Supplementary Materials

Forensic Epigenetics for Casework: A Systematic Scoping Review of DNA Methylation-Centred Applications and Validation Evidence

Supplementary Tables S1–S11

Supplementary Table S1. Search strategies and retrieval audit

S1A. Database search strategies

Database / search	Date	Search strategy	Records
Scopus - Main search	15 June 2026	TITLE-ABS-KEY(forensic* AND (epigenetic* OR "DNA methylation" OR methylome OR methylation OR epigenomic*) AND ("age estimation" OR "age prediction" OR "body fluid" OR "tissue identification" OR "postmortem interval" OR "post-mortem interval" OR "time since deposition" OR "monozygotic twin*" OR "identical twin*" OR exposure OR trauma OR stress OR validation OR casework)) AND PUBYEAR > 2009 AND (LIMIT-TO(LANGUAGE, "English"))	471
Scopus - age estimation	15 June 2026	TITLE-ABS-KEY(forensic* AND ("DNA methylation" OR epigenetic* OR methylation) AND ("age estimation" OR "age prediction" OR "molecular age" OR "epigenetic clock")) AND PUBYEAR > 2009 AND (LIMIT-TO(LANGUAGE, "English"))	250
Scopus - body fluid/tissue identification	15 June 2026	TITLE-ABS-KEY(forensic* AND ("DNA methylation" OR epigenetic* OR methylation OR "tissue-specific methylation" OR tDMR*) AND ("body fluid" OR "biological fluid" OR blood OR saliva OR semen OR sperm OR vaginal OR menstrual OR "tissue identification")) AND PUBYEAR > 2009 AND (LIMIT-TO(LANGUAGE, "English"))	375
Scopus - PMI/time since deposition	15 June 2026	TITLE-ABS-KEY(forensic* AND ("DNA methylation" OR epigenetic* OR methylation OR "epigenetic clock") AND ("postmortem interval" OR "post-mortem interval" OR PMI OR "time since death" OR "time since deposition")) AND PUBYEAR > 2009 AND (LIMIT-TO(LANGUAGE, "English"))	15
Scopus - monozygotic twins	15 June 2026	TITLE-ABS-KEY(forensic* AND ("DNA methylation" OR epigenetic* OR methylation) AND ("monozygotic twin*" OR "identical twin*" OR "twin differentiation" OR "twin discrimination")) AND PUBYEAR > 2009 AND (LIMIT-TO(LANGUAGE, "English"))	64
Scopus - sequencing/platforms	15 June 2026	TITLE-ABS-KEY(forensic* AND ("DNA methylation" OR epigenetic* OR methylation) AND ("massively parallel sequencing" OR MPS OR NGS OR "next generation sequencing" OR nanopore OR pyrosequencing OR bisulfite OR "enzymatic methyl sequencing" OR EM-seq)) AND PUBYEAR > 2009 AND (LIMIT-TO(LANGUAGE, "English"))	241

Database / search	Date	Search strategy	Records
PubMed/MEDLINE	15 June 2026	(forensic*[Title/Abstract] AND (epigenetic*[Title/Abstract] OR "DNA methylation"[Title/Abstract] OR methylation[Title/Abstract] OR epigenomic*[Title/Abstract]) AND ("age estimation"[Title/Abstract] OR "age prediction"[Title/Abstract] OR "body fluid"[Title/Abstract] OR "tissue identification"[Title/Abstract] OR "postmortem interval"[Title/Abstract] OR "post-mortem interval"[Title/Abstract] OR "time since deposition"[Title/Abstract] OR "monozygotic twin"[Title/Abstract] OR "identical twin"[Title/Abstract] OR exposure[Title/Abstract] OR trauma[Title/Abstract] OR stress[Title/Abstract] OR validation[Title/Abstract] OR casework[Title/Abstract])) AND ("2010/01/01"[Date - Publication] : "3000"[Date - Publication]) AND English[Language]	324
Web of Science Core Collection	15 June 2026	TS=(forensic* AND ("DNA methylation" OR epigenetic* OR methylation) AND ("age estimation" OR "age prediction" OR "body fluid" OR "tissue identification" OR "postmortem interval" OR "post-mortem interval" OR "time since deposition" OR "monozygotic twin" OR "identical twin" OR validation OR casework))	472

All reproducible database searches were limited to publications from 2010 onward and English language; Web of Science limits were applied through interface filters. The 2010 lower bound was applied consistently as a methodological temporal eligibility restriction. No specific biological, historical, or milestone-based rationale was used to define exactly 2010, and relevant earlier literature may therefore be absent. Searches differed across databases: Scopus used one broad cross-application search plus five modular searches that expanded application-specific vocabulary for age estimation, body-fluid/tissue identification, postmortem interval/time since deposition, monozygotic twins, and sequencing/platforms. PubMed/MEDLINE and Web of Science used single combined cross-application queries and did not reproduce those five modules separately. The databases were therefore complementary rather than exact replications, and topic-specific retrieval sensitivity could differ. Google Scholar was not used as a reproducible database search. Contextual comparator sources were used only for conceptual framing and were not added to the search denominator or study-level register.

S1B. Deduplication procedure

Records originating from the six Scopus search components and the two other databases were manually deduplicated in Microsoft Excel, comparing available DOIs and publication metadata (titles, authors and publication years). Multiple bibliographic records referring to the same publication were retained once. This removal of bibliographic duplicates preceded, and was distinct from, subsequent full-text source identity and linked-evidence-unit adjudication. The available retrieval audit does not establish a reliable separate count of within-Scopus module overlaps versus cross-database duplicates; no retrospective breakdown is asserted.

S1C. Reports sought but not retrieved (n = 15)

Bibliographic identities were recovered from the contemporaneous full-text retrieval audit. These records were not assessed for full-text eligibility, were not charted or classified, and contributed no empirical or Category 1–5 counts. Entries below are retrieval-log metadata (not sources cited as scientific support). Turchi (2022) remains unretrieved: a separately identified two-page 2016 ISFG congress report is not the full text of the cited 2022 chapter.

Record (author, year)	Title	Source / publication	DOI
Seashols-Williams 2016	High-throughput miRNA sequencing and identification of biomarkers for forensically relevant biological fluids	ELECTROPHORESIS	10.1002/elps.201600258
Antunes 2019	CHAPTER 11: Epigenetics to Solve Crimes	RSC Detection Science	10.1039/9781788016117-00253
Saiz 2020	Applications of Next-Generation Sequencing in Forensic Field	Forensic DNA Typing: Principles, Applications and Advancements	10.1007/978-981-15-6655-4_23
Venkataramanan 2020	Case study identification of population and age prediction in forensic	International Journal of Medical Toxicology and Legal Medicine	10.5958/0974-4614.2020.00046.7
Noël 2022	Semen	Encyclopedia of Forensic Sciences: Volume 1-4, Third Edition	10.1016/b978-0-12-823677-2.00024-6
Tewari 2023	Detection of forensically relevant body fluids using specific biomarkers through flow cytometry	Journal of Punjab Academy of Forensic Medicine and Toxicology	10.5958/0974-083x.2023.00015.8
Rezaei 2024	Epigenetics and Forensics: Brightening the Future	Current Bioactive Compounds	10.2174/1573407219666230815105041
Albujja 2025	Biological Fluid Identification by Epigenetic Approaches	Advances in Forensic Biology and DNA Typing	10.4324/9781032720890-9
Thakur 2025	Advancements in DNA methylation: A systematic and bibliometric review	AIP Conference Proceedings	10.1063/5.0292668
Chowdhry 2026	Dental Age Assessment: A Global Perspective	Dental Age Assessment: A Global Perspective	10.1007/978-3-032-08788-1
Zapico 2017	Mechanisms linking aging, diseases and biological age estimation	Mechanisms Linking Aging, Diseases and Biological Age Estimation	10.1201/9781315371382
Barbaro 2025	Advances in Forensic Biology and DNA Typing	Advances in Forensic Biology and DNA Typing	10.4324/9781032720890
Zhou 2025	Novel age estimation strategy based on blood transfer RNA-derived small RNAs: a preliminary study	Australian Journal of Forensic Sciences	10.1080/00450618.2025.2596366
Sharma 2026	Metabolomics at the Crossroads of Forensic Toxicology and Precision Diagnostics: Analytical Innovations and Translational Opportunities.	Omics : a journal of integrative biology	10.1177/15578100261447998
Turchi 2022	Massive Parallel Sequencing in Forensic Genetics	Encyclopedia of Forensic Sciences: Volume 1-4, Third Edition	10.1016/b978-0-12-823677-2.00094-5

Supplementary Table S2. Study-level record register and evidence roles (n = 429)

Ref.	Author (year)	Primary application	Molecular stratum	Evidence role	Secondary application / cross-cutting tags
1	Gunn (2014)	Cross-cutting/ethics/legal/field overview	contextual/non-qualifying evidence	Contextual	Ethics/legal/governance
2	Williams (2018)	Cross-cutting/ethics/legal/field overview	contextual/non-qualifying evidence	Contextual	Ethics/legal/governance
3	Rana (2018)	Not applicable	background/secondary	Background/secondary	Ethics/legal/governance

Ref.	Author (year)	Primary application	Molecular stratum	Evidence role	Secondary application / cross-cutting tags
4	Shabani (2018)	Cross-cutting/ethics/legal/field overview	contextual/non-qualifying evidence	Contextual	Ethics/legal/governance
5	Dupras (2018)	Cross-cutting/ethics/legal/field overview	contextual/non-qualifying evidence	Contextual	Exposure/lifestyle/trauma/stress inference
6	Koch (2011)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
7	Huang (2015)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
8	Zbieć-Piekarska (2015)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
9	Pfeifer (2020)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
10	Heidegger (2022)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
11	Frumkin (2011)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
12	Holtkötter (2017)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
13	Vidaki (2017)	Monozygotic twin differentiation	DNA methylation	Empirical primary	Sequencing/platform/method development; Validation/forensic implementation evidence
14	Li (2013)	Monozygotic twin differentiation	DNA methylation	Empirical primary	None
15	Maas (2019)	Other donor-characteristic inference	DNA methylation	Empirical primary	Exposure/lifestyle/trauma/stress inference
16	Vidaki (2023)	Other donor-characteristic inference	DNA methylation	Empirical primary	Age estimation; Exposure/lifestyle/trauma/stress inference; Sequencing/platform/method development; Bioinformatics/machine learning and interpretation; Validation/forensic implementation evidence
17	Choi (2014)	Body fluid/tissue identification	mixed molecular	Empirical primary	Sequencing/platform/method development; Validation/forensic implementation evidence
18	Watanabe (2018)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
19	de Bruin (2025)	Sequencing/platform/method development	mixed molecular	Empirical primary	Age estimation; Bioinformatics/machine learning and interpretation; Validation/forensic implementation evidence
26	Naue (2018)	Cross-cutting/ethics/legal/field overview	contextual/non-qualifying evidence	Contextual	Sequencing/platform/method development
27	Dupras (2019)	Cross-cutting/ethics/legal/field overview	contextual/non-qualifying evidence	Contextual	Ethics/legal/governance
28	Dupras (2020)	Cross-cutting/ethics/legal/field overview	contextual/non-qualifying evidence	Contextual	Ethics/legal/governance
29	Palmour (2026)	Cross-cutting/ethics/legal/field overview	contextual/non-qualifying evidence	Contextual	Ethics/legal/governance
30	Kayser (2026)	Not applicable	background/secondary	Background/secondary	Ethics/legal/governance
32	Kampmann (2024)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
33	Heidegger (2025)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
34	Onofri (2025)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
35	Lee (2022)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
36	Bocklandt (2011)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
37	Bekaert (2015)	Age estimation	DNA methylation	Empirical primary	Sequencing/platform/method development; Bioinformatics/machine learning and interpretation; Validation/forensic implementation evidence
38	Freire-Aradas (2016)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation

Ref.	Author (year)	Primary application	Molecular stratum	Evidence role	Secondary application / cross-cutting tags
39	Aliferi (2018)	Age estimation	DNA methylation	Empirical primary	Sequencing/platform/method development; Bioinformatics/machine learning and interpretation; Validation/forensic implementation evidence
40	Jung (2019)	Age estimation	DNA methylation	Empirical primary	Sequencing/platform/method development; Bioinformatics/machine learning and interpretation; Validation/forensic implementation evidence
41	Xu (2015)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
42	Cho (2017)	Age estimation	DNA methylation	Empirical primary	Sequencing/platform/method development; Bioinformatics/machine learning and interpretation; Validation/forensic implementation evidence
43	Vidaki (2017)	Age estimation	DNA methylation	Empirical primary	Sequencing/platform/method development; Bioinformatics/machine learning and interpretation; Validation/forensic implementation evidence
44	Lee (2018)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
45	Peng (2019)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
46	Dias (2020)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
47	Correia Dias (2020)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
48	Fleckhaus (2020)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
49	Yi (2015)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
50	Park (2016)	Age estimation	DNA methylation	Empirical primary	None
51	Hamano (2017)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
52	Liu (2022)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
53	Kim (2024)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
54	Jung (2016)	Body fluid/tissue identification	DNA methylation	Empirical primary	Sequencing/platform/method development; Validation/forensic implementation evidence
55	Madi (2012)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
56	An (2013)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
57	Lee (2016)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
58	Lee (2015)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
59	Forat (2016)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
60	Vidaki (2017)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
61	Hanson (2014)	Body fluid/tissue identification	transcriptomic/non-coding RNA	Empirical primary	Validation/forensic implementation evidence
62	Antunes (2016)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
63	Dorum (2019)	Body fluid/tissue identification	transcriptomic/non-coding RNA	Empirical primary	Validation/forensic implementation evidence
64	Larue (2013)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
65	Wasserstrom (2013)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
66	Silva (2016)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
67	Li (2020)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
68	Foox (2021)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
69	Sutter (2026)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation

Ref.	Author (year)	Primary application	Molecular stratum	Evidence role	Secondary application / cross-cutting tags
70	Choung (2021)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
71	Lee (2026)	Body fluid/tissue identification	mixed molecular	Empirical primary	Validation/forensic implementation evidence
72	Hashiyada (2019)	Not applicable	background/secondary	Background/secondary	Postmortem interval/time since deposition
73	Bilinsky (2025)	Body fluid/tissue identification	DNA methylation	Empirical primary	Postmortem interval/time since deposition; Sequencing/platform/method development; Validation/forensic implementation evidence
74	Badell (2026)	Not applicable	non-human comparative	Non-human	Postmortem interval/time since deposition
75	Nakatome (2011)	Not applicable	background/secondary	Background/secondary	Exposure/lifestyle/trauma/stress inference; Postmortem interval/time since deposition
76	Sjöholm (2018)	Not applicable	non-human comparative	Non-human	Postmortem interval/time since deposition
77	Bugaoan (2026)	Not applicable	background/secondary	Background/secondary	Postmortem interval/time since deposition
78	Stewart (2015)	Monozygotic twin differentiation	DNA methylation	Empirical primary	None
79	Xu (2015)	Monozygotic twin differentiation	DNA methylation	Empirical primary	None
80	Du (2015)	Monozygotic twin differentiation	DNA methylation	Empirical primary	Sequencing/platform/method development; Validation/forensic implementation evidence
81	Zhang (2015)	Monozygotic twin differentiation	DNA methylation	Empirical primary	None
82	Vidaki (2018)	Monozygotic twin differentiation	DNA methylation	Empirical primary	None
83	Marqueta-Gracia (2018)	Monozygotic twin differentiation	DNA methylation	Empirical primary	None
84	Wang (2024)	Monozygotic twin differentiation	transcriptomic/non-coding RNA	Empirical primary	Validation/forensic implementation evidence; Sequencing/platform/method development
85	Cho (2025)	Monozygotic twin differentiation	DNA methylation	Empirical primary	None
86	Zeng (2026)	Monozygotic twin differentiation	DNA methylation	Empirical primary	Sequencing/platform/method development; Validation/forensic implementation evidence
87	Wen (2022)	Other donor-characteristic inference	DNA methylation	Empirical primary	Exposure/lifestyle/trauma/stress inference
88	Ambroa-Conde (2024)	Other donor-characteristic inference	DNA methylation	Empirical primary	Age estimation; Exposure/lifestyle/trauma/stress inference; Bioinformatics/machine learning and interpretation; Validation/forensic implementation evidence
89	Philibert (2019)	Not applicable	contextual/non-qualifying evidence	Contextual	Exposure/lifestyle/trauma/stress inference
90	Llobet (2023)	Other donor-characteristic inference	mixed molecular	Empirical primary	Exposure/lifestyle/trauma/stress inference
91	Pośpiech (2024)	Other donor-characteristic inference	DNA methylation	Empirical primary	Exposure/lifestyle/trauma/stress inference
92	Pośpiech (2025)	Other donor-characteristic inference	DNA methylation	Empirical primary	Exposure/lifestyle/trauma/stress inference; Sequencing/platform/method development; Bioinformatics/machine learning and interpretation; Validation/forensic implementation evidence
93	Wang (2024)	Other donor-characteristic inference	DNA methylation	Empirical primary	None
94	Naue (2018)	Sequencing/platform/method development	DNA methylation	Empirical primary	None
95	Di Lena (2021)	Sequencing/platform/method development	DNA methylation	Empirical primary	None
96	Simons (2025)	Sequencing/platform/method development	DNA methylation	Empirical primary	None

Ref.	Author (year)	Primary application	Molecular stratum	Evidence role	Secondary application / cross-cutting tags
97	Turiello (2023)	Sequencing/platform/method development	DNA methylation	Empirical primary	None
98	Dias (2024)	Age estimation	DNA methylation	Empirical primary	Sequencing/platform/method development
99	So (2024)	Sequencing/platform/method development	mixed molecular	Empirical primary	None
100	Poussard (2023)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
101	Lee (2025)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
103	Sarac (2017)	Age estimation	DNA methylation	Empirical primary	Sequencing/platform/method development
104	Fang (2020)	Age estimation	transcriptomic/non-coding RNA	Empirical primary	Sequencing/platform/method development
107	Li (2011)	Monozygotic twin differentiation	DNA methylation	Empirical primary	Validation/forensic implementation evidence
108	Lee (2012)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
109	Weidner (2014)	Age estimation	DNA methylation	Empirical primary	Exposure/lifestyle/trauma/stress inference; Sequencing/platform/method development; Validation/forensic implementation evidence
110	Vidaki (2016)	Body fluid/tissue identification	DNA methylation	Empirical primary	Sequencing/platform/method development; Validation/forensic implementation evidence
111	Lee (2020)	Age estimation	DNA methylation	Empirical primary	Sequencing/platform/method development; Bioinformatics/machine learning and interpretation; Validation/forensic implementation evidence
112	Anaya (2021)	Age estimation	DNA methylation	Empirical primary	Sequencing/platform/method development; Bioinformatics/machine learning and interpretation; Validation/forensic implementation evidence
113	Koop (2021)	Age estimation	DNA methylation	Empirical primary	Postmortem interval/time since deposition; Sequencing/platform/method development; Bioinformatics/machine learning and interpretation; Validation/forensic implementation evidence
114	Ambroa-Conde (2022)	Age estimation	DNA methylation	Empirical primary	Body fluid/tissue identification; Sequencing/platform/method development; Bioinformatics/machine learning and interpretation; Validation/forensic implementation evidence
115	Schuetter (2024)	Not applicable	background/secondary	Background/secondary	Exposure/lifestyle/trauma/stress inference; Sequencing/platform/method development; Bioinformatics/machine learning and interpretation
116	Jung (2024)	Age estimation	DNA methylation	Empirical primary	Sequencing/platform/method development; Bioinformatics/machine learning and interpretation; Validation/forensic implementation evidence
117	Paparazzo (2025)	Age estimation	DNA methylation	Empirical primary	Sequencing/platform/method development; Bioinformatics/machine learning and interpretation; Validation/forensic implementation evidence
118	Sutter (2025)	Age estimation	DNA methylation	Empirical primary	Sequencing/platform/method development; Validation/forensic implementation evidence
119	Beentjes (2026)	Sequencing/platform/method development	DNA methylation	Empirical primary	Age estimation; Body fluid/tissue identification; Bioinformatics/machine learning and interpretation; Validation/forensic implementation evidence
120	Tiras (2026)	Age estimation	DNA methylation	Empirical primary	Sequencing/platform/method development; Bioinformatics/machine learning and interpretation; Validation/forensic implementation evidence
121	Park (2026)	Body fluid/tissue identification	mixed molecular	Empirical primary	Sequencing/platform/method development; Validation/forensic implementation evidence
122	Freire-Aradas (2023)	Age estimation	DNA methylation	Empirical primary	Body fluid/tissue identification; Sequencing/platform/method development; Bioinformatics/machine learning and interpretation; Validation/forensic implementation evidence
123	Watanabe (2023)	Body fluid/tissue identification	DNA methylation	Empirical primary	Sequencing/platform/method development; Validation/forensic implementation evidence
124	Chen (2025)	Age estimation	DNA methylation	Empirical primary	Sequencing/platform/method development; Bioinformatics/machine learning and interpretation; Validation/forensic implementation evidence
125	Yi (2014)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation

Ref.	Author (year)	Primary application	Molecular stratum	Evidence role	Secondary application / cross-cutting tags
126	Bekaert (2015)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
127	Huang (2015)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
128	Lee (2015)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
129	Silva (2015)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
130	Zbieć-Piekarska (2015)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
131	Giuliani (2016)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
132	Hamano (2016)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
133	Mawlood (2016)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
134	Zubakov (2016)	Age estimation	mixed molecular	Empirical primary	Bioinformatics/machine learning and interpretation
135	Alghanim (2017)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
136	Alsaleh (2017)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
137	Fleckhaus (2017)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
138	Goel (2017)	Not applicable	background/secondary	Background/secondary	Age estimation; Bioinformatics/machine learning and interpretation
139	Hong (2017)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
140	Li (2017)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
141	Naue (2017)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
142	Thong (2017)	Age estimation	DNA methylation	Empirical primary	Validation/forensic implementation evidence
143	Feng (2018)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
144	Guevara (2018)	Not applicable	background/secondary	Background/secondary	Age estimation; Bioinformatics/machine learning and interpretation
145	Horvath (2018)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
146	Shi (2018)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
147	Smeers (2018)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
148	Spólnicka (2018)	Age estimation	DNA methylation	Empirical primary	Validation/forensic implementation evidence
149	Alsaleh (2019)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
150	Bell (2019)	Not applicable	background/secondary	Background/secondary	Age estimation; Bioinformatics/machine learning and interpretation
151	Hong (2019)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
152	Khan (2019)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
153	Li (2019)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
154	McCord (2019)	Not applicable	background/secondary	Background/secondary	Body fluid/tissue identification; Age estimation; Exposure/lifestyle/trauma/stress inference
155	Wagner (2019)	Not applicable	background/secondary	Background/secondary	Age estimation; Bioinformatics/machine learning and interpretation
156	Xie (2019)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
157	Xin (2019)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
158	Zolotarenko (2019)	Not applicable	background/secondary	Background/secondary	Age estimation; Bioinformatics/machine learning and interpretation
159	Becker (2020)	Not applicable	other-molecular comparator	Comparator	Age estimation; Bioinformatics/machine learning and interpretation
160	Correia Dias (2020)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation

Ref.	Author (year)	Primary application	Molecular stratum	Evidence role	Secondary application / cross-cutting tags
161	Freire-Aradas (2020)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
162	Gopalan (2019)	Age estimation	DNA methylation	Empirical primary	Validation/forensic implementation evidence; Bioinformatics/machine learning and interpretation
163	Heidegger (2020)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
164	Karir (2020)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
165	Kondo (2020)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
166	Lau (2020)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
167	Montesanto (2020)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
168	Márquez-Ruiz (2020)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
169	Pan (2020)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
170	Wei (2020)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
171	Yudianto (2020)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
172	Al-Ghanmy (2021)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
173	Amiri Roudbar (2021)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
174	Zapico (2021)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
175	Correia Dias (2021)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
176	Fan (2021)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
177	Guan (2021)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
178	Keerthana (2021)	Not applicable	excluded	Excluded	Age estimation; Bioinformatics/machine learning and interpretation
179	Lemesh (2021)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
180	Piniewska-Róg (2021)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
181	Pisarek (2021)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
182	Schwender (2021)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
183	So (2021)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
184	Sukawutthiya (2021)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
185	Thong (2021)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
186	Vidaki (2021)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
187	Woźniak (2021)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
188	Xiao (2021)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
189	Yudianto (2021)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
190	Zhang (2021)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
191	Aliferi (2022)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
192	Correia Dias (2022)	Not applicable	background/secondary	Background/secondary	Age estimation; Bioinformatics/machine learning and interpretation
193	Correia Dias (2022)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
194	Freire-Aradas (2022)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation

Ref.	Author (year)	Primary application	Molecular stratum	Evidence role	Secondary application / cross-cutting tags
195	Han (2022)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
196	Ho Lee (2022)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
197	Lucknuch (2022)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
198	Manco (2022)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
199	Mayer (2022)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
200	Ogata (2022)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
201	Oka (2022)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
202	Ye (2022)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
203	Carlsen (2023)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
204	Cui (2023)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
205	Fleckhaus (2023)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
206	Fokias (2023)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
207	Fokias (2023)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
208	Hong (2023)	Sequencing/platform/method development	DNA methylation	Empirical primary	Age estimation; Bioinformatics/machine learning and interpretation
209	Huang (2023)	Not applicable	background/secondary	Background/secondary	Age estimation; Bioinformatics/machine learning and interpretation
210	Jiang (2023)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
211	Kotková (2023)	Not applicable	background/secondary	Background/secondary	Age estimation; Bioinformatics/machine learning and interpretation
212	Onofri (2023)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
213	Pośpiech (2023)	Sequencing/platform/method development	DNA methylation	Empirical primary	Age estimation; Bioinformatics/machine learning and interpretation
214	Refn (2023)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
215	Varshavsky (2023)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
216	Wang (2023)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
217	Xiao (2023)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
218	Yang (2023)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
219	Er (2024)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
220	Filoglu (2024)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
221	Ji (2024)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
222	Marcante (2024)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
223	Noroozi (2024)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
224	Pinprasert (2024)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
225	Shiga (2024)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
226	Soedarsono (2024)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
227	Yamagishi (2024)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation

Ref.	Author (year)	Primary application	Molecular stratum	Evidence role	Secondary application / cross-cutting tags
228	Anand (2025)	Not applicable	contextual/non-qualifying evidence	Contextual	Age estimation; Bioinformatics/machine learning and interpretation
229	Boullón-Cassau (2025)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
230	Collins (2025)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
231	Correia Dias (2025)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
232	Gao (2025)	Age estimation	mixed molecular	Empirical primary	Bioinformatics/machine learning and interpretation
233	Grignani (2025)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
234	Jung (2025)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
235	Li (2025)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
236	Liu (2025)	Not applicable	background/secondary	Background/secondary	Age estimation; Bioinformatics/machine learning and interpretation
237	Mathew (2025)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
238	Refn (2025)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
239	Sutter (2025)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
240	Verstraeten (2025)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
241	Wan (2025)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
242	Yang (2025)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
243	Zhu (2025)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
244	Andrejevic (2026)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
245	Can (2026)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
246	Chen (2026)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
247	Fakhr (2026)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
248	Lee (2026)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
249	Liu (2026)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
250	Manco (2026)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
251	Oka (2026)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
252	Pisarek-Pacek (2026)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
253	Poggiali (2026)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
254	So (2026)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
255	Sutter (2026)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
256	Tsutsumi (2026)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
257	Zhang (2026)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
258	Zhao (2026)	Age estimation	DNA methylation	Empirical primary	Bioinformatics/machine learning and interpretation
259	Ma (2013)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
260	Balamurugan (2014)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
261	Bartling (2014)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
262	Park (2014)	Body fluid/tissue identification	DNA methylation	Empirical primary	None

Ref.	Author (year)	Primary application	Molecular stratum	Evidence role	Secondary application / cross-cutting tags
263	Antunes (2015)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
264	Bai (2015)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
265	Fu (2015)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
266	Taki (2015)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
267	Wang (2015)	Not applicable	background/secondary	Background/secondary	Body fluid/tissue identification; Validation/forensic implementation evidence
268	Antunes (2016)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
269	Lin (2016)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
270	Lin (2016)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
271	Watanabe (2016)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
272	Watanabe (2016)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
273	Fachet (2017)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
274	Naue (2018)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
275	Samsuwan (2018)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
276	Fang (2019)	Body fluid/tissue identification	transcriptomic/non-coding RNA	Empirical primary	None
277	Gauthier (2019)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
278	Tian (2019)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
279	Xie (2019)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
280	Alghanim (2020)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
281	Ghai (2020)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
282	Kader (2020)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
283	Liu (2020)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
284	Tian (2020)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
285	Watanabe (2020)	Sequencing/platform/method development	mixed molecular	Empirical primary	Body fluid/tissue identification
286	Xie (2020)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
287	Antunes (2021)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
288	Doi (2021)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
289	Fujimoto (2021)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
290	Gomaa (2021)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
291	Li (2021)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
292	Liu (2021)	Body fluid/tissue identification	transcriptomic/non-coding RNA	Empirical primary	Validation/forensic implementation evidence
293	Abouelkeir (2022)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
294	Huang (2022)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
295	Li (2022)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence

Ref.	Author (year)	Primary application	Molecular stratum	Evidence role	Secondary application / cross-cutting tags
296	Lin (2022)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
297	Watanabe (2022)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
298	Fang (2023)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
299	Fang (2023)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
300	Fernandez-Tejero (2023)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
301	Konrad (2023)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
302	Konrad (2023)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
303	Rhodes (2023)	Body fluid/tissue identification	transcriptomic/non-coding RNA	Empirical primary	Validation/forensic implementation evidence
304	Silva (2023)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
305	Wang (2023)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
306	Altmeyer (2024)	Body fluid/tissue identification	transcriptomic/non-coding RNA	Empirical primary	Validation/forensic implementation evidence
307	Ghemrawi (2024)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
308	Kim (2024)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
309	Li (2024)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
310	Rothe (2024)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
311	Tang (2024)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
312	Balamurugan (2025)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
313	Hsu (2025)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
314	Li (2025)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
315	Mizrachi (2025)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
316	Wen (2025)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
317	Zhao (2025)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
318	Konrad (2026)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
319	Schmelzer (2026)	Body fluid/tissue identification	DNA methylation	Empirical primary	Validation/forensic implementation evidence
320	Schmelzer (2026)	Body fluid/tissue identification	mixed molecular	Empirical primary	Validation/forensic implementation evidence
321	Singh (2026)	Body fluid/tissue identification	transcriptomic/non-coding RNA	Empirical primary	Validation/forensic implementation evidence
322	Tang (2026)	Body fluid/tissue identification	DNA methylation	Empirical primary	None
323	Xu (2026)	Body fluid/tissue identification	mixed molecular	Empirical primary	Validation/forensic implementation evidence
324	Zhang (2018)	Body fluid/tissue identification	transcriptomic/non-coding RNA	Empirical primary	Validation/forensic implementation evidence
325	Liu (2019)	Body fluid/tissue identification	transcriptomic/non-coding RNA	Empirical primary	Validation/forensic implementation evidence
326	Samie (2022)	Not applicable	other-molecular comparator	Comparator	Body fluid/tissue identification; Validation/forensic implementation evidence

Ref.	Author (year)	Primary application	Molecular stratum	Evidence role	Secondary application / cross-cutting tags
327	Li (2026)	Body fluid/tissue identification	transcriptomic/non-coding RNA	Empirical primary	Validation/forensic implementation evidence
328	Xu (2012)	Sequencing/platform/method development	DNA methylation	Empirical primary	None
329	Zhang (2013)	Sequencing/platform/method development	DNA methylation	Empirical primary	None
330	Pandeshwar (2014)	Not applicable	background/secondary	Background/secondary	Body fluid/tissue identification
331	Dumache (2015)	Not applicable	background/secondary	Background/secondary	Sequencing/platform/method development
332	Kovatsi (2015)	Not applicable	background/secondary	Background/secondary	Ethics/legal/governance
333	Kreutz (2015)	Not applicable	background/secondary	Background/secondary	Sequencing/platform/method development
334	Dumache (2016)	Not applicable	background/secondary	Background/secondary	Body fluid/tissue identification
335	Margiotta (2016)	Not applicable	background/secondary	Background/secondary	Exposure/lifestyle/trauma/stress inference
336	Park (2017)	Monozygotic twin differentiation	DNA methylation	Empirical primary	None
337	Freire-Aradas (2018)	Age estimation	DNA methylation	Empirical primary	None
338	Hunter (2018)	Not applicable	background/secondary	Background/secondary	Exposure/lifestyle/trauma/stress inference
339	Ito (2018)	Not applicable	non-human comparative	Non-human	Sequencing/platform/method development
340	Park (2018)	Sequencing/platform/method development	DNA methylation	Empirical primary	None
341	Yao (2018)	Not applicable	other-molecular comparator	Comparator	Sequencing/platform/method development
342	Zubakov (2018)	Not applicable	other-molecular comparator	Comparator	Body fluid/tissue identification
343	Zapico (2019)	Not applicable	background/secondary	Background/secondary	Age estimation
344	Fang (2019)	Monozygotic twin differentiation	transcriptomic/non-coding RNA	Empirical primary	None
345	Hasnain (2019)	Not applicable	background/secondary	Background/secondary	Ethics/legal/governance
346	Mitjans (2019)	Not applicable	excluded	Excluded	Exposure/lifestyle/trauma/stress inference
347	Richards (2019)	Sequencing/platform/method development	DNA methylation	Empirical primary	Age estimation; Monozygotic twin differentiation
348	Xiao (2019)	Monozygotic twin differentiation	transcriptomic/non-coding RNA	Empirical primary	None
349	Liu (2020)	Not applicable	contextual/non-qualifying evidence	Contextual	Exposure/lifestyle/trauma/stress inference
350	Rao (2020)	Not applicable	background/secondary	Background/secondary	Sequencing/platform/method development
351	Sakurada (2020)	Not applicable	background/secondary	Background/secondary	Sequencing/platform/method development
352	Williams (2020)	Not applicable	background/secondary	Background/secondary	Ethics/legal/governance
353	Womersley (2020)	Not applicable	excluded	Excluded	Exposure/lifestyle/trauma/stress inference
354	Cho (2021)	Other donor-characteristic inference	DNA methylation	Empirical primary	Exposure/lifestyle/trauma/stress inference

Ref.	Author (year)	Primary application	Molecular stratum	Evidence role	Secondary application / cross-cutting tags
355	Haddrill (2021)	Not applicable	background/secondary	Background/secondary	Exposure/lifestyle/trauma/stress inference
356	Hao (2021)	Age estimation	DNA methylation	Empirical primary	Sequencing/platform/method development
357	Liu (2021)	Not applicable	contextual/non-qualifying evidence	Contextual	Exposure/lifestyle/trauma/stress inference
358	Naue (2021)	Age estimation	DNA methylation	Empirical primary	Sequencing/platform/method development
359	Planterose Jiménez (2021)	Monozygotic twin differentiation	DNA methylation	Empirical primary	None
360	Romanos (2021)	Monozygotic twin differentiation	DNA methylation	Empirical primary	None
361	Turrina (2021)	Monozygotic-twin legal/contextual analysis	contextual/non-qualifying evidence	Contextual	Monozygotic twin differentiation
362	Xulu (2021)	Not applicable	excluded	Excluded	Exposure/lifestyle/trauma/stress inference
363	Attia (2022)	Not applicable	background/secondary	Background/secondary	Age estimation
364	Becker (2022)	Age estimation	DNA methylation	Empirical primary	None
365	Carratto (2022)	Not applicable	background/secondary	Background/secondary	Sequencing/platform/method development
366	Christiansen (2022)	Sequencing/platform/method development	DNA methylation	Empirical primary	None
367	Elkins (2022)	Not applicable	background/secondary	Background/secondary	Sequencing/platform/method development
368	Konrad (2022)	Sequencing/platform/method development	DNA methylation	Empirical primary	None
369	Liang (2022)	Not applicable	other-molecular comparator	Comparator	Exposure/lifestyle/trauma/stress inference
370	Mazdai (2022)	Not applicable	excluded	Excluded	Exposure/lifestyle/trauma/stress inference
371	Wang (2022)	Age estimation	transcriptomic/non-coding RNA	Empirical primary	Sequencing/platform/method development
372	Al-Snan (2023)	Not applicable	background/secondary	Background/secondary	Ethics/legal/governance
373	Dash (2023)	Not applicable	background/secondary	Background/secondary	Sequencing/platform/method development
374	Fang (2023)	Age estimation	transcriptomic/non-coding RNA	Empirical primary	Sequencing/platform/method development
375	Ghai (2023)	Not applicable	background/secondary	Background/secondary	Sequencing/platform/method development
376	Kim (2023)	Monozygotic twin differentiation	DNA methylation	Empirical primary	None
377	Piccinini (2023)	Not applicable	contextual/non-qualifying evidence	Contextual	Exposure/lifestyle/trauma/stress inference
378	Shabalala (2023)	Sequencing/platform/method development	mixed molecular	Empirical primary	None
379	Skrant (2023)	Not applicable	background/secondary	Background/secondary	Monozygotic twin differentiation
380	Song (2023)	Not applicable	other-molecular comparator	Comparator	Sequencing/platform/method development
381	Wohlfahrt (2023)	Not applicable	other-molecular comparator	Comparator	Sequencing/platform/method development
382	Aourangzaib (2024)	Not applicable	background/secondary	Background/secondary	Monozygotic twin differentiation

Ref.	Author (year)	Primary application	Molecular stratum	Evidence role	Secondary application / cross-cutting tags
383	El-Hossary (2024)	Monozygotic twin differentiation	DNA methylation	Empirical primary	None
384	Hamza (2024)	Not applicable	background/secondary	Background/secondary	Sequencing/platform/method development
385	Oscandar (2024)	Age estimation	DNA methylation	Empirical primary	None
386	Sapozhnikov (2024)	Not applicable	background/secondary	Background/secondary	Age estimation
387	Daimi (editor) (2025)	Not applicable	background/secondary	Background/secondary	Ethics/legal/governance
388	Al Qaderi (2025)	Age estimation	DNA methylation	Empirical primary	None
389	Alwis (2025)	Not applicable	background/secondary	Background/secondary	Postmortem interval/time since deposition
390	Dash (2025)	Not applicable	background/secondary	Background/secondary	Body fluid/tissue identification
391	Gao (2025)	Not applicable	background/secondary	Background/secondary	Sequencing/platform/method development
392	Ghemrawi (2025)	Not applicable	background/secondary	Background/secondary	Body fluid/tissue identification
393	Huang (2025)	Other donor-characteristic inference	DNA methylation	Empirical primary	Exposure/lifestyle/trauma/stress inference
394	Kleenayoon (2025)	Not applicable	background/secondary	Background/secondary	Postmortem interval/time since deposition
395	Lu (2025)	Age estimation	transcriptomic/non-coding RNA	Empirical primary	Sequencing/platform/method development; Bioinformatics/machine learning and interpretation
396	Manco (2025)	Not applicable	background/secondary	Background/secondary	Postmortem interval/time since deposition
397	Ochana (2025)	Not applicable	background/secondary	Background/secondary	Exposure/lifestyle/trauma/stress inference
398	Poggiali (2025)	Sequencing/platform/method development	DNA methylation	Empirical primary	None
399	Qian (2025)	Age estimation	DNA methylation	Empirical primary	None
400	Simons (2025)	Sequencing/platform/method development	DNA methylation	Empirical primary	None
401	Vajpayee (2025)	Not applicable	background/secondary	Background/secondary	Sequencing/platform/method development
402	Wang (2025)	Monozygotic twin differentiation	transcriptomic/non-coding RNA	Empirical primary	None
403	Williams (2025)	Not applicable	background/secondary	Background/secondary	Monozygotic twin differentiation
404	Wulandari (2025)	Age estimation	DNA methylation	Empirical primary	Sequencing/platform/method development
405	Abdelaal (2026)	Not applicable	background/secondary	Background/secondary	Exposure/lifestyle/trauma/stress inference
406	Castagnola (2026)	Not applicable	contextual/non-qualifying evidence	Contextual	Exposure/lifestyle/trauma/stress inference
407	Colloca (2026)	Other donor-characteristic inference	DNA methylation	Empirical primary	Exposure/lifestyle/trauma/stress inference
408	Dash (2026)	Not applicable	background/secondary	Background/secondary	Monozygotic twin differentiation
409	Gaudi (2026)	Not applicable	background/secondary	Background/secondary	Exposure/lifestyle/trauma/stress inference
410	Marszałek (2026)	Other donor-characteristic inference	DNA methylation	Empirical primary	Exposure/lifestyle/trauma/stress inference
411	Sacco (2026)	Sequencing/platform/method development	DNA methylation	Empirical primary	None

Ref.	Author (year)	Primary application	Molecular stratum	Evidence role	Secondary application / cross-cutting tags
412	Shin (2026)	Not applicable	contextual/non-qualifying evidence	Contextual	Exposure/lifestyle/trauma/stress inference
413	Tyagi (2026)	Not applicable	background/secondary	Background/secondary	Ethics/legal/governance
414	Wang (2026)	Not applicable	background/secondary	Background/secondary	Postmortem interval/time since deposition
415	Kayser (2015)	Not applicable	background/secondary	Background/secondary	Sequencing/platform/method development
416	Sinnamon (2015)	Not applicable	background/secondary	Background/secondary	Exposure/lifestyle/trauma/stress inference
417	Cho (2017)	Not applicable	other-molecular comparator	Comparator	Age estimation
418	Pozhitkov (2017)	Not applicable	excluded	Excluded	Postmortem interval/time since deposition
419	Abbott (2018)	Not applicable	background/secondary	Background/secondary	Age estimation
420	Cassina (2018)	Not applicable	background/secondary	Background/secondary	Ethics/legal/governance
421	McCord (2018)	Not applicable	background/secondary	Background/secondary	Ethics/legal/governance
422	Raine (2018)	Not applicable	background/secondary	Background/secondary	Exposure/lifestyle/trauma/stress inference
423	Zapico (2019)	Not applicable	background/secondary	Background/secondary	Sequencing/platform/method development
424	Dragovich (2019)	Not applicable	background/secondary	Background/secondary	Exposure/lifestyle/trauma/stress inference
425	Fox (2020)	Not applicable	excluded	Excluded	Exposure/lifestyle/trauma/stress inference
426	Graça (2020)	Not applicable	background/secondary	Background/secondary	Monozygotic twin differentiation
427	Pośpiech (2020)	Not applicable	other-molecular comparator	Comparator	Exposure/lifestyle/trauma/stress inference
428	Rocchi (2021)	Not applicable	background/secondary	Background/secondary	Sequencing/platform/method development
429	Wang (2021)	Not applicable	other-molecular comparator	Comparator	Exposure/lifestyle/trauma/stress inference
430	Elkins (2022)	Not applicable	background/secondary	Background/secondary	Ethics/legal/governance
431	Vuk-Pavlović (2022)	Not applicable	background/secondary	Background/secondary	Ethics/legal/governance
432	Wang (2022)	Age estimation	transcriptomic/non-coding RNA	Empirical primary	Sequencing/platform/method development; Bioinformatics/machine learning and interpretation
433	Meng (2023)	Not applicable	other-molecular comparator	Comparator	None
434	Gouello (2024)	Not applicable	other-molecular comparator	Comparator	Body fluid/tissue identification
435	Afrifah (2025)	Not applicable	background/secondary	Background/secondary	Ethics/legal/governance
436	Hänggi (2025)	Age estimation	transcriptomic/non-coding RNA	Empirical primary	Sequencing/platform/method development; Bioinformatics/machine learning and interpretation
437	Tian (2025)	Monozygotic twin differentiation	transcriptomic/non-coding RNA	Empirical primary	Validation/forensic implementation evidence; Sequencing/platform/method development
438	Chen (2026)	Age estimation	transcriptomic/non-coding RNA	Empirical primary	Sequencing/platform/method development
439	Lei (2026)	Not applicable	background/secondary	Background/secondary	Ethics/legal/governance

Ten reports are intentionally cross-listed in Tables S2 and S3 (7 excluded and 3 non-human) to preserve their final study-level roles; they do not contribute to the evidence-map or empirical totals. Database retrieval source(s) for the 429 study-level register records are provided in the sortable XLSX companion.

Supplementary Table S3. Full-text reports excluded or classified as non-qualifying (n = 115)

Ref.	Author (year)	Reason for exclusion / non-qualification
74	Badell (2026)	Six pig carcasses generated repeated tissue samples and an internally split ElasticNet PMI model. The small animal-level sample, repeated measures, lack of human validation and absence of external testing preclude Category 3 human forensic evidence.
76	Sjöholm (2018)	The study examines post-mortem and post-sampling effects in rat brain. It contains no human forensic inference model and does not estimate PMI.
178	Keerthana (2021)	Source identity and reporting did not establish an independently verifiable unique empirical evidence unit; the record was excluded without implying research misconduct.
339	Ito (2018)	The model was developed from 20 chimpanzee blood samples for wildlife conservation and animal-age estimation. Human forensic relevance is indirect.
346	Mitjans (2019)	The study does not evaluate a direct forensic epigenetic endpoint and therefore did not meet the review eligibility criteria.
353	Womersley (2020)	The study does not evaluate a direct forensic epigenetic endpoint and therefore did not meet the review eligibility criteria.
362	Xulu (2021)	The study does not evaluate a direct forensic epigenetic endpoint and therefore did not meet the review eligibility criteria.
370	Mazdai (2022)	The study does not evaluate a direct forensic epigenetic endpoint and therefore did not meet the review eligibility criteria.
418	Pozhitkov (2017)	The study does not evaluate a direct forensic epigenetic endpoint and therefore did not meet the review eligibility criteria.
425	Fox (2020)	The study does not evaluate a direct forensic epigenetic endpoint and therefore did not meet the review eligibility criteria.
440	No named author (2011)	Editorial/news item with no primary, validation, methodological, or implementation evidence relevant to the review question.
441	Barash (2011)	Letter to the editor on artificial DNA/authentication; not primary forensic epigenetic evidence.
442	Berglund (2011)	NGS review for human history/forensics; no methylation or forensic epigenetic method evidence.
443	Gomes (2011)	Body-fluid/tissue markers paper focuses on DNA/mRNA skin assays rather than methylation/epigenetic markers.
444	Thanakiatkrai (2011)	Nucleosome-protection STR degradation study; does not evaluate an epigenetic marker/application for forensic inference.
445	Burgess (2013)	Research highlight/commentary on Hannum et al.; not primary evidence.
446	Nayarisseri (2013)	Whole-exome sequencing review for molecular diagnostics; not forensic epigenetics.
447	Fine (2014)	Clinical/personal-genomics discussion of population epigenetics without meaningful forensic epigenetic validation/application evidence.
448	Lee (2014)	Forensic DNA quantification review; relevant to forensic DNA workflow generally but not to epigenetic methods.
449	Prinz (2014)	Generic forensic-genetics, congress, editorial, or platform overview without DNA methylation or other relevant epigenetic evidence.
450	Yang (2014)	Protein, spectroscopy, or immunoassay study without an eligible epigenetic method or target.
451	Song (2015)	Fetal ABO genotyping; no forensic epigenetic application.
452	Branicki (2016)	Generic forensic-genetics, congress, editorial, or platform overview without DNA methylation or other relevant epigenetic evidence.
453	Liu (2017)	Genetic-marker study focused on STRs, SNPs, mtDNA, or other sequence variants without relevant epigenetic evidence.
454	Wolak (2019)	Generic forensic-genetics, congress, editorial, or platform overview without DNA methylation or other relevant epigenetic evidence.
455	Daca-Roszak (2019)	mRNA/transcriptomic study without DNA methylation or an eligible non-coding RNA forensic epigenetic endpoint.
456	Mela (2019)	FASD/mental-health review with epigenetic discussion but no forensic epigenetic casework or evidential application.
457	Perez-Toralla (2019)	Circulating cell-free DNA extraction platform; no forensic epigenetic validation/application.
	Thong (2019)	Corrigendum only; not primary evidence.
	Richards (2020)	Correction notice only; not primary evidence.
458	Daigneault (2020)	Bovine spermatozoa study; non-human evidence without a human forensic epigenetic endpoint.
459	Neves (2021)	Adverse-childhood-experience epigenomics meta-analysis; clinical/developmental focus without forensic evidential application.
460	Siahaan (2021)	Oral surgery morphological/molecular findings; no DNA methylation or relevant epigenetic data.

Ref.	Author (year)	Reason for exclusion / non-qualification
461	Carratto (2023)	Genetic-marker study focused on STRs, SNPs, mtDNA, or other sequence variants without relevant epigenetic evidence.
462	Lee (2023)	Generic forensic-genetics, congress, editorial, or platform overview without DNA methylation or other relevant epigenetic evidence.
463	Hwa (2024)	Genetic-marker study focused on STRs, SNPs, mtDNA, or other sequence variants without relevant epigenetic evidence.
464	Ochana (2024)	Preprint record duplicates the later peer-reviewed Cell Reports article (Ochana 2025) and was not retained as a separate primary evidence unit.
465	Vidaki (2024)	Generic forensic-genetics, congress, editorial, or platform overview without DNA methylation or other relevant epigenetic evidence.
466	Dash (2025)	Forensic identification review focused on genealogical/kinship solutions, without forensic epigenetic method evidence.
467	Gao (2025)	Proteomic signature of aging in bloodstains; not epigenetic.
468	Gerber (2025)	Species with nucleated red blood cells; not human forensic epigenetic evidence.
469	Okano (2025)	Animal model of child neglect; not human forensic epigenetic application.
470	Shabalala (2025)	Compound genetic-marker review; lacks epigenetic technique or methylation-focused forensic evidence.
471	Sharma (2025)	Generic forensic-genetics, congress, editorial, or platform overview without DNA methylation or other relevant epigenetic evidence.
472	Yilmaz (2025)	Genetic-marker study focused on STRs, SNPs, mtDNA, or other sequence variants without relevant epigenetic evidence.
473	van der Gaag (2025)	Genetic-marker study focused on STRs, SNPs, mtDNA, or other sequence variants without relevant epigenetic evidence.
474	Lee (2026)	Erratum only; not primary evidence.
475	Oprinca-Muja (2026)	Burnout epigenetics review; occupational/psychiatric focus without forensic evidential relevance.
476	Meyer (2010)	Forensic toxicology metabolism study; biochemical methylation reactions are not DNA methylation/epigenetic analysis.
477	Sajantila (2010)	Toxicology or drug-metabolism study without a forensic epigenetic method or endpoint.
478	Kuharić (2011)	Uses epigenetic/non-metric anatomical traits, not molecular epigenetics or DNA methylation.
479	Branicki (2015)	Generic forensic-genetics, congress, editorial, or platform overview without DNA methylation or other relevant epigenetic evidence.
480	Danaher (2015)	mRNA/transcriptomic study without DNA methylation or an eligible non-coding RNA forensic epigenetic endpoint.
481	Jeelani (2015)	Oral medicine review; no meaningful forensic epigenetic method or validation content.
	Forat (2016)	Correction notice only; not primary evidence.
482	Wink (2016)	Forensic toxicology metabolism study; no DNA methylation or epigenetic forensic application.
483	Hanson (2017)	mRNA/transcriptomic study without DNA methylation or an eligible non-coding RNA forensic epigenetic endpoint.
484	Pozhitkov (2017)	Postmortem gene-expression review; forensic-adjacent but transcriptomic rather than epigenetic validation evidence.
485	Blackman (2018)	mRNA/transcriptomic study without DNA methylation or an eligible non-coding RNA forensic epigenetic endpoint.
486	Dorum (2018)	mRNA/transcriptomic study without DNA methylation or an eligible non-coding RNA forensic epigenetic endpoint.
487	Holtkötter (2018)	Protein, spectroscopy, or immunoassay study without an eligible epigenetic method or target.
488	Stafford-Allen (2018)	mRNA/transcriptomic study without DNA methylation or an eligible non-coding RNA forensic epigenetic endpoint.
489	de Beijer (2018)	Protein, spectroscopy, or immunoassay study without an eligible epigenetic method or target.
490	Albani (2019)	mRNA/transcriptomic study without DNA methylation or an eligible non-coding RNA forensic epigenetic endpoint.
491	Dobay (2019)	Microbiome, rRNA, or bacterial-marker study without an eligible epigenetic method or target.
492	Huang (2019)	Microbiome, rRNA, or bacterial-marker study without an eligible epigenetic method or target.
493	López (2019)	Microbiome, rRNA, or bacterial-marker study without an eligible epigenetic method or target.
494	Kuffel (2020)	HLA/STR forensic mixture aid; not an epigenetic method.

Ref.	Author (year)	Reason for exclusion / non-qualification
495	Ohta (2020)	Microbiome, rRNA, or bacterial-marker study without an eligible epigenetic method or target.
496	Sharma (2020)	Protein, spectroscopy, or immunoassay study without an eligible epigenetic method or target.
497	Bonicelli (2021)	Bone matrix/rib age-at-death study; no epigenetic method.
498	Das (2021)	Vibrational spectroscopy review for semen analysis; no methylation/epigenetic technique.
499	Haas (2021)	mRNA/transcriptomic study without DNA methylation or an eligible non-coding RNA forensic epigenetic endpoint.
500	Salzmann (2021)	Microbiome, rRNA, or bacterial-marker study without an eligible epigenetic method or target.
501	Sharma (2021)	Protein, spectroscopy, or immunoassay study without an eligible epigenetic method or target.
502	Taylor (2021)	Criminology or psychology study without a forensic epigenetic method or endpoint.
503	Tian (2021)	mRNA/transcriptomic study without DNA methylation or an eligible non-coding RNA forensic epigenetic endpoint.
504	Wang (2021)	Transcriptome study of Chrysomyia pupae; forensic entomology context but not human forensic epigenetics.
505	Jin (2022)	mRNA/transcriptomic study without DNA methylation or an eligible non-coding RNA forensic epigenetic endpoint.
506	Layne (2022)	mRNA/transcriptomic study without DNA methylation or an eligible non-coding RNA forensic epigenetic endpoint.
507	Lehmann-Leo (2022)	Renal glomerulosclerosis/intima-media age assessment; no epigenetic method.
508	Lewis (2022)	Microbiome, rRNA, or bacterial-marker study without an eligible epigenetic method or target.
509	Miller (2022)	Book chapter on childhood memory development; it does not address forensic epigenetic applications, validation, casework, or relevant DNA methylation evidence.
510	Nogueira (2022)	Genetic-marker study focused on STRs, SNPs, mtDNA, or other sequence variants without relevant epigenetic evidence.
511	Xiao (2022)	mRNA/transcriptomic study without DNA methylation or an eligible non-coding RNA forensic epigenetic endpoint.
512	Dass (2023)	Microbial species body-fluid identification review; no DNA methylation or relevant epigenetic data.
513	Fu (2023)	Microbiome, rRNA, or bacterial-marker study without an eligible epigenetic method or target.
514	Hayes (2024)	Toxicology history/background source without forensic epigenetic method or validation value.
515	Kayser (2023)	Genetic-marker study focused on STRs, SNPs, mtDNA, or other sequence variants without relevant epigenetic evidence.
516	Yu (2023)	Microbiome, rRNA, or bacterial-marker study without an eligible epigenetic method or target.
517	Zhong (2023)	Genetic-marker study focused on STRs, SNPs, mtDNA, or other sequence variants without relevant epigenetic evidence.
518	Appel (2024)	Skeletal aging/cause-of-death pilot without epigenetic method.
519	Dorum (2024)	mRNA/transcriptomic study without DNA methylation or an eligible non-coding RNA forensic epigenetic endpoint.
520	Giovannini (2024)	Maternal opioid/FASD clinical-toxicological review; no forensic epigenetic validation or casework implementation content.
521	Haymer (2024)	Forensic entomology molecular markers review; no relevant epigenetic application.
522	Li (2024)	Genetic-marker study focused on STRs, SNPs, mtDNA, or other sequence variants without relevant epigenetic evidence.
523	Xiao (2024)	mRNA/transcriptomic study without DNA methylation or an eligible non-coding RNA forensic epigenetic endpoint.
524	Zhang (2024)	Microbiome, rRNA, or bacterial-marker study without an eligible epigenetic method or target.
525	Chen (2025)	Protein glycosylation for monozygotic twins; not epigenetic.
526	Ferorelli (2025)	FASD disability/clinical-forensic perspective without forensic epigenetic method evidence.
527	Fonseca (2025)	Genetic-marker study focused on STRs, SNPs, mtDNA, or other sequence variants without relevant epigenetic evidence.
528	Helander (2025)	Methamphetamine/metabolite interpretation study; no DNA methylation or relevant epigenetic data.
529	Hänggi (2025)	mRNA/transcriptomic study without DNA methylation or an eligible non-coding RNA forensic epigenetic endpoint.

Ref.	Author (year)	Reason for exclusion / non-qualification
530	Kula (2025)	Lucilia sericata entomology/cuticular chemistry; no human forensic epigenetic method.
531	Liu (2025)	mRNA/transcriptomic study without DNA methylation or an eligible non-coding RNA forensic epigenetic endpoint.
532	Orr (2025)	Forensic entomology blow-fly heritability study; animal/insect study without epigenetic forensic biomarker application.
533	Su (2025)	Microbiome, rRNA, or bacterial-marker study without an eligible epigenetic method or target.
534	Swayambhu (2025)	Microbiome, rRNA, or bacterial-marker study without an eligible epigenetic method or target.
535	Chen (2026)	mRNA/transcriptomic study without DNA methylation or an eligible non-coding RNA forensic epigenetic endpoint.
536	Elliott (2026)	Protein, spectroscopy, or immunoassay study without an eligible epigenetic method or target.
537	Gameli (2026)	Designer benzodiazepine metabolism study; no epigenetic method relevant to the review question.
538	Kumari (2026)	CRISPR-Cas9 forensic DNA review; not epigenetic/methylation evidence.
539	Sessa (2026)	Physical appearance/low-template review; no DNA methylation or relevant epigenetic application captured.
540	Shehata (2026)	Proteomic workflow for body-fluid classification; useful to body-fluid field but not epigenetic.
541	Wen (2026)	Genetic-marker study focused on STRs, SNPs, mtDNA, or other sequence variants without relevant epigenetic evidence.

Supplementary Table S4. Validation evidence and Category assignment for empirical primary studies (n = 322)

Ref.	Author (year)	Primary application	Category	Validation evidence / rationale	Minimum requirements before implementation
6	Koch (2011)	Age estimation	**Category 3 - Pre-implementation validation**	The five-CpG signature was tested across eight independent datasets and multiple tissues.	Translate to targeted forensic assay and validate on forensic sample types
7	Huang (2015)	Age estimation	**Category 3 - Pre-implementation validation**	The assay and chronological-age model were developed using blood samples and evaluated on a separate set of 40 blood specimens not used for model derivation; twenty corresponding bloodstain specimens and six additional fresh/older stain pairs were also tested (including storage for up to four months). This supports independently evaluated, casework-relevant bloodstain performance (C3), but not receiving-laboratory transfer, broadly representative degraded/low-template evaluation, or a documented routine forensic implementation package.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
8	Zbieć-Piekarska (2015)	Age estimation	**Category 3 - Pre-implementation validation**	Independent 124-sample validation plus 5-15-year bloodstains.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
9	Pfeifer (2020)	Age estimation	**Category 4 - Advanced validation evidence under defined conditions**	A receiving laboratory tested the published Bekaert blood and buccal models directly, documented poor transfer, and retrained local models. The retrained blood model was subsequently evaluated on 206 Bekaert blood records external to the local retraining set, while the retrained buccal model was evaluated on 49 additional local buccal samples; the publication does not report how the 100/49 buccal split was selected. Postmortem dried blood, storage/fresh-blood comparisons and broad age ranges were also examined. This supports Category 4 advanced transfer validation under defined conditions.	Finalise jurisdiction-specific SOPs, reporting language, uncertainty thresholds, proficiency testing and ongoing QA before routine implementation.
10	Heidegger (2022)	Age estimation	**Category 4 - Advanced validation evidence under defined conditions**	Five VISAGE laboratories evaluated ET-13 with methylation standards, semen extracts and FTA-card stains, including reproducibility, concordance and a sensitivity series down to 1 ng. Most markers/samples met the read-depth threshold to 10 ng, whereas every 1-ng sample showed at least two marker dropouts (36 total). This is advanced inter-laboratory developmental validation under defined conditions, but 1 ng was tested rather than demonstrated as an acceptable sensitivity limit; ET-5 remained preliminary.	Finalise jurisdiction-specific SOPs, reporting language, uncertainty thresholds, proficiency testing and ongoing QA before routine implementation.
11	Frumkin (2011)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Foundational assay with mixture experiments and forensic-oriented technical testing.	Broaden tissue panel, define thresholds, test degraded/low-template stains and inter-lab reproducibility
12	Holtkötter (2017)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Thirteen published markers were screened, a four-marker SNaPshot multiplex was developed, and mixtures plus five blinded mock stains were correctly interpreted. The work provides substantial single-laboratory pre-implementation evidence, but no external or inter-laboratory validation. Category 3 is therefore supported, not Category 4.	Finalise SOPs, proficiency testing, reporting language, contamination/degradation limits, and jurisdiction-specific legal and reporting requirements, where applicable.
13	Vidaki (2017)	Monozygotic twin differentiation	**Category 3 - Pre-implementation validation**	Discovery and technical validation were followed by analysis of trace-type blood DNA in a defined forensic scenario.	Large monozygotic-twin (MZ) cohorts, cross-tissue/cross-platform validation and probabilistic interpretation
14	Li (2013)	Monozygotic twin differentiation	**Category 1 - Exploratory discovery**	Descriptive methylation-profile differences without validated discrimination assay.	larger longitudinal twin cohorts, reproducibility and operational thresholds; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
15	Maas (2019)	Other donor-characteristic inference	**Category 3 - Pre-implementation validation**	Finite smoking panel validated in independent data.	confounding control, ethical/legal governance and validated individual-level interpretive limits; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation

Ref.	Author (year)	Primary application	Category	Validation evidence / rationale	Minimum requirements before implementation
16	Vidaki (2023)	Other donor-characteristic inference	**Category 2 - Initial technical evidence**	Original model/method study with internal training/test or cross-validation, limited sensitivity/low-input assessment, but without the independent and representative validation breadth required for Category 3.	External validation, age/sex/population confounding, likelihood ratio/uncertainty framework and legal limits
17	Choi (2014)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Forensic-like robustness supports Category 3, but the evidence is mixed methylation/microbiome rather than methylation-only.	Validate across populations, microbiome variability, mixtures, aged/degraded stains and laboratories
18	Watanabe (2018)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	The study demonstrates a novel principle without a broad validation programme.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
19	de Bruin (2025)	Sequencing/platform/method development	**Category 2 - Initial technical evidence**	Original model/method study with forensic relevance mentioned or limited forensic-like material, limited aged/degraded-material assessment, limited mixture-related assessment, but without the independent and representative validation breadth required for Category 3.	Assess low-template/degraded/mixture samples, depth thresholds and operational reproducibility
32	Kampmann (2024)	Age estimation	**Category 4 - Advanced validation evidence under defined conditions**	Five forensic laboratories applied a common bisulfite-pyrosequencing protocol and an existing five-locus model to 49 new blood samples. The collaborative exercise demonstrated inter-laboratory feasibility and identified platform and quality-control limitations. It provides advanced validation under defined conditions, but no casework stains, degradation study or routine-use documentation.	Finalise jurisdiction-specific SOPs, reporting language, uncertainty thresholds, proficiency testing and ongoing QA before routine implementation.
33	Heidegger (2025)	Age estimation	**Category 4 - Advanced validation evidence under defined conditions**	Six laboratories completed two technical phases and three governmental laboratories evaluated 160 blood and 100 buccal samples independent of the original VISAGE model sets. Sensitivity was maintained to 5 ng, but a laboratory-specific blood bias required in-house model validation. This supports Category 4, not routine implementation.	Finalise jurisdiction-specific SOPs, reporting language, uncertainty thresholds, proficiency testing and ongoing QA before routine implementation.
34	Onofri (2025)	Age estimation	**Category 4 - Advanced validation evidence under defined conditions**	The Ge.F.I. exercise standardised a five-locus SNaPshot assay across laboratories, compared fresh blood with dried spots and quantified laboratory/instrument effects. Six laboratories provided four replicate measurements for each of 22 donors; replicates were averaged to one subject-level record per laboratory before leave-one-out cross-validation. Phase II data were first aligned to Phase III using locus-specific regressions on chronological age. The report does not state that these alignment regressions were re-estimated within each LOO-CV iteration; therefore the reported cross-validated MAD should be interpreted as performance after the study's reported preprocessing rather than as a fully nested validation of the complete pipeline. This limitation does not negate the collaborative/inter-laboratory evidence supporting C4.	Finalise jurisdiction-specific SOPs, reporting language, uncertainty thresholds, proficiency testing and ongoing QA before routine implementation.
35	Lee (2022)	Age estimation	**Category 4 - Advanced validation evidence under defined conditions**	Twelve laboratories evaluated two age-prediction multiplexes and a body-fluid assay through a tiered full-workflow exercise using standardised, partly undisclosed samples. The study identified analyzer-, primer- and input-volume effects while retaining useful age estimates. This supports Category 4, with age estimation as the primary endpoint and body-fluid typing as an enabling secondary endpoint.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
36	Bocklandt (2011)	Age estimation	**Category 3 - Pre-implementation validation**	Discovery in twin samples followed by replication in an unrelated male/female population supports independent model validation.	Validate across tissues, populations, degraded traces, low DNA input, mixtures and lab platforms
37	Bekaert (2015)	Age estimation	**Category 2 - Initial technical evidence**	A quadratic four-gene pyrosequencing model was fitted to 50 buccal swabs and reported an apparent mean absolute deviation of 3.32 years, but no independent test set, cross-validation, sensitivity, casework or external validation was described. This short method-development contribution supports Category 2.	External validation across populations and casework-like stains/remains
38	Freire-Aradas (2016)	Age estimation	**Category 3 - Pre-implementation validation**	Large training data, cross-validation and independent 104-twin test set.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.

Ref.	Author (year)	Primary application	Category	Validation evidence / rationale	Minimum requirements before implementation
39	Aliferi (2018)	Age estimation	**Category 3 - Pre-implementation validation**	Independent blind testing plus analytical sensitivity supports Category 3.	External validation, degraded stains, mixtures and calibration across populations/tissues
40	Jung (2019)	Age estimation	**Category 3 - Pre-implementation validation**	Independent test sets across blood, saliva and buccal samples.	Validate on aged/degraded stains, mixtures and independent populations
41	Xu (2015)	Age estimation	**Category 2 - Initial technical evidence**	The small validation set and absence of forensic stains or robustness testing do not support Category 3.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
42	Cho (2017)	Age estimation	**Category 3 - Pre-implementation validation**	Independent validation of published age-prediction approaches.	Broader external validation across age ranges and populations; casework-like sample robustness; calibration and reporting of prediction uncertainty.
43	Vidaki (2017)	Age estimation	**Category 3 - Pre-implementation validation**	Pre-implementation evidence is supported; no inter-laboratory or routine implementation evidence.	External validation, population calibration, degradation/mixture tests and reporting uncertainty
44	Lee (2018)	Age estimation	**Category 3 - Pre-implementation validation**	Casework-oriented concordance and sensitivity testing support Category 3.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
45	Peng (2019)	Age estimation	**Category 3 - Pre-implementation validation**	Two independent time-series bloodstain batches under room-temperature conditions.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
46	Dias (2020)	Age estimation	**Category 3 - Pre-implementation validation**	Cross-population replication and direct postmortem evaluation support Category 3.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
47	Correia Dias (2020)	Age estimation	**Category 3 - Pre-implementation validation**	Replication plus an independent test set supports Category 3, despite modest sample size.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
48	Fleckhaus (2020)	Age estimation	**Category 3 - Pre-implementation validation**	Low-input multiplex strategy tested under forensic-relevant conditions.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
49	Yi (2015)	Age estimation	**Category 3 - Pre-implementation validation**	Independent 65-donor validation after marker discovery.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
50	Park (2016)	Age estimation	**Category 3 - Pre-implementation validation**	535-sample training and independent 230-sample validation.	Robustness, low-template/degraded/mixed-sample testing, and uncertainty reporting are required before casework implementation.
51	Hamano (2017)	Age estimation	**Category 3 - Pre-implementation validation**	Cigarette-butt/saliva forensic-like application and robustness testing.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
52	Liu (2022)	Body fluid/tissue identification	**Category 4 - Advanced validation evidence under defined conditions**	Six ISO 17025 forensic laboratories blindly tested nine mock sexual-assault samples using their own routine extraction and quantification workflows. The 3-plex HhaI MSRE-PCR correctly identified spermatozoa, including semen–saliva and semen–blood mixtures. This is inter-laboratory Category 4 evidence; the study does not establish routine implementation.	Finalise SOPs, proficiency testing, reporting language, contamination/degradation limits, and jurisdiction-specific legal and reporting requirements, where applicable.
53	Kim (2024)	Body fluid/tissue identification	**Category 4 - Advanced validation evidence under defined conditions**	The study combined EPIC-array marker discovery, multiplex SNaPshot development, Asian autopsy-sample validation, sensitivity and mixture experiments, and an independent German autopsy cohort. Correct tissue calls were 92.5% externally, with lung and kidney-cortex limitations. This meets Category 4; postmortem sampling alone is not degradation testing.	Finalise SOPs, proficiency testing, reporting language, contamination/degradation limits, and jurisdiction-specific legal and reporting requirements, where applicable.

Ref.	Author (year)	Primary application	Category	Validation evidence / rationale	Minimum requirements before implementation
54	Jung (2016)	Body fluid/tissue identification	**Category 4 - Advanced validation evidence under defined conditions**	Seven laboratories completed increasingly complex tasks spanning capillary electrophoresis, SBE, PCR, bisulfite conversion and extraction, using known and blinded single-source and mixed body-fluid samples. Six laboratories produced consistent interpretations. This is a collaborative Category 4 exercise; fixed DNA inputs do not constitute a sensitivity study.	Define cross-laboratory error rates and thresholds, extend representative sensitivity/robustness testing, and establish laboratory SOPs and reporting rules.
55	Madi (2012)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	Original model/method study with limited sensitivity/low-input assessment, forensic relevance mentioned or limited forensic-like material, limited mixture-related assessment, but without the independent and representative validation breadth required for Category 3.	Independent validation; quantified sensitivity and specificity; mixture, aged/degraded-stain, low-input, and threshold studies.
56	An (2013)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Multi-fluid assay validation and aged-stain testing support Category 3.	Full validation of thresholds, mixtures, aged stains and cross-lab performance
57	Lee (2016)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Large multi-fluid dataset plus aged and artificial casework samples.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
58	Lee (2015)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Large marker-development dataset with aged and artificial casework samples.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
59	Forat (2016)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Environmental and mixture robustness support Category 3.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
60	Vidaki (2017)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Forensic-like and stability testing support Category 3.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
61	Hanson (2014)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	The study develops a logistic-regression menstrual-blood assay, reports sub-ng RNA sensitivity, admixed-sample testing and menstrual-cycle evaluation. It is not DNA-methylation evidence.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
62	Antunes (2016)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	Limited marker-level proof of concept does not support Category 3.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
63	Dorum (2019)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Mock casework testing supports Category 3 within a separate transcriptomic stratum.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
64	Larue (2013)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Broad single-laboratory developmental validation supports Category 3.	Independent validation and SOP-level interpretation rules
65	Wasserstrom (2013)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	The assay was tested on 135 reference body-fluid samples, 33 actual police casework samples and mock semen-containing vaginal swabs, with successful results down to approximately 148 pg in casework extracts. This is substantial single-laboratory casework-oriented validation, but not inter-laboratory validation or documented routine use.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
66	Silva (2016)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Broad developmental validation supports Category 3.	Finalise SOPs, proficiency testing, reporting language, contamination/degradation limits, and jurisdiction-specific legal and reporting requirements, where applicable.

Ref.	Author (year)	Primary application	Category	Validation evidence / rationale	Minimum requirements before implementation
67	Li (2020)	Age estimation	**Category 3 - Pre-implementation validation**	The semen model was developed in 38 donors and tested in 17 donors across liquid semen, fresh stains, one-month aged stains and semen-vaginal mixtures, with differential-lysis experiments and application to an actual rape case. This supports pre-implementation evidence in a single laboratory.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
68	Foox (2021)	Age estimation	**Category 3 - Pre-implementation validation**	The study tested actual and mock crime-scene blood, including a sample stored for more than 20 years and low-input sequencing.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
69	Sutter (2026)	Age estimation	**Category 3 - Pre-implementation validation**	Five bone types, environmental exposure simulations, and two actual casework samples directly tested forensic transferability and limitations.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
70	Choung (2021)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Twenty-two samples from 18 forensic cases plus sensitivity testing.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
71	Lee (2026)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Two actual casework samples were examined using STR/Y-STR profiling, bisulfite SNaPshot body-fluid typing and EPIC-array deconvolution, age clocks and smoking prediction. The samples included a blood–saliva or upper-gastrointestinal mixture and severe degradation. This is casework-level pre-implementation evidence supporting Category 3, but a single interpretative case is not a validation programme or routine implementation.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
73	Bilinsky (2025)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Four brain-specific methylation loci were tested across human tissues, burned and outdoor air-dried samples, and 10%/50% brain-tissue mixtures. The assay retained discrimination under the tested forensic-like conditions, supporting single-laboratory pre-implementation evidence but not inter-laboratory or routine implementation.	Independent lab validation, tissue spectrum expansion and thresholds for low-template casework
78	Stewart (2015)	Monozygotic twin differentiation	**Category 2 - Initial technical evidence**	HRM proof-of-concept assay.	larger longitudinal twin cohorts, reproducibility and operational thresholds; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
79	Xu (2015)	Monozygotic twin differentiation	**Category 2 - Initial technical evidence**	LINE-1 marker technical study.	larger longitudinal twin cohorts, reproducibility and operational thresholds; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
80	Du (2015)	Monozygotic twin differentiation	**Category 1 - Exploratory discovery**	Original exploratory/discovery study without a sufficiently validated model, independent test set, or broader forensic robustness programme.	Large independent MZ cohorts, multi-tissue testing, forensic samples and statistical interpretation
81	Zhang (2015)	Monozygotic twin differentiation	**Category 1 - Exploratory discovery**	Longitudinal/descriptive twin methylation evidence.	larger longitudinal twin cohorts, reproducibility and operational thresholds; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
82	Vidaki (2018)	Monozygotic twin differentiation	**Category 2 - Initial technical evidence**	Forensic-trace proof of concept in one twin pair.	larger longitudinal twin cohorts, reproducibility and operational thresholds; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
83	Marqueta-Gracia (2018)	Monozygotic twin differentiation	**Category 2 - Initial technical evidence**	PCR-HRM twin discrimination assay development.	larger longitudinal twin cohorts, reproducibility and operational thresholds; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation

Ref.	Author (year)	Primary application	Category	Validation evidence / rationale	Minimum requirements before implementation
84	Wang (2024)	Monozygotic twin differentiation	**Category 3 - Pre-implementation validation**	The study contains more than internal discovery: it validates candidates in additional twin pairs and tests forensic-scenario sample types.	larger longitudinal twin cohorts, reproducibility and operational thresholds; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
85	Cho (2025)	Monozygotic twin differentiation	**Category 3 - Pre-implementation validation**	Independent replication supports Category 3.	larger longitudinal twin cohorts, reproducibility and operational thresholds; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
86	Zeng (2026)	Monozygotic twin differentiation	**Category 2 - Initial technical evidence**	Original model/method study with limited sensitivity/low-input assessment, forensic relevance mentioned or limited forensic-like material, limited aged/degraded-material assessment, limited mixture-related assessment, but without the independent and representative validation breadth required for Category 3.	Larger MZ cohorts, degraded/trace validation, error rates and probabilistic reporting
87	Wen (2022)	Other donor-characteristic inference	**Category 2 - Initial technical evidence**	Single-population smoking model with internal testing.	confounding control, ethical/legal governance and validated individual-level interpretive limits; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
88	Ambroa-Conde (2024)	Other donor-characteristic inference	**Category 3 - Pre-implementation validation**	Tobacco/alcohol models were evaluated with independent test sets in addition to internal model development.	Validate on forensic traces, populations, time since behaviour, confounders, and jurisdiction-specific legal and reporting requirements, where applicable.
90	Llobet (2023)	Other donor-characteristic inference	**Category 2 - Initial technical evidence**	Internal multi-trait prediction models.	confounding control, ethical/legal governance and validated individual-level interpretive limits; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
91	Pośpiech (2024)	Other donor-characteristic inference	**Category 3 - Pre-implementation validation**	Large cohort plus independent 100-sample smoking test set.	confounding control, ethical/legal governance and validated individual-level interpretive limits; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
92	Pośpiech (2025)	Other donor-characteristic inference	**Category 3 - Pre-implementation validation**	A smoking classifier developed in 200 buccal samples was validated in an independent set of 80 samples.	Forensic traces, degradation, mixed samples, confounders and ethical/legal interpretation
93	Wang (2024)	Other donor-characteristic inference	**Category 3 - Pre-implementation validation**	The study developed a targeted DNA-methylation height-prediction model with validation beyond initial discovery, supporting Category 3 within the broader donor-characteristic inference area. Routine forensic implementation is not documented.	Independent external validation across populations, sexes, age groups and relevant tissues; robustness to low-template, degraded and mixed samples; calibration, uncertainty and reporting standards.
94	Naue (2018)	Sequencing/platform/method development	**Category 2 - Initial technical evidence**	Small cross-tissue proof of concept without an endpoint validation set supports Category 2.	application-specific forensic validation on realistic samples; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
95	Di Lena (2021)	Sequencing/platform/method development	**Category 2 - Initial technical evidence**	Software/webserver resource; no pre-implementation forensic validation.	application-specific forensic validation on realistic samples; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
96	Simons (2025)	Sequencing/platform/method development	**Category 2 - Initial technical evidence**	Independent benchmarking of conversion methods.	application-specific forensic validation on realistic samples; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
97	Turiello (2023)	Sequencing/platform/method development	**Category 2 - Initial technical evidence**	Original bisulfite-conversion device/method study.	application-specific forensic validation on realistic samples; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
98	Dias (2024)	Age estimation	**Category 2 - Initial technical evidence**	Internal cross-validation/holdout in one 58-sample cohort; no independent external validation.	application-specific forensic validation on realistic samples; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation

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99	So (2024)	Sequencing/platform/method development	**Category 3 - Pre-implementation validation**	Independent platform-transfer evaluation supports Category 3 for method implementation.	application-specific forensic validation on realistic samples; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
100	Poussard (2023)	Age estimation	**Category 4 - Advanced validation evidence under defined conditions**	A receiving forensic laboratory adapted published saliva/buccal age-prediction models from SNaPshot to pyrosequencing, established trueness/sensitivity/repeatability using methylation standards, and then evaluated the published tissue-specific and multitissue models in 115 French donors. The donor cohort was used for performance evaluation rather than for setting the analytical adaptation conditions. This explicit cross-platform transportability study, combined with technical validation and prediction-limit analysis, supports Category 4 under defined conditions despite the single-laboratory design.	Inter-laboratory replication; degraded/low-template and mixed-trace validation; broader population transfer; laboratory-specific SOPs, proficiency testing, uncertainty/reporting limits and evidence of routine implementation.
101	Lee (2025)	Age estimation	**Category 2 - Initial technical evidence**	Lee et al. (2025) developed bisulfite-MPS semen-age models after marker discovery and reported a 7:3 training/test split (111/48 for the Korean-marker analysis). Multiple candidate regressions were evaluated using training- and test-set performance; ridge and elastic-net models were subsequently highlighted as preferred (Methods §2.7; Results §§3.4–3.7). Although the test samples were distinct from the training set, no additional untouched validation of the selected models after this comparison was documented. Sensitivity and reproducibility checks were targeted rather than broad independent casework validation. C2 therefore reflects the reported model-comparison sequence, not demonstrated data leakage or a general exclusion of internal held-out validation from C3.	Finalise jurisdiction-specific SOPs, reporting language, uncertainty thresholds, proficiency testing and ongoing QA before routine implementation.
103	Sarac (2017)	Age estimation	**Category 2 - Initial technical evidence**	The study developed an age and body-mass-index prediction model from peripheral-blood methylation data. The model remained internally evaluated and supports Category 2 for age estimation.	Independent validation in representative populations and forensic sample types; robustness to low-template, degraded and mixed samples; calibration and uncertainty reporting.
104	Fang (2020)	Age estimation	**Category 2 - Initial technical evidence**	The study used massively parallel sequencing to select bloodstain miRNA markers and developed machine-learning age-prediction models. Evaluation remained within the study cohort and supports Category 2.	application-specific forensic validation on realistic samples; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
107	Li (2011)	Monozygotic twin differentiation	**Category 1 - Exploratory discovery**	22 monozygotic-twin pairs; discovery evidence without independent or casework validation.	Validate markers across more MZ pairs, tissues, ages, environments and forensic samples
108	Lee (2012)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	Original model/method study with forensic relevance mentioned or limited forensic-like material, limited aged/degraded-material assessment, but without the independent and representative validation breadth required for Category 3.	Validate on individual, aged, degraded and mixed forensic stains with thresholds
109	Weidner (2014)	Age estimation	**Category 2 - Initial technical evidence**	Original model/method study with internal training/test or cross-validation, limited aged/degraded-material assessment, but without the independent and representative validation breadth required for Category 3.	Forensic sample validation, population calibration and cross-platform testing
110	Vidaki (2016)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Large stain validation, stability assessment, and sensitivity down to approximately 50 pg provide forensic robustness evidence.	Independent and inter-laboratory validation; defined sensitivity and specificity; mixture/degradation testing; interpretation thresholds and reporting limits.
111	Lee (2020)	Age estimation	**Category 3 - Pre-implementation validation**	Marker discovery in skeletal remains was followed by targeted testing in an independent set of 30 skeletal remains.	Optimize bone protocols and validate marker panels in large independent skeletal cohorts
112	Anaya (2021)	Age estimation	**Category 3 - Pre-implementation validation**	Direct postmortem material and independent testing support Category 3.	External validation, PMI/decomposition stratification and uncertainty reporting
113	Koop (2021)	Age estimation	**Category 3 - Pre-implementation validation**	The age model was evaluated directly in postmortem buccal samples spanning different stages of decomposition.	Multi-marker models, larger cohorts and standardised postmortem condition reporting
114	Ambroa-Conde (2022)	Age estimation	**Category 3 - Pre-implementation validation**	Independent additional-set validation and low-input evaluation support Category 3.	Mixtures, aged stains, external population validation and SOP thresholds

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116	Jung (2024)	Age estimation	**Category 3 - Pre-implementation validation**	Deceased costal-cartilage model with independent external Polish dataset.	Validate on decomposed/burnt samples and independent laboratories with uncertainty reporting
117	Paparazzo (2025)	Age estimation	**Category 3 - Pre-implementation validation**	Reproducibility in an independent population and cross-platform consistency support Category 3.	Evaluate degraded/low-template/mixture stains and inter-lab SOPs
118	Sutter (2025)	Age estimation	**Category 3 - Pre-implementation validation**	Cross-technology evaluation with biological replicates across four tissues.	Larger cohorts, degraded/low-template samples and clear technology-specific SOPs
119	Beentjes (2026)	Sequencing/platform/method development	**Category 2 - Initial technical evidence**	Original technical, model-development, association, or proof-of-concept study without sufficiently broad independent, forensic-like, or transferability validation for Category 3.	Validate read-depth thresholds, low-input performance, more fluids, mixtures, degraded samples and model calibration
120	Tiras (2026)	Age estimation	**Category 1 - Exploratory discovery**	Original exploratory/discovery study without a sufficiently validated model, independent test set, or broader forensic robustness programme.	Develop targeted model, validate independently, test low-template/degraded forensic samples
121	Park (2026)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Single-source and 33 mixture samples using methylation-linked microhaplotypes/SNPs.	Expand marker set, model allele dropout/zygosity, test degraded/low-template casework and external validation
122	Freire-Aradas (2023)	Age estimation	**Category 3 - Pre-implementation validation**	Independent testing of a direct forensic tissue endpoint supports Category 3.	Inter-lab validation, degraded/burnt remains and formal interpretation thresholds
123	Watanabe (2023)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Mock forensic and mixture testing support Category 3.	Inter-lab validation, more substrates, degraded samples and interpretation thresholds
124	Chen (2025)	Age estimation	**Category 3 - Pre-implementation validation**	Direct human skeletal material and held-out testing support Category 3.	Independent cohorts, degraded/burnt remains, cross-bone validation and uncertainty reporting
125	Yi (2014)	Age estimation	**Category 3 - Pre-implementation validation**	Candidate markers were replicated in an additional general-population sample and combined in an age-prediction model.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
126	Bekaert (2015)	Age estimation	**Category 3 - Pre-implementation validation**	The assay was evaluated in living and deceased blood, teeth, and cross-validation, providing broader tissue and forensic-context evidence.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
127	Huang (2015)	Age estimation	**Category 2 - Initial technical evidence**	Marker screening and pyrosequencing provide initial technical evidence only.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
128	Lee (2015)	Age estimation	**Category 2 - Initial technical evidence**	Original technical, model-development, association, or proof-of-concept study without sufficiently broad independent, forensic-like, or transferability validation for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
129	Silva (2015)	Age estimation	**Category 2 - Initial technical evidence**	Original model/method study with internal training/test or cross-validation, but without the independent and representative validation breadth required for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
130	Zbieć-Piekarska (2015)	Age estimation	**Category 3 - Pre-implementation validation**	Model development in 300 samples followed by an independent 120-sample test set supports pre-implementation validation.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
131	Giuliani (2016)	Age estimation	**Category 2 - Initial technical evidence**	Original technical, model-development, association, or proof-of-concept study without sufficiently broad independent, forensic-like, or transferability validation for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
132	Hamano (2016)	Age estimation	**Category 3 - Pre-implementation validation**	Living and deceased blood were evaluated, with a 74-sample training set and an additional independent 30-sample test set.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
133	Mawlood (2016)	Age estimation	**Category 2 - Initial technical evidence**	Original model/method study with limited mixture-related assessment, but without the independent and representative validation breadth required for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.

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134	Zubakov (2016)	Age estimation	**Category 3 - Pre-implementation validation**	Candidate biomarkers were validated in independent samples using alternative technologies and combined-marker models.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
135	Alghanim (2017)	Age estimation	**Category 2 - Initial technical evidence**	Marker evaluation/model development without external validation.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
136	Alsaleh (2017)	Age estimation	**Category 2 - Initial technical evidence**	Model developed from repository data and tested in a small independent dataset.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
137	Fleckhaus (2017)	Age estimation	**Category 2 - Initial technical evidence**	Transferability testing across three ancestry groups; short format limits appraisal.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
139	Hong (2017)	Age estimation	**Category 3 - Pre-implementation validation**	Marker discovery used an initial 54-saliva methylation-array cohort. Targeted model development then used 113 samples from a separate 226-sample cohort, with final performance evaluated in the other 113 samples held out from model construction; additional sensitivity testing examined varying DNA inputs. This staged discovery plus held-out endpoint validation supports Category 3, but no external laboratory/population transfer was demonstrated.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
140	Li (2017)	Age estimation	**Category 2 - Initial technical evidence**	Original semen age-marker testing in 38 donors; limited validation breadth.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
141	Naue (2017)	Age estimation	**Category 3 - Pre-implementation validation**	The MPS/random-forest model used 208 training and 104 test samples with additional marker and sensitivity evaluation.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
142	Thong (2017)	Age estimation	**Category 3 - Pre-implementation validation**	Independent testing plus bloodstain and low-template robustness testing exceed ordinary internal model development and support Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
143	Feng (2018)	Age estimation	**Category 2 - Initial technical evidence**	Original model/method study with internal training/test or cross-validation, but without the independent and representative validation breadth required for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
145	Horvath (2018)	Age estimation	**Category 2 - Initial technical evidence**	The paper develops a skin-and-blood epigenetic clock and notes possible forensic use, but its main analyses concern progeria, ex vivo cells and general biological ageing.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
146	Shi (2018)	Age estimation	**Category 2 - Initial technical evidence**	Original model/method study with internal training/test or cross-validation, but without the independent and representative validation breadth required for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
147	Smeers (2018)	Age estimation	**Category 2 - Initial technical evidence**	Original model/method study with forensic relevance mentioned or limited forensic-like material, but without the independent and representative validation breadth required for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
148	Spólnicka (2018)	Age estimation	**Category 3 - Pre-implementation validation**	The study provides independent disease/confounder testing of age markers beyond routine internal model development, supporting Category 3 but not Category 4.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
149	Alsaleh (2019)	Age estimation	**Category 2 - Initial technical evidence**	Original model/method study with internal training/test or cross-validation, but without the independent and representative validation breadth required for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
151	Hong (2019)	Age estimation	**Category 2 - Initial technical evidence**	Original model/method study with internal training/test or cross-validation, forensic relevance mentioned or limited forensic-like material, but without the independent and representative validation breadth required for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.

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152	Khan (2019)	Age estimation	**Category 2 - Initial technical evidence**	Original model/method study with forensic relevance mentioned or limited forensic-like material, but without the independent and representative validation breadth required for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
153	Li (2019)	Age estimation	**Category 2 - Initial technical evidence**	Original technical, model-development, association, or proof-of-concept study without sufficiently broad independent, forensic-like, or transferability validation for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
156	Xie (2019)	Age estimation	**Category 2 - Initial technical evidence**	Database-led marker selection plus 20 stored bloodstains.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
157	Xin (2019)	Age estimation	**Category 2 - Initial technical evidence**	Original model/method study with internal training/test or cross-validation, but without the independent and representative validation breadth required for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
160	Correia Dias (2020)	Age estimation	**Category 3 - Pre-implementation validation**	The deceased-blood model was evaluated in an independent 19-sample test set.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
161	Freire-Aradas (2020)	Age estimation	**Category 2 - Initial technical evidence**	Original model/method study with internal training/test or cross-validation, limited sensitivity/low-input assessment, but without the independent and representative validation breadth required for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
162	Gopalan (2019)	Age estimation	**Category 2 - Initial technical evidence**	The 2020 American Journal of Physical Anthropology item is an AAPA meeting abstract of the same work, not a separate full empirical publication. The complete 2019 bioRxiv preprint (doi:10.1101/801647) was therefore treated as the controlling source and counted once as a single empirical evidence unit. That report contains 32 newly generated bone specimens plus 133 previously published bone donors. All newly generated forensic samples failed post-assay array quality control and were excluded from subsequent modelling; the age model was developed on the merged retained data using an internal training/test split. These features support Category 2, not Category 3.	Translate the model to a validated forensic assay; test representative forensic, degraded, low-template and population-transfer conditions; define uncertainty and reporting thresholds.
163	Heidegger (2020)	Age estimation	**Category 2 - Initial technical evidence**	Original model/method study with limited sensitivity/low-input assessment, limited aged/degraded-material assessment, but without the independent and representative validation breadth required for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
164	Karir (2020)	Age estimation	**Category 2 - Initial technical evidence**	Original technical, model-development, association, or proof-of-concept study without sufficiently broad independent, forensic-like, or transferability validation for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
165	Kondo (2020)	Age estimation	**Category 2 - Initial technical evidence**	Small 29-tooth single-marker model without independent validation.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
166	Lau (2020)	Age estimation	**Category 2 - Initial technical evidence**	Original model/method study with internal training/test or cross-validation, but without the independent and representative validation breadth required for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
167	Montesanto (2020)	Age estimation	**Category 3 - Pre-implementation validation**	Independent test-set validation supports Category 3.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
168	Márquez-Ruiz (2020)	Age estimation	**Category 2 - Initial technical evidence**	Original technical, model-development, association, or proof-of-concept study without sufficiently broad independent, forensic-like, or transferability validation for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
169	Pan (2020)	Age estimation	**Category 3 - Pre-implementation validation**	Independent 80-sample validation set after 230-sample training.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.

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170	Wei (2020)	Age estimation	**Category 2 - Initial technical evidence**	Original model/method study with internal training/test or cross-validation, but without the independent and representative validation breadth required for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
171	Yudianto (2020)	Age estimation	**Category 1 - Exploratory discovery**	Only ten bloodstain samples were analysed, split by sex, using a global CpG-count-derived methylation percentage rather than a validated locus-specific age model. Correlations were significant only in five male samples, and the authors acknowledged low external validity. This is Category 1 exploratory evidence.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
172	Al-Ghanmy (2021)	Age estimation	**Category 2 - Initial technical evidence**	Internal resampling without an independent forensic validation set supports Category 2.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
173	Amiri Roudbar (2021)	Age estimation	**Category 2 - Initial technical evidence**	Original technical, model-development, association, or proof-of-concept study without sufficiently broad independent, forensic-like, or transferability validation for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
174	Zapico (2021)	Age estimation	**Category 2 - Initial technical evidence**	Original model/method study with forensic relevance mentioned or limited forensic-like material, but without the independent and representative validation breadth required for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
175	Correia Dias (2021)	Age estimation	**Category 2 - Initial technical evidence**	Original model/method study with internal training/test or cross-validation, but without the independent and representative validation breadth required for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
176	Fan (2021)	Age estimation	**Category 2 - Initial technical evidence**	Original model/method study with internal training/test or cross-validation, but without the independent and representative validation breadth required for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
177	Guan (2021)	Age estimation	**Category 2 - Initial technical evidence**	Direct postmortem material is relevant, but the design lacks independent or broad robustness validation.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
179	Lemesh (2021)	Age estimation	**Category 2 - Initial technical evidence**	Large internal model-development study without independent or casework validation.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
180	Piniewska-Róg (2021)	Age estimation	**Category 2 - Initial technical evidence**	Original technical, model-development, association, or proof-of-concept study without sufficiently broad independent, forensic-like, or transferability validation for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
181	Pisarek (2021)	Age estimation	**Category 3 - Pre-implementation validation**	Independent marker/model validation supports Category 3.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
182	Schwender (2021)	Age estimation	**Category 3 - Pre-implementation validation**	Independent 46-sample validation set.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
183	So (2021)	Age estimation	**Category 2 - Initial technical evidence**	Original model/method study with internal training/test or cross-validation, but without the independent and representative validation breadth required for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
184	Sukawutthiya (2021)	Age estimation	**Category 3 - Pre-implementation validation**	The ELOVL2 assay included postmortem blood, a validation subset, and low-input/sensitivity assessment.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
185	Thong (2021)	Age estimation	**Category 3 - Pre-implementation validation**	A large blood cohort, model comparison, held-out evaluation, and an experimentally defined bisulfite-input threshold support Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
186	Vidaki (2021)	Age estimation	**Category 3 - Pre-implementation validation**	The male-specific model was tested in additional and external datasets beyond the initial discovery material.	Independent replication, targeted assay development and forensic validation before any casework consideration.

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187	Woźniak (2021)	Age estimation	**Category 3 - Pre-implementation validation**	Multi-tissue held-out testing and analytical sensitivity support Category 3.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
188	Xiao (2021)	Age estimation	**Category 2 - Initial technical evidence**	Original model/method study with internal training/test or cross-validation, forensic relevance mentioned or limited forensic-like material, limited mixture-related assessment, but without the independent and representative validation breadth required for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
189	Yudianto (2021)	Age estimation	**Category 1 - Exploratory discovery**	The article inconsistently reports 40 versus 30 bite-mark samples; correlation analysis was presented without a reproducibly validated age model. The internal sample-size discrepancy remains unresolved.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
190	Zhang (2021)	Age estimation	**Category 2 - Initial technical evidence**	Original technical, model-development, association, or proof-of-concept study without sufficiently broad independent, forensic-like, or transferability validation for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
191	Aliferi (2022)	Age estimation	**Category 3 - Pre-implementation validation**	Marker selection from large public datasets was followed by in-house MPS validation and minimal-DNA sensitivity assessment.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
193	Correia Dias (2022)	Age estimation	**Category 2 - Initial technical evidence**	Bone and tooth age models were developed from small cohorts using bisulfite Sanger sequencing and multiplex SNaPshot, with internal cross-validation and split-sample testing. The materials are forensically relevant, but no independent external cohort, sensitivity study or inter-laboratory validation was performed. Category 2 is supported.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
194	Freire-Aradas (2022)	Age estimation	**Category 3 - Pre-implementation validation**	Seven-CpG blood models were trained on 895 Spanish samples and evaluated on an independent 152-sample test set, with additional training-size analysis. This supports pre-implementation model validation, but the study did not test forensic stains, low-input material, degradation, mixtures or inter-laboratory reproducibility.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
195	Han (2022)	Age estimation	**Category 3 - Pre-implementation validation**	Held-out validation and bloodstain robustness support Category 3.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
196	Ho Lee (2022)	Age estimation	**Category 2 - Initial technical evidence**	Method adaptation and internal evaluation do not provide sufficient independent validation for Category 3.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
197	Lucknuch (2022)	Age estimation	**Category 2 - Initial technical evidence**	Original technical, model-development, association, or proof-of-concept study without sufficiently broad independent, forensic-like, or transferability validation for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
198	Manco (2022)	Age estimation	**Category 2 - Initial technical evidence**	Original technical, model-development, association, or proof-of-concept study without sufficiently broad independent, forensic-like, or transferability validation for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
199	Mayer (2022)	Age estimation	**Category 2 - Initial technical evidence**	Original technical, model-development, association, or proof-of-concept study without sufficiently broad independent, forensic-like, or transferability validation for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
200	Ogata (2022)	Age estimation	**Category 2 - Initial technical evidence**	Original technical, model-development, association, or proof-of-concept study without sufficiently broad independent, forensic-like, or transferability validation for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
201	Oka (2022)	Age estimation	**Category 2 - Initial technical evidence**	Population-comparison study without a validated forensic prediction model.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
202	Ye (2022)	Age estimation	**Category 3 - Pre-implementation validation**	Training cohort plus blood, fresh-bloodstain and aged-bloodstain validation sets.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.

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203	Carlsen (2023)	Age estimation	**Category 3 - Pre-implementation validation**	Model development and cut-off selection were confined to 161 training samples using repeated 10-fold cross-validation; final performance was then evaluated in a separate 69-sample validation set that was not used for model fitting or hyperparameter selection. This clearly held-out endpoint validation supports Category 3, while external population/laboratory transfer and forensic-trace robustness were not tested.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
204	Cui (2023)	Age estimation	**Category 2 - Initial technical evidence**	Original model/method study with forensic relevance mentioned or limited forensic-like material, but without the independent and representative validation breadth required for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
205	Fleckhaus (2023)	Age estimation	**Category 3 - Pre-implementation validation**	Cross-population transferability testing.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
206	Fokias (2023)	Age estimation	**Category 2 - Initial technical evidence**	Original model/method study with internal training/test or cross-validation, but without the independent and representative validation breadth required for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
207	Fokias (2023)	Age estimation	**Category 2 - Initial technical evidence**	Original model/method study with internal training/test or cross-validation, but without the independent and representative validation breadth required for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
208	Hong (2023)	Sequencing/platform/method development	**Category 2 - Initial technical evidence**	The primary contribution is platform harmonisation, not independent validation of an age endpoint.	Finalise jurisdiction-specific SOPs, reporting language, uncertainty thresholds, proficiency testing and ongoing QA before routine implementation.
210	Jiang (2023)	Age estimation	**Category 3 - Pre-implementation validation**	Training/test model and male-female mixture evaluation.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
212	Onofri (2023)	Age estimation	**Category 2 - Initial technical evidence**	Pilot model with pseudoreplicated technical observations, not independent validation.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
213	Pośpiech (2023)	Sequencing/platform/method development	**Category 2 - Initial technical evidence**	Protocol comparison in only ten blood samples; no endpoint-level external validation.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
214	Refn (2023)	Age estimation	**Category 2 - Initial technical evidence**	Original model/method study with limited sensitivity/low-input assessment, but without the independent and representative validation breadth required for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
215	Varshavsky (2023)	Age estimation	**Category 3 - Pre-implementation validation**	The small-marker machine-learning model was tested across multiple independent datasets and diverse cohorts.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
216	Wang (2023)	Age estimation	**Category 2 - Initial technical evidence**	Original technical, model-development, association, or proof-of-concept study without sufficiently broad independent, forensic-like, or transferability validation for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
217	Xiao (2023)	Age estimation	**Category 3 - Pre-implementation validation**	Independent validation and matrix-specific testing support Category 3.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
218	Yang (2023)	Age estimation	**Category 3 - Pre-implementation validation**	Bloodstain-specific robustness and held-out testing support Category 3.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
219	Er (2024)	Age estimation	**Category 3 - Pre-implementation validation**	Direct robustness testing under simulated forensic conditions supports Category 3.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.

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220	Filoglu (2024)	Age estimation	**Category 2 - Initial technical evidence**	Original model/method study with limited sensitivity/low-input assessment, but without the independent and representative validation breadth required for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
221	Ji (2024)	Age estimation	**Category 3 - Pre-implementation validation**	Training/test sets, sensitivity and male-female mixed bloodstain testing.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
222	Marcante (2024)	Age estimation	**Category 2 - Initial technical evidence**	Original model/method study with internal training/test or cross-validation, forensic relevance mentioned or limited forensic-like material, limited aged/degraded-material assessment, but without the independent and representative validation breadth required for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
223	Noroozi (2024)	Age estimation	**Category 1 - Exploratory discovery**	Nearly 1000 samples were used to compare epigenetic clocks and associations with lifestyle and sociodemographic factors. The study informs confounding and biological ageing, but does not validate a defined crime-scene or casework age-inference workflow.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
224	Pinprasert (2024)	Age estimation	**Category 2 - Initial technical evidence**	Original model/method study with internal training/test or cross-validation, limited aged/degraded-material assessment, limited mixture-related assessment, but without the independent and representative validation breadth required for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
225	Shiga (2024)	Age estimation	**Category 2 - Initial technical evidence**	Internal LOOCV and assay-quality assessment do not constitute pre-implementation forensic validation.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
226	Soedarsono (2024)	Age estimation	**Category 2 - Initial technical evidence**	Original technical, model-development, association, or proof-of-concept study without sufficiently broad independent, forensic-like, or transferability validation for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
227	Yamagishi (2024)	Age estimation	**Category 3 - Pre-implementation validation**	The ELOVL2 interval-age models were tested in independent populations and forensically relevant bloodstain material.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
229	Boullón-Cassau (2025)	Age estimation	**Category 3 - Pre-implementation validation**	Legal-age prediction was evaluated on a large independent twin-based test design with extensive validation analyses.	Independent replication, targeted assay development and forensic validation before any casework consideration.
230	Collins (2025)	Age estimation	**Category 2 - Initial technical evidence**	Single-cohort saliva clock development.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
231	Correia Dias (2025)	Age estimation	**Category 3 - Pre-implementation validation**	Deceased blood and bone cohorts with training/validation splits and forensic-context samples.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
232	Gao (2025)	Age estimation	**Category 3 - Pre-implementation validation**	Training/validation design and bloodstain evaluation; report as mixed-omics, not methylation-only.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
233	Grignani (2025)	Age estimation	**Category 3 - Pre-implementation validation**	A model trained in living donors was applied to 29 identified burnt human remains, directly testing a difficult forensic matrix.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
234	Jung (2025)	Age estimation	**Category 3 - Pre-implementation validation**	Costal-cartilage age prediction used separate training and test sets, low-input evaluation, and additional tissue testing.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
235	Li (2025)	Age estimation	**Category 2 - Initial technical evidence**	Original model/method study with internal training/test or cross-validation, but without the independent and representative validation breadth required for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.

Ref.	Author (year)	Primary application	Category	Validation evidence / rationale	Minimum requirements before implementation
237	Mathew (2025)	Age estimation	**Category 3 - Pre-implementation validation**	The selected CpGs and machine-learning models were evaluated in independent datasets spanning populations and health conditions.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
238	Refn (2025)	Age estimation	**Category 3 - Pre-implementation validation**	Independent evaluation of a published panel plus sensitivity testing.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
239	Sutter (2025)	Age estimation	**Category 3 - Pre-implementation validation**	The established forensic age tool was challenged in 100 cancer patients against 102 healthy controls, providing direct confounder validation.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
240	Verstraeten (2025)	Age estimation	**Category 3 - Pre-implementation validation**	Cross-platform implementation and held-out testing support Category 3.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
241	Wan (2025)	Age estimation	**Category 2 - Initial technical evidence**	Original technical, model-development, association, or proof-of-concept study without sufficiently broad independent, forensic-like, or transferability validation for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
242	Yang (2025)	Age estimation	**Category 3 - Pre-implementation validation**	Postmortem skeletal-muscle samples underwent genome-wide discovery, targeted NGS/SBE validation, and age-model construction.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
243	Zhu (2025)	Age estimation	**Category 3 - Pre-implementation validation**	Independent cohort and multi-centre casework-sample testing support Category 3; the assay was not independently run by multiple laboratories.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
244	Andrejevic (2026)	Age estimation	**Category 3 - Pre-implementation validation**	Held-out and forensic-like testing support Category 3.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
245	Can (2026)	Age estimation	**Category 2 - Initial technical evidence**	Original technical, model-development, association, or proof-of-concept study without sufficiently broad independent, forensic-like, or transferability validation for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
246	Chen (2026)	Age estimation	**Category 3 - Pre-implementation validation**	The multi-tissue model was tested in an independent set of forensically relevant chewed-gum samples.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
247	Fakhr (2026)	Age estimation	**Category 3 - Pre-implementation validation**	The ddPCR assay combined held-out and cross-validation with analytical sensitivity and multiplex-performance testing.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
248	Lee (2026)	Age estimation	**Category 3 - Pre-implementation validation**	Independent and mixture testing support Category 3, although sample numbers are limited.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
249	Liu (2026)	Age estimation	**Category 3 - Pre-implementation validation**	Independent forensic-matrix validation supports Category 3.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
250	Manco (2026)	Age estimation	**Category 2 - Initial technical evidence**	Sixty-two women with overweight or obesity were analysed by ddPCR to develop FHL2-based age models and assess obesity-related error. The work provides initial technical/confounder evidence without external validation.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
251	Oka (2026)	Age estimation	**Category 3 - Pre-implementation validation**	Training and independent test sets in tooth-root material.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
252	Pisarek-Pacek (2026)	Age estimation	**Category 3 - Pre-implementation validation**	Independent and cross-platform validation support Category 3.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.

Ref.	Author (year)	Primary application	Category	Validation evidence / rationale	Minimum requirements before implementation
253	Poggiali (2026)	Age estimation	**Category 2 - Initial technical evidence**	The study demonstrates feasibility but lacks an independent or casework validation phase.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
254	So (2026)	Age estimation	**Category 3 - Pre-implementation validation**	Independent population validation supports Category 3.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
255	Sutter (2026)	Age estimation	**Category 3 - Pre-implementation validation**	Two age tools were compared across three biogeographic populations and three sample types, providing transferability evidence.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
256	Tsutsumi (2026)	Age estimation	**Category 2 - Initial technical evidence**	Original technical, model-development, association, or proof-of-concept study without sufficiently broad independent, forensic-like, or transferability validation for Category 3.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
257	Zhang (2026)	Age estimation	**Category 3 - Pre-implementation validation**	Large methylome screening was followed by a multi-tissue multiplex ddPCR assay and predictive-model evaluation across blood, saliva and buccal samples.	Translate model to validated forensic assay; test forensic-like, degraded, low-template and population-transfer conditions; define uncertainty and thresholds.
258	Zhao (2026)	Age estimation	**Category 3 - Pre-implementation validation**	Held-out testing and broad analytical robustness support Category 3.	Broader external/inter-laboratory validation, defined limits of use, uncertainty reporting, robustness testing and SOP/proficiency framework.
259	Ma (2013)	Body fluid/tissue identification	**Category 1 - Exploratory discovery**	The two-page study discovers six blood-specific tDMRs and reports quantitative differences among blood, saliva, semen and vaginal fluid, but does not validate a reportable assay, thresholds, mixtures or independent reproducibility.	larger independent forensic-like validation; body-fluid specificity across populations and substrates; mixture/low-template/degradation testing; operational interpretation framework
260	Balamurugan (2014)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	Marker/assay development without broader validation.	larger independent forensic-like validation; body-fluid specificity across populations and substrates; mixture/low-template/degradation testing; operational interpretation framework
261	Bartling (2014)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	Original model/method study with limited sensitivity/low-input assessment, but without the independent and representative validation breadth required for Category 3.	larger independent forensic-like validation; body-fluid specificity across populations and substrates; mixture/low-template/degradation testing; operational interpretation framework
262	Park (2014)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	Body-fluid marker discovery/technical confirmation.	larger independent forensic-like validation; body-fluid specificity across populations and substrates; mixture/low-template/degradation testing; operational interpretation framework
263	Antunes (2015)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	Pyrosequencing marker evaluation.	larger independent forensic-like validation; body-fluid specificity across populations and substrates; mixture/low-template/degradation testing; operational interpretation framework
264	Bai (2015)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	Original technical, model-development, association, or proof-of-concept study without sufficiently broad independent, forensic-like, or transferability validation for Category 3.	larger independent forensic-like validation; body-fluid specificity across populations and substrates; mixture/low-template/degradation testing; operational interpretation framework
265	Fu (2015)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	Four-marker assay preliminarily evaluated in 40 samples; no external validation.	larger independent forensic-like validation; body-fluid specificity across populations and substrates; mixture/low-template/degradation testing; operational interpretation framework
266	Taki (2015)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	Salivary cellular/extracellular DNA characterisation; limited endpoint validation.	larger independent forensic-like validation; body-fluid specificity across populations and substrates; mixture/low-template/degradation testing; operational interpretation framework

Ref.	Author (year)	Primary application	Category	Validation evidence / rationale	Minimum requirements before implementation
268	Antunes (2016)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	Single-laboratory HRM method development with limited validation breadth.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
269	Lin (2016)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Developmental validation breadth supports Category 3.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
270	Lin (2016)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Mixture and non-probative sample testing support Category 3.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
271	Watanabe (2016)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Aged stains up to 29 years and multiple body-fluid testing.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
272	Watanabe (2016)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Aged-stain and mixture-oriented testing support Category 3.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
273	Fachet (2017)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Mixture testing and aged stains up to five months provide pre-implementation robustness evidence.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
274	Naue (2018)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	The study directly quantified performance and interpretative limits in minimal-trace DNA conditions.	larger independent forensic-like validation; body-fluid specificity across populations and substrates; mixture/low-template/degradation testing; operational interpretation framework
275	Samsuwan (2018)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	The brain-tissue assay was evaluated in tissues from 108 autopsies, aged samples and minimal-DNA conditions.	larger independent forensic-like validation; body-fluid specificity across populations and substrates; mixture/low-template/degradation testing; operational interpretation framework
276	Fang (2019)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	MicroRNA expression study; it cannot support methylation-specific counts.	larger independent forensic-like validation; body-fluid specificity across populations and substrates; mixture/low-template/degradation testing; operational interpretation framework
277	Gauthier (2019)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	A four-marker bisulfite-pyrosequencing multiplex was developed on 78 body-fluid samples and evaluated on an internal 46-sample test set. The study did not directly test mixtures, low-template input, degradation, casework stains or external transfer; these were identified as future work. Category 2 is therefore appropriate.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
278	Tian (2019)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	Two ARMS-PCR multiplexes targeting four published CpG sites were tested on five samples per body-fluid type. The assay demonstrated marker-specific methylation patterns and capillary-electrophoresis feasibility, but no independent set, mixtures, sensitivity, casework or external validation. Category 2 method-development evidence is appropriate.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
279	Xie (2019)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Reports 80 samples, mixtures, low input and degraded material in a two-page format.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines

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280	Alghanim (2020)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	Marker development in 89 samples; mixtures were discussed, not tested.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
281	Ghai (2020)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Marker panel with casework-oriented and aged/degraded sample evaluation.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
282	Kader (2020)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Body-fluid markers were tested across ethnicity, age and disease strata to evaluate transferability and confounding.	larger independent forensic-like validation; body-fluid specificity across populations and substrates; mixture/low-template/degradation testing; operational interpretation framework
283	Liu (2020)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Broad sensitivity, mixture and case-oriented testing support Category 3.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
284	Tian (2020)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Independent and extensive robustness testing support Category 3.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
285	Watanabe (2020)	Sequencing/platform/method development	**Category 2 - Initial technical evidence**	The main endpoint is extraction-method performance, not validation of a body-fluid classifier.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
286	Xie (2020)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	Preliminary method development without broad validation supports Category 2.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
287	Antunes (2021)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	Bioinformatic discovery and limited HRM confirmation; mixtures/degradation not actually validated.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
288	Doi (2021)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	Single-marker/limited-cohort development does not support Category 3.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
289	Fujimoto (2021)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Extensive mixture evaluation supports Category 3.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
290	Gomaa (2021)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Mixed-fluid crime-scene simulations.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
291	Li (2021)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	112 reference samples, sensitivity and semen-containing mixture deconvolution.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines

Ref.	Author (year)	Primary application	Category	Validation evidence / rationale	Minimum requirements before implementation
292	Liu (2021)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	This is a primary miRNA RT-qPCR classification study, not a DNA-methylation study. Seven algorithms were evaluated on 605 body-fluid samples using repeated random splits, cross-validation and perturbation analyses. Because testing remained internal and no casework, mixture or external validation was performed, Category 2 applies in the transcriptomic/non-coding RNA stratum.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
293	Abouelkeir (2022)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Fresh/aged semen and multiple mixed-fluid groups provide relevant robustness testing.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
294	Huang (2022)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Independent and robustness testing support Category 3.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
295	Li (2022)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Broad validation under relevant conditions supports Category 3.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
296	Lin (2022)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	The co-amplification system was tested on 65 reference samples, sensitivity and female-DNA mixtures, and nine non-probative samples from seven sexual-assault cases. No inter-laboratory implementation evidence is reported.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
297	Watanabe (2022)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Mixture and forensic-stain evaluation support Category 3.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
298	Fang (2023)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Independent new-sample model evaluation and robustness support Category 3.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
299	Fang (2023)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	Internal marker validation and very small held-out fraction without external robustness testing.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
300	Fernandez-Tejero (2023)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	Skin/sweat marker and HRM assay development without external or broad forensic validation.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
301	Konrad (2023)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	Nasal-marker development with incomplete discrimination and no mixture validation.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
302	Konrad (2023)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	Workflow/marker development without sufficient independent or inter-laboratory validation.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
303	Rhodes (2023)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	A 355-sample dataset, ten-fold cross-validation, unknown samples, biological-cycle testing and compromised samples support pre-implementation evidence. Mixed-sample classification remains untested.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines

Ref.	Author (year)	Primary application	Category	Validation evidence / rationale	Minimum requirements before implementation
304	Silva (2023)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	Original model/method study with forensic relevance mentioned or limited forensic-like material, but without the independent and representative validation breadth required for Category 3.	larger independent forensic-like validation; body-fluid specificity across populations and substrates; mixture/low-template/degradation testing; operational interpretation framework
305	Wang (2023)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Large independent mixture test sets support Category 3.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
306	Altmeyer (2024)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	Only six samples per body fluid were used for marker confirmation and clustering. No validated prediction model, mixture study or inter-laboratory exercise was performed.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
307	Ghemrawi (2024)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	Original model/method study with forensic relevance mentioned or limited forensic-like material, limited mixture-related assessment, but without the independent and representative validation breadth required for Category 3.	larger independent forensic-like validation; body-fluid specificity across populations and substrates; mixture/low-template/degradation testing; operational interpretation framework
308	Kim (2024)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Cross-platform and robustness assessment support Category 3.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
309	Li (2024)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Developmental validation breadth supports Category 3.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
310	Rothe (2024)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Robust validation supports Category 3; archived GEDNAP samples do not by themselves create an inter-laboratory exercise.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
311	Tang (2024)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Extensive mixture and donor-linkage testing supports Category 3.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
312	Balamurugan (2025)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	Small marker-development study lacks broad validation.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
313	Hsu (2025)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Condition-specific robustness supports Category 3.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
314	Li (2025)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Broad single-laboratory validation supports Category 3.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
315	Mizrachi (2025)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Complex mixture deconvolution provides pre-implementation evidence, although external validation is absent.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines

Ref.	Author (year)	Primary application	Category	Validation evidence / rationale	Minimum requirements before implementation
316	Wen (2025)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Direct mixture testing supports Category 3.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
317	Zhao (2025)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	Marker screening and internal test split without external/forensic robustness validation.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
318	Konrad (2026)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	453 samples and blinded validation of additional age-sensitive workflow markers.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
319	Schmelzer (2026)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Independent validation and extensive mixture testing support Category 3.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
320	Schmelzer (2026)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	The study developed bisulfite-MPS and FDSTools workflows linking STR/iSNP alleles to methylation in seven body fluids and one 1:1 semen–saliva mixture. Known tDMPs were confirmed, but STR-flanking sites lacked exclusive discrimination and further unbalanced, low-template and degraded testing was deferred. Category 2 technical feasibility is supported.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
321	Singh (2026)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	Original model/method study with limited sensitivity/low-input assessment, forensic relevance mentioned or limited forensic-like material, but without the independent and representative validation breadth required for Category 3.	larger independent forensic-like validation; body-fluid specificity across populations and substrates; mixture/low-template/degradation testing; operational interpretation framework
322	Tang (2026)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Relevant field-oriented robustness supports Category 3.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
323	Xu (2026)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	The 5-plex ddPCR/random-forest method was developed from 115 samples, then tested on 25 additional donor samples, 45 substrate samples, 15 six-year aged samples and sensitivity series. This supports pre-implementation evidence in a single laboratory. It does not test mixed body fluids or inter-laboratory reproducibility, and it combines miRNA with bacterial 16S rDNA rather than DNA methylation.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
324	Zhang (2018)	Body fluid/tissue identification	**Category 3 - Pre-implementation validation**	Robust transcriptomic testing supports Category 3 in a separate stratum.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
325	Liu (2019)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	Marker-characterisation evidence is technical rather than pre-implementation validation.	external/inter-laboratory validation; predefined thresholds/likelihood reporting; degraded, low-template and mixture limits; workflow compatibility with STR/MPS pipelines
327	Li (2026)	Body fluid/tissue identification	**Category 2 - Initial technical evidence**	RT-qPCR tsRNA assay, not DNA methylation.	larger independent forensic-like validation; body-fluid specificity across populations and substrates; mixture/low-template/degradation testing; operational interpretation framework
328	Xu (2012)	Sequencing/platform/method development	**Category 2 - Initial technical evidence**	Bisulfite sequencing method for microvolume dried blood spots.	application-specific forensic validation on realistic samples; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation

Ref.	Author (year)	Primary application	Category	Validation evidence / rationale	Minimum requirements before implementation
329	Zhang (2013)	Sequencing/platform/method development	**Category 2 - Initial technical evidence**	Five imprinted-gene SNPs were analysed after bisulfite treatment in pooled samples, 133 heterozygous individuals and selected trios. The work demonstrates technical feasibility, not endpoint implementation.	application-specific forensic validation on realistic samples; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
336	Park (2017)	Monozygotic twin differentiation	**Category 1 - Exploratory discovery**	Genome-wide 450K profiling of 12 monozygotic-twin pairs identified pair-specific differentially methylated CpGs and six recurrent candidates present in only one-third of pairs. No targeted assay, independent cohort or forensic trace testing followed. The authors explicitly called for technical and large-cohort validation, supporting Category 1 discovery evidence.	larger longitudinal twin cohorts, reproducibility and operational thresholds; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
337	Freire-Aradas (2018)	Age estimation	**Category 3 - Pre-implementation validation**	Independent young-donor test set supports pre-implementation evidence.	Robustness, low-template/degraded/mixed-sample testing, and uncertainty reporting are required before casework implementation.
340	Park (2018)	Sequencing/platform/method development	**Category 2 - Initial technical evidence**	Primer-design/software method with experimental validation.	application-specific forensic validation on realistic samples; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
344	Fang (2019)	Monozygotic twin differentiation	**Category 1 - Exploratory discovery**	MicroRNA markers, not DNA methylation.	larger longitudinal twin cohorts, reproducibility and operational thresholds; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
347	Richards (2019)	Sequencing/platform/method development	**Category 2 - Initial technical evidence**	The exact full article reports original empirical data from 28 donors aged 22–62 years, including five monozygotic-twin pairs. Four bisulfite-converted targeted MPS assays were developed for blood and semen age estimation and buccal-sample twin differentiation. Age models were assessed by leave-one-out cross-validation only; no independent cohort, external laboratory, degraded-trace, mixture, or casework validation was reported. The study therefore supports Category 2 method development, not Category 3.	Larger independent cohorts; degraded/trace and mixture testing; external/inter-laboratory transfer; reporting thresholds and uncertainty.
348	Xiao (2019)	Monozygotic twin differentiation	**Category 1 - Exploratory discovery**	Descriptive miRNA twin-profile study.	larger longitudinal twin cohorts, reproducibility and operational thresholds; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
354	Cho (2021)	Other donor-characteristic inference	**Category 2 - Initial technical evidence**	Seven hundred Korean participants were divided into 490 training and 210 test samples. The methylation/genetic BMI models showed limited accuracy, providing initial technical evidence rather than implementation support.	confounding control, ethical/legal governance and validated individual-level interpretive limits; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
356	Hao (2021)	Age estimation	**Category 3 - Pre-implementation validation**	A ten-CpG hair-follicle SNaPshot model was trained on 90 samples and tested on a randomized 40-sample holdout. The study also assessed inputs down to 0.2 ng converted DNA, single-hair STR plus methylation analysis, species specificity, hair color and body site. This supports Category 3 age-estimation evidence, but not external validation.	application-specific forensic validation on realistic samples; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
358	Naue (2021)	Age estimation	**Category 2 - Initial technical evidence**	Pilot study of age-associated methylation in plucked hair using massively parallel sequencing. The evaluation remained internal and supports Category 2.	Independent validation in larger hair cohorts; assessment of root condition, storage, low-template and degraded samples; calibration and uncertainty reporting.
359	Planterose Jiménez (2021)	Monozygotic twin differentiation	**Category 1 - Exploratory discovery**	Epigenome-wide descriptive twin variation.	larger longitudinal twin cohorts, reproducibility and operational thresholds; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
360	Romanos (2021)	Monozygotic twin differentiation	**Category 2 - Initial technical evidence**	Small targeted twin-discrimination study.	larger longitudinal twin cohorts, reproducibility and operational thresholds; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation

Ref.	Author (year)	Primary application	Category	Validation evidence / rationale	Minimum requirements before implementation
364	Becker (2022)	Age estimation	**Category 1 - Exploratory discovery**	Population methylation comparison; no forensic predictor.	confounding control, ethical/legal governance and validated individual-level interpretive limits; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
366	Christiansen (2022)	Sequencing/platform/method development	**Category 2 - Initial technical evidence**	The study assessed EPIC-array reproducibility across low DNA inputs and showed reduced reproducibility at the lowest quantities. This provides initial technical evidence for platform performance but not external forensic validation, supporting Category 2.	Independent and inter-laboratory replication; predefined quality-control thresholds; evaluation across relevant low-template, degraded and mixed forensic samples; reporting limits before implementation.
368	Konrad (2022)	Sequencing/platform/method development	**Category 1 - Exploratory discovery**	Method pitfall/artefact paper.	application-specific forensic validation on realistic samples; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
371	Wang (2022)	Age estimation	**Category 3 - Pre-implementation validation**	The study used circRNA sequencing, public miRNA-expression datasets, RT-qPCR validation, and separate screening, validation, modelling, and held-out test sets. The absence of external or inter-laboratory validation limits the evidence to Category 3.	application-specific forensic validation on realistic samples; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
374	Fang (2023)	Age estimation	**Category 3 - Pre-implementation validation**	The study combined piRNA and miRNA markers in 240 blood samples, with separate training and validation sets, to develop an age-prediction model for aged blood. The absence of inter-laboratory validation limits the evidence to Category 3.	application-specific forensic validation on realistic samples; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
376	Kim (2023)	Monozygotic twin differentiation	**Category 2 - Initial technical evidence**	Targeted twin methylome profiling.	larger longitudinal twin cohorts, reproducibility and operational thresholds; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
378	Shabalala (2023)	Sequencing/platform/method development	**Category 1 - Exploratory discovery**	Population variation study, not endpoint validation.	application-specific forensic validation on realistic samples; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
383	El-Hossary (2024)	Monozygotic twin differentiation	**Category 1 - Exploratory discovery**	Single monozygotic-triplet exploratory study.	larger longitudinal twin cohorts, reproducibility and operational thresholds; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
385	Oscandar (2024)	Age estimation	**Category 1 - Exploratory discovery**	Three freshly extracted teeth were assessed by CBCT and ELOVL2 pyrosequencing using published equations. Methylation values were mostly 0–3%, the sample age span was narrow, and the authors acknowledged invalid or unverified regression transfer and no definitive accuracy conclusion. This is Category 1 preliminary evidence.	Robustness, low-template/degraded/mixed-sample testing, and uncertainty reporting are required before casework implementation.
388	Al Qaderi (2025)	Age estimation	**Category 2 - Initial technical evidence**	The study reports a CpG-based machine-learning age model with internal technical evaluation but no independent external or casework validation, supporting Category 2.	Independent validation; testing on low-template, degraded and mixed samples; calibration and uncertainty reporting before casework implementation.
393	Huang (2025)	Other donor-characteristic inference	**Category 2 - Initial technical evidence**	Brain tissues from 53 deceased individuals were used to derive an alcohol-intake methylation index and distinguish ingestion from postmortem fermentation. This is initial technical evidence without external validation.	confounding control, ethical/legal governance and validated individual-level interpretive limits; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
395	Lu (2025)	Age estimation	**Category 2 - Initial technical evidence**	The study is original and model-based but rests on internal development/testing; it supports Category 2 rather than Category 3.	application-specific forensic validation on realistic samples; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
398	Poggiali (2025)	Sequencing/platform/method development	**Category 2 - Initial technical evidence**	Controlled low-quality/low-input EPIC platform evaluation.	application-specific forensic validation on realistic samples; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation

Ref.	Author (year)	Primary application	Category	Validation evidence / rationale	Minimum requirements before implementation
399	Qian (2025)	Age estimation	**Category 3 - Pre-implementation validation**	The 10-CpG age model was tested in an independent 648-sample Chinese set and a multi-ancestry public dataset, supporting Category 3 while showing reduced accuracy across populations.	External and inter-laboratory validation across populations, tissues and age ranges; casework-like low-template, degraded and mixed-sample testing; calibration and uncertainty reporting.
400	Simons (2025)	Sequencing/platform/method development	**Category 2 - Initial technical evidence**	The smMIP study developed and optimised a targeted methylation approach but found substantial probe-dependent coverage and limited specificity and uniformity. It provides initial method-development evidence and supports Category 2.	Improved probe specificity and uniformity; independent replication; validation across relevant DNA inputs and forensic sample conditions; predefined quality-control and reporting limits.
402	Wang (2025)	Monozygotic twin differentiation	**Category 2 - Initial technical evidence**	Small twin cohorts support technical evidence but not Category 3 validation.	larger longitudinal twin cohorts, reproducibility and operational thresholds; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
404	Wulandari (2025)	Age estimation	**Category 1 - Exploratory discovery**	Two prehistoric Pawon teeth were destructively analysed by ELOVL2 pyrosequencing after CBCT. DNA was low quantity, methylation was 0% at every CpG, no replicate was possible, and a modern regression was applied with substantial methodological uncertainty. The study is an archaeological case application and supports Category 1 only.	application-specific forensic validation on realistic samples; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
407	Colloca (2026)	Other donor-characteristic inference	**Category 2 - Initial technical evidence**	Italian age/smoking replication with internal cross-validation.	confounding control, ethical/legal governance and validated individual-level interpretive limits; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
410	Marszałek (2026)	Other donor-characteristic inference	**Category 3 - Pre-implementation validation**	Independent 112-sample validation of published BMI models.	confounding control, ethical/legal governance and validated individual-level interpretive limits; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
411	Sacco (2026)	Sequencing/platform/method development	**Category 2 - Initial technical evidence**	Method-development study using fragment termini to infer methylation.	application-specific forensic validation on realistic samples; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
432	Wang (2022)	Age estimation	**Category 2 - Initial technical evidence**	The source supports original circRNA age-model development, but the validation structure remains internal and does not support Category 3.	application-specific forensic validation on realistic samples; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
436	Hänggi (2025)	Age estimation	**Category 2 - Initial technical evidence**	This is original mRNA age-estimation work with internal technical/model evaluation, but it is not DNA-methylation evidence and does not reach Category 3.	application-specific forensic validation on realistic samples; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
437	Tian (2025)	Monozygotic twin differentiation	**Category 3 - Pre-implementation validation**	The source describes more than ordinary internal model development: it includes validation in additional MZT material plus bloodstain and stability testing.	larger longitudinal twin cohorts, reproducibility and operational thresholds; robustness, low-template/degraded/mixed-sample testing and reporting uncertainty before casework implementation
438	Chen (2026)	Age estimation	**Category 3 - Pre-implementation validation**	The lncRNA study enrolled 127 participants in the training cohort and 154 in a separate test cohort; four training-cohort outliers were removed before subsequent feature selection/model development. The test cohort was used during model development and parameter optimisation. Final models were then evaluated in two independently sourced public cohorts (GSE124326 and GSE177044). However, cross-dataset ComBat correction incorporated known chronological age as a biological covariate. The authors explicitly state that the resulting external accuracy represents an idealized evaluation scenario because age would be unavailable in real forensic prediction. The external cohorts therefore support Category 3 as external-cohort evaluation beyond internal model development, but not independent validation of the entire prospective prediction pipeline. Absence of laboratory transfer, inter-laboratory validation and representative forensic-trace robustness keeps the study below C4.	application-specific forensic validation on realistic samples; assay/laboratory transfer; robustness, low-template/degraded/mixed-sample testing; uncertainty and reporting limits before casework implementation

Supplementary Table S5. Evidence distributions and report accounting

S5A. Validation Category distribution by primary application (n = 322)

Primary application	n	Category 1	Category 2	Category 3	Category 4	Category 5
Age estimation	177	7	75	88	7	0
Body fluid/tissue identification	92	1	33	55	3	0
Monozygotic twin differentiation	21	9	8	4	0	0
Sequencing/platform/method development	20	2	17	1	0	0
Other donor-characteristic inference	12	0	6	6	0	0
Overall qualifying empirical evidence	322	19	139	154	10	0

S5B. Molecular-stratum distribution among empirical primary studies (n = 322)

Molecular stratum	n	%
DNA methylation	288	89.4%
Mixed molecular	12	3.7%
Transcriptomic/non-coding RNA	22	6.8%

S5C. Study-level evidence roles (n = 429)

Evidence role	n
Empirical primary	322
Contextual	16
Background/secondary	69
Comparator	12
Non-human	3
Excluded	7
Total study-level register	429

The 7 excluded and 3 non-human records are intentionally cross-listed in Tables S2 and S3 to document their final study-level roles; they do not contribute to evidence-map or empirical totals.

Supplementary Table S5 (continued)

S5D. Cross-cutting descriptive tags among empirical primary studies (non-additive)

Cross-cutting tag	n	Category 1	Category 2	Category 3	Category 4	Category 5
Bioinformatics/machine learning and interpretation	165	4	74	80	7	0
Validation/forensic implementation evidence	85	4	24	54	3	0

Cross-cutting tag counts are non-additive and must not be summed to the empirical denominator.

S5E. Report-level accounting

Disposition	n
Full-text reports assessed	596
Included in evidence map	338
Empirical primary studies	322
Contextual records	16
Retained outside the evidence map	143
Represented in S2 (background/secondary + comparators)	81
Listed separately in S8	62
Excluded/non-qualifying full-text reports	115

S5F. Empirical primary application by molecular stratum (n = 322)

Mutually exclusive dominant primary applications and molecular strata. These counts describe the retrieved methylation-centred corpus; transcriptomic/non-coding RNA records were selectively captured without a dedicated RNA search block.

Dominant primary application	DNA methylation	Mixed molecular	Transcriptomic/non-coding RNA	Total
Age estimation	168	2	7	177
Body fluid/tissue identification	77	5	10	92
Monozygotic twin differentiation	16	0	5	21
Sequencing/platform/method development	16	4	0	20
Other donor-characteristic inference	11	1	0	12
Total	288	12	22	322

Supplementary Table S6. Primary discrimination principles, methodological tags, and readout/platform frequencies

S6A. Primary discrimination principle among identifiable methylation workflows (n = 272)

Principle	n	%
Chemical conversion (predominantly bisulfite)	243	89.3%
Methylation-sensitive or methylation-dependent restriction digestion	18	6.6%
Enzymatic conversion	1	0.4%
Direct native-DNA methylation detection	3	1.1%
Affinity/enrichment-based methylation capture	1	0.4%
Native-DNA indirect methylation inference (fragmentomics)	1	0.4%
Hybrid/comparative multiple principles	5	1.8%

S6B. Analytical-workflow status among empirical primary studies (n = 322)

Workflow status	n	%
Identifiable methylation workflow	272	84.5%
Non-methylation study	23	7.1%
Computational reuse/no new assay	26	8.1%
Unresolved analytical workflow	1	0.3%

S6C. Non-additive methylation-method tags (n = 322)

Methodological tag	n	%
Chemical conversion	248	77.0%
MSRE	19	5.9%
Direct native-DNA detection	3	0.9%
Enzymatic conversion	3	0.9%
Affinity/enrichment	1	0.3%
MDRE	8	2.5%
Native-DNA fragmentomics	1	0.3%

S6D. Non-additive readout/platform tags (n = 322)

Readout / platform	n	%
MPS/NGS/targeted sequencing	61	18.9%
Methylation microarray	44	13.7%
Pyrosequencing	80	24.8%
SNaPshot/SBE-capillary electrophoresis	59	18.3%
qPCR/ddPCR/MSP/HRM	66	20.5%
Capillary electrophoresis/fragment analysis	98	30.4%
MassARRAY/Agena EpiTYPER	14	4.3%
Other expression/readout or not reported	36	11.2%

Readout / platform	n	%
Nanopore/direct single-molecule	3	0.9%
Computational/public-data modelling	104	32.3%
Lateral-flow/dipstick readout	1	0.3%

MSRE and MDRE are restriction-digestion approaches and are not coded as enzymatic conversion. Method and readout/platform tags are non-additive. Quantification-only qPCR, methods merely cited, and reused arrays/sequencing datasets are not counted as generated platforms; reused/public-data analyses are coded only in their dedicated tag. Zeng 2026 remains unresolved and is not assigned a definitive analytical principle or readout/platform.

Abbreviations: MSRE, methylation-sensitive restriction enzyme; MDRE, methylation-dependent restriction enzyme; MPS/NGS, massively parallel/next-generation sequencing; SBE, single-base extension; qPCR, quantitative PCR; ddPCR, droplet digital PCR; MSP, methylation-specific PCR; HRM, high-resolution melting.

Supplementary Table S7. Study-level technology coding for empirical primary studies (n = 322)

Ref.	Author (year)	Primary application	Primary discrimination principle	Non-additive methodological tags	Non-additive readout/platform tags
6	Koch (2011)	Age estimation	Computational reuse of existing methylation data — assay not performed/reported	Computational/public-data modelling	Computational/public-data modelling
7	Huang (2015)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
8	Zbieć-Piekarska (2015)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
9	Pfeifer (2020)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
10	Heidegger (2022)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; Capillary electrophoresis/fragment analysis; Other expression/readout or not reported
11	Frumkin (2011)	Body fluid/tissue identification	Methylation-sensitive or methylation-dependent restriction digestion	MSRE	Capillary electrophoresis/fragment analysis; Computational/public-data modelling
12	Holtkötter (2017)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
13	Vidaki (2017)	Monozygotic twin differentiation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray; qPCR/ddPCR/MSP/HRM
14	Li (2013)	Monozygotic twin differentiation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray; Capillary electrophoresis/fragment analysis
15	Maas (2019)	Other donor-characteristic inference	Computational reuse of existing methylation data — assay not performed/reported	Computational/public-data modelling	Computational/public-data modelling
16	Vidaki (2023)	Other donor-characteristic inference	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing
17	Choi (2014)	Body fluid/tissue identification	Methylation-sensitive or methylation-dependent restriction digestion	MSRE	Capillary electrophoresis/fragment analysis
18	Watanabe (2018)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing; qPCR/ddPCR/MSP/HRM; Other expression/readout or not reported
19	de Bruin (2025)	Sequencing/platform/method development	Direct native-DNA methylation detection	Direct native-DNA detection	Methylation microarray; Nanopore/direct single-molecule
32	Kampmann (2024)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
33	Heidegger (2025)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing
34	Onofri (2025)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
35	Lee (2022)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
36	Bocklandt (2011)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray; Pyrosequencing; MassARRAY/Agena EpiTYPER
37	Bekaert (2015)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
38	Freire-Aradas (2016)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MassARRAY/Agena EpiTYPER; Computational/public-data modelling
39	Aliferi (2018)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; Computational/public-data modelling
40	Jung (2019)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing; SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
41	Xu (2015)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray; MassARRAY/Agena EpiTYPER
42	Cho (2017)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Other expression/readout or not reported

Ref.	Author (year)	Primary application	Primary discrimination principle	Non-additive methodological tags	Non-additive readout/platform tags
43	Vidaki (2017)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; Computational/public-data modelling
44	Lee (2018)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
45	Peng (2019)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MassARRAY/Agena EpiTYPER; Computational/public-data modelling
46	Dias (2020)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
47	Correia Dias (2020)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Capillary electrophoresis/fragment analysis; Other expression/readout or not reported; Computational/public-data modelling
48	Fleckhaus (2020)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
49	Yi (2015)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MassARRAY/Agena EpiTYPER
50	Park (2016)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing; Computational/public-data modelling
51	Hamano (2017)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM
52	Liu (2022)	Body fluid/tissue identification	Methylation-sensitive or methylation-dependent restriction digestion	MSRE; MDRE	Capillary electrophoresis/fragment analysis
53	Kim (2024)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis; Computational/public-data modelling
54	Jung (2016)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
55	Madi (2012)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
56	An (2013)	Body fluid/tissue identification	Methylation-sensitive or methylation-dependent restriction digestion	MSRE	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis; Other expression/readout or not reported
57	Lee (2016)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray; SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis; Computational/public-data modelling
58	Lee (2015)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray; SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis; Other expression/readout or not reported
59	Forat (2016)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; Methylation microarray; SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis; Other expression/readout or not reported
60	Vidaki (2017)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
61	Hanson (2014)	Body fluid/tissue identification	Non-methylation empirical study	RNA expression	qPCR/ddPCR/MSP/HRM
62	Antunes (2016)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
63	Dorum (2019)	Body fluid/tissue identification	Non-methylation empirical study	RNA expression	MPS/NGS/targeted sequencing
64	Larue (2013)	Body fluid/tissue identification	Methylation-sensitive or methylation-dependent restriction digestion	MSRE	Capillary electrophoresis/fragment analysis
65	Wasserstrom (2013)	Body fluid/tissue identification	Methylation-sensitive or methylation-dependent restriction digestion	MSRE	Capillary electrophoresis/fragment analysis

Ref.	Author (year)	Primary application	Primary discrimination principle	Non-additive methodological tags	Non-additive readout/platform tags
66	Silva (2016)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing; Capillary electrophoresis/fragment analysis
67	Li (2020)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
68	Foox (2021)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing
69	Sutter (2026)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; Computational/public-data modelling
70	Choung (2021)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
71	Lee (2026)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray; SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
73	Bilinsky (2025)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Capillary electrophoresis/fragment analysis; Computational/public-data modelling
78	Stewart (2015)	Monozygotic twin differentiation	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM
79	Xu (2015)	Monozygotic twin differentiation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
80	Du (2015)	Monozygotic twin differentiation	Affinity/enrichment-based methylation capture	Affinity/enrichment	MPS/NGS/targeted sequencing; qPCR/ddPCR/MSP/HRM
81	Zhang (2015)	Monozygotic twin differentiation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray
82	Vidaki (2018)	Monozygotic twin differentiation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray; qPCR/ddPCR/MSP/HRM
83	Marqueta-Gracia (2018)	Monozygotic twin differentiation	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM
84	Wang (2024)	Monozygotic twin differentiation	Non-methylation empirical study	RNA expression	MPS/NGS/targeted sequencing; qPCR/ddPCR/MSP/HRM
85	Cho (2025)	Monozygotic twin differentiation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray; Pyrosequencing
86	Zeng (2026)	Monozygotic twin differentiation	UNRESOLVED — analytical principle/readout conflict	Unresolved	Not assigned - unresolved workflow
87	Wen (2022)	Other donor-characteristic inference	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
88	Ambroa-Conde (2024)	Other donor-characteristic inference	Computational reuse of existing methylation data — assay not performed/reported	Computational/public-data modelling	Computational/public-data modelling
90	Llobet (2023)	Other donor-characteristic inference	Computational reuse of existing methylation data — assay not performed/reported	Computational/public-data modelling	Computational/public-data modelling
91	Pośpiech (2024)	Other donor-characteristic inference	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray
92	Pośpiech (2025)	Other donor-characteristic inference	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray
93	Wang (2024)	Other donor-characteristic inference	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; Computational/public-data modelling
94	Naue (2018)	Sequencing/platform/method development	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; Other expression/readout or not reported
95	Di Lena (2021)	Sequencing/platform/method development	Computational reuse of existing methylation data — assay not performed/reported	Computational/public-data modelling	Computational/public-data modelling
96	Simons (2025)	Sequencing/platform/method development	Hybrid/comparative multiple principles	Chemical conversion; Enzymatic conversion	qPCR/ddPCR/MSP/HRM
97	Turiello (2023)	Sequencing/platform/method development	Hybrid/comparative multiple principles	Chemical conversion; Enzymatic conversion	Pyrosequencing; qPCR/ddPCR/MSP/HRM
98	Dias (2024)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM

Ref.	Author (year)	Primary application	Primary discrimination principle	Non-additive methodological tags	Non-additive readout/platform tags
99	So (2024)	Sequencing/platform/method development	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
100	Poussard (2023)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
101	Lee (2025)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; Methylation microarray
103	Sarac (2017)	Age estimation	Computational reuse of existing methylation data — assay not performed/reported	Computational/public-data modelling	Computational/public-data modelling
104	Fang (2020)	Age estimation	Non-methylation empirical study	RNA expression	MPS/NGS/targeted sequencing; qPCR/ddPCR/MSP/HRM; Computational/public-data modelling
107	Li (2011)	Monozygotic twin differentiation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray; Capillary electrophoresis/fragment analysis
108	Lee (2012)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM; Other expression/readout or not reported
109	Weidner (2014)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing; Computational/public-data modelling
110	Vidaki (2016)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
111	Lee (2020)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray; SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
112	Anaya (2021)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing; Computational/public-data modelling
113	Koop (2021)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
114	Ambroa-Conde (2022)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
116	Jung (2024)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing
117	Paparazzo (2025)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray; SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
118	Sutter (2025)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis; Computational/public-data modelling
119	Beentjes (2026)	Sequencing/platform/method development	Direct native-DNA methylation detection	Direct native-DNA detection	Methylation microarray; Nanopore/direct single-molecule
120	Tiras (2026)	Age estimation	Direct native-DNA methylation detection	Direct native-DNA detection	Nanopore/direct single-molecule; Computational/public-data modelling
121	Park (2026)	Body fluid/tissue identification	Enzymatic conversion	Enzymatic conversion	MPS/NGS/targeted sequencing; Methylation microarray; Computational/public-data modelling
122	Freire-Aradas (2023)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing
123	Watanabe (2023)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM; Capillary electrophoresis/fragment analysis
124	Chen (2025)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
125	Yi (2014)	Age estimation	Methylation-sensitive or methylation-dependent restriction digestion	Chemical conversion; MSRE	MassARRAY/Agena EpiTYPER; Other expression/readout or not reported; Computational/public-data modelling
126	Bekaert (2015)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing; Computational/public-data modelling
127	Huang (2015)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing; Computational/public-data modelling

Ref.	Author (year)	Primary application	Primary discrimination principle	Non-additive methodological tags	Non-additive readout/platform tags
128	Lee (2015)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis; Computational/public-data modelling
129	Silva (2015)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
130	Zbieć-Piekarska (2015)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
131	Giuliani (2016)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MassARRAY/Agena EpiTYPER
132	Hamano (2016)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM
133	Mawlood (2016)	Age estimation	Methylation-sensitive or methylation-dependent restriction digestion	MSRE; MDRE	qPCR/ddPCR/MSP/HRM
134	Zubakov (2016)	Age estimation	Hybrid/comparative multiple principles	Differential methylation hybridisation; Chemical conversion	Methylation microarray; Other expression/readout or not reported; Computational/public-data modelling
135	Alghanim (2017)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
136	Alsaleh (2017)	Age estimation	Computational reuse of existing methylation data — assay not performed/reported	Computational/public-data modelling	Computational/public-data modelling
137	Fleckhaus (2017)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
139	Hong (2017)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray; SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
140	Li (2017)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
141	Naue (2017)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; Computational/public-data modelling
142	Thong (2017)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
143	Feng (2018)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing; MassARRAY/Agena EpiTYPER
145	Horvath (2018)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray; Computational/public-data modelling
146	Shi (2018)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray; qPCR/ddPCR/MSP/HRM
147	Smeers (2018)	Age estimation	Computational reuse of existing methylation data — assay not performed/reported	Computational/public-data modelling	Computational/public-data modelling
148	Spólnicka (2018)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing; Computational/public-data modelling
149	Alsaleh (2019)	Age estimation	Computational reuse of existing methylation data — assay not performed/reported	Computational/public-data modelling	Computational/public-data modelling
151	Hong (2019)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; Computational/public-data modelling
152	Khan (2019)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Other expression/readout or not reported; Computational/public-data modelling
153	Li (2019)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MassARRAY/Agena EpiTYPER
156	Xie (2019)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
157	Xin (2019)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM; Other expression/readout or not reported
160	Correia Dias (2020)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Capillary electrophoresis/fragment analysis; Other expression/readout or not reported

Ref.	Author (year)	Primary application	Primary discrimination principle	Non-additive methodological tags	Non-additive readout/platform tags
161	Freire-Aradas (2020)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; Pyrosequencing; SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis; MassARRAY/Agena EpiTYPER; Computational/public-data modelling
162	Gopalan (2019)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray; Computational/public-data modelling
163	Heidegger (2020)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; Capillary electrophoresis/fragment analysis; Other expression/readout or not reported
164	Karir (2020)	Age estimation	Computational reuse of existing methylation data — assay not performed/reported	Computational/public-data modelling	Computational/public-data modelling
165	Kondo (2020)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM
166	Lau (2020)	Age estimation	Computational reuse of existing methylation data — assay not performed/reported	Computational/public-data modelling	Computational/public-data modelling
167	Montesanto (2020)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing; MassARRAY/Agena EpiTYPER
168	Márquez-Ruiz (2020)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing; qPCR/ddPCR/MSP/HRM
169	Pan (2020)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
170	Wei (2020)	Age estimation	Computational reuse of existing methylation data — assay not performed/reported	Computational/public-data modelling	Computational/public-data modelling
171	Yudianto (2020)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Other expression/readout or not reported
172	Al-Ghanmy (2021)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing; Computational/public-data modelling
173	Amiri Roudbar (2021)	Age estimation	Computational reuse of existing methylation data — assay not performed/reported	Computational/public-data modelling	Computational/public-data modelling
174	Zapico (2021)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
175	Correia Dias (2021)	Age estimation	Computational reuse of existing methylation data — assay not performed/reported	Computational/public-data modelling	Computational/public-data modelling
176	Fan (2021)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing; Computational/public-data modelling
177	Guan (2021)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Computational/public-data modelling
179	Lemesh (2021)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis; Computational/public-data modelling
180	Piniewska-Róg (2021)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing
181	Pisarek (2021)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; Methylation microarray; Pyrosequencing; Computational/public-data modelling
182	Schwender (2021)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing; SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis; Computational/public-data modelling
183	So (2021)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
184	Sukawutthiya (2021)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
185	Thong (2021)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing

Ref.	Author (year)	Primary application	Primary discrimination principle	Non-additive methodological tags	Non-additive readout/platform tags
186	Vidaki (2021)	Age estimation	Computational reuse of existing methylation data — assay not performed/reported	Computational/public-data modelling	Computational/public-data modelling
187	Woźniak (2021)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; Capillary electrophoresis/fragment analysis; Other expression/readout or not reported
188	Xiao (2021)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray; Pyrosequencing
189	Yudianto (2021)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Other expression/readout or not reported
190	Zhang (2021)	Age estimation	Computational reuse of existing methylation data — assay not performed/reported	Computational/public-data modelling	Computational/public-data modelling
191	Aliferi (2022)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing
193	Correia Dias (2022)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis; Other expression/readout or not reported
194	Freire-Aradas (2022)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MassARRAY/Agena EpiTYPER
195	Han (2022)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
196	Ho Lee (2022)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM
197	Lucknuch (2022)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
198	Manco (2022)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM
199	Mayer (2022)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
200	Ogata (2022)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM
201	Oka (2022)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM
202	Ye (2022)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis; Computational/public-data modelling
203	Carlsen (2023)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
204	Cui (2023)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM
205	Fleckhaus (2023)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
206	Fokias (2023)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
207	Fokias (2023)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
208	Hong (2023)	Sequencing/platform/method development	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
210	Jiang (2023)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis; Computational/public-data modelling
212	Onofri (2023)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
213	Pośpiech (2023)	Sequencing/platform/method development	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; Methylation microarray
214	Refn (2023)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray

Ref.	Author (year)	Primary application	Primary discrimination principle	Non-additive methodological tags	Non-additive readout/platform tags
215	Varshavsky (2023)	Age estimation	Computational reuse of existing methylation data — assay not performed/reported	Computational/public-data modelling	Computational/public-data modelling
216	Wang (2023)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; Pyrosequencing
217	Xiao (2023)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis; Computational/public-data modelling
218	Yang (2023)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
219	Er (2024)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
220	Filoglu (2024)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
221	Ji (2024)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing; Computational/public-data modelling
222	Marcante (2024)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
223	Noroozi (2024)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray; Other expression/readout or not reported
224	Pinprasert (2024)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing; Computational/public-data modelling
225	Shiga (2024)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing; qPCR/ddPCR/MSP/HRM
226	Soedarsono (2024)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM; Computational/public-data modelling
227	Yamagishi (2024)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing; Computational/public-data modelling
229	Boullón-Cassau (2025)	Age estimation	Computational reuse of existing methylation data — assay not performed/reported	Computational/public-data modelling	Computational/public-data modelling
230	Collins (2025)	Age estimation	Computational reuse of existing methylation data — assay not performed/reported	Computational/public-data modelling	Computational/public-data modelling
231	Correia Dias (2025)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM
232	Gao (2025)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM
233	Grignani (2025)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
234	Jung (2025)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
235	Li (2025)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing
237	Mathew (2025)	Age estimation	Computational reuse of existing methylation data — assay not performed/reported	Computational/public-data modelling	Computational/public-data modelling
238	Refn (2025)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing
239	Sutter (2025)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing
240	Verstraeten (2025)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing
241	Wan (2025)	Age estimation	Computational reuse of existing methylation data — assay not performed/reported	Computational/public-data modelling	Computational/public-data modelling
242	Yang (2025)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Capillary electrophoresis/fragment analysis; MPS/NGS/targeted sequencing; SNaPshot/SBE-capillary electrophoresis; Computational/public-data modelling

Ref.	Author (year)	Primary application	Primary discrimination principle	Non-additive methodological tags	Non-additive readout/platform tags
243	Zhu (2025)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; Computational/public-data modelling
244	Andrejevic (2026)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis; Computational/public-data modelling
245	Can (2026)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
246	Chen (2026)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Computational/public-data modelling
247	Fakhr (2026)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM; Computational/public-data modelling
248	Lee (2026)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
249	Liu (2026)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis; Computational/public-data modelling
250	Manco (2026)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM
251	Oka (2026)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM; Computational/public-data modelling
252	Pisarek-Pacek (2026)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; Methylation microarray; Computational/public-data modelling
253	Poggiali (2026)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray; Computational/public-data modelling
254	So (2026)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis; Computational/public-data modelling
255	Sutter (2026)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis; Computational/public-data modelling
256	Tsutsumi (2026)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM; Computational/public-data modelling
257	Zhang (2026)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM
258	Zhao (2026)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing; Computational/public-data modelling
259	Ma (2013)	Body fluid/tissue identification	Hybrid/comparative multiple principles	MSRE	MassARRAY/Agena EpiTYPER
260	Balamurugan (2014)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing; Capillary electrophoresis/fragment analysis
261	Bartling (2014)	Body fluid/tissue identification	Methylation-sensitive or methylation-dependent restriction digestion	MSRE; MDRE	MPS/NGS/targeted sequencing
262	Park (2014)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray; Pyrosequencing; Computational/public-data modelling
263	Antunes (2015)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
264	Bai (2015)	Body fluid/tissue identification	Methylation-sensitive or methylation-dependent restriction digestion	MSRE; MDRE	qPCR/ddPCR/MSP/HRM; Other expression/readout or not reported
265	Fu (2015)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
266	Taki (2015)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Other expression/readout or not reported

Ref.	Author (year)	Primary application	Primary discrimination principle	Non-additive methodological tags	Non-additive readout/platform tags
268	Antunes (2016)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM
269	Lin (2016)	Body fluid/tissue identification	Methylation-sensitive or methylation-dependent restriction digestion	MSRE	Capillary electrophoresis/fragment analysis; Computational/public-data modelling
270	Lin (2016)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; qPCR/ddPCR/MSP/HRM; Capillary electrophoresis/fragment analysis; Computational/public-data modelling
271	Watanabe (2016)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM; Capillary electrophoresis/fragment analysis
272	Watanabe (2016)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM; Capillary electrophoresis/fragment analysis; Other expression/readout or not reported
273	Fachet (2017)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM
274	Naue (2018)	Body fluid/tissue identification	Computational reuse of existing methylation data — assay not performed/reported	Computational/public-data modelling	Computational/public-data modelling
275	Samsuwan (2018)	Body fluid/tissue identification	Hybrid/comparative multiple principles	Chemical conversion; post-bisulfite restriction digestion	Other expression/readout or not reported; Computational/public-data modelling
276	Fang (2019)	Body fluid/tissue identification	Non-methylation empirical study	RNA expression	MPS/NGS/targeted sequencing; qPCR/ddPCR/MSP/HRM
277	Gauthier (2019)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
278	Tian (2019)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Capillary electrophoresis/fragment analysis; Computational/public-data modelling
279	Xie (2019)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis; Computational/public-data modelling
280	Alghanim (2020)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray; Pyrosequencing; qPCR/ddPCR/MSP/HRM
281	Ghai (2020)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM; Other expression/readout or not reported
282	Kader (2020)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Other expression/readout or not reported
283	Liu (2020)	Body fluid/tissue identification	Methylation-sensitive or methylation-dependent restriction digestion	MSRE; MDRE	Capillary electrophoresis/fragment analysis; Other expression/readout or not reported; Computational/public-data modelling
284	Tian (2020)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Capillary electrophoresis/fragment analysis; Other expression/readout or not reported
285	Watanabe (2020)	Sequencing/platform/method development	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
286	Xie (2020)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis; Computational/public-data modelling
287	Antunes (2021)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing; qPCR/ddPCR/MSP/HRM; Computational/public-data modelling
288	Doi (2021)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Capillary electrophoresis/fragment analysis; Computational/public-data modelling
289	Fujimoto (2021)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM; Capillary electrophoresis/fragment analysis

Ref.	Author (year)	Primary application	Primary discrimination principle	Non-additive methodological tags	Non-additive readout/platform tags
290	Gomaa (2021)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM; Other expression/readout or not reported
291	Li (2021)	Body fluid/tissue identification	Methylation-sensitive or methylation-dependent restriction digestion	MSRE; MDRE	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
292	Liu (2021)	Body fluid/tissue identification	Non-methylation empirical study	RNA expression	qPCR/ddPCR/MSP/HRM
293	Abouelkeir (2022)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM
294	Huang (2022)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
295	Li (2022)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Capillary electrophoresis/fragment analysis
296	Lin (2022)	Body fluid/tissue identification	Methylation-sensitive or methylation-dependent restriction digestion	MSRE; MDRE	Capillary electrophoresis/fragment analysis
297	Watanabe (2022)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; Methylation microarray
298	Fang (2023)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis; Computational/public-data modelling
299	Fang (2023)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray; Pyrosequencing
300	Fernandez-Tejero (2023)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray; qPCR/ddPCR/MSP/HRM
301	Konrad (2023)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
302	Konrad (2023)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
303	Rhodes (2023)	Body fluid/tissue identification	Non-methylation empirical study	RNA expression	qPCR/ddPCR/MSP/HRM; Capillary electrophoresis/fragment analysis
304	Silva (2023)	Body fluid/tissue identification	Computational reuse of existing methylation data — assay not performed/reported	Computational/public-data modelling	Computational/public-data modelling
305	Wang (2023)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
306	Altmeyer (2024)	Body fluid/tissue identification	Non-methylation empirical study	RNA expression	qPCR/ddPCR/MSP/HRM; Capillary electrophoresis/fragment analysis
307	Ghemrawi (2024)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing; Capillary electrophoresis/fragment analysis
308	Kim (2024)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
309	Li (2024)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
310	Rothe (2024)	Body fluid/tissue identification	Methylation-sensitive or methylation-dependent restriction digestion	MSRE; MDRE	Capillary electrophoresis/fragment analysis; Computational/public-data modelling
311	Tang (2024)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; Capillary electrophoresis/fragment analysis
312	Balamurugan (2025)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing; Computational/public-data modelling
313	Hsu (2025)	Body fluid/tissue identification	Methylation-sensitive or methylation-dependent restriction digestion	MSRE	Capillary electrophoresis/fragment analysis
314	Li (2025)	Body fluid/tissue identification	Methylation-sensitive or methylation-dependent restriction digestion	MSRE	Capillary electrophoresis/fragment analysis

Ref.	Author (year)	Primary application	Primary discrimination principle	Non-additive methodological tags	Non-additive readout/platform tags
315	Mizrachi (2025)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; Capillary electrophoresis/fragment analysis; Computational/public-data modelling
316	Wen (2025)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; Capillary electrophoresis/fragment analysis
317	Zhao (2025)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing; Computational/public-data modelling
318	Konrad (2026)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
319	Schmelzer (2026)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
320	Schmelzer (2026)	Body fluid/tissue identification	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing
321	Singh (2026)	Body fluid/tissue identification	Non-methylation empirical study	RNA expression	qPCR/ddPCR/MSP/HRM
322	Tang (2026)	Body fluid/tissue identification	Methylation-sensitive or methylation-dependent restriction digestion	MSRE	Lateral-flow/dipstick readout
323	Xu (2026)	Body fluid/tissue identification	Non-methylation empirical study	RNA expression; Microbial 16S-rDNA	qPCR/ddPCR/MSP/HRM
324	Zhang (2018)	Body fluid/tissue identification	Non-methylation empirical study	RNA expression	qPCR/ddPCR/MSP/HRM; Capillary electrophoresis/fragment analysis; Other expression/readout or not reported
325	Liu (2019)	Body fluid/tissue identification	Non-methylation empirical study	RNA expression	qPCR/ddPCR/MSP/HRM; Capillary electrophoresis/fragment analysis; Other expression/readout or not reported
327	Li (2026)	Body fluid/tissue identification	Non-methylation empirical study	RNA expression	qPCR/ddPCR/MSP/HRM; Capillary electrophoresis/fragment analysis; Other expression/readout or not reported
328	Xu (2012)	Sequencing/platform/method development	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM; Other expression/readout or not reported
329	Zhang (2013)	Sequencing/platform/method development	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing; SNaPshot/SBE-capillary electrophoresis; Capillary electrophoresis/fragment analysis
336	Park (2017)	Monozygotic twin differentiation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray
337	Freire-Aradas (2018)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MassARRAY/Agena EpiTYPER; Computational/public-data modelling
340	Park (2018)	Sequencing/platform/method development	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM; Other expression/readout or not reported
344	Fang (2019)	Monozygotic twin differentiation	Non-methylation empirical study	RNA expression	MPS/NGS/targeted sequencing; qPCR/ddPCR/MSP/HRM
347	Richards (2019)	Sequencing/platform/method development	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing
348	Xiao (2019)	Monozygotic twin differentiation	Non-methylation empirical study	RNA expression	Other expression/readout or not reported
354	Cho (2021)	Other donor-characteristic inference	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
356	Hao (2021)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Capillary electrophoresis/fragment analysis; SNaPshot/SBE-capillary electrophoresis
358	Naue (2021)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing
359	Planterose Jiménez (2021)	Monozygotic twin differentiation	Computational reuse of existing methylation data — assay not performed/reported	Computational/public-data modelling	Computational/public-data modelling

Ref.	Author (year)	Primary application	Primary discrimination principle	Non-additive methodological tags	Non-additive readout/platform tags
360	Romanos (2021)	Monozygotic twin differentiation	Chemical conversion (predominantly bisulfite)	Chemical conversion	qPCR/ddPCR/MSP/HRM; Capillary electrophoresis/fragment analysis
364	Becker (2022)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
366	Christiansen (2022)	Sequencing/platform/method development	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray
368	Konrad (2022)	Sequencing/platform/method development	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
371	Wang (2022)	Age estimation	Non-methylation empirical study	RNA expression	MPS/NGS/targeted sequencing; qPCR/ddPCR/MSP/HRM; Computational/public-data modelling
374	Fang (2023)	Age estimation	Non-methylation empirical study	RNA expression	MPS/NGS/targeted sequencing; qPCR/ddPCR/MSP/HRM
376	Kim (2023)	Monozygotic twin differentiation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray; Computational/public-data modelling
378	Shabalala (2023)	Sequencing/platform/method development	Chemical conversion (predominantly bisulfite)	Chemical conversion	Other expression/readout or not reported
383	El-Hossary (2024)	Monozygotic twin differentiation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray
385	Oscandar (2024)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
388	Al Qaderi (2025)	Age estimation	Computational reuse of existing methylation data — assay not performed/reported	Computational/public-data modelling	Computational/public-data modelling
393	Huang (2025)	Other donor-characteristic inference	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing
395	Lu (2025)	Age estimation	Non-methylation empirical study	RNA expression	MPS/NGS/targeted sequencing; Computational/public-data modelling
398	Poggiali (2025)	Sequencing/platform/method development	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray
399	Qian (2025)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Methylation microarray; Computational/public-data modelling
400	Simons (2025)	Sequencing/platform/method development	Chemical conversion (predominantly bisulfite)	Chemical conversion	MPS/NGS/targeted sequencing; Methylation microarray
402	Wang (2025)	Monozygotic twin differentiation	Non-methylation empirical study	RNA expression	MPS/NGS/targeted sequencing; qPCR/ddPCR/MSP/HRM
404	Wulandari (2025)	Age estimation	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
407	Colloca (2026)	Other donor-characteristic inference	Chemical conversion (predominantly bisulfite)	Chemical conversion	Pyrosequencing
410	Marszałek (2026)	Other donor-characteristic inference	Computational reuse of existing methylation data — assay not performed/reported	Computational/public-data modelling	Computational/public-data modelling
411	Sacco (2026)	Sequencing/platform/method development	Native-DNA indirect methylation inference (fragmentomics)	Native-DNA fragmentomics	MPS/NGS/targeted sequencing; Computational/public-data modelling
432	Wang (2022)	Age estimation	Non-methylation empirical study	RNA expression	MPS/NGS/targeted sequencing; qPCR/ddPCR/MSP/HRM
436	Hänggi (2025)	Age estimation	Non-methylation empirical study	RNA expression	MPS/NGS/targeted sequencing
437	Tian (2025)	Monozygotic twin differentiation	Non-methylation empirical study	RNA expression	MPS/NGS/targeted sequencing; qPCR/ddPCR/MSP/HRM
438	Chen (2026)	Age estimation	Non-methylation empirical study	RNA expression	Computational/public-data modelling

Supplementary Table S8. Secondary/non-primary reports retained outside the evidence map and not represented in the study-level register (n = 62)

Ref.	Author (year)	Role / disposition
542	An (2012)	Review for citation tracking only
543	Gršković (2013)	Review for citation tracking only
544	Hannum (2013)	Background/context only
545	Vidaki (2013)	Review for citation tracking only
546	Kader (2015)	Review for citation tracking only
547	Relton (2015)	Background/context only
548	Sijen (2015)	Review for citation tracking only
549	Lee (2016)	Review for citation tracking only
550	Freire-Aradas (2017)	Review for citation tracking only
551	Jung (2017)	Review for citation tracking only
552	Kader (2017)	Background/context only
553	Santurro (2017)	Background/context only
554	Vidaki (2017)	Background/context only
555	Parson (2018)	Review for citation tracking only
556	Richards (2018)	Review for citation tracking only
557	Vidaki (2018)	Review for citation tracking only
558	Bacquet (2019)	Review for citation tracking only
559	Hartomo (2019)	Background/context only
560	Meng (2019)	Review for citation tracking only
561	Suttipasit (2019)	Background/context only
562	Kader (2020)	Review for citation tracking only
563	Koop (2020)	Review for citation tracking only
564	Maulani (2020)	Review for citation tracking only
565	Nilendu (2020)	Background/context only
566	Suma (2020)	Review for citation tracking only
567	Wang (2020)	Review for citation tracking only
568	Åsenius (2020)	Background/context only
569	Böhme (2021)	Review for citation tracking only
570	Phulari (2021)	Review for citation tracking only
571	Sijen (2021)	Review for citation tracking only
572	Simpson (2021)	Background/context only
573	Faress (2023)	Review for citation tracking only
574	Huang (2023)	Review for citation tracking only
575	Kattamreddy (2023)	Review for citation tracking only
576	Naue (2023)	Review for citation tracking only
577	Paparazzo (2023)	Review for citation tracking only
578	Refn (2023)	Review for citation tracking only
579	Wang (2023)	Review for citation tracking only
580	Castagnola (2024)	Review for citation tracking only
581	Gerra (2024)	Review for citation tracking only
582	Prastyo (2024)	Review for citation tracking only
583	Procopio (2024)	Background/context only
584	Song (2024)	Review for citation tracking only
585	Syvänen (2024)	Background/context only
586	Ferreira (2025)	Background/context only
587	Gemmati (2025)	Background/context only
588	Grassi (2025)	Review for citation tracking only

Ref.	Author (year)	Role / disposition
589	Liu (2025)	Review for citation tracking only
590	Marcante (2025)	Review for citation tracking only
591	Rojas-Torres (2025)	Review for citation tracking only
592	Yang (2025)	Review for citation tracking only
593	Macfarlane (2026)	Review for citation tracking only
594	Wang (2026)	Background/context only
595	Zaatar (2026)	Review for citation tracking only
596	Zar (2026)	Review for citation tracking only
597	Zupanič Pajnič (2026)	Review for citation tracking only
598	Gilardi (2018)	Background/context only
599	Ghemrawi (2023)	Background/context only
600	Hu (2024)	Background/context only
601	Rawat (2016)	Review for citation tracking only
602	Ghai (2019)	Background/context only
603	Mishra (2022)	Review for citation tracking only

Supplementary Table S9. Operational classification decision guide and worked boundary examples

Supplementary Table S9 translates the author-defined Categories 1–5 in Table 2 into an operational decision guide rather than a numerical score. Worked examples, including Chen et al. (2026; long non-coding RNA age-estimation study, Ref. 438) at Category 3 and Poussard et al. (2023) at Category 4, illustrate how external cohort assessment and receiving-laboratory evaluation are considered alongside their interpretative limitations. The unit of classification remains the individual empirical study/report. A category describes the evidence documented for that report, not necessarily successful transfer or suitability for routine use; an observed failure of transportability differs from testing that was not reported. Evidence was considered only to the extent documented in the report or, for Category 5, in clearly linked indexed and retrievable sources concerning the same method and laboratory workflow. "Not reported" was not treated as proof that an activity had not occurred, only that it could not support assignment to a higher category.

S9A. Operational decision guide

Category	Minimum documented basis	Alternative qualifying evidence patterns	Why evidence remains below the next category	Treatment of missing or ambiguous reporting
C1 Exploratory discovery	Original empirical discovery, association, descriptive evidence, or initial proof of concept relevant to a qualifying forensic endpoint.	Marker discovery; descriptive association; initial proof-of-concept experiment; early biological signal characterisation.	No sufficiently developed assay/model or internal technical-performance evidence to support C2.	Unreported technical development or validation is not assumed. The report remains C1 unless higher-category evidence is documented.
C2 Initial technical evidence	A defined assay, model, or workflow with internal performance evidence, cross-validation, or a development-stage training/test evaluation in which the test data contribute to feature selection, model fitting, parameter tuning, or iterative model choice; limited technical testing may also support C2.	Internal model performance; cross-validation; training/test evaluation used during model development or tuning; assay development with limited sensitivity/repeatability testing; limited technical robustness studies.	Evidence remains mainly within the development setting, without sufficient independent/external validation or broader representative forensic testing to support C3.	Unreported independent datasets, forensic-like testing, or external validation are not treated as absent, but cannot be used to justify C3.
C3 Pre-implementation validation	Evidence beyond development-stage internal performance, through an independent/external dataset, a clearly held-out validation set not used for feature selection/model fitting/tuning, broader technical validation, or evaluation with relevant forensic or forensic-like samples, while important gaps remain.	Independent external dataset; genuinely held-out endpoint-validation set; substantial single-laboratory developmental validation; blinded or forensic-like samples; broader sensitivity/robustness/mixture testing; representative sample evaluation. External-cohort evaluation can contribute to C3 even when preprocessing limits prospective independence, but any outcome-informed preprocessing must be disclosed and prevents that evidence from being described as validation of an independently deployable prediction pipeline.	Validation remains limited in transferability, inter-laboratory reproducibility, representative breadth, uncertainty/interpretation, or implementation evidence. Ordinary single-laboratory external validation or local reimplementation without an explicit transportability question and separated performance verification does not automatically establish C4.	If the advanced transfer, collaborative, or broader external evidence required for C4 is not documented, the report remains C3 even when the reported performance is strong.
C4 Advanced validation evidence under defined conditions (evaluation, not proof of success)	A defined assay/model with evidence materially beyond ordinary C3 pre-implementation validation and with explicit limitations under the conditions tested.	(a) A receiving-laboratory transportability evaluation of a published assay/model in which the transfer question is explicit, any required analytical adaptation is established separately from performance evaluation, and performance is verified on data not used to set that adaptation; failed direct transfer or retraining is not mandatory. (b) Collaborative/inter-laboratory evaluation of a substantial workflow with reproducibility or concordance evidence. (c) Strong independent external validation combined with multiple meaningful representative-sample, sensitivity, mixture, robustness, or interpretative tests. A single-laboratory reimplementation remains C3 when it mainly demonstrates local feasibility or when adaptation and performance evaluation cannot be separated; a single-laboratory cross-platform receiving-lab study can reach C4 when it explicitly evaluates portability of a published inference workflow and documents meaningful transfer limitations under defined conditions. No single performance metric is sufficient.	The publication does not document routine forensic casework implementation with the full local-validation, SOP, QA, interpretation/reporting, and limits-of-use package required for C5.	Advanced qualifying evidence must be documented. A missing inter-laboratory study does not by itself preclude C4 when another advanced qualifying pattern is documented; conversely, an unreported advanced feature is not assumed.

Category	Minimum documented basis	Alternative qualifying evidence patterns	Why evidence remains below the next category	Treatment of missing or ambiguous reporting
C5 Documented routine forensic implementation	Published, indexed, and retrievable documentation that a defined method has entered routine forensic casework following laboratory-specific validation, with SOPs, QA conditions, defined interpretation/reporting rules, and documented limits of use.	The required implementation elements may be documented in one integrated report or, in principle, across clearly linked indexed/retrievable reports concerning the same defined method and laboratory workflow. All required implementation elements must be collectively documented. Candidate report links were considered only when apparent during source-identity checks, full-text charting or reference-list examination and supported by a shared method and laboratory workflow; no corpus-wide reconstruction of all method families was undertaken.	Not applicable as a higher category. C5 does not imply universal admissibility, accreditation, universal transferability, or proof of use outside the documented corpus.	If any required implementation element is not documented, C5 is not assigned. This is a statement about the retrievable evidence, not proof that operational use does not exist elsewhere.

Note: "Alternative qualifying evidence patterns" are not additive points. The table describes documentary routes that can support a category when considered in the context of the complete study. A random split within a development dataset is insufficient on its own for C3 when the test partition informs feature selection, tuning or model comparison. A genuinely untouched endpoint-validation set may support C3 when the model and preprocessing choices have been fixed before that set is evaluated, even if the validation set originates from the same source population; this alone does not demonstrate transferability to other populations or laboratories. Broader, representative forensic-like technical testing remains an alternative documentary route to C3. The route to C4 must document a defined advanced external/receiving-laboratory, collaborative/inter-laboratory, or otherwise sufficiently broad endpoint-specific evaluation; a numerically strong internal model fit alone is not enough. In an adverse transfer study, the fact of independent evaluation and its poor result must be recorded separately. Category 5 is the exception in requiring the full implementation package specified above. High analytical accuracy alone does not determine C3, C4, or C5.

S9B. Worked boundary examples

Boundary	Study	Evidence documented	Decisive distinction	Assigned category	Why the higher category was not assigned / was supported
C3-C4	Koch (2011) [6]	Five-CpG age signature evaluated across eight independent datasets and multiple tissues.	Strong independent biological/model validation, but no receiving-laboratory transfer of a defined forensic assay/workflow and no collaborative/inter-laboratory implementation-oriented evaluation.	C3	Independent datasets support pre-implementation validation, but the documented evidence does not reach the advanced transfer/reproducibility patterns used for C4.
C2–C3	Huang (2015) [7]	After model development, 40 separate blood specimens were used for validation. Bloodstain results were compared in 20 paired blood/bloodstain samples and six further pairs included stored stains.	A separate validation blood set and actual bloodstain-condition testing add documentary validation evidence beyond internal model-fit estimates.	C3	C3 is supported by this separately evaluated cohort and stain testing; C4 was not assigned because the report did not demonstrate receiving-laboratory transfer or a comparative/inter-laboratory advanced validation package.
C3-C4	Pfeifer (2020) [9]	A receiving laboratory tested published blood and buccal age models on large independent cohorts, documented poor direct transfer, retrained the models, and tested them on external or held-out data; postmortem dried blood, storage intervals, and fresh-blood comparisons were included.	Direct receiving-laboratory transferability was tested and limitations were exposed, followed by adaptation and verification under defined conditions.	C4	The transfer/adaptation design provides advanced external validation beyond ordinary single-laboratory independent validation, while still falling short of routine implementation.
C3-C4	Holtkötter (2017) [12]	Thirteen published markers were screened; a four-marker SNaPshot multiplex was developed; mixtures and five blinded mock stains were interpreted correctly.	Substantial single-laboratory pre-implementation evidence, but no external or inter-laboratory validation.	C3	Mock stains and mixtures strengthen the validation package but do not by themselves establish cross-laboratory transfer or reproducibility.
C3-C4	Jung (2016) [54]	Seven laboratories completed increasingly complex tasks from capillary electrophoresis through bisulfite conversion and extraction using known/blinded single-source and mixed body-fluid samples; six laboratories produced consistent interpretations.	A collaborative multi-laboratory workflow directly tested between-laboratory reproducibility and interpretation across increasingly complete analytical steps.	C4	The inter-laboratory collaborative design supports advanced validation under defined conditions; routine implementation, sensitivity breadth, and SOP/reporting infrastructure were not established.
C3-C4	Poussard (2023) [100]	A receiving forensic laboratory transferred published Jung saliva/buccal age models from a SNaPshot workflow to pyrosequencing, optimized the analytical workflow using methylation standards, assessed trueness/sensitivity/repeatability, and then evaluated the published models in saliva and buccal swabs from 115 French donors.	The study explicitly addressed cross-platform transportability of a published inference workflow. Analytical adaptation was established with standards before donor-level performance evaluation, and the new donor cohort was used to test prediction performance and limitations; a failed direct-transfer stage or model retraining is not required by the general C4 rule.	C4	The receiving-laboratory cross-platform design plus technical validation and donor-level performance/uncertainty evaluation reaches advanced validation under defined conditions. It remains below C5 because it is single-laboratory and does not document routine use, inter-laboratory reproducibility, mixtures/degraded traces, or the full local SOP/QA/reporting package.

Boundary	Study	Evidence documented	Decisive distinction	Assigned category	Why the higher category was not assigned / was supported
C2–C3	Lee (2025) [101]	EPIC marker discovery and bisulfite-MPS semen-age modelling; 111/48 training/test partition for Korean markers, with several candidate regressions evaluated on training and test sets; preferred models highlighted after performance comparisons, alongside targeted technical checks.	The test samples were distinct from training, but the article compares test-set performance across candidate regression models and then identifies preferred regressions; no further untouched endpoint test of the selected models is documented.	C2	C2 retained because the final preferred models were not evaluated on a further untouched endpoint-validation set after the reported model-comparison process. Targeted sensitivity/reproducibility checks do not establish broader independent forensic-trace validation. No leakage is inferred, and genuinely held-out internal validation can support C3 under S9A.
C2–C3	Chen (2026; lncRNA age model) [438]	Independently sourced external cohorts were used to evaluate a long non-coding RNA-based chronological-age model. ComBat preprocessing included known chronological age as a biological covariate.	The external-cohort evaluation supports C3 as a documented evaluation design, but the outcome-informed batch correction requires the unknown forensic prediction target and is not a deployable prospective workflow.	C3	C3 reflects external-cohort evaluation under outcome-informed preprocessing; no evidence of a fully prospectively valid pipeline was established. C4 was not supported by independent receiving-laboratory implementation-oriented or comparable advanced evaluation.

These examples illustrate the documentary distinctions applied at the C2–C3 and C3–C4 boundaries. They do not imply that the number of datasets, laboratories, or tested samples is by itself determinative; category assignment reflects the type, independence, transferability, forensic representativeness, reproducibility, and interpretative scope of the evidence documented in the individual report. The Lee (2025) test partition contributed to the comparison and selection of preferred regressions, without subsequent untouched validation (C2); Chen (2026; lncRNA study) used external cohorts but outcome-informed preprocessing (C3). The higher category thus indicates a different documented evaluation design, not more credible prospective prediction.

Supplementary Table S10. Detailed characterization and qualifying evaluation routes of the 10 Category 4 studies

Category 4 remains a study/report-level classification. Table S10A characterises the ten studies assigned to this category, including the receiving-laboratory evaluation by Poussard et al. (2023). Supplementary Table S11 distinguishes independent biological samples from repeated technical measurements and multiple participating laboratories. Fields marked “not reported” or “not tested” describe the published evidence and do not establish what a laboratory may have done outside the report. Performance values are source-specific and were not pooled.

S10A. Detailed advanced-evaluation characteristics

Study / application	Assay or model / intended use	Samples, tissue and population information	Independence / laboratory participation	Performance / uncertainty	Forensic conditions actually tested	Remaining limitations before routine implementation
9. Pfeifer (2020) – Age estimation	Published four-gene pyrosequencing age models for blood and buccal cells; test cross-laboratory transfer and recalibrate locally.	151 postmortem blood samples (1 day–96 y) and 149 buccal swabs (13 days–95 y) collected locally; 100 buccal samples used for initial local model evaluation and 49 additional buccal samples later used as a test set. Twenty-one fresh-blood samples were analysed for fresh-versus-stored/postmortem comparison. The retrained blood model was also evaluated against 206 online Bekaert blood records.	Receiving laboratory independent of the original model developers. Published models were first transferred directly and then locally retrained. For post-retraining evaluation, the blood model was applied to the 206 Bekaert blood records, which were external to the local retraining set but derive from the original published study; the buccal model was evaluated on 49 additional local samples not used in the 100-sample retraining/evaluation set. The publication does not specify how the 100/49 local buccal split was selected.	Direct-transfer MAD 9.84 y (blood). For the initial buccal application, the source is internally inconsistent: the abstract reports MAD 8.32 y, whereas the Results section reports 8.68 y for the 100-sample application. Apparent fit after local retraining: MAD 5.55 y (blood) and 4.65 y (buccal). Post-retraining evaluation: MAD 6.49 y on the 206 Bekaert blood records and 4.47 y on the 49 buccal test samples. Duplicate methylation measurements showed small mean differences at tested CpGs.	Dried postmortem blood, storage intervals, fresh-blood comparison, broad age ranges; local buccal samples. Mixtures/low-template challenge not a major component.	Single receiving laboratory. Blood post-retraining evaluation used the original Bekaert study data rather than a new third cohort; buccal post-retraining evaluation used 49 local samples, but the split-selection procedure was not reported. The source itself reports 8.32 y in the abstract and 8.68 y in the Results for the initial buccal MAD; both values are retained here rather than silently resolving the discrepancy. Local SOPs/calibration, reportable uncertainty, low-template/mixture robustness, proficiency testing and ongoing QA remain necessary.

Study / application	Assay or model / intended use	Samples, tissue and population information	Independence / laboratory participation	Performance / uncertainty	Forensic conditions actually tested	Remaining limitations before routine implementation
10. Heidegger (2022) – Semen age estimation	VISAGE Enhanced Tool ET-13 targeted bisulfite-MPS assay; six CpGs feed the semen age model.	Overall 99 assay-validation preparations; concordance DNA and FTA-card stains from two semen donors (33 and 42 y), methylation standards and species controls. Population transfer was not the focus.	Five VISAGE consortium laboratories performed one MiSeq FGx validation run each; collaborative developmental validation.	Mean SD at the 50% methylation standard ≈2.8%; extract-versus-stain mean differences were small. In the sensitivity series, most markers/samples met the 1000-read threshold down to 10 ng, with isolated 10-ng dropouts; all 1-ng samples had read depths below threshold at ≥2 markers (36 dropouts total). Methylation variability increased below 50 ng. Mean age deviation across concordance/mock stains was 5.4 y and 2.0 y for the two donors.	FTA-card semen stains, sensitivity series (50/20/10/1 ng), concordance samples, species specificity, cross-laboratory workflow.	Very limited donor-level stain set. The assay was challenged down to 1 ng, but 1 ng did not demonstrate acceptable sensitivity because every sample showed multiple marker dropouts; the authors stated that further semen studies were needed to define sensitivity for final age prediction. Broader population/casework validation, local SOPs, uncertainty thresholds and proficiency/QA remain required; ET-5 remained preliminary.
32. Kampmann (2024) – Age estimation	Five-CpG bisulfite-pyrosequencing protocol (ELOVL2, C1orf132, TRIM59, KLF14, FHL2) on PyroMark Q48 with an existing age model.	49 peripheral-blood donors aged 18–64 y plus methylation controls; each laboratory analysed 5–15 samples and controls; samples/controls were run in triplicate. Detailed population composition was not a central reported variable.	Five forensic genetic laboratories applied a common protocol in a collaborative exercise.	Overall MAD 3.62 y. The exercise demonstrated comparability while identifying QC/platform effects and failed/check run issues.	Inter-laboratory blood testing and technical controls; no aged/degraded trace or mixed-sample challenge.	Limited age range and sample size; no casework stains/degradation study; broader population transfer, failure criteria, uncertainty/reporting, local validation and proficiency/QA needed.
33. Heidegger (2025) – Blood/buccal age estimation	VISAGE Enhanced Tool targeted MPS assay plus published blood and buccal age-prediction models.	Technical phases used methylation controls plus blood/saliva; model evaluation used 160 blood and 100 buccal samples independent of the original VISAGE testing sets.	Six laboratories conducted technical reproducibility/concordance/sensitivity testing; three governmental laboratories evaluated model performance.	Sensitivity maintained to 5 ng. MAE 3.95 y (blood) and 4.41 y (buccal); one laboratory showed systematic blood-age underestimation, and excluding it reduced blood MAE to 3.1 y (N=89).	Inter-lab technical testing, saliva used to mimic casework material, low-input assessment, independent model testing in governmental laboratories.	Laboratory-specific blood bias demonstrates need for in-house model validation; degraded/mixed trace performance and routine reporting/QA remain to be established locally.
34. Onofri (2025) – Age estimation	Ge.F.I. standardized bisulfite-conversion SBE/SNaPshot assay at five loci with laboratory-specific calibration.	22 healthy Italian volunteers; fresh peripheral blood and mock-casework dried blood spots. Six laboratories contributed four replicate measurements per subject/laboratory (two bisulfite conversions × two PCR/SBE replicates), for 528 replicate records. For age-model analyses, the four measurements were averaged to one subject-level record per laboratory (22 records/lab).	Ten Ge.F.I. laboratories participated across three phases; participation varied by phase. Six laboratories contributed complete/nearly complete final quantitative data. The same 22-subject panel was analysed independently by the participating laboratories. Before model fitting, Phase II methylation values were aligned to Phase III using locus-specific regressions on chronological age. After replicate averaging, LOO-CV was applied separately to each 22-record laboratory dataset, omitting one subject-level record at a time. The report does not state that the phase-alignment regressions were re-estimated within each LOO-CV iteration.	Mean laboratory-specific MAD was 3.07 y before cross-validation and 4.41 y with subject-level LOO-CV. For each subject, the study also calculated a 95% confidence interval around the mean predicted age across six laboratories; CI widths ranged from 2.43 to 8.82 y, with an average width of 5.24 y. This is uncertainty around the cross-laboratory mean prediction, not a prediction interval for a future single case. A one-way ANOVA on residuals attributed 33.8% of variance to laboratory effects. Because the reported age-based phase alignment is not described as nested within each LOO-CV iteration, the 4.41-y value should not be interpreted as validation of a completely preprocessing-independent future-case pipeline.	Protocol set-up, fresh-versus-blood-spot comparison, intra-/inter-laboratory variability, multiple analyzers and replicate testing.	Only 22 subjects were available, making performance estimates sensitive to influential observations. Repeated measurements improve assessment of technical reproducibility but do not enlarge the independent donor sample. Phase II-to-III alignment used chronological-age regressions and the publication does not document whether this preprocessing was re-estimated within each LOO-CV fold; this creates a possible optimism risk in whole-pipeline predictive performance, not proof of leakage or an error in the authors' code. No aged/degraded, low-template or mixture validation; local calibration, case-level uncertainty/reporting rules, SOP/proficiency testing and routine implementation remain necessary.

Study / application	Assay or model / intended use	Samples, tissue and population information	Independence / laboratory participation	Performance / uncertainty	Forensic conditions actually tested	Remaining limitations before routine implementation
35. Lee (2022) – Age estimation (primary); body-fluid typing (secondary)	Two SNaPshot age-prediction multiplexes (semen; blood/saliva) plus a methylation SNaPshot body-fluid-identification assay.	Each laboratory received 24 standardized test samples derived from blood, saliva and semen; sample origin/age information was progressively disclosed or withheld according to four tasks. Population composition was not the principal validation variable.	Twelve forensic laboratories completed a full-workflow collaborative exercise with different local instruments/reagents/conditions.	Mean absolute age-prediction error across participant data: 2.7 y semen, 5.0 y blood, 3.8 y saliva. Body-fluid identification was mostly conclusive (98%). Analyzer type, PCR buffer and high bisulfite-DNA input materially affected measurements.	Four increasingly complex tasks spanning pre-converted DNA to extraction from dried swabs; undisclosed body-fluid/age characteristics in later tasks.	Standardized exercise rather than routine casework; local analyzer/workflow effects, local validation, SOPs, failure criteria, uncertainty/reporting rules and proficiency/QA remain necessary.
52. Liu (2022) – Spermatozoa identification	3-plex HhaI MSRE-PCR combining digestive control, sperm-specific methylated marker and SRY.	Nine blinded volunteer-derived samples: two semen, two saliva, one blood and four two-fluid mixtures (semen-saliva 1:10/1:100; semen-blood 1:5/1:50).	Six of eight invited Taiwanese forensic laboratories participated (three central, three local); all routinely performed casework DNA analysis and were ISO 17025:2017 accredited.	All six laboratories produced concordant expected sperm-identification results. Study also identified the need for laboratory-appropriate analytical thresholds.	Blind mock sexual-assault samples, mixtures and each laboratory's own routine presumptive tests, extraction and quantification workflow.	Mock rather than actual case material; local internal validation/threshold setting, broader proficiency testing, reporting rules and longitudinal QA remain required.
53. Kim (2024) – Organ/tissue identification	EPIC-array discovery followed by forward/reverse methylation-SNaPshot multiplex assays for organ-tissue identification.	Discovery/validation used Korean/Asian autopsy tissues; multiplex evaluation included 88 autopsy samples from 10 Asian individuals. Independent German comparison used 80 autopsy samples from 10 individuals.	Development in Korea followed by independent inter-laboratory comparison in Germany; sensitivity and mixture experiments were also included.	Internal multiplex: 100% correct presence detection for nine tissue types in 88 samples, with two lung samples also indicating blood. German comparison: 74/80 (92.5%) correct across eight tissue types; six samples failed correct classification due mainly to target-signal dropouts.	Autopsy tissue matrices, independent geographic/laboratory transfer, threshold evaluation, sensitivity and mixture testing.	Lung/kidney-cortex and threshold/dropout effects; postmortem tissue use does not itself demonstrate degradation robustness. Broader inter-lab error characterization, SOPs and QA still required.
54. Jung (2016) – Body-fluid identification	Seven-CpG methylation SNaPshot multiplex for blood, saliva, semen and vaginal fluid.	30 prepared specimens distributed after testing; donor demographics were not a primary reported characteristic. Samples included known/unknown single-source and mixed body-fluid materials.	Seven laboratories completed four progressively complex tasks from capillary analysis to extraction/bisulfite/full workflow.	Six laboratories generated consistent body-fluid typing results for bisulfite-converted/genomic samples; one laboratory failed to establish appropriate capillary conditions. All laboratories concurred on interpretation of produced methylation profiles.	Known and blinded source material, mixtures, staged inter-lab workflow including extraction and bisulfite conversion.	Inter-lab measurement variation increased with workflow complexity; formal interpretive guidelines, sensitivity/error-rate characterization, local SOPs and proficiency/QA remained incomplete.
100. Poussard (2023) – Saliva/buccal age estimation	Published Jung tissue-specific and multitissue age-prediction models; receiving-laboratory transfer from SNaPshot to a locally optimized pyrosequencing workflow.	Saliva and two buccal swabs from each of 115 French volunteers aged 0–88 y. Analytical standards were used for trueness and for sensitivity/repeatability testing at 300/150/75/37.5 ng DNA input.	Single independent receiving forensic laboratory (IRCGN). Analytical adaptation and optimization were performed using methylation standards and assay conditions; the 115-donor cohort was then used for model-performance evaluation. No inter-laboratory phase was included.	MAE 3.5 y for the saliva model, 3.9 y for the buccal model and 3.2 y for the multitissue model. Approximate 95% prediction intervals were ±9 y for saliva and ±10 y for the other models; performance deteriorated at age extremes. A 75-ng bisulfite-conversion input was selected as the practical compromise.	Cross-platform assay transfer, trueness, sensitivity, repeatability, saliva/buccal donor samples and model prediction-limit analysis. No mixtures, aged/degraded trace challenge or multi-laboratory reproducibility study.	Single receiving laboratory; high DNA input relative to routine STR work; reduced utility at youngest/oldest ages; broader population transfer, degraded/low-template and mixture testing, inter-laboratory reproducibility, local SOP/QA/proficiency and routine implementation remain to be established.

Abbreviations: MAD, mean absolute deviation; MAE, mean absolute error; CI, confidence interval; MPS, massively parallel sequencing; SBE, single-base extension; MSRE-PCR, methylation-sensitive restriction enzyme PCR; SOP, standard operating procedure; QA, quality assurance. The fields summarize what was explicitly documented in each publication and do not imply application-wide validation or routine implementation.

S10B. Qualifying advanced-evaluation route for each C4 report (n = 10)

These are descriptive documentary routes to C4, not additional categorical scores or indicators of successful validation. Source-specific methods, outcomes and limitations remain in S10A above.

C4 report	Qualifying C4 evidence route	Interpretive boundary
Pfeifer (2020) [9]	Independent receiving-laboratory transfer and adaptation of published blood/buccal age	Direct transfer failed; retraining and reuse of originating model

	models	data constrain claims
Heidegger (2022) [10]	Five-laboratory collaborative assay-level developmental evaluation (VISAGE ET-13)	Donor-level stain series limited; 1-ng challenge produced marker dropouts
Kampmann (2024) [32]	Five-laboratory collaborative blood-age assay/model exercise	49 donors; no aged, degraded or mixed casework stains
Heidegger (2025) [33]	Multi-laboratory assay testing and separate model evaluation at governmental laboratories	Systematic age bias in one participating laboratory
Onofri (2025) [34]	Multi-phase Ge.F.I. laboratory collaboration assessing assay reproducibility and age-model performance	22 biological donors, repeated technical observations; age-informed alignment may affect cross-validation
Lee (2022) [35]	Twelve-laboratory, staged blinded full-workflow collaborative exercise	Shared standardised samples, not independent routine casework submissions
Liu (2022) [52]	Six-laboratory blinded collaborative sperm-identification exercise	Nine mock specimens only; routine thresholds and local validation still needed
Kim (2024) [53]	Independent Korean-to-German inter-laboratory organ/tissue assay comparison	80 tissue specimens from 10 donors; threshold/dropout errors
Jung (2016) [54]	Seven-laboratory staged collaborative body-fluid assay evaluation	Shared prepared samples and incomplete quantitative interpretation thresholds
Poussard (2023) [100]	Independent receiving-laboratory cross-platform model transfer with separate donor-cohort evaluation	Single receiving laboratory; no degraded/mixed material or casework implementation

Supplementary Table S11. Category 4 evaluation-chain relationships and non-independence considerations (n = 10)

This comparison describes reported relationships among the ten Category 4 studies; it does not attempt to reconstruct every assay/model network or provide an independent-method count. "Independent" refers to the actual dimension of independence reported: source institution, donor cohort, evaluation material, or laboratory. Shared workflow families do not imply shared donors, and multi-laboratory technical repetitions do not add independent biological subjects. Unreported lineage or reuse was not coded as absent reuse. Detailed experimental descriptions remain in S10.

C4 report / citation	Assay/model family or report relationship	Biological versus technical evaluation unit	Independence and transferability caveat
9. Pfeifer (2020)	Published Bekaert blood/buccal pyrosequencing models assessed and locally recalibrated by a receiving laboratory.	151 postmortem blood and 149 buccal collections; distinct 100/49 local buccal portions; original Bekaert data used for the blood post-retraining check.	Cross-laboratory model origin is documented, but the blood post-retraining test returns to the published development source; a new independent third laboratory/cohort is not demonstrated.
10. Heidegger (2022)	VISAGE Enhanced Tool semen assay/ET-13, within the same broader VISAGE programme as Heidegger 2025, which concerns other tissues/models.	Five laboratories; 99 assay-validation preparations include standards and repeated technical materials; two semen donors for concordance.	Repeated assay preparations and shared VISAGE programme participation do not constitute 99 independent biological donors or an independent evidence chain for each related report.
32. Kampmann (2024)	Five-CpG PyroMark Q48 age protocol and existing age model evaluated in a five-laboratory collaboration.	49 blood donors aged 18–64 y; individual laboratories tested allocated samples plus controls, with technical triplicates.	A common model and shared donor set underlie the multi-lab exercise; technical triplicates do not multiply biological sample independence. Broader model-family lineage was not systematically mapped.
33. Heidegger (2025)	VISAGE Enhanced Tool blood/buccal models; linked research programme to Heidegger 2022 semen testing, but tissue-specific endpoints differ.	Six laboratories in technical phases; three laboratories tested age models on 160 blood and 100 buccal samples independent of the original VISAGE testing sets.	Independence of model-evaluation samples is reported, whereas the publications are related within the VISAGE development network; systematic blood-age bias at one laboratory limits transfer claims.
34. Onofri (2025)	Ge.F.I. five-locus bisulfite/SNaPshot blood age workflow developed and studied collaboratively.	22 biological donors with fresh blood and mock stains; six laboratories contributed four technical replicate measurements per subject/laboratory.	The 528 technical replicate data points described in the analysis are not 528 independent donors; calibration and validation results remain linked to the same small subject panel.
35. Lee (2022)	SNaPshot multiplexes combining body-fluid identification as secondary task with age-estimation models in a distinct collaborative evaluation.	Twelve laboratories each received 24 standardised test samples of blood, saliva and semen, some blinded in later stages.	Repeat evaluation of standardised materials across laboratories is not a set of independent sample collections; overlap with other methylation-assay development chains was not exhaustively quantified.
52. Liu (2022)	Three-plex HhaI MSRE-PCR sperm-identification workflow assessed in multiple forensic laboratories.	Nine standardised blinded mock samples circulated among six participating laboratories.	Agreement across laboratories is evidence of reproducibility on shared prepared mock materials, not six independent clinical/forensic cohorts or routine submissions.
53. Kim (2024)	EPIC-derived organ/tissue CpG markers transferred to a methylation SNaPshot multiplex and compared in Germany.	Asian development/multiplex material including 88 tissue samples; independent German comparison used 80 tissue samples from 10 individuals.	The German laboratory comparison is a documented external condition, but 80 tissue specimens are not 80 independent donors; tissue- and threshold-specific errors persist.
54. Jung (2016)	Seven-CpG SNaPshot body-fluid assay, staged collaborative verification across tasks.	Thirty shared prepared specimens covering known/unknown fluids and mixtures assessed through stages by seven laboratories.	Increasing analytical task complexity does not increase the number of independent donor cohorts. A complete cross-study linkage to later published fluid-typing implementations was not established.
100. Poussard (2023)	Published Jung saliva/buccal age models adapted in a new forensic laboratory from SNaPshot to pyrosequencing; distinct from the Jung (2016) body-fluid collaborative study.	One receiving laboratory; analytical standards were used for adaptation; a separate 115-donor saliva/buccal cohort for performance evaluation.	Cross-platform transfer and a new cohort were documented, but no second receiving laboratory, broad forensic degraded/mixture series or routine use is established.

Notes: C4 is a report-level category documenting an advanced evaluation design; the validation-chain comparison does not classify assay/model families as operationally validated. Laboratory counts and technical replicates must not be added to biologically independent sample counts. Distinctions such as "not reported", "not examined" and "unsatisfactory result" should be retained rather than converted to a single missing-value assumption. References correspond to the unified bibliography in the main manuscript.