQUENCE
81337	SMN1 (SURVIVAL OF MOTOR NEURON 1, TELOMERIC) (EG, SPINAL MUSCULAR ATROPHY) GENE ANALYSIS; KNOWN FAMILIAL SEQUENCE VARIANT(S)
81338	MPL (MPL PROTO-ONCOGENE, THROMBOPOIETIN RECEPTOR) (EG, MYELOPROLIFERATIVE DISORDER) GENE ANALYSIS; COMMON VARIANTS (EG, W515A, W515K, W515L, W515R)
81339	MPL (MPL PROTO-ONCOGENE, THROMBOPOIETIN RECEPTOR) (EG, MYELOPROLIFERATIVE DISORDER) GENE ANALYSIS; SEQUENCE ANALYSIS, EXON 10
81340	TRB@ (T CELL ANTIGEN RECEPTOR, BETA) (EG, LEUKEMIA AND LYMPHOMA), GENE REARRANGEMENT ANALYSIS TO DETECT ABNORMAL CLONAL POPULATION(S); USING AMPLIFICATION METHODOLOGY (EG, POLYMERASE CHAIN REACTION)
81341	TRB@ (T CELL ANTIGEN RECEPTOR, BETA) (EG, LEUKEMIA AND LYMPHOMA), GENE REARRANGEMENT ANALYSIS TO DETECT ABNORMAL CLONAL POPULATION(S); USING DIRECT PROBE METHODOLOGY (EG, SOUTHERN BLOT)
81342	TRG@ (T CELL ANTIGEN RECEPTOR, GAMMA) (EG, LEUKEMIA AND LYMPHOMA), GENE REARRANGEMENT ANALYSIS, EVALUATION TO DETECT ABNORMAL CLONAL POPULATION(S)
81343	PPP2R2B (PROTEIN PHOSPHATASE 2 REGULATORY SUBUNIT BBETA) (EG, SPINOCEREBELLAR ATAXIA) GENE ANALYSIS, EVALUATION TO DETECT ABNORMAL

CODE	DESCRIPTION
	(EG, EXPANDED) ALLELES
81344	TBP (TATA BOX BINDING PROTEIN) (EG, SPINOCEREBELLAR ATAXIA) GENE ANALYSIS, EVALUATION TO DETECT ABNORMAL (EG, EXPANDED) ALLELES
81345	TERT (TELOMERASE REVERSE TRANSCRIPTASE) (EG, THYROID CARCINOMA, GLIOBLASTOMA MULTIFORME) GENE ANALYSIS, TARGETED SEQUENCE ANALYSIS (EG, PROMOTER REGION)
81346	TYMS (THYMIDYLATE SYNTHETASE) (EG, 5-FLUOROURACIL/5-FU DRUG METABOLISM), GENE ANALYSIS, COMMON VARIANT(S) (EG, TANDEM REPEAT VARIANT)
81347	SF3B1 (SPLICING FACTOR [3B] SUBUNIT B1) (EG, MYELODYSPLASTIC SYNDROME/ACUTE MYELOID LEUKEMIA) GENE ANALYSIS, COMMON VARIANTS (EG, A672T, E622D, L833F, R625C, R625L)
81348	SRSF2 (SERINE AND ARGININE-RICH SPLICING FACTOR 2) (EG, MYELODYSPLASTIC SYNDROME, ACUTE MYELOID LEUKEMIA) GENE ANALYSIS, COMMON VARIANTS (EG, P95H, P95L)
81350	UGT1A1 (UDP GLUCURONOSYLTRANSFERASE 1 FAMILY, POLYPEPTIDE A1) (EG, DRUG METABOLISM, HEREDITARY UNCONJUGATED HYPERBILIRUBINEMIA [GILBERT SYNDROME]) GENE ANALYSIS, COMMON VARIANTS (EG, *28, *36, *37)
81351	TP53 (TUMOR PROTEIN 53) (EG, LI-FRAUMENI SYNDROME) GENE ANALYSIS; FULL GENE SEQUENCE
81352	TP53 (TUMOR PROTEIN 53) (EG, LI-FRAUMENI SYNDROME) GENE ANALYSIS; TARGETED SEQUENCE ANALYSIS (EG, 4 ONCOLOGY)
81353	TP53 (TUMOR PROTEIN 53) (EG, LI-FRAUMENI SYNDROME) GENE ANALYSIS; KNOWN FAMILIAL VARIANT
81355	VKORC1 (VITAMIN K EPOXIDE REDUCTASE COMPLEX, SUBUNIT 1) (EG, WARFARIN METABOLISM), GENE ANALYSIS, COMMON VARIANT(S) (EG, -1639G>A, C.173+1000C>T)
81357	U2AF1 (U2 SMALL NUCLEAR RNA AUXILIARY FACTOR 1) (EG, MYELODYSPLASTIC SYNDROME, ACUTE MYELOID LEUKEMIA) GENE ANALYSIS, COMMON VARIANTS (EG, S34F, S34Y, Q157R, Q157P)
81360	ZRSR2 (ZINC FINGER CCCH-TYPE, RNA BINDING MOTIF AND SERINE/ARGININE-RICH 2) (EG, MYELODYSPLASTIC SYNDROME, ACUTE MYELOID LEUKEMIA) GENE ANALYSIS, COMMON VARIANT(S) (EG, E65FS, E122FS, R448FS)
81361	HBB (HEMOGLOBIN, SUBUNIT BETA) (EG, SICKLE CELL ANEMIA, BETA THALASSEMIA, HEMOGLOBINOPATHY); COMMON VARIANT(S) (EG, HBS, HBC, HBE)
81362	HBB (HEMOGLOBIN, SUBUNIT BETA) (EG, SICKLE CELL ANEMIA, BETA THALASSEMIA, HEMOGLOBINOPATHY); KNOWN FAMILIAL VARIANT(S)
81363	HBB (HEMOGLOBIN, SUBUNIT BETA) (EG, SICKLE CELL ANEMIA, BETA

CODE	DESCRIPTION
	THALASSEMIA, HEMOGLOBINOPATHY); DUPLICATION/DELETION VARIANT(S)
81364	HBB (HEMOGLOBIN, SUBUNIT BETA) (EG, SICKLE CELL ANEMIA, BETA THALASSEMIA, HEMOGLOBINOPATHY); FULL GENE SEQUENCE
81401	MOLECULAR PATHOLOGY PROCEDURE, LEVEL 2 (EG, 2-10 SNPS, 1 METHYLATED VARIANT, OR 1 SOMATIC VARIANT [TYPICALLY USING NONSEQUENCING TARGET VARIANT ANALYSIS], OR DETECTION OF A DYNAMIC MUTATION DISORDER/TRIPLET REPEAT)
81402	MOLECULAR PATHOLOGY PROCEDURE, LEVEL 3 (EG, >10 SNPS, 2-10 METHYLATED VARIANTS, OR 2-10 SOMATIC VARIANTS [TYPICALLY USING NON-SEQUENCING TARGET VARIANT ANALYSIS], IMMUNOGLOBULIN AND T-CELL RECEPTOR GENE REARRANGEMENTS, DUPLICATION/DELETION VARIANTS OF 1 EXON, LOSS OF HETEROZYGOSITY [LOH], UNIPARENTAL DISOMY [UPD])
81403	MOLECULAR PATHOLOGY PROCEDURE, LEVEL 4 (EG, ANALYSIS OF SINGLE EXON BY DNA SEQUENCE ANALYSIS, ANALYSIS OF >10 AMPLICONS USING MULTIPLEX PCR IN 2 OR MORE INDEPENDENT REACTIONS, MUTATION SCANNING OR DUPLICATION/DELETION VARIANTS OF 2-5 EXONS)
81404	MOLECULAR PATHOLOGY PROCEDURE, LEVEL 5 (EG, ANALYSIS OF 2-5 EXONS BY DNA SEQUENCE ANALYSIS, MUTATION SCANNING OR DUPLICATION/DELETION VARIANTS OF 6-10 EXONS, OR CHARACTERIZATION OF A DYNAMIC MUTATION DISORDER/TRIPLET REPEAT BY SOUTHERN BLOT ANALYSIS) UGT1A1 (UDP GLUCURONOSYLTRANSFERASE 1 FAMILY, POLYPEPTIDE A1) (EG, HEREDITARY UNCONJUGATED HYPERBILIRUBINEMIA [CRIGLER-NAJJAR SYNDROME]) FULL GENE SEQUENCE
81405	MOLECULAR PATHOLOGY PROCEDURE, LEVEL 6 (EG, ANALYSIS OF 6-10 EXONS BY DNA SEQUENCE ANALYSIS, MUTATION SCANNING OR DUPLICATION/DELETION VARIANTS OF 11-25 EXONS, REGIONALLY TARGETED CYTOGENOMIC ARRAY ANALYSIS)
81406	MOLECULAR PATHOLOGY PROCEDURE, LEVEL 7 (EG, ANALYSIS OF 11-25 EXONS BY DNA SEQUENCE ANALYSIS, MUTATION SCANNING OR DUPLICATION/DELETION VARIANTS OF 26-50 EXONS, CYTOGENOMIC ARRAY ANALYSIS FOR NEOPLASIA)
81407	MOLECULAR PATHOLOGY PROCEDURE, LEVEL 8 (EG, ANALYSIS OF 26-50 EXONS BY DNA SEQUENCE ANALYSIS, MUTATION SCANNING OR DUPLICATION/DELETION VARIANTS OF >50 EXONS, SEQUENCE ANALYSIS OF MULTIPLE GENES ON ONE PLATFORM) APOB (APOLIPOPROTEIN B) (EG, FAMILIAL HYPERCHOLESTEROLEMIA TYPE B) FULL GENE SEQUENCE
81408	MOLECULAR PATHOLOGY PROCEDURE, LEVEL 9 (EG, ANALYSIS OF >50 EXONS IN A SINGLE GENE BY DNA SEQUENCE ANALYSIS)
81410	AORTIC DYSFUNCTION OR DILATION (EG, MARFAN SYNDROME, LOEYS DIETZ SYNDROME, EHLER DANLOS SYNDROME TYPE IV, ARTERIAL TORTUOSITY SYNDROME); GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE SEQUENCING

CODE	DESCRIPTION
	OF AT LEAST 9 GENES, INCLUDING FBN1, TGFBR1, TGFBR2, COL3A1, MYH11, ACTA2, SLC2A10, SMAD3, AND MYLK
81411	AORTIC DYSFUNCTION OR DILATION (EG, MARFAN SYNDROME, LOEYS DIETZ SYNDROME, EHLER DANLOS SYNDROME TYPE IV, ARTERIAL TORTUOSITY SYNDROME); DUPLICATION/DELETION ANALYSIS PANEL, MUST INCLUDE ANALYSES FOR TGFBR1, TGFBR2, MYH11, AND COL3A1
81412	ASHKENAZI JEWISH ASSOCIATED DISORDERS (EG, BLOOM SYNDROME, CANAVAN DISEASE, CYSTIC FIBROSIS, FAMILIAL DYSAUTONOMIA, FANCONI ANEMIA GROUP C, GAUCHER DISEASE, TAY-SACHS DISEASE), GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE SEQUENCING OF AT LEAST 9 GENES, INCLUDING ASPA, BLM, CFTR, FANCC, GBA, HEXA, IKBKAP, MCOLN1, AND SMPD1
81413	CARDIAC ION CHANNELOPATHIES (EG, BRUGADA SYNDROME, LONG QT SYNDROME, SHORT QT SYNDROME, CATECHOLAMINERGIC POLYMORPHIC VENTRICULAR TACHYCARDIA); GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE SEQUENCING OF AT LEAST 10 GENES, INCLUDING ANK2, CASQ2, CAV3, KCNE1, KCNE2, KCNH2, KCNJ2, KCNQ1, RYR2, AND SCN5A
81414	CARDIAC ION CHANNELOPATHIES (EG, BRUGADA SYNDROME, LONG QT SYNDROME, SHORT QT SYNDROME, CATECHOLAMINERGIC POLYMORPHIC VENTRICULAR TACHYCARDIA); DUPLICATION/DELETION GENE ANALYSIS PANEL, MUST INCLUDE ANALYSIS OF AT LEAST 2 GENES, INCLUDING KCNH2 AND KCNQ1
81415	EXOME (EG, UNEXPLAINED CONSTITUTIONAL OR HERITABLE DISORDER OR SYNDROME); SEQUENCE ANALYSIS
81416	EXOME (EG, UNEXPLAINED CONSTITUTIONAL OR HERITABLE DISORDER OR SYNDROME); SEQUENCE ANALYSIS, EACH COMPARATOR EXOME (EG, PARENTS, SIBLINGS) (LIST SEPARATELY IN ADDITION TO CODE FOR PRIMARY PROCEDURE)
81417	EXOME (EG, UNEXPLAINED CONSTITUTIONAL OR HERITABLE DISORDER OR SYNDROME); RE-EVALUATION OF PREVIOUSLY OBTAINED EXOME SEQUENCE (EG, UPDATED KNOWLEDGE OR UNRELATED CONDITION/SYNDROME)
81419	EPILEPSY GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE ANALYSES FOR ALDH7A1, CACNA1A, CDKL5, CHD2, GABRG2, GRIN2A, KCNQ2, MECP2, PCDH19, POLG, PRRT2, SCN1A, SCN1B, SCN2A, SCN8A, SLC2A1, SLC9A6, STXBP1, SYNGAP1, TCF4, TPP1, TSC1, TSC2, AND ZEB2
81420	FETAL CHROMOSOMAL ANEUPLOIDY (EG, TRISOMY 21, MONOSOMY X) GENOMIC SEQUENCE ANALYSIS PANEL, CIRCULATING CELL-FREE FETAL DNA IN MATERNAL BLOOD, MUST INCLUDE ANALYSIS OF CHROMOSOMES 13, 18, AND 21
81422	FETAL CHROMOSOMAL MICRODELETION(S) GENOMIC SEQUENCE ANALYSIS (EG, DIGEORGE SYNDROME, CRI-DU-CHAT SYNDROME), CIRCULATING CELL-FREE FETAL DNA IN MATERNAL BLOOD
81425	GENOME (EG, UNEXPLAINED CONSTITUTIONAL OR HERITABLE DISORDER OR SYNDROME); SEQUENCE ANALYSIS

CODE	DESCRIPTION
81426	GENOME (EG, UNEXPLAINED CONSTITUTIONAL OR HERITABLE DISORDER OR SYNDROME); SEQUENCE ANALYSIS, EACH COMPARATOR GENOME (EG, PARENTS, SIBLINGS) (LIST SEPARATELY IN ADDITION TO CODE FOR PRIMARY PROCEDURE)
81427	GENOME (EG, UNEXPLAINED CONSTITUTIONAL OR HERITABLE DISORDER OR SYNDROME); RE-EVALUATION OF PREVIOUSLY OBTAINED GENOME SEQUENCE (EG, UPDATED KNOWLEDGE OR UNRELATED CONDITION/SYNDROME)
81430	HEARING LOSS (EG, NONSYNDROMIC HEARING LOSS, USHER SYNDROME, PENDRED SYNDROME); GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE SEQUENCING OF AT LEAST 60 GENES, INCLUDING CDH23, CLRN1, GJB2, GPR98, MTRNR1, MYO7A, MYO15A, PCDH15, OTOF, SLC26A4, TMC1, TMPRSS3, USH1C, USH1G, USH2A, AND WFS1
81431	HEARING LOSS (EG, NONSYNDROMIC HEARING LOSS, USHER SYNDROME, PENDRED SYNDROME); DUPLICATION/DELETION ANALYSIS PANEL, MUST INCLUDE COPY NUMBER ANALYSES FOR STRC AND DFNB1 DELETIONS IN GJB2 AND GJB6 GENES
81432	HEREDITARY BREAST CANCER-RELATED DISORDERS (EG, HEREDITARY BREAST CANCER, HEREDITARY OVARIAN CANCER, HEREDITARY ENDOMETRIAL CANCER); GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE SEQUENCING OF AT LEAST 10 GENES, ALWAYS INCLUDING BRCA1, BRCA2, CDH1, MLH1, MSH2, MSH6, PALB2, PTEN, STK11, AND TP53
81433	HEREDITARY BREAST CANCER-RELATED DISORDERS (EG, HEREDITARY BREAST CANCER, HEREDITARY OVARIAN CANCER, HEREDITARY ENDOMETRIAL CANCER); DUPLICATION/DELETION ANALYSIS PANEL, MUST INCLUDE ANALYSES FOR BRCA1, BRCA2, MLH1, MSH2, AND STK11
81434	HEREDITARY RETINAL DISORDERS (EG, RETINITIS PIGMENTOSA, LEBER CONGENITAL AMAUROSIS, CONE-ROD DYSTROPHY), GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE SEQUENCING OF AT LEAST 15 GENES, INCLUDING ABCA4, CNGA1, CRB1, EYS, PDE6A, PDE6B, PRPF31, PRPH2, RDH12, RHO, RP1, RP2, RPE65, RPGR, AND USH2A
81435	HEREDITARY COLON CANCER DISORDERS (EG, LYNCH SYNDROME, PTEN HAMARTOMA SYNDROME, COWDEN SYNDROME, FAMILIAL ADENOMATOSIS POLYPOSIS); GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE SEQUENCING OF AT LEAST 10 GENES, INCLUDING APC, BMPR1A, CDH1, MLH1, MSH2, MSH6, MUTYH, PTEN, SMAD4, AND STK11
81436	HEREDITARY COLON CANCER DISORDERS (EG, LYNCH SYNDROME, PTEN HAMARTOMA SYNDROME, COWDEN SYNDROME, FAMILIAL ADENOMATOSIS POLYPOSIS); DUPLICATION/DELETION ANALYSIS PANEL, MUST INCLUDE ANALYSIS OF AT LEAST 5 GENES, INCLUDING MLH1, MSH2, EPCAM, SMAD4, AND STK11
81437	HEREDITARY NEUROENDOCRINE TUMOR DISORDERS (EG, MEDULLARY THYROID CARCINOMA, PARATHYROID CARCINOMA, MALIGNANT PHEOCHROMOCYTOMA OR PARAGANGLIOMA); GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE

CODE	DESCRIPTION
	SEQUENCING OF AT LEAST 6 GENES, INCLUDING MAX, SDHB, SDHC, SDHD, TMEM127, AND VHL
81438	HEREDITARY NEUROENDOCRINE TUMOR DISORDERS (EG, MEDULLARY THYROID CARCINOMA, PARATHYROID CARCINOMA, MALIGNANT PHEOCHROMOCYTOMA OR PARAGANGLIOMA); DUPLICATION/DELETION ANALYSIS PANEL, MUST INCLUDE ANALYSES FOR SDHB, SDHC, SDHD, AND VHL
81439	HEREDITARY CARDIOMYOPATHY (EG, HYPERTROPHIC CARDIOMYOPATHY, DILATED CARDIOMYOPATHY, ARRHYTHMOGENIC RIGHT VENTRICULAR CARDIOMYOPATHY), GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE SEQUENCING OF AT LEAST 5 CARDIOMYOPATHY-RELATED GENES (EG, DSG2, MYBPC3, MYH7, PKP2, TTN)
81440	NUCLEAR ENCODED MITOCHONDRIAL GENES (EG, NEUROLOGIC OR MYOPATHIC PHENOTYPES), GENOMIC SEQUENCE PANEL, MUST INCLUDE ANALYSIS OF AT LEAST 100 GENES, INCLUDING BCS1L, C10ORF2, COQ2, COX10, DGUOK, MPV17, OPA1, PDSS2, POLG, POLG2, RRM2B, SCO1, SCO2, SLC25A4, SUCLA2, SUCLG1, TAZ, TK2, AND TYMP
81442	NOONAN SPECTRUM DISORDERS (EG, NOONAN SYNDROME, RADIO-FACIO-CUTANEOUS SYNDROME, COSTELLO SYNDROME, LEOPARD SYNDROME, NOONAN-LIKE SYNDROME), GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE SEQUENCING OF AT LEAST 12 GENES, INCLUDING BRAF, CBL, HRAS, KRAS, MAP2K1, MAP2K2, NRAS, PTPN11, RAF1, RIT1, SHOC2, AND SOS1
81443	GENETIC TESTING FOR SEVERE INHERITED CONDITIONS (EG, CYSTIC FIBROSIS, ASHKENAZI JEWISH-ASSOCIATED DISORDERS [EG, BLOOM SYNDROME, CANAVAN DISEASE, FANCONI ANEMIA TYPE C, MUCOLIPIDOSIS TYPE VI, GAUCHER DISEASE, TAY-SACHS DISEASE], BETA HEMOGLOBINOPATHIES, PHENYLKETONURIA, GALACTOSEMIA), GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE SEQUENCING OF AT LEAST 15 GENES (EG, ACADM, ARSA, ASPA, ATP7B, BCKDHA, BCKDHB, BLM, CFTR, DHCR7, FANCC, G6PC, GAA, GALT, GBA, GBE1, HBB, HEXA, IKBKAP, MCOLN1, PAH)
81448	HEREDITARY PERIPHERAL NEUROPATHIES (EG, CHARCOT-MARIE-TOOTH, SPASTIC PARAPLEGIA), GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE SEQUENCING OF AT LEAST 5 PERIPHERAL NEUROPATHY-RELATED GENES (EG, BSCL2, GJB1, MFN2, MPZ, REEP1, SPAST, SPG11, SPTLC1)
81460	WHOLE MITOCHONDRIAL GENOME (EG, LEIGH SYNDROME, MITOCHONDRIAL ENCEPHALOMYOPATHY, LACTIC ACIDOSIS, AND STROKE-LIKE EPISODES [MELAS], MYOCLONIC EPILEPSY WITH RAGGED-RED FIBERS [MERFF], NEUROPATHY, ATAXIA, AND RETINITIS PIGMENTOSA [NARP], LEBER HEREDITARY OPTIC NEUROPATHY [LHON]), GENOMIC SEQUENCE, MUST INCLUDE SEQUENCE ANALYSIS OF ENTIRE MITOCHONDRIAL GENOME WITH HETEROPLASMY DETECTION
81465	WHOLE MITOCHONDRIAL GENOME LARGE DELETION ANALYSIS PANEL (EG, KEARNS-SAYRE SYNDROME, CHRONIC PROGRESSIVE EXTERNAL OPHTHALMOPLEGIA), INCLUDING HETEROPLASMY DETECTION, IF PERFORMED

CODE	DESCRIPTION
81470	X-LINKED INTELLECTUAL DISABILITY (XLID) (EG, SYNDROMIC AND NON-SYNDROMIC XLID); GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE SEQUENCING OF AT LEAST 60 GENES, INCLUDING ARX, ATRX, CDKL5, FGD1, FMR1, HUWE1, IL1RAPL, KDM5C, L1CAM, MECP2, MED12, MID1, OCRL, RPS6KA3, AND SLC16A2
81471	X-LINKED INTELLECTUAL DISABILITY (XLID) (EG, SYNDROMIC AND NON-SYNDROMIC XLID); DUPLICATION/DELETION GENE ANALYSIS, MUST INCLUDE ANALYSIS OF AT LEAST 60 GENES, INCLUDING ARX, ATRX, CDKL5, FGD1, FMR1, HUWE1, IL1RAPL, KDM5C, L1CAM, MECP2, MED12, MID1, OCRL, RPS6KA3, AND SLC16A2

Group 2 Paragraph:

For tests billed under the Not Otherwise Classified (NOC) CPT® code 81479:

Tests billed under the NOC CPT® code 81479 that are used for germline testing and are further defined by a unique identifier (such as a Z-Identifier code) are limited to once per lifetime, as are such tests that are duplicative.

If non-duplicative testing of such a test is considered medically reasonable and necessary, please use a -77 modifier to trigger a medical review.

Group 2 Codes:

CODE	DESCRIPTION
81479	UNLISTED MOLECULAR PATHOLOGY PROCEDURE

CPT/HCPCS Modifiers

Group 1 Paragraph:

N/A

Group 1 Codes:

CODE	DESCRIPTION
77	REPEAT PROCEDURE BY ANOTHER PHYSICIAN: THE PHYSICIAN MAY NEED TO INDICATE THAT A BASIC PROCEDURE OR SERVICE PERFORMED BY ANOTHER PHYSICIAN HAD TO BE REPEATED. THIS SITUATION MAY BE REPORTED BY ADDING MODIFIER -77 TO THE REPEATED PROCEDURE/SERVICE OR THE SEPARATE FIVE DIGIT MODIFIER CODE 09977 MAY BE USED.

ICD-10-CM Codes that Support Medical Necessity

Group 1 Paragraph:

N/A

Group 1 Codes:

CODE	DESCRIPTION
XX000	Not Applicable

ICD-10-CM Codes that DO NOT Support Medical Necessity

Group 1 Paragraph:

N/A

Group 1 Codes:

N/A

Additional ICD-10 Information

N/A

Bill Type Codes

Contractors may specify Bill Types to help providers identify those Bill Types typically used to report this service. Absence of a Bill Type does not guarantee that the article does not apply to that Bill Type. Complete absence of all Bill Types indicates that coverage is not influenced by Bill Type and the article should be assumed to apply equally to all claims.

CODE	DESCRIPTION
999x	Not Applicable

Revenue Codes

Contractors may specify Revenue Codes to help providers identify those Revenue Codes typically used to report this service. In most instances Revenue Codes are purely advisory. Unless specified in the article, services reported under other Revenue Codes are equally subject to this coverage determination. Complete absence of all Revenue Codes indicates that coverage is not influenced by Revenue Code and the article should be assumed to apply equally to all Revenue Codes.

N/A

Other Coding Information

Group 1 Paragraph:

N/A

Group 1 Codes:

CODE

N/A

Revision History Information

REVISION HISTORY DATE	REVISION HISTORY NUMBER	REVISION HISTORY EXPLANATION
01/01/2021	R1	<p>Under CPT/HCPCS Codes Group 1: Added 81168, 81191, 81192, 81193, 81194, 81278, 81279, 81338, 81339, 81347, 81348, 81351, 81352, 81353, 81357, 81360, 81419.</p> <p>This revision is due to the Q1 2021 CPT/HCPCS Code Update and is effective for dates of service on or after 01/01/2021.</p>

Associated Documents

Related Local Coverage Documents

LCDs

[L38353 - MolDX: Repeat Germline Testing](#)

Related National Coverage Documents

N/A

Statutory Requirements URLs

N/A

Rules and Regulations URLs

N/A

CMS Manual Explanations URLs

N/A

Other URLs

N/A

Public Versions

UPDATED ON	EFFECTIVE DATES	STATUS
02/05/2021	01/01/2021 - N/A	Currently in Effect (This Version)

UPDATED ON	EFFECTIVE DATES	STATUS
06/02/2020	08/03/2020 - N/A	Superseded

Keywords

N/A