

06, Feb 2026

severity	code	details	expression
12 error	invalid	Not a valid date/time format: '2025-10-13T00:00:00:00'	[Bundle.entry[4].resource/*Specimen/null*/.receivedTime]
17 information	business-rule	Reference to draft CodeSystem https://fhir.nwgenomics.nhs.uk/CodeSystem/GenomicClinicalIndication 0.1.0	[Bundle.entry[5].resource/*ServiceRequest/null*/.reasonCode[0]]
25 information	structure	Details for urn:uuid:b3e369a1-c150-4eae-87e9-c4985dc0f53f matching against profile http://hl7.org/fhir/StructureDefinition/Specimen 4.0.1	[Bundle.entry[6].resource/*DiagnosticReport/null*/.specimen[0]]
30 information	informational	Entry 'urn:uuid:4504b6c7-5ed8-4e2d-bab0-3979d115528d' 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]]
31 information	informational	This element does not match any known slice defined in the profile https://fhir.nwgenomics.nhs.uk/StructureDefinition/DiagnosticReport 0.1.0 (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]]
32 information	informational	This element does not match any known slice defined in the profile https://fhir.nwgenomics.nhs.uk/StructureDefinition/DiagnosticReport 0.1.0 (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]]
19 information	structure	Details for urn:uuid:b3e369a1-c150-4eae-87e9-c4985dc0f53f matching against profile http://hl7.org/fhir/StructureDefinition/Specimen 4.0.1	[Bundle.entry[5].resource/*ServiceRequest/null*/.specimen[0]]
22 information	code-invalid	None of the codings provided are in the value set 'LOINC Diagnostic Report Codes' (http://hl7.org/fhir/ValueSet/report-codes 4.0.1), 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]
24 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	[Bundle.entry[6].resource/*DiagnosticReport/null*/.subject.identifier.type]

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23 warning	invalid	<p>what is suitable) (codes = <a href="http://terminology.hl7.org/CodeSystem/v2-0203#NH">http://terminology.hl7.org/CodeSystem/v2-0203#NH</a>)</p> <p>value should not start or finish with whitespace 'Factor II deficiency (Single gene sequencing &gt;=10 amplicons)'</p> <p>Unknown Code 'R112.1' in the CodeSystem '<a href="https://fhir.nhs.uk/CodeSystem/England-GenomicTestDirectory">https://fhir.nhs.uk/CodeSystem/England-GenomicTestDirectory</a>' version '0.1.0' - note that the code system is labeled as a fragment, so the code may be valid in some other fragment</p>	[Bundle.entry[6].resource/*DiagnosticReport/null*/.code.coding[1].display]
21 warning	code-invalid	<p>Unknown Code 'R112' in the CodeSystem '<a href="https://fhir.nwgenomics.nhs.uk/CodeSystem/GenomicClinicalIndication">https://fhir.nwgenomics.nhs.uk/CodeSystem/GenomicClinicalIndication</a>' version '0.1.0' - note that the code system is labeled as a fragment, so the code may be valid in some other fragment</p> <p>None of the codings provided are in the value set 'IdentifierType' (<a href="http://hl7.org/fhir/ValueSet/identifier-type">http://hl7.org/fhir/ValueSet/identifier-type</a> 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 = <a href="http://terminology.hl7.org/CodeSystem/v2-0203#NH">http://terminology.hl7.org/CodeSystem/v2-0203#NH</a>)</p>	[Bundle.entry[6].resource/*DiagnosticReport/null*/.code.coding[1].code]
18 warning	code-invalid	<p>value should not start or finish with whitespace 'Factor II deficiency (Single gene sequencing &gt;=10 amplicons)'</p> <p>Unknown Code 'R112.1' in the CodeSystem '<a href="https://fhir.nhs.uk/CodeSystem/England-GenomicTestDirectory">https://fhir.nhs.uk/CodeSystem/England-GenomicTestDirectory</a>' version '0.1.0' - note that the code system is labeled as a fragment, so the code may be valid in some other fragment</p> <p>None of the codings provided are in the value set 'IdentifierType' (<a href="http://hl7.org/fhir/ValueSet/identifier-type">http://hl7.org/fhir/ValueSet/identifier-type</a> 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 = <a href="http://terminology.hl7.org/CodeSystem/v2-0203#NH">http://terminology.hl7.org/CodeSystem/v2-0203#NH</a>)</p>	[Bundle.entry[5].resource/*ServiceRequest/null*/.reasonCode[0].coding[0].code]
16 warning	code-invalid	<p>value should not start or finish with whitespace 'Factor II deficiency (Single gene sequencing &gt;=10 amplicons)'</p> <p>Unknown Code 'R112.1' in the CodeSystem '<a href="https://fhir.nhs.uk/CodeSystem/England-GenomicTestDirectory">https://fhir.nhs.uk/CodeSystem/England-GenomicTestDirectory</a>' version '0.1.0' - note that the code system is labeled as a fragment, so the code may be valid in some other fragment</p> <p>None of the codings provided are in the value set 'IdentifierType' (<a href="http://hl7.org/fhir/ValueSet/identifier-type">http://hl7.org/fhir/ValueSet/identifier-type</a> 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 = <a href="http://terminology.hl7.org/CodeSystem/v2-0203#NH">http://terminology.hl7.org/CodeSystem/v2-0203#NH</a>)</p>	[Bundle.entry[5].resource/*ServiceRequest/null*/.subject.identifier.type]
15 warning	invalid	<p>value should not start or finish with whitespace 'Factor II deficiency (Single gene sequencing &gt;=10 amplicons)'</p> <p>Unknown Code 'R112.1' in the CodeSystem '<a href="https://fhir.nhs.uk/CodeSystem/England-GenomicTestDirectory">https://fhir.nhs.uk/CodeSystem/England-GenomicTestDirectory</a>' version '0.1.0' - note that the code system is labeled as a fragment, so the code may be valid in some other fragment</p> <p>None of the codings provided are in the value set 'IdentifierType' (<a href="http://hl7.org/fhir/ValueSet/identifier-type">http://hl7.org/fhir/ValueSet/identifier-type</a> 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 = <a href="http://terminology.hl7.org/CodeSystem/v2-0203#NH">http://terminology.hl7.org/CodeSystem/v2-0203#NH</a>)</p>	[Bundle.entry[5].resource/*ServiceRequest/null*/.code.coding[0].display]
14 warning	code-invalid	<p>value should not start or finish with whitespace 'Factor II deficiency (Single gene sequencing &gt;=10 amplicons)'</p> <p>Unknown Code 'R112.1' in the CodeSystem '<a href="https://fhir.nhs.uk/CodeSystem/England-GenomicTestDirectory">https://fhir.nhs.uk/CodeSystem/England-GenomicTestDirectory</a>' version '0.1.0' - note that the code system is labeled as a fragment, so the code may be valid in some other fragment</p> <p>None of the codings provided are in the value set 'IdentifierType' (<a href="http://hl7.org/fhir/ValueSet/identifier-type">http://hl7.org/fhir/ValueSet/identifier-type</a> 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 = <a href="http://terminology.hl7.org/CodeSystem/v2-0203#NH">http://terminology.hl7.org/CodeSystem/v2-0203#NH</a>)</p>	[Bundle.entry[5].resource/*ServiceRequest/null*/.code.coding[0].code]
11 warning	code-invalid	<p>value should not start or finish with whitespace 'Factor II deficiency (Single gene sequencing &gt;=10 amplicons)'</p> <p>Unknown Code 'R112.1' in the CodeSystem '<a href="https://fhir.nhs.uk/CodeSystem/England-GenomicTestDirectory">https://fhir.nhs.uk/CodeSystem/England-GenomicTestDirectory</a>' version '0.1.0' - note that the code system is labeled as a fragment, so the code may be valid in some other fragment</p> <p>None of the codings provided are in the value set 'IdentifierType' (<a href="http://hl7.org/fhir/ValueSet/identifier-type">http://hl7.org/fhir/ValueSet/identifier-type</a> 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 = <a href="http://terminology.hl7.org/CodeSystem/v2-0203#NH">http://terminology.hl7.org/CodeSystem/v2-0203#NH</a>)</p>	[Bundle.entry[4].resource/*Specimen/null*/.subject.identifier.type]
6 warning	code-invalid	<p>value should not start or finish with whitespace 'Factor II deficiency (Single gene sequencing &gt;=10 amplicons)'</p> <p>Unknown Code 'R112.1' in the CodeSystem '<a href="https://fhir.nhs.uk/CodeSystem/England-GenomicTestDirectory">https://fhir.nhs.uk/CodeSystem/England-GenomicTestDirectory</a>' version '0.1.0' - note that the code system is labeled as a fragment, so the code may be valid in some other fragment</p> <p>None of the codings provided are in the value set 'IdentifierType' (<a href="http://hl7.org/fhir/ValueSet/identifier-type">http://hl7.org/fhir/ValueSet/identifier-type</a> 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 = <a href="http://terminology.hl7.org/CodeSystem/v2-0203#NH">http://terminology.hl7.org/CodeSystem/v2-0203#NH</a>)</p>	[Bundle.entry[3].resource/*DocumentReference/null*/.subject.identifier.type]

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1 warning	code-invalid	<p>None of the codings provided are in the value set 'IdentifierType' (<a href="http://hl7.org/fhir/ValueSet/identifier-type">http://hl7.org/fhir/ValueSet/identifier-type</a> 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 = <a href="http://terminology.hl7.org/CodeSystem/v2-0203#NH">http://terminology.hl7.org/CodeSystem/v2-0203#NH</a>)</p>	[Bundle.entry[1].resource/*Patient/null*/.identifier[0].type]