

06, Feb 2026

severity	code	details	expression
29 information	informational	This element does not match any known slice defined in the profile https://fhir.nwgenomics.nhs.uk/StructureDefinition/DiagnosticReport0.1.0 (this may not be a problem, but you should check that it's not intended to match a slice)	[Bundle.entry[6].resource.code.coding[0]]
28 information	informational	This element does not match any known slice defined in the profile https://fhir.nwgenomics.nhs.uk/StructureDefinition/DiagnosticReport0.1.0 (this may not be a problem, but you should check that it's not intended to match a slice)	[Bundle.entry[6].resource.resultsInterpreter[0]]
27 information	informational	Entry 'urn:uuid:dff0b8e5-a42d-4ad0-952e-b7c20c143877' isn't reachable by traversing forwards from the MessageHeader. Check that this is meant to be included (needed to process the message)	[Bundle.entry[8]]
20 information	code-invalid	None of the codings provided are in the value set 'LOINC Diagnostic Report Codes' (http://hl7.org/fhir/ValueSet/report-codes4.0.1), and a coding is recommended to come from this value set (codes = https://fhir.nwgenomics.nhs.uk/CodeSystem/IGEAP#CCP19v1_R112 , https://fhir.nhs.uk/CodeSystem/England-GenomicTestDirectory#R112.1)	[Bundle.entry[6].resource/*DiagnosticReport/null*/.code]
16 information	business-rule	Reference to draft CodeSystem https://fhir.nwgenomics.nhs.uk/CodeSystem/GenomicClinicalIndication0.1.0	[Bundle.entry[5].resource/*ServiceRequest/null*/.reasonCode[0]]
21 warning	invalid	value should not start or finish with whitespace 'Factor II deficiency (Single gene sequencing >=10 amplicons)'	[Bundle.entry[6].resource/*DiagnosticReport/null*/.code.coding[1].display]
22 warning	code-invalid	None of the codings provided are in the value set 'IdentifierType' (http://hl7.org/fhir/ValueSet/identifier-type4.0.1), and a coding should come from this value set unless it has no suitable code (note that the validator cannot judge what is suitable) (codes = http://terminology.hl7.org/CodeSystem/v2-0203#NH)	[Bundle.entry[6].resource/*DiagnosticReport/null*/.subject.identifier.type]
19 warning	code-invalid	Unknown Code 'R112.1' in the CodeSystem ' https://fhir.nhs.uk/CodeSystem/England-GenomicTestDirectory ' version '0.1.0' - note that the code system is labeled as a fragment, so the code may be valid in some other fragment	[Bundle.entry[6].resource/*DiagnosticReport/null*/.code.coding[1].code]

severity	code	details	expression
15 warning	code-invalid	None of the codings provided are in the value set 'IdentifierType' (http://hl7.org/fhir/ValueSet/identifier-type 4.0.1), and a coding should come from this value set unless it has no suitable code (note that the validator cannot judge what is suitable) (codes = http://terminology.hl7.org/CodeSystem/v2-0203#NH) Unknown Code 'R112' in the CodeSystem ' https://fhir.nwgenomics.nhs.uk/CodeSystem/GenomicClinicalIndication ' version '0.1.0' - note that the code system is labeled as a fragment, so the code may be valid in some other fragment	[Bundle.entry[5].resource/*ServiceRequest/null*/.subject.identifier.type]
17 warning	code-invalid	value should not start or finish with whitespace 'Factor II deficiency (Single gene sequencing >=10 amplicons)' Unknown Code 'R112.1' in the CodeSystem ' https://fhir.nhs.uk/CodeSystem/England-GenomicTestDirectory ' version '0.1.0' - note that the code system is labeled as a fragment, so the code may be valid in some other fragment	[Bundle.entry[5].resource/*ServiceRequest/null*/.code.coding[0].display]
14 warning	invalid	Unknown Code 'R112.1' in the CodeSystem ' https://fhir.nhs.uk/CodeSystem/England-GenomicTestDirectory ' version '0.1.0' - note that the code system is labeled as a fragment, so the code may be valid in some other fragment	[Bundle.entry[5].resource/*ServiceRequest/null*/.code.coding[0].code]
13 warning	code-invalid	None of the codings provided are in the value set 'IdentifierType' (http://hl7.org/fhir/ValueSet/identifier-type 4.0.1), and a coding should come from this value set unless it has no suitable code (note that the validator cannot judge what is suitable) (codes = http://terminology.hl7.org/CodeSystem/v2-0203#NH)	[Bundle.entry[4].resource/*Specimen/null*/.subject.identifier.type]
11 warning	code-invalid	None of the codings provided are in the value set 'IdentifierType' (http://hl7.org/fhir/ValueSet/identifier-type 4.0.1), and a coding should come from this value set unless it has no suitable code (note that the validator cannot judge what is suitable) (codes = http://terminology.hl7.org/CodeSystem/v2-0203#NH)	[Bundle.entry[3].resource/*DocumentReference/null*/.subject.identifier.type]
6 warning	code-invalid	None of the codings provided are in the value set 'IdentifierType' (http://hl7.org/fhir/ValueSet/identifier-type 4.0.1), and a coding should come from this value set unless it has no suitable code (note that the validator cannot judge what is suitable) (codes = http://terminology.hl7.org/CodeSystem/v2-0203#NH)	[Bundle.entry[1].resource/*Patient/null*/.identifier[0].type]
1 warning	code-invalid	None of the codings provided are in the value set 'IdentifierType' (http://hl7.org/fhir/ValueSet/identifier-type 4.0.1), and a coding should come from this value set unless it has no suitable code (note that the validator cannot judge what is suitable) (codes = http://terminology.hl7.org/CodeSystem/v2-0203#NH)	