

Culturomics & Media Navigator

User Manual — Software Version V0.309

GMExpression

Edition 1.0 · August 2026

Contents

Document Control and Notices	5
Document identification	5
Intended use statement	5
Biosafety notice	5
Conventions used in this manual	6
1. Introduction	7
1.1 Purpose of this manual	7
1.2 What the toolkit is	7
1.3 Intended users	8
1.4 Primary application directions	8
1.5 Scope limitations — what the toolkit is not	8
1.6 Database composition at a glance	9
1.7 Data provenance and the source hierarchy	10
1.8 Privacy, connectivity, and data handling	11
2. Getting Started	12
2.1 Access and system requirements	12
2.2 Application layout	12
2.3 The core workflow in five steps	15
2.4 First-run walkthrough	15
2.5 Keyboard operation and accessibility	16
3. Definitions, Nomenclature and Abbreviations	17
3.1 Using the built-in glossary	17
3.2 Oxygen requirement classes	17
3.3 Gram stain classes	19
3.4 Growth environment descriptors	20
3.5 Biosafety terminology	21
3.6 Isolation objectives	22
3.7 Culture media — abbreviations and full names	23
3.8 Analytical, diagnostic and typing methods	26
3.9 Metabolic and physiological terms	28
3.10 Clinical and antimicrobial resistance terms	29
3.11 Databases, nomenclature authorities and standards	31
3.12 Taxonomic qualifiers	32
3.13 Reagents and selective agents	32
3.14 Units and measurements	34
4. Instructions for Use — Core Functions	35
4.1 Task 1 — Locating an organism by name	35
4.2 Task 2 — Locating an organism by taxonomy	36
4.3 Task 3 — Selecting the isolation objective	36
4.4 Task 4 — Running the analysis and reading the result	37
4.4.1 The organism identity header [12]	37
4.4.2 The recommended medium [13]	38
4.4.3 The standard formulation [14]	38

4.4.4 Critical culture parameters [15]	38
4.4.5 Authorised references	39
4.4.6 What to do when no result appears	39
4.5 Task 5 — Searching for a culture medium by name	39
4.6 Task 6 — Determining whether a medium is suitable for a given organism	40
4.6.1 Procedure	41
4.6.2 Worked example	42
4.7 Task 7 — Saving and exporting a result	43
5. Extended Functionality	44
5.1 Symbiotic (cross-feeding) analysis	44
5.1.1 Purpose and scientific rationale	44
5.1.2 Procedure	44
5.1.3 How the analysis works	45
5.1.4 Reading the results panel	46
5.1.5 Worked example	47
5.1.6 Coverage and limitations	47
5.2 Sporulation-cultivation protocols	48
5.2.1 Purpose	48
5.2.2 Availability	48
5.2.3 Protocol selection	48
5.2.4 Protocol structure	49
5.3 Handling tips and cautions engine	49
5.3.1 Purpose	49
5.3.2 Severity grades	49
5.3.3 What triggers a tip	50
5.3.4 Using the panel	50
5.4 Detection and diagnosis methods engine	50
5.4.1 Purpose	50
5.4.2 Method classes	50
5.4.3 Method content	51
5.4.4 Universal and specific methods	51
5.5 Derived workflows	51
5.5.1 Comparing the cultivation envelope of a single organism	51
5.5.2 Designing a defined synthetic consortium	52
5.5.3 Rationalising a media inventory	52
5.5.4 Troubleshooting a failed cultivation	52
5.5.5 Selecting a supplement in place of a partner organism	52
5.5.6 Biosafety triage before specimen work	52
5.5.7 Training and competency assessment	52
6. Symbol and Indicator Guide	54
6.1 Complete symbol reference	54
6.2 Where each symbol appears	54
6.3 Reading the indicators as a set	55
6.4 Colour semantics	55
7. Taxonomy and Classification	56
7.1 Three parallel classification schemes	56
7.2 The eleven groups	56
7.3 Group contents in outline	57
7.4 The ten categories	57
7.5 Nomenclature conventions and cautions	58
8. Methodology Reference	59
8.1 The three media classes	59
8.1.1 Primary isolation media	59
8.1.2 Selective media	59
8.1.3 Enrichment media	60
8.2 Anaerobic cultivation technique	60

8.2.1 Equipment tiers	60
8.2.2 Pre-reduction	60
8.2.3 The resazurin read-out	61
8.2.4 Chemical reductants	61
8.2.5 Gas phases	61
8.3 Special atmospheres and extreme conditions	61
8.4 Detection and identification approaches	62
8.4.1 The identification cascade	62
8.4.2 16S rRNA gene amplification	62
8.4.3 Staining methods	63
8.4.4 Quality control	63
9. Data Model, Provenance and Contribution	65
9.1 Record structure	65
9.1.1 The organism record	65
9.1.2 The physiological metadata record	66
9.1.3 The biosafety record	66
9.1.4 The group assignment	66
9.2 Integrity validation	66
9.3 Submitting a new organism	67
10. Troubleshooting	68
10.1 Interface behaviour	68
10.2 Result content	68
10.3 Cultivation failures	69
11. Limitations, Verification Duty and Safety	71
11.1 Database limitations	71
11.2 Derived-output limitations	71
11.3 The user's verification duty	71
11.4 Safety obligations	72
11.5 Regulatory position	72
12. Version and Document Control	73
12.1 Software version applicable to this manual	73
12.2 Features introduced since earlier releases	73
12.3 Keeping this manual current	73
12.4 Manual revision history	74
12.5 Feedback and corrections	74
Appendix A — Complete Organism Index	75
Group 1 — Gut Commensals & SCFA Producers	75
Group 2 — Enteric & Foodborne Pathogens	80
Group 3 — Respiratory, Wound & Soft Tissue Pathogens	82
Group 4 — Zoonotic, Vector-Borne & Systemic Pathogens	83
Group 5 — Oral Microbiome & Upper GI Tract	84
Group 6 — Biotechnology, Industrial & Research Models	86
Group 7 — Food Processing & Fermentation	87
Group 8 — Soil, Environmental & Spore-Forming Organisms	88
Group 9 — Extremophiles	89
Group 10 — Chemolithotrophs, Gas Metabolism & Photolithotrophs	89
Group 11 — Pathogenic Fungi (Eukaryota)	90
Appendix B — Shared Media Index	92
Appendix C — Metabolite Ontology Reference	94
Appendix D — Oxygen Compatibility Matrix	95
Appendix E — Authoritative Sources and Standards	96
Biosafety	96

Culture collections and media	96
Nomenclature and taxonomy	96
Sequence and literature databases	97
Clinical and methodological standards	97
Foundational methods cited within the database	97
Disclaimer	98

Document Control and Notices

Document identification

Field	Value
Document title	Culturomics & Media Navigator — User Manual
Document edition	1.0
Date of issue	August 2026
Applies to software version	V0.309
Database revision at time of writing	455 organism profiles · 11 groups · 67 subgroups
Issuing organisation	GMExpression
Product URL	https://shop.gmexpression.com/Culturomics-and-Media-Navigator.html
Document status	Released

Intended use statement

For Research Use Only.

The Culturomics & Media Navigator is a bibliographic and decision-support reference tool for laboratory professionals. **It is not a medical device.** It is not intended for clinical diagnosis, patient management, therapeutic decision-making, or any purpose that directly affects patient care. It has not been evaluated or cleared by any regulatory authority for diagnostic use.

All culture media formulations, growth parameters, biosafety classifications, and detection methods presented by the toolkit must be independently verified against the cited primary source and against the user's own institutional standard operating procedures before laboratory use.

Biosafety notice

Biosafety level (BSL) assignments in the toolkit are provided as an orientation aid only. They do **not** substitute for a documented, protocol-driven institutional risk assessment as required by the CDC/NIH *Biosafety in Microbiological and Biomedical Laboratories* (BMBL), 6th Edition (revised June 2020), the WHO *Laboratory Biosafety Manual*, 4th Edition (2020), or the equivalent national or institutional framework applicable in the user's jurisdiction.

Where the toolkit displays **BSL: Unknown**, no biosafety record exists for that organism in the database. The organism must be treated as potentially hazardous and the biosafety level established locally before any material is handled.

Certain organisms in the database are regulated as select agents or their national equivalents. Possession, use, and transfer of these organisms are subject to

statutory control. The toolkit does not track, and cannot advise on, the user's regulatory obligations.

Conventions used in this manual

Convention	Meaning
Bold	An on-screen control, button, field, or panel name exactly as it appears in the application
<i>Italic</i>	Scientific binomial names, and emphasis
Monospace	Database keys, field names, literal values, and text to be typed
[1] [2] [3]	Numbered callouts referring to Figure 1
CRITICAL	An instruction whose omission may cause organism death, invalid results, or a biosafety breach
CAUTION	An instruction whose omission commonly causes cultivation failure or misinterpretation
NOTE	Supporting information

1. Introduction

1.1 Purpose of this manual

This manual describes the complete operation of the GMExpression **Culturomics & Media Navigator**, software version V0.309. It is written for laboratory professionals who need to determine how to cultivate, enrich, select for, or detect a specific microorganism, and who require the underlying evidence to be traceable to authoritative primary sources.

The manual covers:

- the scientific scope and organisational logic of the underlying database;
- the meaning of every indicator, badge, symbol, and abbreviation used in the interface;
- step-by-step procedures for all core and extended functions;
- the algorithms behind the derived outputs, so that results can be interpreted with appropriate scientific reserve;
- the limitations of the tool and the verification duties that fall to the user.

Readers who wish to begin immediately should read Section 2.3 (the five-step core workflow) and Section 2.4 (a worked example), then use Sections 3 and 6 as reference.

1.2 What the toolkit is

The Culturomics & Media Navigator is a browser-based, client-side reference application that maps microorganisms to validated cultivation strategies. For any organism in its database it returns:

1. **Organism identity** — current binomial nomenclature with recognised synonyms, functional category, biosafety classification, and a concise phenotypic and ecological description.
2. **A recommended culture medium**, selected according to the user's stated isolation objective, with the complete formulation expressed per litre, preparation notes, and the critical cultivation parameters (atmosphere, incubation temperature and duration, pH, and objective-specific parameters such as reductant concentration, inhibitor loading, or expected colony morphology).
3. **Handling tips and cautions**, generated from the organism's physiological metadata and from the composition of the selected medium, and graded by severity.
4. **Detection and diagnosis methods**, spanning culture-based, staining, molecular, biochemical, immunological, and imaging approaches, with primer sequences and stepwise protocols where applicable.

Beyond single-organism lookup, the toolkit supports **reverse enquiry** (which organisms does a given medium support?) and **metabolic interaction analysis** (which organisms are plausible cross-feeding partners for a given target?).

Every record is bound to at least one authorised primary reference — a DSMZ type-strain medium, an NCBI/NIH database record, an IJSEM species description, a CLSI or EUCAST guideline, an ISO standard, or a PubMed-indexed peer-reviewed publication.

1.3 Intended users

The toolkit is designed for, and this manual is written for, the following readers:

User group	Typical application
Microbiologists and culturomics researchers	Recovering fastidious, oxygen-sensitive, or previously uncultured taxa from complex communities; designing enrichment cascades
Molecular biologists	Selecting propagation and expression-host media; establishing pure cultures upstream of nucleic acid or protein work
Clinical and diagnostic laboratory scientists	Confirming primary isolation and selective media for enteric, respiratory, wound, oral, and zoonotic pathogens; retrieving companion detection methodology
Hospital clinicians with laboratory liaison duties	Understanding what a laboratory can and cannot recover, and over what timescale, for a suspected organism
Biotechnology and fermentation scientists	Media selection for industrial platform strains, expression hosts, and starter cultures
Food and environmental microbiologists	Starter culture and spoilage organism cultivation; ripening flora; spore-former management
Biosafety officers and laboratory managers	Orientation on containment expectations and handling constraints prior to formal risk assessment
Educators and trainees	Teaching media design rationale, selective agent function, and anaerobic technique

A working knowledge of aseptic technique, general microbiological practice, and the biosafety framework applicable in the user's jurisdiction is assumed throughout.

1.4 Primary application directions

The toolkit is optimised for six recurring laboratory questions:

1. **"How do I grow this organism?"** — forward lookup from organism to medium and conditions (Section 4.4).
2. **"What grows on this medium?"** — reverse lookup from medium to organism set, used to rationalise a media inventory or to interpret mixed growth (Section 4.5).
3. **"Is this medium appropriate for my organism?"** — a structured suitability judgement combining curated evidence with a physiological compatibility check (Section 4.6).
4. **"What should I co-culture this organism with?"** — metabolic cross-feeding analysis for consortium and co-culture design (Section 5.1).
5. **"How do I confirm the identity of what I have grown?"** — retrieval of the companion detection and identification panel (Section 5.4).
6. **"What will go wrong, and how do I avoid it?"** — severity-graded handling cautions derived from organism physiology and medium composition (Section 5.3).

1.5 Scope limitations — what the toolkit is not

Understanding the boundaries of the tool is a prerequisite for using it safely.

- **It is not a diagnostic algorithm.** It does not accept clinical signs, specimen types, or patient data, and it does not propose a differential diagnosis.

- **It is not a substitute for the primary literature.** The formulations are curated summaries. Where a protocol will be adopted into routine use, the cited source must be retrieved and read.
- **It does not perform antimicrobial susceptibility interpretation.** Antimicrobials appear in the database only as selective agents within media formulations, at concentrations chosen to inhibit competing flora. These are not therapeutic or breakpoint concentrations, and must never be read as such.
- **It is not a strain-level resource.** Records are held at species or species-group level. Strain-to-strain variation in nutritional requirement, oxygen tolerance, and antimicrobial resistance is real and is not modelled.
- **It does not guarantee coverage.** Absence of an organism, or of a medium, from the database is not evidence that the organism cannot be cultured or that the medium is unsuitable. It reflects the current state of curation only.
- **Its interaction predictions are heuristics.** The symbiosis engine ranks plausibility from curated annotations; it does not measure or demonstrate interaction (Section 5.1.6).

1.6 Database composition at a glance

The figures below were derived directly from the database shipped with software version V0.309. Every one of the 455 organism records carries a complete physiological metadata record and a biosafety record, and every record supplies all three media classes.

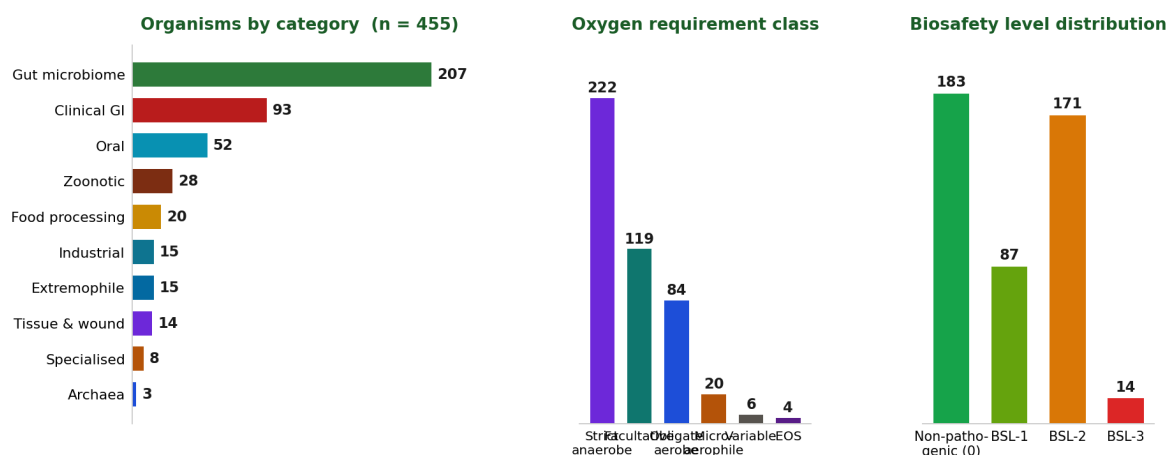


Figure 6 — Database composition, V0.309 (values derived directly from the shipped database; every organism carries a metadata and biosafety record).

Summary metrics

Metric	Value
Organism profiles	455
Organisational groups	11
Subgroups	67
Functional categories	10
Media entries (455 × 3 classes)	1,365
Distinct medium names after normalisation	943
Media shared by three or more organisms	53
Organisms with a physiological metadata record	455 / 455
Organisms with a biosafety record	455 / 455
Organisms flagged as endospore-formers	33
Glossary terms embedded in the application	133

Distribution by functional category

Category	Organisms	Share
Gut microbiome — culturomics	207	45.5 %
Clinical GI pathogens	93	20.4 %
Oral microbiome	52	11.4 %
Zoonotic and systemic pathogens	28	6.2 %
Food processing and fermentation	20	4.4 %
Industrial / bioengineering	15	3.3 %
Extremophiles / autotrophs	15	3.3 %
Tissue and wound pathogens	14	3.1 %
Specialised / fastidious	8	1.8 %
Archaea / methanogens	3	0.7 %

The distribution reflects the toolkit's origin in gastrointestinal culturomics. Coverage is deepest for gut commensals, enteric pathogens, and the oral microbiome; it is deliberately representative rather than exhaustive for environmental, extremophile, and fungal taxa.

Distribution by oxygen requirement

Class	Code	Organisms
Strict anaerobe	S	222
Facultative anaerobe	F	119
Obligate aerobe	A	84
Microaerophile	M	20
Variable / not applicable	X	6
Extreme oxygen-sensitive (EOS)	E	4

Just under half the database consists of strict anaerobes. Users whose laboratory lacks a controlled anaerobic workstation should read Section 8.2 before attempting recovery of these organisms.

Distribution by biosafety level

Classification	Organisms
Non-pathogenic (GRAS / no documented human pathogenicity)	183
BSL-1	87
BSL-2	171
BSL-3	14

1.7 Data provenance and the source hierarchy

Every organism record must cite at least one primary reference. The accepted source hierarchy, in descending order of authority, is:

1. **DSMZ** type-strain medium formulations (Deutsche Sammlung von Mikroorganismen und Zellkulturen).
2. **NCBI / NIH** database records, including GenBank accessions and taxonomic records.
3. **IJSEM / IJSB** species descriptions — the journals of record for validly published prokaryotic names.
4. **CLSI** and **EUCAST** standards and guidelines.
5. **ISO** standards, where an internationally standardised method exists.
6. **WHO** publications, principally for biosafety and risk-group classification.
7. **PubMed-indexed peer-reviewed publications**.
8. **ATCC** and **JCM** culture collection records.
9. **LPSN** (List of Prokaryotic Names with Standing in Nomenclature) for current nomenclature.

Encyclopaedic websites, general textbooks, and commercial kit inserts are **not** accepted as primary sources for database entries.

The source or sources for the displayed medium are shown in the **Authorised References & Database Sources** block at the foot of the result panel. Where sources conflict on a formulation detail, the curation policy is to exclude the conflicting datum rather than to average or arbitrate between sources; this is why some parameter fields carry ranges rather than point values.

1.8 Privacy, connectivity, and data handling

The application is delivered as a single self-contained page and executes entirely in the user's browser.

- The embedded Content Security Policy sets `connect-src 'none'`, which blocks all outbound network requests from application scripts. No search term, organism selection, or analysis result is transmitted to GMEExpression or to any third party.
- The database is embedded in the page. Once the page has loaded, all lookup, cross-reference, and symbiosis functions operate offline.
- No user account is required, and no personal data is collected by the application.
- Framing is disabled (`frame-ancestors 'none'`) and object embedding is blocked, reducing the risk of clickjacking or embedded-content attacks.
- Externally sourced assets are limited to web fonts and the GMEExpression logo image.

These properties make the toolkit suitable for use inside restricted hospital and institutional networks. Users in regulated environments should nonetheless confirm the page against their own local policy before deployment.

2. Getting Started

2.1 Access and system requirements

Requirement	Specification
Access	Open https://shop.gmexpression.com/Culturomics-and-Media-Navigator.html in a web browser. No login, licence key, or installation is required.
Browser	Any current version of Chrome, Edge, Firefox, or Safari. JavaScript must be enabled; the application is inoperable without it.
Display	A viewport of 1,100 px or wider presents the intended two-column layout. Below approximately 740 px the layout reflows to a single column, and the sidebar appears above the result panel.
Network	Required only for the initial page load. All analysis thereafter is local.
Printing	Any system print path. A dedicated print stylesheet reformats the result for A4 portrait output (Section 4.7).

NOTE — The page is large because the entire curated database is embedded in it. Initial load on a constrained connection may take several seconds. Once loaded, response is immediate.

2.2 Application layout

The interface is a two-column working surface beneath a fixed header. Figure 1 maps every control referenced in this manual. The numbered callouts are used throughout Sections 4 and 5.

Culturomics & Media Navigator

455 Organism Profiles · 11 groups · 67 subgroups

9 Save & Export

10 Glossary

11 Submit Profile

1 MEDIA SELECTION

1 SEARCH ORGANISM

e.g. Akkermansia, E. coli, MRSA...

2 TARGET ORGANISM

S P Faecalibacterium prausnitzii

3 ISOLATION OBJECTIVE

Primary Isolation

4 Analysis & Match

6 Symbiotic Analysis

7 INDICATOR KEY

BIOSAFETY

▲▲▲▲▲

OXYGEN REQUIREMENT

E S M F A

GRAM STAIN

P N X

GROWTH-ENVIRONMENT BADGES

SCFA · ACID · ALK · HAL · AUTO · THERM · HYD ...

8 ORGANISM CATEGORIES

Gut Microbiome

Clinical GI Pathogens

Tissue & Wound Pathogens

Archaea / Methanogen

Fastidious / Dark Matter

Industrial / Bioengineering

Extreme Environments

Food Processing

5 GUT MICROBIOME

12 Faecalibacterium prausnitzii

Non-Pathogenic

Gram-Positive

Strict Anaerobe (EOS)

Butyrate Producer

13 RECOMMENDED CULTURE MEDIUM

YCFA Medium + 30 mM Sodium Acetate

STANDARD FORMULATION (PER LITRE)

Casitone

10.0 g

Yeast Extract

2.5 g

Sodium Acetate

1.64 g

± 30 mM

// Autoclave 121 °C / 15 min under N₂

14 CRITICAL CULTURE PARAMETERS

ATMOSPHERE

< 0.5 ppm O₂

INCUBATION

37 °C, 7-14 d

pH

6.8-7.0

REDUCTANT

L-Cysteine 1 g/L

15 HANDLING TIPS & CAUTIONS

CRITICAL — EOS organism — Coy chamber < 0.5 ppm O₂ mandatory

CAUTION — Pre-reduce medium ≥ 24 h; discard if resazurin is pink

NOTE — SCFA-dependent — VFA mix required in the formulation

17 DETECTION & DIAGNOSIS METHODS

MOLECULAR

16S rRNA — 27F / 1492R universal primers

STAINING

Gram stain — Gram-positive rods; may stain variably

CULTURE

YCFA agar, 7-14 d anaerobic; convex translucent colonies

Figure 1 — Application layout map. Numbered callouts are referenced throughout Sections 4 and 5.

Header controls

Callout	Control	Function
[9]	Save & Export	Opens the browser print dialogue with the print stylesheet applied (Section 4.7)
[10]	Glossary	Opens the searchable glossary of 133 terms (Section 3.1)
[11]	Submit Profile	Opens the contributor guide for proposing a new organism (Section 9.3)

Left column — control panels

Callout	Control	Function
[1]	Search Organism field	Free-text search across names, synonyms, traits, and category labels (Section 4.1)
[2]	Target Organism dropdown	Grouped, browsable list of all 455 organisms (Section 4.2)
[3]	Isolation Objective dropdown	Selects which medium class is returned (Section 4.3)

Callout	Control	Function
[4]	Analysis & Match button	Executes the lookup and populates the result panel (Section 4.4)
[5]	Information icon on the Media Selection header	Opens the Media Cross-Reference panel for reverse lookup (Section 4.5)
[6]	Symbiotic Analysis button	Opens the metabolic interaction panel for the selected organism (Section 5.1)
[7]	Indicator Key card	Static legend for all symbols (Section 6)
[8]	Information icon on the Organism Categories header	Opens the Organism Taxonomy & Classification browser (Section 7)

Right column — result panels

Callout	Panel region	Content
[12]	Organism identity header	Category badge, biosafety triangle and banner, binomial name, trait chips, description
[13]	Recommended culture medium	Name of the medium matched to the selected objective
[14]	Standard formulation	Complete per-litre formulation with preparation notes
[15]	Critical culture parameters	Atmosphere, incubation, pH, and objective-specific parameters
—	Authorised references	Primary sources for the displayed record
[16]	Handling Tips & Cautions	Severity-graded practical warnings (Section 5.3)
[17]	Detection & Diagnosis Methods	Identification and confirmation panel (Section 5.4)

Before an analysis is run, the right column shows a placeholder prompt. It is replaced by the result panels when **Analysis & Match** is clicked.

2.3 The core workflow in five steps

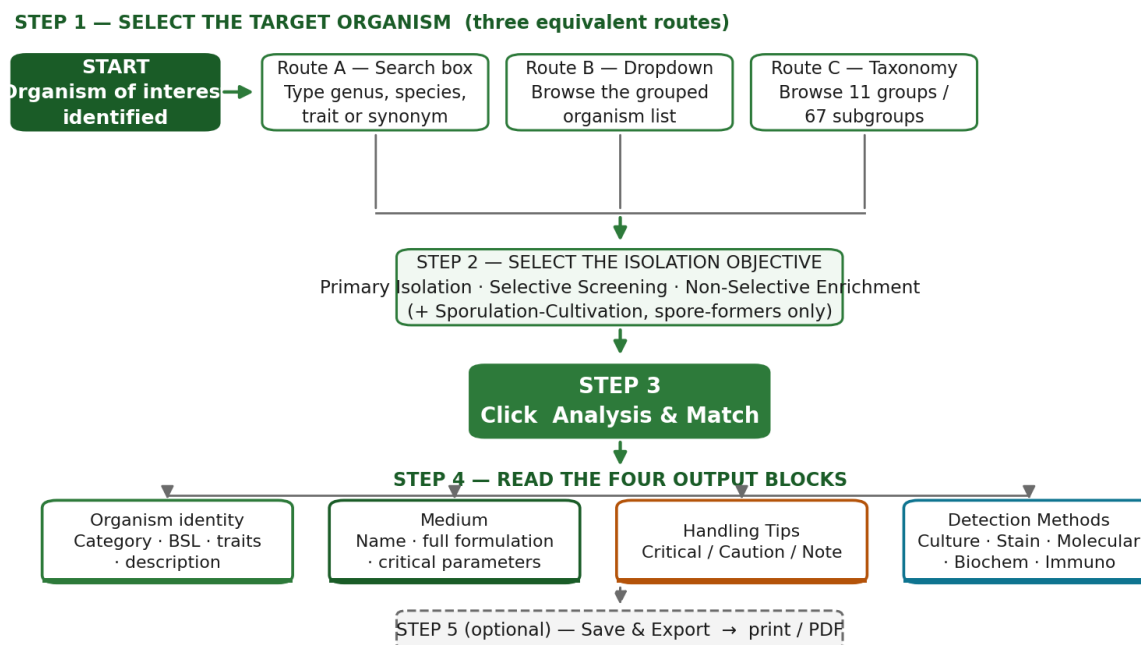


Figure 2 — Core analysis workflow.

The core workflow is invariant:

1. **Select the target organism** by one of three equivalent routes — the search field, the grouped dropdown, or the taxonomy browser.
2. **Select the isolation objective** — this determines which of the three (or, for spore-formers, four) media classes is returned.
3. **Click Analysis & Match.**
4. **Read the four output blocks** — identity, medium, handling cautions, detection methods.
5. **Save or export** the result, if a bench record is required.

Steps 1 and 2 are order-independent, with one exception noted in Section 4.3: the **Sporulation-Cultivation** objective is only offered once a spore-forming organism has been selected.

2.4 First-run walkthrough

The following worked example exercises the whole workflow. It uses *Faecalibacterium prausnitzii*, an extreme oxygen-sensitive gut commensal, because it demonstrates the highest-severity handling output.

Step 1 — select the organism. Click into the **Search Organism** field [1] and type *prausnitzii*. A result list appears beneath the field. Click the entry *Faecalibacterium prausnitzii*. The **Target Organism** control [2] updates to show the name preceded by two indicator marks: a violet circle marked S and a rose hexagon marked P.

Step 2 — read the indicators before proceeding. The violet S circle denotes a strict anaerobe; the rose P hexagon denotes a Gram-positive organism. These indicators are visible before analysis is run precisely so that the user can judge feasibility in advance. If the laboratory cannot deliver a strictly anaerobic atmosphere, work should stop here.

Step 3 — select the isolation objective. Open the **Isolation Objective** dropdown [3] and confirm that **Primary Isolation** is selected.

Step 4 — run the analysis. Click **Analysis & Match** [4]. The right column populates.

Step 5 — read the identity header [12]. The category badge reads *Gut Microbiome — Culturomics*. The biosafety triangle points upward and is green, and the banner reads *Non-Pathogenic*. The binomial appears in italic, followed by trait chips including *Strict Anaerobe (EOS)*, *Butyrate Producer*, and *Acetate-Dependent*. Read the italic description beneath: it establishes the organism’s ecological role and clinical relevance.

Step 6 — read the medium [13]** [14] [15]** The recommended medium is *YCFA Medium + 30 mM Sodium Acetate*. The formulation block lists every component per litre; lines beginning with // are preparation notes, not ingredients. The parameter grid gives an atmosphere of < 0.5 ppm O₂, incubation at 37 °C, 7–14 d, pH 6.8–7.0, and a reductant specification.

Step 7 — read the handling cautions [16]. Note the summary counts at the top of the panel. Items graded **CRITICAL** must be satisfied; for this organism they include the requirement for an anaerobic chamber. Items graded **CAUTION** and **NOTE** follow.

Step 8 — read the detection panel [17]. Methods are grouped by type. For this organism the panel includes universal 16S rRNA amplification with primer sequences, Gram staining guidance, and culture-based identification criteria.

Step 9 — extend the analysis (optional). With the organism still selected, click **Symbiotic Analysis** [6]. A panel opens showing that this organism *produces* butyrate and *requires* acetate, followed by ranked candidate cross-feeding partners — acetate producers that share its anaerobic niche.

Step 10 — export (optional). Click **Save & Export** [9] to produce a printable record.

2.5 Keyboard operation and accessibility

Action	Key
Close any open modal panel (taxonomy, glossary, submission guide, symbiosis)	Esc
Activate a focused list item, partner card, or organism link	Enter or Space
Move between controls	Tab / Shift + Tab

Modal panels trap keyboard focus while open and restore focus to the invoking control on close. Dropdowns and result lists carry ARIA listbox and option roles. Every result list entry is individually focusable.

CAUTION — Colour is used to encode oxygen class, Gram reaction, biosafety level, and caution severity. All four encodings are redundantly carried by a letter, a shape, or a text label, so that the interface remains usable without colour discrimination. Users should nonetheless read the text label rather than relying on colour alone.

3. Definitions, Nomenclature and Abbreviations

3.1 Using the built-in glossary

The application carries an embedded glossary of **133 terms** across eleven subject categories, opened by the **Glossary** button **[10]** in the header. It is searchable, and the search matches the abbreviation, the expanded term, and the definition text.

Glossary category	Terms	Covered in this manual
Indicator symbols	26	Sections 3.2–3.5, 6
Culture media	24	Section 3.7
Analytical techniques	21	Section 3.8
Clinical and resistance	19	Section 3.10
Metabolic terms	9	Section 3.9
Reagents and selective agents	9	Section 3.13
Biosafety	6	Section 3.5
Databases and nomenclature	6	Section 3.11
Units and measurements	5	Section 3.14
Oxygen requirements	4	Section 3.2
Taxonomic qualifiers	4	Section 3.12

The sections below reproduce and extend that content in a form suitable for offline reference and for induction training.

3.2 Oxygen requirement classes

Oxygen classification is the single most consequential parameter in the database. It determines the atmosphere, the equipment, the medium preparation route, and in many cases whether recovery is possible at all in a given laboratory.

Code	Class	Definition and operational consequence
E	Extreme oxygen-sensitive anaerobe (EOS)	Killed by more than approximately 0.5 ppm O ₂ . Handling is confined to an anaerobic chamber of the Coy type, with a palladium catalyst and an H ₂ /N ₂ /CO ₂ atmosphere. Media must be pre-reduced inside the chamber before inoculation. Brief exposure to air during plate transfer is sufficient to abolish recovery.
S	Strict (obligate) anaerobe	Cannot tolerate more than approximately 2 % O ₂ . Recoverable in an anaerobic chamber or in a sealed jar with a gas-generating sachet. Dies on prolonged air exposure, but tolerates the brief handling required for plate transfer.
M	Microaerophile	Requires oxygen, but at 2–10 %, below the atmospheric 21 %, and generally with elevated CO ₂ at 5–10 %. Requires a microaerobic gas-generating system or a controlled-atmosphere incubator. Will not grow either aerobically or strictly anaerobically.
F	Facultative anaerobe	Grows with or without oxygen, switching between aerobic respiration and fermentation. Culturable under either atmosphere, though colony morphology, pigment production, and growth rate frequently differ between the two.
A	Obligate aerobe	Requires at least approximately 10 % O ₂ . Strictly aerobic incubation.

Code	Class	Definition and operational consequence
X	Variable / not applicable	The oxygen relationship is variable, undefined in the source literature, or the classification does not apply. Establish the requirement from the primary reference before proceeding.

Related terms

- **Aerotolerant anaerobe** — an organism with a fermentative metabolism that does not use oxygen but survives exposure to it. The database does not maintain a separate code for this state; such organisms appear as S or F according to the source description.
- **Capnophile** — an organism requiring elevated CO₂. This is recorded in the atmosphere parameter of the medium rather than as a separate oxygen code.

3.3 Gram stain classes

Code	Class	Definition
P	Gram-positive	Thick peptidoglycan cell wall, approximately 20–80 nm. Retains the crystal violet-iodine complex during decolourisation and appears purple. Includes the Firmicutes (<i>Bacillus</i> , <i>Clostridium</i> , <i>Staphylococcus</i> , <i>Streptococcus</i>) and the Actinobacteria.
N	Gram-negative	Thin peptidoglycan layer, approximately 1–3 nm, enclosed by an outer membrane bearing lipopolysaccharide (endotoxin). Decolourised during staining and counterstained pink or red by safranin. Includes the Proteobacteria and Bacteroidetes.
X	Gram-variable / not applicable	Archaea (pseudomurein or S-layer, no classical peptidoglycan), fungi (chitinous cell wall), and organisms whose Gram reaction is unreliable. The Gram stain is not diagnostically informative for these groups.

CAUTION — A Gram-positive organism may stain Gram-variable or falsely Gram-negative in old cultures, in sporulating cultures, and in several anaerobic genera. A discordant Gram

result should prompt re-staining from a fresh culture before the identification is revised.

3.4 Growth environment descriptors

These badges are additive and appear only when the corresponding trait applies to the organism. Each represents a non-negotiable cultivation constraint.

Badge	Full term	Requirement
SCFA	SCFA-dependent	Requires exogenous short-chain fatty acids (acetate, propionate, butyrate). The medium must carry a volatile fatty acid (VFA) supplement.
ACID	Acidophile	Optimal growth below approximately pH 5.0–6.5. Media must be acidified and buffered accordingly.
ALK	Alkaliphile	Optimal growth above approximately pH 8.5–9.0. Requires carbonate/bicarbonate-buffered alkaline media.
HAL	Halophile	Requires 2–10 % NaCl. Standard media must be salt-supplemented.
E-HAL	Extreme halophile	Requires more than 15 % NaCl, up to near-saturation at approximately 30 %.
AUTO	Obligate autotroph	Principally haloarchaea. Derives all carbon from CO ₂ fixation and cannot use organic carbon. Requires a mineral salts medium with an inorganic electron donor.
MIX	Mixotroph / facultative autotroph	Grows autotrophically or heterotrophically, switching according to substrate availability.
THERM	Thermophile	Optimum 55–80 °C. Gelrite replaces agar as the solidifying agent above approximately 60 °C.
H-THM	Hyperthermophile	Optimum above 80 °C. Cultivation above 100 °C requires sealed serum vials or pressurised vessels.
HYD	Hydrogenophile	Uses molecular hydrogen as electron donor. Requires an H ₂ -containing gas phase.

Badge	Full term	Requirement
METH	Methanotroph	Uses methane as sole carbon and energy source. Requires a CH ₄ /air atmosphere.
AMPH	Ammoniaphile	Uses ammonia as sole energy source via nitrification. Mineral salts medium with NH ₄ ⁺ .
SDPH	Sulphidophile	Uses hydrogen sulfide or reduced sulfur compounds as electron donor. Media contain Na ₂ S or thiosulfate.
MTRO	Methyлотroph	Uses C ₁ compounds (methanol, methylamine, formaldehyde) as sole carbon and energy source. Not all methyлотrophs oxidise methane.

3.5 Biosafety terminology

Term	Expansion	Definition
BSL	Biosafety Level	Classification defining containment, personal protective equipment, and practices required to handle an agent safely.
BMBL	<i>Biosafety in Microbiological and Biomedical Laboratories</i>	The CDC/NIH reference standard for United States laboratory biosafety, 6th Edition, revised June 2020. Defines BSL-1 to BSL-4 and the agent summary statements.
WHO LBM	<i>WHO Laboratory Biosafety Manual</i>	The World Health Organization's international biosafety reference, 4th Edition (2020), defining risk groups and biosafety practice.
Select agent	CDC/USDA Select Agent	A biological agent or toxin judged to pose a severe threat to public, animal, or plant health. Possession, use, and transfer are statutorily regulated (in the United States, under 42 CFR Part 73 and 9 CFR Part 121).

Term	Expansion	Definition
BSC	Biological Safety Cabinet	Ventilated enclosure providing containment. A Class II Type A2 cabinet protects operator, product, and environment through HEPA-filtered inward and exhaust airflow.
PPE	Personal Protective Equipment	Protective clothing, gloves, eye protection, and respiratory protection worn to reduce exposure.

Biosafety levels as applied in the toolkit

Displayed	Meaning	Typical practice
Non-Pathogenic	No documented human pathogenicity; GRAS organisms, environmental saprophytes, non-pathogenic commensals	Standard laboratory practice
BSL-1	Not known to consistently cause disease in healthy adults	Standard microbiological practice; open bench acceptable
BSL-2	Moderate potential hazard	Class II BSC for aerosol-generating procedures; laboratory coat, gloves, eye protection; autoclave waste
BSL-3	Serious or potentially lethal disease, with aerosol transmission potential	Dedicated BSL-3 facility; controlled access, double-door entry, directional airflow, HEPA exhaust; full PPE; may also be a regulated select agent
BSL: Unknown	No record exists in the database	Treat as potentially hazardous; establish the level locally before handling

3.6 Isolation objectives

The **Isolation Objective** control determines which medium class is returned. The four objectives are not interchangeable.

Objective	Purpose	Design principle
Primary Isolation	Recover the organism in pure culture, with the highest achievable yield	Nutritionally rich and permissive; no deliberate inhibitors. Maximises recovery but permits competitor growth.

Objective	Purpose	Design principle
Selective Screening	Recover the target from a mixed or heavily contaminated specimen	Contains inhibitors — antimicrobials, bile salts, dyes, elevated salt, extreme pH — that suppress competing flora. Recovery of the target is reduced relative to primary isolation.
Non-Selective Enrichment	Increase the target's population before plating, typically from a low-abundance source	Usually a liquid broth. Amplifies the target and its competitors together; requires subsequent plating and often a defined transfer schedule.
Sporulation-Cultivation	Induce and harvest endospores	Nutrient-limited or specifically formulated to trigger sporulation, followed by a heat-selection step. Offered only for organisms flagged as endospore-formers.

CRITICAL — A selective medium is not a substitute for a primary isolation medium. The inhibitors that suppress competitors also depress the recovery of the target. Where a specimen is expected to yield the organism in near-pure form, the primary isolation medium gives the higher yield and should be preferred.

3.7 Culture media — abbreviations and full names

The media below are those defined in the application glossary. They represent the most frequently recurring formulations across the database.

Abbreviation	Full name	Description
YCFA	Yeast Casitone Fatty Acids medium	The standard strict-anaerobe gut culture medium (Holdeman 1977; DSMZ Medium 337). Contains casitone, yeast extract, Na ₂ CO ₃ , L-cysteine, volatile fatty acids, hemin, and vitamin K1. The primary medium for butyrate-producing Firmicutes and the most widely used medium in this database.
MBM	Mucin-Basal Medium	Minimal anaerobic medium using porcine gastric mucin as sole carbon and nitrogen source. Selective for mucin-degrading gut bacteria such as <i>Akkermansia muciniphila</i> (Derrien et al. 2004).

Abbreviation	Full name	Description
BHI	Brain Heart Infusion	Rich general-purpose medium containing calf brain and beef heart infusion solids, proteose peptone, dextrose, NaCl, and Na ₂ HPO ₄ . Supports most non-fastidious bacteria.
BHIS	Brain Heart Infusion Supplemented	BHI enriched with hemin, vitamin K1, L-cysteine, and resazurin. A non-selective anaerobic medium for obligate anaerobes.
PRAS	Pre-Reduced Anaerobically Sterilised	<i>A preparation method</i> , not a formulation: the medium is sparged with N ₂ /CO ₂ , dispensed under anaerobic gas into sealed tubes, and then autoclaved. Maintains a redox potential below approximately –100 mV. Applied to BHI, PYG, and other broths (Dowell & Hawkins 1977).
GAM	Gifu Anaerobic Medium	Complex anaerobic broth (DSMZ Medium 5) containing peptone, soy peptone, digested serum, yeast extract, liver extract, glucose, and cysteine. Broad-spectrum anaerobe recovery.
BBE	<i>Bacteroides</i> Bile Esculin agar	Selective differential agar for <i>Bacteroides</i> and <i>Parabacteroides</i> . Oxgall inhibits non-Bacteroidaceae; esculin hydrolysis with ferric ammonium citrate produces black colonies; gentamicin suppresses facultative anaerobes.
KVLB	Kanamycin-Vancomycin Laked Blood agar	Highly selective anaerobic agar for <i>Bacteroides</i> , <i>Prevotella</i> , and <i>Porphyromonas</i> . Laked (freeze-thawed) sheep blood releases haemoglobin to support pigmentation reactions.
TSA	Tryptic Soy Agar	Non-selective general-purpose solid medium containing tryptone, soy peptone, NaCl, and agar.
TSBA	Tryptic Soy Blood Agar	TSA supplemented with 5 % defibrinated sheep blood; supports fastidious organisms and permits haemolysis reading.

Abbreviation	Full name	Description
CBA	Columbia Blood Agar	Non-selective blood agar on Columbia agar base with 5 % defibrinated sheep blood. A general-purpose medium for clinical isolate recovery.
MRS	de Man, Rogosa and Sharpe medium	Selective enrichment medium for Lactobacillaceae, at pH 6.2, containing peptone, meat and yeast extracts, glucose, Tween 80, K ₂ HPO ₄ , sodium acetate, triammonium citrate, MgSO ₄ , and MnSO ₄ .
TCBS	Thiosulfate Citrate Bile Salts Sucrose agar	Selective differential agar for <i>Vibrio</i> . Alkaline pH 8.6, bile salts, and thiosulfate suppress non-vibrios; sucrose fermenters such as <i>V. cholerae</i> form yellow colonies.
CHROMagar	Chromogenic differentiation agar	Commercial media containing substrate-linked chromogens that yield species-characteristic colony colours through specific enzyme activity, permitting presumptive identification without biochemical testing.
BCYE	Buffered Charcoal Yeast Extract agar	Selective medium for <i>Legionella</i> . Activated charcoal adsorbs toxic fatty acids; ACES buffer maintains pH 6.9; L-cysteine and iron pyrophosphate are essential growth factors.
LJ	Löwenstein-Jensen medium	Egg-based solid medium for <i>Mycobacterium</i> . Coagulated whole egg provides nutrients; malachite green inhibits most non-mycobacteria. Incubation at 35–37 °C for 4–8 weeks.
7H10 / 7H11	Middlebrook 7H10 / 7H11 agar	Semi-defined mycobacterial agars requiring OADC (oleic acid-albumin-dextrose-catalase) supplementation. 7H11 adds casein hydrolysate for improved recovery of drug-resistant strains.
MTM	Modified Thayer-Martin medium	Selective chocolate agar for pathogenic <i>Neisseria</i> : GC agar base with lysed horse blood, IsoVitaleX, and the VCNT inhibitor mix (vancomycin, colistin, nystatin, trimethoprim).

Abbreviation	Full name	Description
GC Agar	Gonococcal agar	Transparent base medium for <i>Neisseria</i> , requiring blood or IsoVitaleX supplementation for fastidious species.
FAA	Fastidious Anaerobe Agar	Non-selective enriched anaerobic medium containing tryptose, peptone, yeast extract, glucose, NaCl, cysteine, hemin, and vitamin K1. Supports the widest range of obligate anaerobes.
SDA	Sabouraud Dextrose Agar	Standard fungal medium with 40 g/L dextrose and mycological peptone at pH 5.6; the acidic pH inhibits most bacteria.
EYA	Egg Yolk Agar	Differential agar detecting lecithinase (opaque halo), lipase (pearlescent sheen), and proteolysis (clearing) in <i>Clostridium</i> , <i>Bacillus</i> , and related spore-formers. Egg yolk emulsion is added after autoclaving.
RCM	Reinforced Clostridial Medium	Enriched anaerobic medium for clostridia containing beef and yeast extracts, peptone, glucose, sodium acetate, cysteine, starch, and agar.
PYG	Peptone Yeast Glucose broth	The standard VPI anaerobe laboratory broth; a basal enrichment for gut and clinical anaerobes.

Additional media abbreviations occurring in formulations

Abbreviation	Expansion
M2GSC	Modified medium 2 with glucose, soluble starch and cellobiose — rumen and gut anaerobe medium
BSM	<i>Bifidobacterium</i> Selective Medium
LAMVAB	<i>Lactobacillus</i> Anaerobic MRS with Vancomycin and Bromocresol green
XLD	Xylose Lysine Deoxycholate agar
SFM	Soya Flour Mannitol medium — <i>Streptomyces</i> sporulation
DSM	Difco Sporulation Medium — <i>Bacillus</i> sporulation
OADC	Oleic Acid–Albumin–Dextrose–Catalase supplement
VFA	Volatile Fatty Acid supplement mixture

3.8 Analytical, diagnostic and typing methods

Abbreviation	Full name	Definition
MALDI-TOF MS	Matrix-Assisted Laser Desorption/Ionisation Time-of-Flight Mass Spectrometry	Generates a ribosomal protein mass fingerprint from whole cells and matches it against a reference spectral library. Identifies most clinical bacteria within minutes of colony growth.
PCR	Polymerase Chain Reaction	Exponential amplification of a defined DNA sequence using primers, thermostable polymerase, and thermal cycling.
qPCR	Quantitative (real-time) PCR	PCR monitored in real time with fluorescent dyes or hydrolysis probes, permitting quantification of organism load.
16S rRNA	16S ribosomal RNA gene	Approximately 1,550 bp bacterial gene combining conserved and variable regions (V1-V9). Sequencing supports genus- and often species-level assignment and is the universal fallback identification method in this toolkit.
FISH	Fluorescence In Situ Hybridisation	Fluorescently labelled oligonucleotide probes targeting rRNA, used to visualise specific organisms directly in specimens or biofilms without culture.
ELISA	Enzyme-Linked Immunosorbent Assay	Plate-based immunoassay detecting antigens or antibodies via enzyme-conjugated detection and a colorimetric substrate.
LF-ELISA	Lateral Flow ELISA	Rapid point-of-care nitrocellulose strip format producing a visible line.
DFA	Direct Fluorescent Antibody	Immunofluorescence using fluorophore-conjugated antibodies to detect antigen directly in specimens or cultures.
MPN	Most Probable Number	Statistical estimate of viable organism concentration derived from serial dilution and multiple-tube results.
CFU	Colony-Forming Unit	A single viable cell or clump producing one visible colony; the unit of viable count.
MIC	Minimum Inhibitory Concentration	Lowest antimicrobial concentration visibly inhibiting growth after overnight incubation.

Abbreviation	Full name	Definition
MBC	Minimum Bactericidal Concentration	Lowest concentration killing at least 99.9 % of the inoculum; always at or above the MIC.
EUCAST	European Committee on Antimicrobial Susceptibility Testing	Publishes European clinical breakpoints and epidemiological cut-off values.
CLSI	Clinical and Laboratory Standards Institute	Publishes United States reference methods and breakpoints.
PFGE	Pulsed-Field Gel Electrophoresis	Separation of large chromosomal restriction fragments under alternating fields; a reference typing method for outbreak investigation.
WGS	Whole Genome Sequencing	Complete genome determination, providing definitive typing, resistance and virulence gene profiling, and phylogenetic placement.
MLST	Multi-Locus Sequence Typing	Allelic profiling at seven housekeeping loci, assigning a sequence type for epidemiological comparison.
VITEK	VITEK 2 automated system	Automated identification and susceptibility platform using miniaturised biochemical cards with turbidimetric reading.
API	Analytical Profile Index	Manual miniaturised biochemical identification strips read after 18–48 h.
BACTEC	BACTEC blood culture system	Automated blood culture platform detecting CO ₂ production by fluorescence.
MGIT	Mycobacteria Growth Indicator Tube	Liquid mycobacterial culture with an oxygen-quenched fluorescent indicator; detects growth in a mean of 11–14 days against 3–4 weeks for solid media.

3.9 Metabolic and physiological terms

Abbreviation	Full name	Definition
SCFA	Short-Chain Fatty Acid	Fatty acids of six carbons or fewer — acetate, propionate, butyrate, valerate — produced by anaerobic fermentation of dietary fibre. Butyrate is the principal energy substrate of colonocytes.

Abbreviation	Full name	Definition
VFA	Volatile Fatty Acid	The volatile subset of SCFAs (acetic, propionic, isobutyric, butyric, isovaleric, valeric). Supplied as a defined mixture in YCFA and related media.
BCFA	Branched-Chain Fatty Acid	Isobutyric, isovaleric, and 2-methylbutyric acids, derived from fermentation of valine, leucine, and isoleucine. Markers of proteolytic fermentation.
HMO	Human Milk Oligosaccharide	Complex non-digestible carbohydrates of human milk, selectively fermented by infant-associated <i>Bifidobacterium</i> .
FMT	Faecal Microbiota Transplantation	Transfer of processed donor stool to restore a dysbiotic microbiome; established therapy for recurrent <i>C. difficile</i> infection.
IBD	Inflammatory Bowel Disease	Crohn's disease and ulcerative colitis; characterised by dysbiosis, mucosal inflammation, and immune dysregulation.
IBS	Irritable Bowel Syndrome	Functional gastrointestinal disorder without structural pathology, associated with microbiome alterations.
GRAS	Generally Recognised As Safe	United States FDA classification for substances and organisms considered safe for their intended use in food.
PHB	Polyhydroxybutyrate	Intracellular polyester storage polymer accumulated under nutrient limitation; a bioplastic precursor.
PUL	Polysaccharide Utilisation Locus	Co-regulated gene cluster encoding the machinery for binding, degrading, and importing a specific glycan; the basis of glycan foraging in <i>Bacteroides</i> .

3.10 Clinical and antimicrobial resistance terms

Abbreviation	Full name	Definition
MRSA	Methicillin-Resistant <i>Staphylococcus aureus</i>	<i>S. aureus</i> carrying <i>mecA</i> or <i>mecC</i> , encoding PBP2a and conferring resistance to essentially all β -lactams.

Abbreviation	Full name	Definition
VRE	Vancomycin-Resistant <i>Enterococcus</i>	<i>E. faecium</i> or <i>E. faecalis</i> carrying <i>vanA</i> / <i>vanB</i> , conferring high-level vancomycin resistance.
ESBL	Extended-Spectrum β -Lactamase	Plasmid-encoded enzymes (TEM, SHV, CTX-M families) hydrolysing extended-spectrum cephalosporins and penicillins.
KPC	<i>Klebsiella pneumoniae</i> Carbapenemase	Ambler class A serine carbapenemase conferring carbapenem resistance across multiple Enterobacteriaceae.
NDM	New Delhi Metallo- β -Lactamase	Ambler class B zinc-dependent carbapenemase conferring pan-carbapenem resistance.
CRE	Carbapenem-Resistant Enterobacteriaceae	Enterobacteriaceae resistant to carbapenems via KPC, NDM, OXA-48, VIM, or IMP enzymes; associated with high bloodstream infection mortality.
MDR	Multidrug-Resistant	Non-susceptible to at least one agent in three or more antimicrobial categories.
XDR	Extensively Drug-Resistant	Non-susceptible to all but two or fewer antimicrobial categories.
PDR	Pan-Drug-Resistant	Non-susceptible to all agents in all categories tested.
HACEK	<i>Haemophilus</i> , <i>Aggregatibacter</i> , <i>Cardiobacterium</i> , <i>Eikenella</i> , <i>Kingella</i>	Slow-growing fastidious Gram-negative organisms of the oral flora, associated with subacute infective endocarditis.
NVS	Nutritionally Variant Streptococci	<i>Granulicatella</i> and <i>Abiotrophia</i> species requiring exogenous pyridoxal or L-cysteine; fail to grow on unsupplemented blood agar.
CDI	<i>Clostridioides difficile</i> Infection	Toxin-mediated colitis; the leading cause of antibiotic-associated diarrhoea. TcdA and TcdB disrupt the colonocyte cytoskeleton.
CAP	Community-Acquired Pneumonia	Pneumonia acquired outside hospital or within 48 h of admission.
HAP	Hospital-Acquired Pneumonia	Pneumonia developing 48 h or more after admission; associated with MDR organisms.

Abbreviation	Full name	Definition
UTI	Urinary Tract Infection	Infection of the urethra, bladder, ureter, or kidney.
BSI	Bloodstream Infection	Viable organisms in blood confirmed by culture; primary or secondary to a defined source.
HUS	Haemolytic Uraemic Syndrome	Microangiopathic haemolytic anaemia, thrombocytopenia, and acute kidney injury; most often following Shiga toxin-producing <i>E. coli</i> infection.
STEC	Shiga Toxin-Producing <i>Escherichia coli</i>	<i>E. coli</i> carrying <i>stx1</i> and/or <i>stx2</i> ; O157:H7 is the prototypic serotype.
ESKAPE	<i>Enterococcus</i> , <i>Staphylococcus</i> , <i>Klebsiella</i> , <i>Acinetobacter</i> , <i>Pseudomonas</i> , <i>Enterobacter</i>	Six priority nosocomial pathogens with high resistance rates, framed as a development priority by Rice (2008).

3.11 Databases, nomenclature authorities and standards

Abbreviation	Full name	Role
DSMZ	Deutsche Sammlung von Mikroorganismen und Zellkulturen	German culture collection; maintains type strains and the authoritative numbered medium formulations cited throughout the database.
ATCC	American Type Culture Collection	United States biological resource centre; reference strains and validated culture conditions.
NCBI	National Center for Biotechnology Information	Hosts GenBank, PubMed, and the NCBI Taxonomy database.
LPSN	List of Prokaryotic Names with Standing in Nomenclature	Authoritative registry of validly published prokaryotic names under the International Code of Nomenclature of Prokaryotes.
IJSEM	International Journal of Systematic and Evolutionary Microbiology	Journal of record for new prokaryotic species descriptions.
JCM	Japan Collection of Microorganisms	RIKEN biological resource centre; type strains with DSMZ cross-accessions.
ISO	International Organization for Standardization	Source of standardised microbiological methods, particularly in food and water testing.
WHO	World Health Organization	Source of the <i>Laboratory Biosafety Manual</i> and risk-group classifications.

3.12 Taxonomic qualifiers

Qualifier	Expansion	Meaning
emend.	emendation	Formal correction or expansion of a species or genus description without a change of name.
subsp.	subspecies	Rank below species, used where populations show consistent heritable differences — for example <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> .
serovar	serological variety	Variant defined by surface antigens (O, H, K) detected by agglutination; extensively used in <i>Salmonella</i> and <i>E. coli</i> .
biovar	biological variety	Variant defined by biochemical or physiological characteristics rather than antigens.
sp. / spp.	species (singular / plural)	An unidentified species, or several species, of the named genus.
comb. nov.	combinatio nova	A new combination, indicating a taxon transferred to a different genus.

NOTE on nomenclature drift — Prokaryotic nomenclature is revised continually. Several organisms in the database carry names that have been reassigned since their original description; where a widely used former name persists in the literature, the record shows both — for example *Roseburia intestinalis* / *Eubacterium rectale*, or *Fructilactobacillus sanfranciscensis* (formerly *Lactobacillus sanfranciscensis*). The search function indexes the whole name string, so either form retrieves the record. Confirm current standing against LPSN before publication.

3.13 Reagents and selective agents

Reagent	Chemical identity	Function
Esculin	6,7-Dihydroxycoumarin-6-glucoside	Hydrolysed by β -glucosidase to esculetin, which chelates Fe^{3+} to form a black complex. Differential indicator in BBE, bile esculin, and chromogenic agars.
Bile salts	Cholate / deoxycholate mixture	Detergents inhibiting Gram-positives and fastidious Gram-negatives by membrane disruption. Selective component of MacConkey, TCBS, and BBE.

Reagent	Chemical identity	Function
Crystal violet	Gentian violet	Triphenylmethane dye inhibiting Gram-positives at low concentration; used in MacConkey to permit Enterobacteriaceae growth selectively.
Cetrimide	Cetyltrimethylammonium bromide (CTAB)	Cationic detergent permitting <i>P. aeruginosa</i> growth while inhibiting most other organisms.
Cefoxitin	Second-generation cephalosporin	Used at 4 µg/mL in chromogenic MRSA media to detect <i>mecA/mecC</i> -mediated resistance; preferred over oxacillin for resistance induction.
Hemin	Iron-protoporphyrin IX	Essential growth factor for many anaerobes and capnophiles; the X factor requirement of <i>Haemophilus</i> . Supplies bioavailable iron.
Vitamin K1	Phylloquinone	Growth factor for pigmented anaerobes; standard co-supplement with hemin in anaerobic media.
IsoVitaleX / CVA	Defined vitamin supplement	Supplies NAD (V factor), cocarboxylase, glutamine, adenine, cystine, cysteine, guanine, thiamine pyrophosphate, PABA, and B ₁₂ for fastidious <i>Neisseria</i> and <i>Haemophilus</i> .
Resazurin	7-Hydroxy-3H-phenoxazin-3-one-10-oxide	Redox indicator: blue when oxidised, pink on partial reduction, colourless when fully reduced. Confirms that an anaerobic medium is adequately pre-reduced.
L-Cysteine HCl	—	The standard chemical reductant in anaerobic media, typically at 0.3–1.0 g/L.
Sodium sulfide (Na₂S)	—	A stronger reductant used for extremely oxygen-sensitive organisms; toxic and malodorous, requiring fume extraction.
Tween 80	Polysorbate 80	Non-ionic surfactant supplying oleic acid as a growth factor in MRS; also disperses mycobacterial clumps in 7H9 broth.

CRITICAL — Resazurin is the operator’s direct read-out of medium redox state. A medium showing pink coloration has been oxidised and must not be used for strict or extreme anaerobes. This single observation prevents a large proportion of anaerobic cultivation failures.

3.14 Units and measurements

Unit	Expansion	Notes
µg/mL	Micrograms per millilitre	Standard concentration unit for antimicrobials; numerically equal to mg/L. Used for oxygen measurement in anaerobic chambers, for example < 0.5 ppm O ₂ . Viable count density.
ppm	Parts per million	
CFU/mL	Colony-forming units per millilitre	
IU	International Unit	Standardised biological activity unit, used for some antimicrobial preparations. Turbidimetric growth measure. For <i>E. coli</i> , OD ₆₀₀ ≈ 0.1 corresponds to roughly 10 ⁸ CFU/mL; the relationship is species- and instrument-dependent and must be calibrated locally. Unit of redox potential (Eh). Strict anaerobe media typically require below –100 mV.
OD₆₀₀	Optical density at 600 nm	
mV	Millivolt	
v/v, w/v	Volume per volume, weight per volume	Supplement concentration conventions used in formulations.

4. Instructions for Use — Core Functions

This section describes the seven core tasks. Callout numbers in circles refer to Figure 1.

4.1 Task 1 — Locating an organism by name

Purpose. To find an organism when its name, or part of its name, is known.

Procedure

1. Click into the **Search Organism** field [1].
2. Begin typing. Results appear after a short pause; the application waits approximately 150 ms after the last keystroke before searching, so that typing is not interrupted.
3. Review the result list beneath the field. Each entry shows the binomial in italic and a coloured category badge.
4. Click an entry, or focus it with Tab and press Enter, to select it. The list closes and the **Target Organism** control [2] updates.
5. To clear the search, click the clear (×) button at the right of the field.

What the search matches

The search examines three fields for every record:

- the full scientific name, including any parenthetical synonyms;
- the complete trait list;
- the category label.

It does **not** search medium names, formulations, or the descriptive introduction. To search by medium name, use the Media Cross-Reference panel (Section 4.5).

Query normalisation

Full stops and commas are removed from both the query and the indexed text, and runs of whitespace are collapsed to a single space. The comparison is case-insensitive and matches any substring.

You type	Interpreted as	Result
E. coli	e coli	Matches <i>Escherichia coli</i> records
E.coli	ecoli	No match — the removed full stop closes the gap
coli	coli	Matches all <i>coli</i> records
MRSA	mrsa	Matches via the trait list
butyrate	butyrate	Matches every organism carrying a butyrate-related trait
Lachnospiraceae	lachnospiraceae	Matches every member of the family, because family names are held as traits

CAUTION — Typing an abbreviated genus with no space, as in *E.coli*, will return no result. Type either the full genus or the species epithet alone.

Result limits

The list displays at most 40 entries. Where more records match, a line above the list reports the number shown against the total — for example *Showing 40 of 63 matches*. Add characters to narrow the query. If nothing matches, the message *No organisms matched your search* is displayed.

Productive search strategies

Goal	Query approach
A specific species	The species epithet alone is usually the fastest and least error-prone route
All members of a genus	The genus name
All members of a family	The family name, which is stored as a trait
All organisms sharing a phenotype	A trait phrase such as Butyrate Producer, Mucin Degradar, Spore
All organisms of an oxygen class	Strict Anaerobe, Microaerophile, Facultative
Resistance phenotypes	MRSA, VRE, ESBL

4.2 Task 2 — Locating an organism by taxonomy

Purpose. To browse the database when the organism's name is not known, or to survey what is available in a functional area.

Route A — the grouped dropdown

1. Click the **Target Organism** control [2]. A panel opens listing all 455 organisms.
2. Entries are arranged under group headings that mirror the organisational structure described in Section 7.
3. Each entry is preceded by its oxygen circle and Gram hexagon, allowing feasibility to be judged during browsing.
4. Click an entry to select it.

Route B — the taxonomy browser

1. Click the information icon [8] on the **Organism Categories** card header. The **Organism Taxonomy & Classification** panel opens.
2. A table of contents lists the 11 groups. Within each group, organisms are arranged into subgroups reflecting phylogenetic and functional clustering.
3. Click any organism name. The panel closes and that organism becomes the selected target.
4. Press Esc, or click outside the panel, to close it without changing the selection.

NOTE — The taxonomy browser is the most efficient route when the requirement is functional rather than nominal — for example, “*show me the butyrate producers*” or “*what oral anaerobes are covered*”.

4.3 Task 3 — Selecting the isolation objective

Purpose. To specify which class of medium the analysis should return.

Procedure

1. Click the **Isolation Objective** control [3].
2. Select one of the available objectives.
3. The control label updates to show the selection.

Available objectives

Objective	Availability
Primary Isolation	Always available
Selective Screening	Always available
Non-Selective Enrichment	Always available
Sporulation-Cultivation	Appears only when the selected organism is flagged as an endospore-former

All 455 organisms carry a complete set of primary, selective, and enrichment media, so the first three objectives always return a result.

The sporulation objective

The fourth objective is offered for the 33 organisms recorded as endospore-formers. The list is regenerated each time the target organism changes, so the objective appears and disappears as the selection moves between spore-forming and non-spore-forming organisms.

CAUTION — If **Sporulation-Cultivation** was selected for a spore-former and the target is then changed to a non-spore-former, the objective is withdrawn from the list. Confirm the objective before clicking **Analysis & Match**; if the current objective is no longer valid, the application displays an explanatory message rather than a result.

Choosing the right objective

Situation	Objective
Pure or near-pure material; maximum recovery required	Primary Isolation
Mixed specimen; target is a minority population	Selective Screening
Target is present at very low abundance	Non-Selective Enrichment, then plate onto the primary medium
Spore preparation, heat-resistance testing, or long-term stock	Sporulation-Cultivation
Uncertain	Run all three in turn and compare. The three results together describe the organism's full cultivation envelope.

4.4 Task 4 — Running the analysis and reading the result

Procedure

1. Confirm the target organism [2] and objective [3].
2. Click **Analysis & Match** [4].
3. The placeholder is replaced by the result panels.

4.4.1 The organism identity header [12]

Read this block in the following order.

a. Category badge. A coloured label giving the functional category — for example *Gut Microbiome* — *Culturomics*, *Clinical GI Pathogen*, *Oral Microbiome*. This orients the record but carries no cultivation instruction.

b. Biosafety triangle and banner. Immediately left of the organism name. An **upward** green triangle indicates a non-pathogenic or BSL-1 organism; a **downward** amber or red triangle indicates BSL-2 or BSL-3. The banner beneath states the classification in words. Where the triangle is grey and the banner reads *BSL: Unknown — verify before handling*, no biosafety record exists and the level must be established locally.

c. Scientific name. Displayed in italic, following current nomenclature. Where a widely used synonym exists it is shown alongside.

d. Trait chips. Four to eight concise descriptors. By convention the first two are the Gram reaction and the oxygen class, followed by defining metabolic or taxonomic features. The trait list is the substrate for the symbiosis engine (Section 5.1) and for much of the handling and detection logic.

e. Description. Two to five sentences on ecological niche, clinical or industrial relevance, and defining metabolic features.

4.4.2 The recommended medium [13]

A single medium name, matched to the selected objective. Where a DSMZ medium number or a standard abbreviation exists, it is included in the name.

CRITICAL — The medium shown corresponds to the objective currently selected. Changing the objective changes the medium. When transcribing a formulation to the bench, record the objective alongside it.

4.4.3 The standard formulation [14]

The complete formulation per litre, in a fixed-width block.

- Component names are dot-aligned to their quantities.
- Lines beginning with // are **preparation notes**, not ingredients. They carry sterilisation conditions, pH adjustment steps, post-autoclave additions, and pre-reduction requirements.
- Arrows such as ← 30 mM give the molar equivalent of a mass quantity where the molarity is the biologically meaningful figure.
- Where a formulation builds on a base medium, the base is named as its own line item.

CRITICAL — Preparation notes are as binding as the ingredient list. A component listed as a post-autoclave addition will be destroyed if autoclaved. A medium requiring 24 h pre-reduction will not support an extreme oxygen-sensitive organism if inoculated immediately after preparation.

4.4.4 Critical culture parameters [15]

A grid of key-value pairs. Three keys are always present:

Parameter	Content
Atmosphere	Gas composition, for example < 0.5 ppm O ₂ , 5 % CO ₂ / N ₂ balance, Aerobic
Incubation	Temperature and duration, for example 37 °C, 7–14 d
pH	Value or range

Additional keys appear according to the medium and objective:

Key	Typical content
Reductant	Chemical reductant and concentration
Inhibitor / Inhibitors	Selective agents and concentrations
Carbon	Defined carbon source where it is the selective principle
Supplement	Serum, filtrate, growth factor, or vitamin addition
Colony	Expected colony morphology on the medium

Key	Typical content
Format	For enrichment media, the physical format and transfer schedule

CAUTION — The incubation duration is a minimum, not a maximum. Fastidious and slow-growing organisms in this database include entries requiring 14–21 days; mycobacterial media require 4–8 weeks. Plates discarded at 48 h will be falsely reported as no growth.

4.4.5 Authorised references

The primary sources for the record, semicolon-separated. Retrieve and read these before adopting a protocol into routine use.

4.4.6 What to do when no result appears

Message	Cause	Action
<i>No database entry found for organism...</i>	No organism is selected, or the selection is invalid	Select an organism using [1] or [2]
<i>No [objective] media defined for...</i>	The record lacks a medium for that objective	Select a different objective
<i>...is not marked as a spore-former...</i>	Sporulation requested for a non-spore-former	Select a different objective
<i>Select an organism first, then click Symbiotic Analysis</i>	Symbiosis requested with no target selected	Select an organism first

4.5 Task 5 — Searching for a culture medium by name

Purpose. To answer the reverse question: *given this medium, which organisms does the database associate with it, and in what role?*

Procedure

1. Click the information icon **[5]** on the **Media Selection** card header. The **Media Cross-Reference** panel opens.
2. The panel header reports the index size — the number of distinct media and the number of organisms indexed.
3. On opening, all media are listed in descending order of the number of organisms using them, so the most widely used media appear first.
4. Type a medium name or fragment into the search field. **At least two characters are required.** Results refresh after a short pause.
5. Each result card shows the medium name, the number of organisms using it, and the list of those organisms. Each organism is tagged with the role the medium plays for it — [primary], [selective], or [enrichment].
6. Click any organism name. The panel closes, that organism is selected, and a full analysis runs immediately.
7. Press Esc, or click outside the panel, to close it.

How medium names are matched

Before indexing and before comparison, medium names are normalised: converted to lower case, parenthetical content removed, and whitespace runs collapsed. This means that *YCFA Agar* and *YCFA Agar (modified)* index to the same entry, and that a query need not reproduce punctuation.

You type	Behaviour
ycfa	Matches every medium whose normalised name contains ycfa
blood agar	Matches Blood Agar, Columbia Blood Agar, Laked Blood Agar, and similar
bhi	Matches BHI, BHIS, PRAS BHI, and related entries
y	No search — a minimum of two characters is required

Result limits. At most 50 media cards are rendered. Where more match, a line reports *Showing 50 of N media. Refine your search.*

Applications of reverse lookup

Application	Method
Media inventory rationalisation	Identify the media supporting the largest number of target organisms and stock those preferentially. YCFA agar alone serves 72 organisms in this database; PRAS BHI broth serves 52.
Interpreting mixed growth	Where a plate yields unexpected colonies, list the organisms the database associates with that medium as a starting hypothesis set.
Assessing selectivity	A medium associated with many organisms under [primary] is permissive. A medium associated with few, and chiefly under [selective], is narrow.
Substituting a medium	Search for a medium already held in stock and check whether the target organism appears in its list.
Training	Compare the organism sets of a selective medium and its parent base medium to demonstrate the effect of the selective agents.

4.6 Task 6 — Determining whether a medium is suitable for a given organism

This is the composite question the toolkit is most often used to answer, and it requires evidence from more than one panel. Figure 3 sets out the procedure.

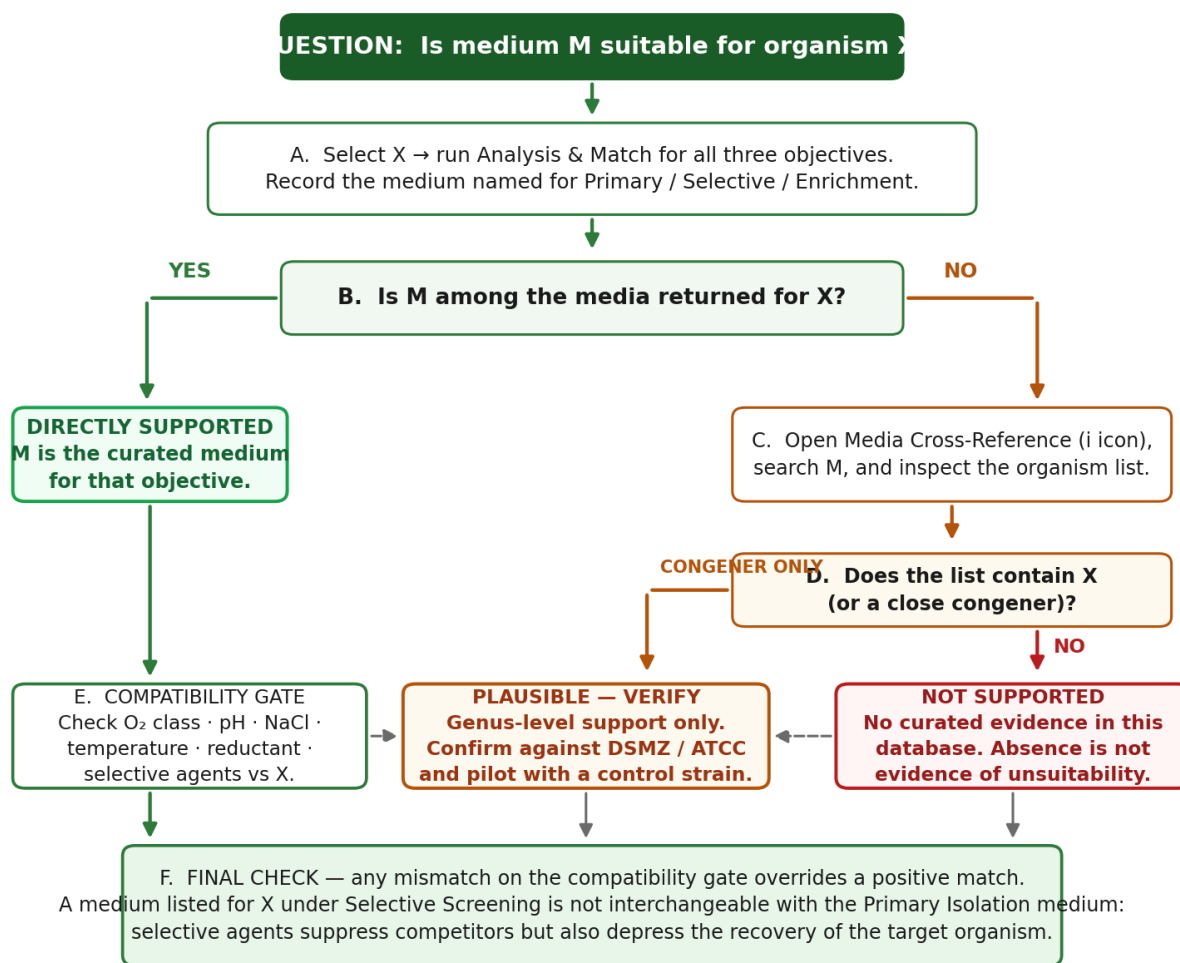


Figure 3 — Decision procedure for judging medium suitability (Section 4.6).

4.6.1 Procedure

Step A — establish the curated recommendations. Select the organism. Run **Analysis & Match** three times, once for each of Primary Isolation, Selective Screening, and Non-Selective Enrichment. Record the medium named each time. These three media constitute the database’s positive evidence for that organism.

Step B — test for a direct match. If the medium under consideration appears among the three, the answer is **directly supported**: the medium is the curated recommendation for that objective, traceable to the cited source. Proceed to Step E.

Step C — perform a reverse lookup. If the medium does not appear, open the **Media Cross-Reference** panel [5] and search for it. Read the organism list.

Step D — assess the reverse-lookup result.

- **The organism appears in the list.** This should not occur if Step B was performed correctly for all three objectives; if it does, re-check the objective under which the medium is listed.
- **A congener appears — the same genus, or a closely related genus in the same family.** The result is **plausible but unverified**. Genus-level support is a reasonable basis for a pilot experiment but not for a routine protocol. Confirm against DSMZ or ATCC records for the specific species and run a control strain in parallel.
- **Neither the organism nor a congener appears.** The medium is **not supported by this database** for that organism. Note carefully that absence is not evidence of unsuitability — it reflects the current state of curation only.

Step E — apply the compatibility gate. Independently of the curated evidence, verify that the medium does not violate any of the organism’s physiological constraints. Every constraint must pass.

Constraint	Source in the toolkit	Failure mode if violated
Oxygen class	Oxygen circle on the organism	No growth; cell death for E and S organisms
pH	ACID / ALK badges; pH parameter of the medium	No growth, or growth of contaminants only
Salinity	HAL / E-HAL badges	Osmotic lysis, or failure to grow
Temperature	THERM / H-THM badges; incubation parameter	No growth; agar melts above approximately 60 °C
Carbon source	AUTO / MIX / METH / MTRO badges	No growth on a medium supplying only organic or only inorganic carbon
Reductant	Formulation and Reductant parameter	Redox potential too high for strict anaerobes
Required supplement	SCFA badge; Supplement parameter	No growth where an essential factor is absent
Selective agents	Inhibitors parameter	Target inhibited alongside the competitors

Step F — reach a conclusion.

A failure at the compatibility gate overrides a positive curated match. In practice this arises most often in three situations:

- a medium is listed for the organism under **Selective Screening** and is then used for primary isolation, depressing recovery;
- a base medium is used without its required supplement, most commonly hemin, vitamin K1, or the VFA mixture;
- an anaerobic medium is used without pre-reduction, so that the redox potential is far above the organism’s tolerance.

4.6.2 Worked example

Question: is MacConkey agar suitable for Bacteroides fragilis?

- **Step A.** Select *B. fragilis* and run all three objectives. The recommended media are anaerobic formulations; MacConkey agar is not among them.
- **Step C.** Search macconkey in the Media Cross-Reference panel. The organism list consists of Enterobacteriaceae and related facultative Gram-negatives.
- **Step D.** Neither *B. fragilis* nor a *Bacteroides* congener appears. Not supported.
- **Step E.** The compatibility gate fails on two counts. The oxygen class is S: MacConkey agar is an aerobic plating medium and is not pre-reduced. The medium also contains bile salts and crystal violet at concentrations chosen to select Enterobacteriaceae.
- **Step F.** MacConkey agar is unsuitable. The database’s recommended anaerobic media should be used instead.

Question: is BBE agar suitable for a Parabacteroides species not individually listed?

- **Step C.** Search bbe. The organism list contains 20 organisms, chiefly *Bacteroides* and *Parabacteroides* species, listed under [selective].
- **Step D.** Congener support is present and strong at genus level.
- **Step E.** The compatibility gate passes: the medium is anaerobic, the pH is appropriate, and the selective agents — oxgall and gentamicin — target the flora that *Parabacteroides* is intrinsically resistant to.
- **Step F.** Plausible, and appropriate for a pilot. Confirm against the DSMZ record for the specific species, and run a characterised *Parabacteroides* control on the same batch.

4.7 Task 7 — Saving and exporting a result

Purpose. To produce a bench-usable or archivable record of an analysis.

Procedure

1. Run the analysis so that the result panels are populated.
2. Click **Save & Export [9]**.
3. The browser print dialogue opens with a dedicated print stylesheet applied.
4. Choose a physical printer, or select *Save as PDF / Microsoft Print to PDF* as the destination.

What the print stylesheet does

Change	Effect
Page setup	A4 portrait, approximately 14 mm top and bottom and 12 mm side margins
Removed	Header bar, sidebar, all buttons, and the page footer
Added	A print header giving the product name, software version, the research-use-only statement, and the source databases
Reflowed	The two-column grid collapses to a single column; the parameter grid expands to four columns
Recoloured	Backgrounds are lightened for legibility on paper while the colour semantics of formulation, biosafety, and reference blocks are preserved

CAUTION — The exported record captures a single organism-objective combination. Where a protocol depends on more than one objective, for example an enrichment step followed by plating, export each objective separately and keep them together.

Good practice for bench records

- Annotate the printout with the date, the operator, and the medium batch or lot number.
- Where the printout will be used as a working document, retrieve the cited primary reference and file it alongside.
- Record the software version, shown in the print header, so that the record can be reconciled against future database revisions.

5. Extended Functionality

5.1 Symbiotic (cross-feeding) analysis

5.1.1 Purpose and scientific rationale

Many organisms in this database do not grow well, or at all, in axenic culture on defined media, because in their native environment they depend on metabolites supplied by neighbouring taxa. The classic example in the gut is butyrogenesis: *Faecalibacterium prausnitzii* and several Lachnospiraceae convert exogenous **acetate** to **butyrate** via butyryl-CoA:acetate CoA-transferase, and therefore require an acetate source. In a mixed community that acetate is supplied by bifidobacteria and other acetogens. A second well-characterised example is interspecies hydrogen transfer, in which fermentative organisms release H₂ that hydrogenotrophic methanogens consume, keeping the hydrogen partial pressure low enough for the fermenters' own reactions to remain thermodynamically favourable.

The **Symbiotic Analysis** function identifies candidate partners of this kind. It answers the question: *given this organism, which other organisms in the database are plausible metabolic partners, and what would be exchanged?*

Typical applications:

- designing a defined co-culture or synthetic consortium;
- explaining why an organism grew in a mixed enrichment but failed in pure culture;
- selecting a helper strain to support recovery of a fastidious target;
- identifying which metabolite to add to a medium as a substitute for a partner organism;
- teaching cross-feeding and syntrophy.

5.1.2 Procedure

1. Select a target organism by any route (Sections 4.1–4.2).
2. Click **Symbiotic Analysis [6]**. A panel opens over the page.
3. Read the target's own metabolic profile at the top of the panel.
4. Read the ranked partner list beneath.
5. Click any partner card to close the panel, select that organism, and run a full analysis on it.
6. Press Esc, or click outside the panel, to close.

If no organism is selected, the application displays *Select an organism first, then click Symbiotic Analysis*.

5.1.3 How the analysis works

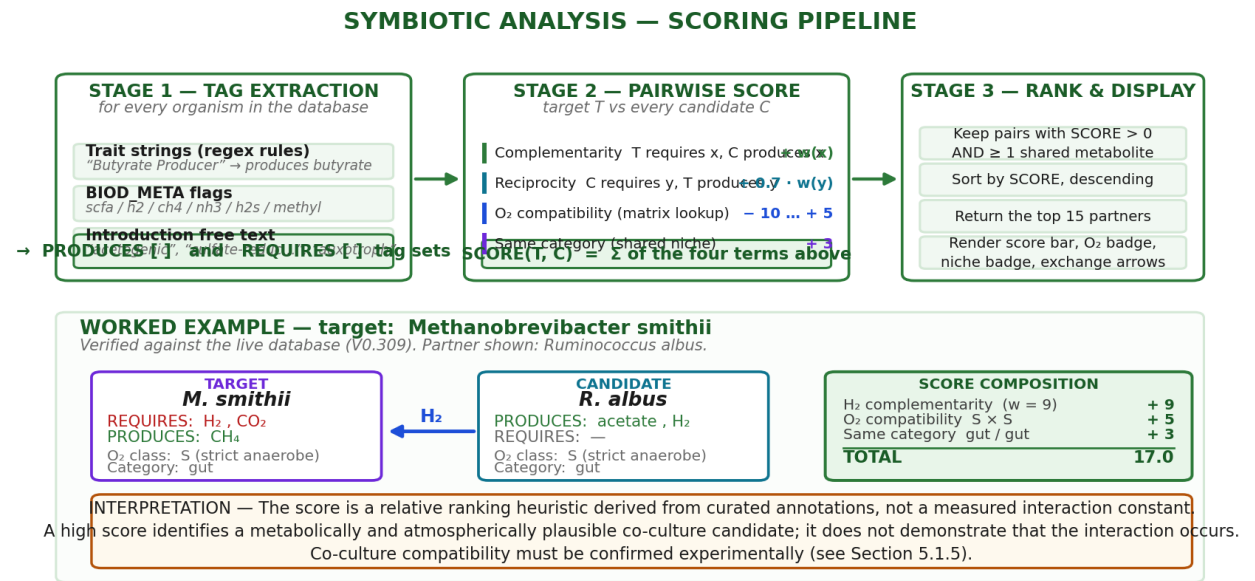


Figure 4 — Symbiotic Analysis scoring pipeline with a worked example.

Stage 1 — metabolic tag extraction. For every organism the application derives two sets — **PRODUCES** and **REQUIRES** — from three independent sources within the record:

Source	Mechanism	Example
Trait strings	Pattern rules matched against the trait list	<i>Butyrate Producer</i> → produces butyrate; <i>Acetate-Dependent</i> → requires acetate; <i>Hydrogenotrophic</i> → requires H2 and C02, produces CH4
Physiological metadata flags	Boolean flags in the metadata record	scfa → produces SCFAs; ch4 → produces CH4, requires H2 and C02; h2s → produces H2S, requires sulfate; methyl → requires methanol
Description text	Case-insensitive keyword scan of the introduction	<i>vitamin K / menaquinone</i> → produces vitamin-K; <i>auxotroph</i> → requires exogenous-vitamins; <i>acetogenic</i> → produces acetate, requires H2 and C02; <i>sulfate-reduc...</i> → requires sulfate and H2, produces H2S

A directional override applies to hydrogen. The h2 flag normally denotes production, but for recognised hydrogenotrophic methanogens it is interpreted as **consumption**, so that *Methanobrevibacter smithii* is correctly modelled as requiring rather than producing H₂.

Stage 2 — pairwise scoring. The target is scored against every other organism in the database. The score is the sum of four terms:

Term	Condition	Contribution
Complementarity	The target <i>requires</i> metabolite x and the candidate <i>produces</i> it	+ $w(x)$, the metabolite's weight
Reciprocity	The candidate <i>requires</i> metabolite y and the target <i>produces</i> it	+ $0.7 \times w(y)$
Oxygen compatibility	Matrix lookup on the two oxygen classes	-10 to +5
Shared niche	Both organisms belong to the same functional category	+ 3

The asymmetry between complementarity and reciprocity is deliberate: the user has asked about the target, so metabolites flowing *toward* the target are weighted more heavily than those flowing away from it.

Metabolite weights encode ecological significance. Butyrate carries the highest weight at 10, reflecting its central role in gut physiology; molecular hydrogen carries 9, reflecting the thermodynamic importance of interspecies hydrogen transfer; acetate carries 8. Minor and ubiquitous metabolites such as CO₂ carry 1. The complete weight table is reproduced in Appendix C.

The oxygen compatibility matrix (Appendix D) applies a strong penalty to atmospherically incompatible pairings. An extreme oxygen-sensitive organism paired with an obligate aerobe scores -10, which in practice removes the pair from consideration regardless of metabolic complementarity. This encodes a physical constraint: two organisms cannot form a co-culture if no single atmosphere supports both.

Stage 3 — filtering, ranking and display. A candidate is retained only if its score is greater than zero **and** at least one metabolite is actually exchanged. A high oxygen-compatibility score alone is therefore insufficient to generate a partner. Surviving candidates are sorted by descending score and the top **15** are displayed.

5.1.4 Reading the results panel

Target profile. The panel opens with the target's name, category, and two chip rows:

- **Produces** — metabolites the organism releases;
- **Requires** — metabolites it depends on.

Where both rows are empty, the panel states that no metabolic cross-feeding data is available for that organism. See Section 5.1.6.

Partner cards. Each card carries:

Element	Meaning
Score bar and number	The composite score. The bar is scaled to the top-ranked partner, so it shows relative standing within this result set only — bars are not comparable between different targets.
Organism name	Click or press Enter to load that organism's full profile.
O₂ badge	A tick badge where the oxygen compatibility term is zero or positive; a cross badge where it is negative. A negative badge means the pair cannot share a single atmosphere and co-culture is not physically achievable under one gas regime.

Element	Meaning
Same niche badge	Shown when both organisms share a functional category, indicating that they plausibly co-occur.
Exchange arrows	metabolite → target denotes a metabolite the partner supplies to the target. target → metabolite denotes a metabolite the target supplies to the partner. Cards showing arrows in both directions represent mutualistic candidates.

5.1.5 Worked example

Selecting *Methanobrevibacter smithii*, the dominant archaeon of the human gut, produces the following.

Target profile. Requires H₂ and CO₂; produces CH₄. This is correct hydrogenotrophic methanogenesis: $4 \text{ H}_2 + \text{CO}_2 \rightarrow \text{CH}_4 + 2 \text{ H}_2\text{O}$.

Top partners. The leading candidates all score 17.0 and include *Ruminococcus albus*, *Ruminococcus champanellensis*, *Ruminococcus bicirculans*, *Prevotella copri*, and *Cloacibacillus evryensis*. All are fibre-fermenting gut anaerobes that release H₂.

Score composition for *R. albus*:

Term	Value
H ₂ complementarity (weight 9)	+ 9
Oxygen compatibility, S × S	+ 5
Shared niche, gut / gut	+ 3
Total	17.0

Interpretation. The result reproduces a genuine and well-documented syntrophy. The methanogen consumes the hydrogen released by cellulolytic fermenters, and by holding the hydrogen partial pressure low it makes the fermenters' own NADH re-oxidation thermodynamically favourable. Both partners are strict anaerobes of the same niche, so a single atmosphere and a single medium base can serve both. This is a sound basis for designing a co-culture experiment.

5.1.6 Coverage and limitations

These constraints are material and must be understood before the function is used.

Coverage. Metabolic tags can be derived for **142 of the 455 organisms**. Of these, **69 organisms return at least one symbiotic partner**. For the remaining organisms the panel reports that no cross-feeding data is available. This is a limitation of annotation depth, not a statement about the organism's biology: an organism with no tags may nonetheless participate in extensive cross-feeding *in vivo*.

Coverage is strongest for gut anaerobes, SCFA producers and consumers, methanogens, and organisms with explicit metabolic traits. It is weakest for clinical pathogens, fungi, and environmental organisms, whose trait annotations describe virulence, taxonomy, or habitat rather than metabolite exchange.

The score is a ranking heuristic, not a measurement. It is computed from curated text annotations. It is not derived from genome-scale metabolic models, flux balance analysis, growth data, or any experimental measurement of interaction. A score of 17.0 does not mean that an interaction of a given magnitude occurs; it means that, within this database and this rule set, the pair ranks highly for metabolic and atmospheric plausibility.

Specific things the model does not capture:

- **Antagonism.** Bacteriocins, organic acid inhibition, competitive exclusion, and contact-dependent killing are not modelled. Two organisms may be perfectly complementary metabolically and still be mutually exclusive in culture.
- **Stoichiometry and kinetics.** The model records that a metabolite is produced, not at what rate, in what quantity, or under what conditions.
- **Regulation.** Production and consumption are frequently conditional on substrate availability, growth phase, and pH; the model treats them as constitutive.
- **Physical and pH compatibility beyond oxygen.** Temperature, pH, and salinity compatibility are not scored. Two organisms may pass the oxygen test yet require incompatible pH optima.
- **Directionality of some flags.** Aside from the explicit hydrogenotroph override, boolean metabolic flags are interpreted as production by default. An organism that consumes a metabolite recorded only by a flag may be misclassified.
- **Strain-level variation.** Cross-feeding capacity varies between strains of the same species; the model operates at species level.

Required verification. A high-scoring pairing is a hypothesis. Before it is relied upon:

1. confirm the metabolic claim against the cited primary reference for both organisms;
2. confirm that a single medium and atmosphere can support both — run **Analysis & Match** on each and compare the parameter grids directly;
3. test the co-culture experimentally, with both monocultures as controls;
4. verify that the predicted metabolite is actually exchanged, for example by quantifying SCFAs by gas chromatography or by measuring headspace H_2 and CH_4 ;
5. check for antagonism by cross-streaking or by spent-medium inhibition assay before committing to a consortium design.

5.2 Sporulation-cultivation protocols

5.2.1 Purpose

To induce, harvest, and quality-control endospores — for long-term stock preparation, heat-resistance testing, spore-based probiotic manufacture, sterilisation validation, or the study of sporulation itself.

5.2.2 Availability

The objective appears only for the **33 organisms** flagged as confirmed endospore-formers. The flag is the single authoritative criterion; the application does not infer spore-forming capacity from family names or trait text, because such inference misclassifies non-spore-forming members of otherwise spore-forming families.

If the objective is requested for an organism that is not so flagged, the application declines and explains why rather than generating a speculative protocol.

5.2.3 Protocol selection

The protocol returned depends on the organism's traits:

Organism type	Protocol	Basis
Aerobic Bacillaceae	Difco Sporulation Medium (DSM) with heat-shock selection	Nutrient downshift into a Mn^{2+} - and Ca^{2+} -supplemented medium triggers synchronised sporulation
Anaerobic Clostridiaceae or Peptostreptococcaceae	Duncan-Strong sporulation medium, anaerobic	Starch- and phosphate-based medium under strict anaerobiosis

Organism type	Protocol	Basis
Streptomycetaceae	Soya Flour Mannitol (SFM) aerial conidia production	Aerial mycelium formation and conidiation
Other confirmed spore-formers	General multi-stage sporulation protocol	Growth phase followed by nutrient limitation

CRITICAL — The *Streptomyces* protocol produces **aerial conidia, not endospores**. Conidia are *not* heat-resistant. The heat-selection and heat-resistance quality control steps used for *Bacillus* and *Clostridium* spores must not be applied to conidia; doing so destroys the preparation and yields a false-negative viable count.

5.2.4 Protocol structure

Each protocol supplies a medium name, a formulation, numbered procedural steps within the formulation block, and a parameter grid covering protocol type, atmosphere, incubation, expected spore yield, quality-control criteria, and storage.

The generic sequence is:

1. **Pre-cultivation** — grow to mid-logarithmic phase in a rich medium.
2. **Transfer** — wash and resuspend in the sporulation medium at a defined starting density.
3. **Sporulation incubation** — typically 48–72 h for *Bacillus*; longer for clostridia.
4. **Monitoring** — phase-contrast microscopy; mature spores are phase-bright.
5. **Heat selection** — for true endospore-formers, typically 80 °C for 10 min, killing vegetative cells and leaving spores viable.
6. **Enumeration and storage** — plate count on a recovery medium, then store as a spore suspension at 4 °C.

CAUTION — Several of the spore-formers in this database are BSL-2 or BSL-3 organisms, and spores are environmentally persistent and readily aerosolised. Spore preparation from *Clostridium botulinum*, *Clostridium tetani*, or *Bacillus anthracis* must be performed only under the containment specified by the institutional risk assessment. Waste must be autoclaved; spores survive many chemical disinfectants that are effective against vegetative cells.

5.3 Handling tips and cautions engine

5.3.1 Purpose

The **Handling Tips & Cautions** panel [16] is generated for every analysis. It converts the organism’s physiological metadata and the composition of the selected medium into specific, actionable bench warnings, and grades them by severity.

5.3.2 Severity grades

Grade	Meaning	Response
CRITICAL	Failure will cause organism death, an invalid result, or a biosafety breach	Must be satisfied before work begins
CAUTION	Failure commonly causes cultivation failure or misinterpretation	Should be satisfied; deviation must be justified
NOTE	Supporting information improving yield or interpretation	Advisory

A summary line at the top of the panel gives the count of each grade. Read that line first: a result carrying three critical items requires different preparation from one carrying none.

5.3.3 What triggers a tip

Tips are generated from several independent inputs, so the panel content changes with the objective as well as with the organism.

Trigger class	Examples
Oxygen class	Chamber requirements for E and S; gas-generation systems for M; the note that F organisms may show different morphology under the two atmospheres
Medium composition	Presence of resazurin triggers the redox-indicator warning; Na ₂ S triggers a toxicity and extraction warning; blood-containing media trigger storage and haemolysis-reading guidance; laked blood triggers a pigmentation note; media that must not be autoclaved trigger a preparation warning
Physiological badges	ACID, ALK, HAL, E-HAL, THERM, H-THM, AUTO, SCFA, HYD, METH, AMPH, SDPH each generate their specific constraint
Biosafety and pathogenicity	Toxin-producing organisms, aerosol-risk organisms requiring a biological safety cabinet, methicillin-resistant strains, and organisms classified as WHO Group 1 carcinogens each generate a dedicated warning
Spore-forming status	Spore persistence, disinfection resistance, and waste handling
Organism-specific rules	A number of organisms carry bespoke warnings — for example the specific containment and antitoxin considerations for <i>C. botulinum</i> and <i>C. tetani</i> , or bait-culture technique for <i>Nocardia</i>

5.3.4 Using the panel

Read the panel **before** preparing media, not after inoculation. Several critical items — pre-reduction time, post-autoclave additions, chamber availability, cabinet requirements — must be acted upon days before the culture is set up.

CAUTION — The panel is generated from the fields present in the record. It is not a complete risk assessment and it does not enumerate every hazard. It supplements, and never replaces, the institutional risk assessment and the laboratory's own standard operating procedures.

5.4 Detection and diagnosis methods engine

5.4.1 Purpose

The **Detection & Diagnosis Methods** panel [17] answers the question that follows successful cultivation: *how do I confirm that what I have grown is what I intended to grow?*

5.4.2 Method classes

Methods are grouped and colour-coded by class. A summary line reports how many methods of each class are present.

Class	Content
Culture	Colony morphology, growth characteristics, differential reactions on the recommended medium
Staining	Gram stain and its expected result; acid-fast staining for mycobacteria; spore staining; fungal stains; archaeal considerations
Molecular	16S rRNA amplification with primer sequences; organism-specific gene targets; qPCR assays; sequencing approaches
Biochemical	Enzyme and substrate utilisation tests; commercial identification systems
Immunological	ELISA, lateral flow, direct fluorescent antibody, agglutination
Imaging	Microscopic morphology and, where relevant, radiological correlates
Other	Methods not falling into the classes above

5.4.3 Method content

Each method card carries a class badge, a title, an explanatory text, and, where applicable:

- **Primer sequences**, given in 5'→3' orientation with the primer name — for example the universal bacterial primers 27F and 1492R, and the V4 region primers 515F and 806R;
- **Stepwise protocols**, presented as numbered steps;
- **A citation** to the source method.

5.4.4 Universal and specific methods

Every organism receives the universal 16S rRNA identification method, since it applies across the bacterial and archaeal domains. Beyond that, methods are selected according to the organism's Gram reaction, oxygen class, taxonomic group, biosafety level, category, and the composition of the selected medium — so a mycobacterium receives acid-fast staining and MGIT culture guidance, a yeast receives fungal stains, and a spore-former receives spore staining.

CAUTION — Detection methods are supplied for laboratory identification of cultured isolates and for research use. They are not validated diagnostic procedures, and they do not carry the performance characteristics, controls, or reporting criteria required for clinical diagnostic reporting. Clinical laboratories must use validated assays under their accredited quality system.

5.5 Derived workflows

Beyond its four documented functions, the toolkit supports a number of derived applications that follow from combining panels. These are legitimate uses that are not signposted in the interface.

5.5.1 Comparing the cultivation envelope of a single organism

Run all three objectives in sequence for one organism and compare the results side by side. The comparison reveals:

- **the permissive envelope** — what the organism needs when nothing competes with it (primary isolation);
- **the selective margin** — which inhibitors it tolerates, and therefore which competitors can be suppressed without losing it (selective screening);
- **the amplification strategy** — what substrate preferentially enriches it from a mixed source (enrichment).

Read together, these define both the organism's nutritional requirements and its intrinsic resistance profile.

5.5.2 Designing a defined synthetic consortium

1. Identify the functional target of the consortium — for example butyrate production.
2. Select a keystone organism performing that function and read its **Requires** list in the symbiosis panel.
3. Use the ranked partners to select organisms supplying each required metabolite.
4. For each candidate, run **Analysis & Match** and compare the parameter grids. Retain only combinations that share a feasible atmosphere, temperature, and pH.
5. Use the **Media Cross-Reference** panel to find a single medium serving as many members as possible.
6. Verify experimentally as set out in Section 5.1.6.

5.5.3 Rationalising a media inventory

Open the **Media Cross-Reference** panel with an empty search field. Media are listed in descending order of use. Compare that ranking against the organisms your laboratory actually works with, and stock preferentially the media with the widest coverage. In this database YCFA agar supports 72 organisms and PRAS BHI broth 52, so a laboratory working across gut anaerobes obtains disproportionate coverage from a small number of base media plus supplements.

5.5.4 Troubleshooting a failed cultivation

Where an organism failed to grow, work back through the record in this order:

1. **Handling tips** [16]**** — was any CRITICAL item unmet?
2. **Parameter grid** [15]**** — was the atmosphere correct? Was the plate discarded before the stated minimum incubation had elapsed?
3. **Formulation** [14]**** — were preparation notes followed? Were post-autoclave additions made? Was the medium pre-reduced for the required time?
4. **Redox state** — was the resazurin pink at the time of inoculation?
5. **Objective** — was a selective medium used where primary isolation was intended?
6. **Symbiosis panel** [6]**** — does the organism require a metabolite that neither the medium nor a partner organism supplied? If so, supplement the medium with that metabolite directly.

5.5.5 Selecting a supplement in place of a partner organism

Where the symbiosis panel shows that a target requires a metabolite, the metabolite can often be supplied chemically instead of biologically. An organism requiring acetate can be cultured on a medium supplemented with sodium acetate rather than co-cultured with an acetogen; the *F. prausnitzii* record demonstrates exactly this design, adding 30 mM sodium acetate to a YCFA base. Reading the symbiosis panel and the formulation together shows the rationale behind such supplements and generalises it to other organisms.

5.5.6 Biosafety triage before specimen work

Before a specimen or panel of organisms is accepted, run each candidate organism and record the biosafety triangle and banner. This yields a rapid inventory of the containment levels involved and flags any organism carrying **BSL: Unknown**, which must be resolved before work proceeds. The result is an input to, not a substitute for, the formal risk assessment.

5.5.7 Training and competency assessment

The database supports structured teaching:

- **Selective agent function** — compare a selective medium with its base medium and read the **Inhibitors** parameter to show what each agent suppresses and why the target survives.
- **Anaerobic technique** — compare the handling tips of an E-class and an F-class organism to demonstrate the practical difference between the two.
- **Nomenclature** — use the records carrying dual names to demonstrate reclassification and its consequences for literature searching.
- **Media design rationale** — use the mucin-based media to demonstrate selection by sole carbon source rather than by chemical inhibition.

6. Symbol and Indicator Guide

6.1 Complete symbol reference

INDICATOR SYMBOL REFERENCE

BIOSAFETY — triangle, left of the organism name		OXYGEN REQUIREMENT — filled circle	
▲ Non-Pathogenic	Not documented human pathogenicity; GRAS / saprophytic	● EOS	< 0.5 ppm O ₂ — anaerobic chamber only
▲ BSL-1	Not known to cause disease in healthy adults	● Strict Anaerobe	2 % O ₂ — chamber or gas-generating jar
▲ BSL-2	Moderate hazard; Class II BSC for aerosol-generating steps	● Microaerophile	10 % O ₂ plus 5–10 % CO ₂
▲ BSL-3	Serious/lethal aerosol-transmissible disease; high containment	● Facultative	Grows aerobically or anaerobically
▲ Unknown	No BSL record — verify before handling	● Obligate Aerobe	10 % O ₂ required
GRAM STAIN — hexagon		CATEGORY — coloured dot / badge	
● Gram-Positive	Thick peptidoglycan (20–80 nm); retains crystal violet	● Gut Microbiome	
● Gram-Negative	Thin peptidoglycan + outer membrane with LPS	● Clinical GI Pathogen	
● Variable / N.A.	Archaea, fungi, or unreliable Gram reaction	● Tissue & Wound Pathogen	
		● Archaea / Methanogen	
		● Specialised / Fastidious	
		● Industrial · Food · Extremophile · Oral · Zoonotic	
GROWTH-ENVIRONMENT BADGES — displayed only when the trait applies			
SCFA	SCFA-dependent — VFA supplement required	ACID	Acidophile — optimum pH < 6.5
ALK	Alkaliphile — optimum pH > 8.5	HAL	Halophile — 2–10 % NaCl
E-HAL	Extreme halophile — > 15 % NaCl	AUTO	Obligate autotroph — CO ₂ sole carbon source
MIX	Mixotroph / facultative autotroph	THERM	Thermophile — 55–80 °C
H-THM	Hyperthermophile — > 80 °C	HYD	Hydrogenophile — H ₂ electron donor
METH	Methanotroph — CH ₄ sole carbon source	AMPH	Ammoniphile — NH ₃ energy source
SDPH	Sulphidophile — H ₂ S electron donor	MTRO	Methylotroph — C ₁ / methanol sole carbon source
READING RULE — Every organism always carries exactly one biosafety triangle, one oxygen circle and one Gram hexagon. Environment badges are additive and may be absent. A badge is a cultivation constraint, not a taxonomic statement: if a badge is shown, the corresponding parameter must be satisfied or growth will fail.			

Figure 5 — Complete indicator symbol reference (Section 6).

6.2 Where each symbol appears

Symbol	Sidebar dropdown	Search results	Result header	Symbiosis panel
Oxygen circle	Yes	—	via trait chip	via O ₂ badge
Gram hexagon	Yes	—	via trait chip	—
Biosafety triangle	—	—	Yes	—
Category badge / dot	Yes (group heading)	Yes	Yes	Yes
Environment badge	Indicator Key only	—	via trait chip	—
Severity bar	—	—	Handling tips	—
Method class badge	—	—	Detection methods	—

The oxygen circle and Gram hexagon appear **before** an analysis is run, in the dropdown and on the selection control. This is deliberate: it allows the user to judge whether the organism is within their laboratory's capability before committing to the lookup.

6.3 Reading the indicators as a set

Every organism carries exactly one biosafety triangle, one oxygen circle, and one Gram hexagon. Environment badges are additive and may be absent. Read them in this order:

1. **Biosafety triangle** — *may I handle this organism here?* An upward green triangle indicates non-pathogenic or BSL-1; a downward amber or red triangle indicates BSL-2 or BSL-3; a grey downward triangle indicates that the level is unrecorded and must be established locally. If the answer is no, stop.
2. **Oxygen circle** — *can I provide the atmosphere?* This is the most common cause of failure. E requires an anaerobic chamber; S requires a chamber or a gas-generating jar; M requires a microaerobic system.
3. **Gram hexagon** — *what will I see down the microscope, and which antimicrobial classes will the medium exploit?* The Gram reaction underlies most selective agent choices.
4. **Environment badges** — *what else must the medium deliver?* Each badge is a hard constraint on pH, salinity, temperature, carbon source, or supplementation.

6.4 Colour semantics

Colour family	Applied to	Meaning
Green	Biosafety triangle, primary interface accents	Safe / permissive / the application's identity colour
Yellow-green	Biosafety triangle	BSL-1
Amber	Biosafety triangle, caution bars, reference block	Caution; moderate hazard
Red	Biosafety triangle, critical bars, Gram-negative hexagon	Highest hazard; critical requirement
Violet / purple	Oxygen circles for E and S, tissue pathogen category	Anaerobic; specialist handling
Blue	Oxygen circle for A, archaea category, note bars	Aerobic; informational
Teal	Oxygen circle for F, detection panel, industrial category	Facultative; identification methods
Rose	Gram-positive hexagon	Gram-positive
Stone / grey	Gram hexagon X, unknown biosafety	Not applicable or unrecorded

CAUTION — Two colour pairings warrant particular attention. The amber and red biosafety triangles both point **downward**, which is the shape cue for “pathogenic”; the green and yellow-green triangles both point **upward**. Users should read the triangle direction, not only its colour. Similarly, the E and S oxygen circles are both violet and differ mainly in depth of shade; read the letter, since the operational difference between them is substantial.

7. Taxonomy and Classification

7.1 Three parallel classification schemes

The application uses three distinct schemes concurrently. Confusing them is a common source of misunderstanding.

Scheme	Purpose	Where seen	Values
Group	Navigation and organisation of the interface	Dropdown headings; taxonomy browser	11 groups, subdivided into 67 subgroups
Category	Functional and clinical labelling; colour coding; a scoring input for the symbiosis engine	Category badge; category dots; search results	10 categories
Biological taxonomy	Scientific classification	Trait chips (family names); the binomial itself	Standard Linnaean ranks

Groups reflect *how a laboratory thinks about its work* — by specimen source and application area. Categories reflect *functional and clinical role*. Neither is a phylogeny. Within a group, subgroups are arranged by phylogenetic and functional clustering, so the subgroup level is where the arrangement comes closest to biological taxonomy.

7.2 The eleven groups

Group	Name	Subgroups	Organisms
1	Gut Commensals & SCFA Producers	9	197
2	Enteric & Foodborne Pathogens	6	49
3	Respiratory, Wound & Soft Tissue Pathogens	7	29
4	Zoonotic, Vector-Borne & Systemic Pathogens	6	33
5	Oral Microbiome & Upper GI Tract	7	62
6	Biotechnology, Industrial & Research Models	5	16
7	Food Processing & Fermentation	8	20
8	Soil, Environmental & Spore-Forming Organisms	3	5
9	Extremophiles	5	12
10	Chemolithotrophs, Gas Metabolism & Photolithotrophs	5	10
11	Pathogenic Fungi (Eukaryota)	6	22
	Total	67	455

NOTE — Group counts and category counts do not correspond. A group is a navigational container; a category is a functional label. For example, Group 1 contains 197 organisms while the gut category contains 207, because a small number of organisms placed in other groups carry the gut category label.

Group order differs between the two navigation routes. The taxonomy browser sorts groups ascending by number, so Group 10 precedes Group 11. The **Target Organism** dropdown presents groups in the order they are defined in the database, in which Group 11 (Pathogenic Fungi) appears *before* Group 10 (Chemolithotrophs), reflecting the order in which the groups were added. Both routes contain the same organisms.

7.3 Group contents in outline

Group 1 — Gut Commensals & SCFA Producers. The largest group. Subgroups cover core butyrate producers; acetate and cross-feeding species; mucosal and polysaccharide degraders; colonic commensals and modulators; spore-forming gut colonisers; gut archaea; obligate intracellular and rare GI pathogens; representatives of novel phyla; and a placeholder for candidate phyla and uncultured “dark matter”.

Group 2 — Enteric & Foodborne Pathogens. Enterobacteriaceae and Gram-negative enteropathogens; *Vibrio* and Aeromonadaceae; anaerobic GI pathogens; hospital-acquired GI pathogens; microaerophilic enteric pathogens; non-spore-forming foodborne pathogens.

Group 3 — Respiratory, Wound & Soft Tissue Pathogens. Anaerobic wound organisms; aerobic Gram-positive rods and diphtheroids; pyogenic cocci and streptococci; Gram-negative respiratory and wound organisms; non-tuberculous mycobacteria and leprosy; the *M. tuberculosis* complex; pathogenic non-*albicans* yeasts.

Group 4 — Zoonotic, Vector-Borne & Systemic Pathogens. BSL-3 organisms and select agents; spirochaetal zoonoses; bite and animal-contact zoonoses; systemic and meningeal pathogens; obligate intracellular tick-borne Rickettsiales; Chlamydiales and mycoplasmas.

Group 5 — Oral Microbiome & Upper GI Tract. Viridans streptococci as early colonisers; cariogenic organisms; red-complex periodontal pathogens; orange-complex and emerging periodontal pathogens; oral microaerophiles; oral anaerobes and commensals; fastidious CO₂-requiring organisms and nutritionally variant streptococci.

Group 6 — Biotechnology, Industrial & Research Models. Genetic model organisms; fermentation and organic acid producers; industrial biosynthesis platforms; rhizosphere and bioengineering organisms; methylotrophic yeast expression hosts.

Group 7 — Food Processing & Fermentation. Dairy starters; vegetable and dough fermentation lactic acid bacteria; probiotic and meat cultures; sourdough specialists; cheese rind and smear-ripening flora; mould-based fermentation; food fermentation yeasts; rare and artisan fermenters.

Group 8 — Soil, Environmental & Spore-Forming Organisms. Spore-forming soil pathogens; soil-origin actinomycetes and mycobacteria; environmental fungi and moulds.

Group 9 — Extremophiles. Extreme and moderate halophiles; alkaliphiles; moderate thermophiles at 55–80 °C; hyperthermophiles above 80 °C; acidophiles.

Group 10 — Chemolithotrophs, Gas Metabolism & Photolithotrophs. H₂-oxidising chemolithotrophs; methanotrophs; nitrifiers; sulfur and denitrifying chemolithotrophs; photolithotrophs.

Group 11 — Pathogenic Fungi. *Candida* species; *Aspergillus* and moulds; encapsulated yeasts; dimorphic systemic fungi; *Pneumocystis* and Mucorales; dermatophytes.

A complete organism-by-organism listing is given in Appendix A.

7.4 The ten categories

Category key	Displayed label	Organisms
gut	Gut Microbiome — Culturomics	207
clinical	Clinical GI Pathogen	93
oral	Oral Microbiome	52

Category key	Displayed label	Organisms
zoonotic	Zoonotic / Systemic Pathogen	28
food	Food Processing	20
industrial	Industrial / Bioengineering	15
extremo	Extremophile / Autotroph	15
tissue	Tissue & Wound Pathogen	14
special	Specialized / Fastidious	8
archaea	Archaea / Methanogen	3

The category is not merely cosmetic: it contributes the *shared niche* term to the symbiosis score (Section 5.1.3), on the reasoning that organisms sharing a functional category are more likely to co-occur and therefore to interact.

7.5 Nomenclature conventions and cautions

- **Binomials** are shown in italic, following current standing in nomenclature.
- **Synonyms** appear within the name field where a superseded name remains in wide use. Both forms are searchable.
- **Species groups** are recorded as a single entry where the source literature treats them together — for example the *Mycobacterium avium* complex.
- **Family names** are stored as traits, which makes family-level searching possible.

CAUTION — Prokaryotic taxonomy is under continuous revision, and several genera represented here have been substantially reorganised in recent years, notably within the Lactobacillaceae and the Clostridiaceae. A name shown in the toolkit may have been superseded since the record was curated. Where nomenclature is material — for publication, for regulatory submission, or for a culture collection deposit — confirm current standing against LPSN and the most recent IJSEM validation lists.

8. Methodology Reference

This section provides the technical background needed to execute the protocols the toolkit returns. It is not a substitute for a laboratory methods text; it establishes the principles that the database's parameters assume.

8.1 The three media classes

8.1.1 Primary isolation media

Design principle. Maximise recovery of the target organism. Nutritionally rich, containing peptones, yeast and meat extracts, defined growth factors (hemin, vitamin K1, cysteine, vitamins), and where necessary blood, serum, or biological filtrates that supply undefined co-factors.

Interpretation. Growth on a primary isolation medium indicates viability and nutritional compatibility. It carries **no** identification information on its own, because the medium is permissive by design.

When to use. For pure or near-pure material; for maximum yield; for viability assessment; for subculture and maintenance.

8.1.2 Selective media

Design principle. Suppress competing flora while permitting the target to grow. Selection is achieved by one or more of:

Mechanism	Examples in this database
Antimicrobial inhibition	Kanamycin/vancomycin for Bacteroidetes; mupirocin for bifidobacteria; vancomycin for lactobacilli; neomycin, rifampicin, fusidic acid, nalidixic acid
Bile salts	Oxgall in BBE; bile salts in MacConkey and TCBS
Dyes	Crystal violet, malachite green, bromocresol green
Extreme pH	Alkaline pH 8.6 in TCBS; acidic pH 5.6 in Sabouraud
Elevated salt or lithium	LiCl in <i>Bifidobacterium</i> selective medium
Sole carbon source	Mucin as sole carbon and nitrogen source; methanol for methylotrophs; CH ₄ for methanotrophs
Physical selection	Heat shock for spore-formers

Interpretation. Growth on a selective medium is *presumptive evidence of identity*, because the medium excludes most non-target organisms. It is not confirmation. Confirmation requires the detection methods panel.

CRITICAL — Selective media reduce recovery of the target as well as of competitors. Quantitative work must not be performed on selective media unless the recovery efficiency has been separately established with a control strain.

8.1.3 Enrichment media

Design principle. Increase the target population before plating. Usually liquid, permitting a larger inoculum volume and a longer effective exposure of the organism to nutrients than a plate surface allows.

Two strategies:

- **Non-selective enrichment** — a rich broth amplifying everything present. Simple, but the target's proportion may fall if competitors grow faster.
- **Substrate-directed enrichment** — a defined substrate that only the target, or a narrow functional group, can use. Prebiotic oligosaccharides for fibre degraders, mucin for mucolytic organisms, glycerol for reuterin producers, and HMO mixtures for infant bifidobacteria all appear in this database.

Critical operational parameter. The **transfer schedule**. Enrichment cultures must be plated or subcultured at defined intervals, given in the **Format** parameter. Left too long, the culture is overgrown by fast-growing competitors and the target is lost; plated too early, insufficient amplification has occurred.

8.2 Anaerobic cultivation technique

Just under half of the organisms in this database are strict or extreme anaerobes, and anaerobic technique failures are the commonest cause of unsuccessful recovery.

8.2.1 Equipment tiers

Tier	Equipment	Achievable O ₂	Suitable for
1	Anaerobic jar with gas-generating sachet	Approximately 1 % or below	S organisms of moderate sensitivity
2	Evacuation-replacement jar with gas mixture	Below 0.5 %	Most S organisms
3	Anaerobic chamber (Coy or equivalent) with palladium catalyst under H ₂ /N ₂ /CO ₂	Below 5 ppm	S organisms, including fastidious ones
4	Anaerobic chamber with continuous O ₂ monitoring, fresh catalyst, and all handling performed inside	Below 0.5 ppm	E (EOS) organisms

CRITICAL — For E-class organisms, every operation — media preparation, pre-reduction, inoculation, incubation, and colony picking — must occur inside the chamber. Transferring a plate through room air, even briefly, is sufficient to abolish recovery.

8.2.2 Pre-reduction

Autoclaving dissolves oxygen into a medium. Reducing agents scavenge it, but the reaction requires time.

1. Prepare and sterilise the medium.
2. Transfer it into the anaerobic environment while still warm.
3. Hold it in the anaerobic atmosphere for the period specified in the preparation notes — commonly 24 h, sometimes longer.
4. Confirm reduction by reading the resazurin indicator before use.

8.2.3 The resazurin read-out

Appearance	Redox state	Action
Colourless	Fully reduced	Use
Faint pink	Partially oxidised	Return to the chamber and re-reduce; do not use for E organisms
Pink or blue	Oxidised	Discard

8.2.4 Chemical reductants

Reductant	Typical concentration	Notes
L-Cysteine hydrochloride	0.3–1.0 g/L	The standard reductant; also a sulfur and nitrogen source Stronger; used for the most oxygen-sensitive organisms. Toxic and malodorous — prepare in a fume hood. Used in thioglycollate broth Occasionally used in defined media
Sodium sulfide (Na ₂ S)	Low millimolar	
Sodium thioglycollate Dithiothreitol	Variable Variable	

8.2.5 Gas phases

Composition	Application
100 % N ₂	Simple anaerobiosis where CO ₂ is not required
80:10:10 N ₂ /CO ₂ /H ₂	Standard anaerobic chamber mixture; H ₂ supports catalytic O ₂ removal
90:10 N ₂ /CO ₂	Where a bicarbonate buffer requires a CO ₂ partial pressure
5–10 % CO ₂ in air	Capnophiles and many oral organisms
5–10 % O ₂ with 5–10 % CO ₂	Microaerophiles
H ₂ /CO ₂ (typically 80:20)	Hydrogenotrophic methanogens and acetogens

CAUTION — Where a medium contains carbonate or bicarbonate buffer, the CO₂ partial pressure is part of the buffering system, not merely an atmosphere. Incubating such a medium without CO₂ causes a pH rise that will inhibit growth.

8.3 Special atmospheres and extreme conditions

Condition	Practical requirement
Thermophily, 55-80 °C	High-temperature incubator; Gelrite in place of agar above approximately 60 °C, since agar melts; sealed vessels to limit evaporation
Hyperthermophily, above 80 °C	Sealed serum vials; pressurised vessels above 100 °C; synthetic seawater bases are common
Extreme halophily	Media prepared with near-saturated salt; note that high-salt media are corrosive to some incubator components and that plates dry rapidly
Alkaliphily	Carbonate/bicarbonate buffering; separate sterilisation of carbonate from other components to avoid precipitation
Acidophily	Acid-stable buffer; agar may hydrolyse at low pH and high temperature, so sterilise the acid component separately
Autotrophy	Mineral salts base with a defined inorganic electron donor and a CO ₂ -containing gas phase; scrupulous exclusion of organic carbon, including from laboratory water and from finger contact

8.4 Detection and identification approaches

8.4.1 The identification cascade

The conventional sequence, from cheapest and fastest to most definitive:

1. **Colony morphology and growth characteristics** — presumptive only, but free and immediate.
2. **Gram stain and microscopy** — establishes cell wall type and morphology in minutes.
3. **Rapid biochemical spot tests** — catalase, oxidase, indole, coagulase; minutes to an hour.
4. **Differential media reactions** — haemolysis, lactose fermentation, esculin hydrolysis, lecithinase.
5. **Commercial biochemical panels** — API strips, VITEK cards; 18-48 h.
6. **MALDI-TOF mass spectrometry** — minutes from a colony, given a suitable reference library. Now the routine identification method in most clinical laboratories.
7. **16S rRNA gene sequencing** — universal; genus-level and often species-level assignment; the fallback where phenotypic methods fail or where the organism is not in the mass spectral library.
8. **Whole genome sequencing** — definitive identification, typing, and resistance and virulence gene profiling.

8.4.2 16S rRNA gene amplification

The universal method offered for every organism in the database.

Primer	Direction	Sequence (5'→3')	Target
27F	Forward	AGAGTTTGATCMTGGCTCAG	Near-full-length amplification
1492R	Reverse	TACGGYTACCTTGTTACGACT	Near-full-length amplification
515F	Forward	GTGYCAGCMGCCGCGGTAA	V4 region
806R	Reverse	GGACTACNVTGGGTWCTAAT	V4 region

Degenerate base codes follow IUPAC convention: M = A/C, Y = C/T, R = A/G, W = A/T, N = any, V = A/C/G.

NOTE — Near-full-length amplification with 27F/1492R gives the best taxonomic resolution for isolate identification. The V4 primers are shorter and better suited to amplicon community profiling on short-read platforms. Choose according to purpose.

CAUTION — 16S rRNA sequencing resolves most genera but cannot reliably separate certain closely related species pairs, notably within the *Bacillus cereus* group, the *Enterobacter cloacae* complex, and several *Streptococcus* and *Mycobacterium* groups. Where species-level assignment is material, use an additional housekeeping gene target, MLST, or whole genome sequencing.

8.4.3 Staining methods

Stain	Application	Principle
Gram	Universal first-line	Differential retention of the crystal violet-iodine complex by thick peptidoglycan
Ziehl-Neelsen / Kinyoun	Mycobacteria, <i>Nocardia</i>	Mycolic acid retains carbol fuchsin against acid-alcohol decolourisation
Auramine-rhodamine	Mycobacterial screening	Fluorochrome binding to mycolic acid; higher throughput than Ziehl-Neelsen
Spore stain (Schaeffer-Fulton)	Endospore-formers	Malachite green penetrates the spore coat under heat and resists water decolourisation
Lactophenol cotton blue	Fungi	Stains chitin and preserves morphology for mounting
Calcofluor white	Fungi	Fluorescent binding to chitin and cellulose
India ink / nigrosin	<i>Cryptococcus</i>	Negative staining reveals the polysaccharide capsule
Giemsa	Intracellular organisms	Stains inclusion bodies and intracellular forms

8.4.4 Quality control

Control	Purpose
Positive control strain	Confirms that the medium supports the target. Essential when preparing a batch of a fastidious or selective medium.
Negative / inhibition control	Confirms that a selective medium actually suppresses the intended competitors.
Sterility control	An uninoculated plate or tube from the batch, incubated alongside.
Redox control	The resazurin indicator, read at the moment of inoculation.
Atmosphere control	An anaerobic indicator strip, or a continuous chamber O ₂ reading.
Batch records	Lot numbers for base medium, blood, serum, and antimicrobial supplements; pH after autoclaving; date of preparation.

CAUTION — Antimicrobial supplements degrade in prepared plates. Selective media containing antibiotics have a materially shorter usable life than their base media, commonly two to four weeks refrigerated depending on the agent. A selective medium that has lost its selective agent behaves as a permissive medium and will yield overgrowth that may be mistaken for a positive result.

9. Data Model, Provenance and Contribution

This section is written for advanced users, database contributors, and reviewers who need to understand how a record is constructed and validated.

9.1 Record structure

Each organism is represented by three co-indexed records sharing a single database key.

9.1.1 The organism record

Field	Requirement	Content
key	Required	Unique identifier in snake_case, no spaces, up to 30 characters
latinName	Required	Full binomial following current nomenclature, with synonyms in parentheses
category	Required	One of the ten category keys (Section 7.4); controls badge colour and contributes to the symbiosis score
traits	Required	Four to eight descriptors, conventionally beginning with the Gram reaction and the oxygen class, then metabolic features and family. Supplies the search index and the symbiosis engine.
intro	Required	60–200 words of plain text on niche, relevance, and metabolic features. Scanned for symbiosis keywords.
media.primary	Required	Medium name, formulation, and parameters
media.selective	Strongly recommended	As above
media.enrichment	Strongly recommended	As above
ref	Required	Semicolon-separated primary references, including a DSMZ or NCBI accession or a PubMed-indexed citation

Each media entry contains a name, a formula (dot-aligned per litre, with preparation notes

on lines beginning with //), and a params object of key-value pairs in which Atmosphere, Incubation, and pH are mandatory.

9.1.2 The physiological metadata record

Field	Requirement	Accepted values
o2	Required	E, S, M, F, A, X
gram	Required	P, N, X
spore	Optional	true for confirmed endospore-formers; unlocks the sporulation objective
scfa	Optional	true where the organism is a primary SCFA producer
ph	Optional	AC acidophile, AL alkaliphile
sal	Optional	HL halophile, EH extreme halophile
carbon	Optional	AU obligate autotroph, MX mixotroph
temp	Optional	TH thermophile, HT hyperthermophile
h2, ch4, nh3, h2s	Optional	true for the corresponding gas metabolism
methyl	Optional	true for methylotrophy

Current population of the optional flags: spore 33, scfa 41, h2s 3, methyl 3, h2 2, ch4 2, nh3 2; sal — EH 5, HL 1; carbon — MX 4, AU 3; temp — HT 4, TH 2; ph — AC 2, AL 2.

The sparse population of these flags is the direct cause of the symbiosis engine's limited coverage (Section 5.1.6). Contributors can materially improve the extended functionality by supplying them.

9.1.3 The biosafety record

A single value per organism: 0 non-pathogenic or GRAS, 1 BSL-1, 2 BSL-2, 3 BSL-3, or null for unknown or unclassified. The record must be verified against the CDC/NIH BMBL 6th Edition or the WHO *Laboratory Biosafety Manual* 4th Edition. All 455 organisms currently carry a value.

CRITICAL — Understating a biosafety level is the most consequential possible data error in this application, because a user may rely on it when planning containment. The curation policy is that a misclassification of a BSL-3 organism as BSL-2 causes immediate rejection of a submission.

9.1.4 The group assignment

Each key appears in exactly one subgroup of one group. This drives the dropdown, the taxonomy browser, and the organism counts. All 455 keys are assigned; there are no orphans.

9.2 Integrity validation

The application runs an automatic consistency check when the page loads. Any inconsistency is written to the browser console and, if present, surfaced in an on-page banner. The checks are:

Check	Detects
Organism → metadata	An organism record with no physiological metadata
Organism → biosafety	An organism record with no biosafety record (would display as <i>BSL: Unknown</i>)
Organism → group	An organism present in the database but absent from all groups, and therefore unreachable by navigation
Group → organism	A group referencing a key that does not exist
Group → metadata / biosafety	A group referencing a key lacking either supporting record
Duplicate group membership	A key appearing in more than one subgroup
Orphaned metadata	A metadata record with no corresponding organism
Orphaned biosafety	A biosafety record with no corresponding organism

The database shipped with V0.309 passes all checks: organism, metadata, biosafety, and group membership counts are all 455, with no orphans and no duplicates.

The three principal data objects are frozen at the top level after load, preventing accidental addition or deletion of records at run time.

9.3 Submitting a new organism

The **Submit Profile** button [11] opens the contributor guide.

Eligibility requirements

1. **Check first.** Search the database, and browse the taxonomy, to confirm the organism is not already present.
2. **Authorised sources only.** Every formulation, growth parameter, and clinical statement must trace to a DSMZ type-strain medium, an NCBI/NIH record, an IJSEM or IJSB species description, a CLSI or EUCAST guideline, an ISO standard, or a PubMed-indexed publication. Encyclopaedic websites, textbooks, and commercial kit inserts are not accepted.
3. **Primary medium is mandatory.** Selective and enrichment media are strongly recommended. Where none is described in the literature, state this explicitly and cite the source. Formulations must give full ingredient quantities per litre; shorthand such as “*base as above*” is not accepted.
4. **Biosafety level must be accurate,** per WHO or CDC classification, and is independently reviewed.
5. **No proprietary or confidential data.** Unpublished internal formulations, trade secrets, and client data must not be submitted.

Submission route. A plain-text template is provided within the guide and can be copied to the clipboard. Complete one file per organism without altering field names, and email it to the submissions address given in the guide, attaching primary reference PDFs where available.

Review process. Submissions are acknowledged, then technically reviewed against the cited sources; inconsistencies are returned for clarification. Approved records are integrated and the handling and detection engines verified against the new metadata before publication. Contributors may request attribution in the reference field.

10. Troubleshooting

10.1 Interface behaviour

Symptom	Probable cause	Resolution
Page loads but no controls respond	JavaScript disabled or blocked	Enable JavaScript; check for a blocking browser extension or enterprise policy
Search returns nothing for a known organism	Query normalisation, most often an abbreviated genus written without a space, as in <i>E.coli</i>	Type the full genus, or the species epithet alone
Search list truncated	More than 40 matches	Add characters; the header line reports the total
Media search does nothing	Fewer than two characters entered	Type at least two characters
Media result list truncated	More than 50 media match	Refine the search; the footer line reports the total
Sporulation objective missing	The selected organism is not flagged as an endospore-former	Only 33 organisms offer this objective
Objective list changed unexpectedly	The objective list is rebuilt when the target organism changes	Re-select the objective after changing organism
Modal will not close	Focus is trapped inside the modal by design	Press Esc, or click outside the panel
Layout appears as one column	Viewport narrower than approximately 740 px	Widen the window, or scroll — the sidebar now sits above the result
Printed output missing panels	The print stylesheet deliberately removes navigation	This is expected; only the result content is printed

10.2 Result content

Symptom	Probable cause	Resolution
<i>No database entry found for organism</i>	No valid organism selected	Select an organism before running the analysis
<i>No [objective] media defined</i>	The record has no medium for that objective	Choose a different objective
<i>...is not marked as a spore-former</i>	Sporulation requested for a non-spore-former	Choose a different objective
<i>Select an organism first</i>	Symbiotic Analysis clicked with no target	Select an organism

Symptom	Probable cause	Resolution
<i>No metabolic cross-feeding data available</i>	The organism yields no metabolic tags; this applies to 313 of 455 organisms	Expected behaviour, not a fault. See Section 5.1.6.
<i>No symbiotic partners identified</i>	Tags exist but no partner exceeds the score threshold	Expected behaviour
Biosafety shows <i>BSL</i> : <i>Unknown</i>	No biosafety record	Establish the level locally before handling. Not currently expected in V0.309, in which all records carry a value.

10.3 Cultivation failures

The table below maps common bench outcomes to the panel that will most often explain them.

Outcome	First checks	Panel
No growth at all	Atmosphere correct? Incubation long enough — was the plate read before the stated minimum? Medium pre-reduced? Resazurin colourless at inoculation?	[15] Parameters, [16] Handling tips
No growth of an anaerobe	Chamber O ₂ within the organism's tolerance? Plates transferred through air? Catalyst fresh? Reductant present at the stated concentration?	[16] Handling tips
Growth of everything except the target	Was a selective medium used where primary isolation was needed? Are the inhibitors appropriate to the competing flora?	[13] Medium, [15] Parameters
Overgrowth on a selective medium	Has the antimicrobial supplement degraded? Check the plate preparation date.	Section 8.4.4
Weak or pinpoint colonies	Required supplement omitted — hemin, vitamin K1, VFA mixture, serum, or filtrate? Incubation curtailed?	[14] Formulation, [16] Handling tips
Growth in mixed culture but not in pure culture	The organism may depend on a cross-fed metabolite. Identify it and supplement the medium directly.	[6] Symbiosis panel
Unexpected colony morphology	For facultative organisms, morphology commonly differs between aerobic and anaerobic incubation.	[15] Parameters
Correct growth, wrong identification	Selective growth is presumptive only. Confirm by an independent method.	[17] Detection methods

Outcome	First checks	Panel
pH drift or medium colour change	Carbonate-buffered medium incubated without the required CO ₂ partial pressure.	[15] Parameters, Section 8.2.5

11. Limitations, Verification Duty and Safety

This section consolidates the constraints stated throughout the manual. It should be read in full before the toolkit is used to inform any laboratory decision.

11.1 Database limitations

- **Coverage is representative, not exhaustive.** 455 organisms, weighted heavily toward gastrointestinal, enteric, and oral microbiology. Absence of an organism is not evidence that it cannot be cultured.
- **Records are at species or species-group level.** Strain-to-strain variation in nutritional requirement, oxygen tolerance, antimicrobial resistance, and cross-feeding capacity is real and is not modelled.
- **Formulations are curated summaries.** They condense a primary source and may omit detail material to a particular application.
- **Nomenclature may lag.** Prokaryotic taxonomy is revised continually.
- **The database is a snapshot.** It reflects curation at the time of the software release, not the current literature.

11.2 Derived-output limitations

- **Handling tips are rule-generated,** from the fields present in the record. The panel is not a complete hazard enumeration and is not a risk assessment.
- **Detection methods are for laboratory identification and research use.** They are not validated diagnostic procedures and carry no performance characteristics, controls, or reporting criteria for clinical use.
- **Symbiosis scores are ranking heuristics** derived from curated text annotations, with coverage for 142 of 455 organisms and partner results for 69. They do not measure interaction and do not model antagonism, stoichiometry, kinetics, regulation, or compatibility on any axis other than oxygen.
- **Sporulation protocols are generic by organism class,** selected from four templates rather than curated per organism.

11.3 The user's verification duty

The toolkit is a starting point for laboratory work, never its authority. Before any protocol is adopted:

1. **Retrieve and read the cited primary reference.** The references block exists for this purpose.
2. **Confirm the biosafety classification** against the institutional risk assessment and the applicable national framework. Never rely on the displayed triangle alone.
3. **Verify the formulation** against the source, particularly the concentration of selective agents and the identity of post-autoclave additions.

4. **Run a positive control strain** when preparing a new batch of any fastidious or selective medium.
5. **Confirm identification independently.** Growth on a selective medium is presumptive, never confirmatory.
6. **Validate locally** before any method enters routine or regulated use.

11.4 Safety obligations

- Work within the containment specified by your institutional biosafety committee, not by this toolkit.
- Treat any organism displayed as **BSL: Unknown** as potentially hazardous until the level is established locally.
- Determine whether any organism you intend to handle is a regulated select agent or national equivalent, and comply with the applicable statutory controls. The toolkit does not track regulatory status.
- Observe the specific hazards of the reagents in the formulations. Sodium sulfide is toxic and malodorous and requires fume extraction. Several selective agents are antimicrobials requiring appropriate handling and disposal.
- Autoclave all waste. Spores of the spore-forming organisms in this database survive many chemical disinfectants effective against vegetative cells.
- Where a medium requires human- or animal-derived components — blood, serum, mucin, faecal filtrate — apply the appropriate biological handling controls and sourcing documentation.

11.5 Regulatory position

The Culturomics & Media Navigator is **For Research Use Only**. It is not a medical device, has not been evaluated by any regulatory authority for diagnostic use, and must not be used for clinical diagnosis, patient management, or therapeutic decision-making. Clinical and diagnostic laboratories may use it as a reference and training aid, but all procedures entering diagnostic service must be validated under the laboratory's own accredited quality management system.

12. Version and Document Control

12.1 Software version applicable to this manual

This edition documents **software version V0.309**, comprising 455 organism profiles across 11 groups and 67 subgroups, with 943 distinct normalised medium names.

12.2 Features introduced since earlier releases

Users familiar with earlier releases should note the following changes, since procedures described in older internal documentation may no longer apply.

Feature	Status in V0.309
Organism count	Expanded to 455
Groups	Expanded to 11, with the addition of oral microbiome, zoonotic and systemic pathogens, and pathogenic fungi
Categories	Expanded to 10, adding oral and zoonotic
Symbiotic Analysis	Introduced
Media Cross-Reference	Introduced
Glossary	Introduced, with 133 terms
Biosafety data	Now a first-class field on every record, with an explicit <i>unknown</i> sentinel
Endospore flag	Now the sole authority for the sporulation objective; inference from family or trait text removed
Database administration panel	Removed from the public interface; contribution is now by the submission route in Section 9.3
Contributor guide	Updated to version 2.0

12.3 Keeping this manual current

The database is expanded and refined continuously. Where this manual and the application disagree, **the application is authoritative** for interface behaviour and for data content; this manual is authoritative for procedure and interpretation.

Users should confirm the software version shown in the application header, or in the print header of an exported record, against the version stated in Section 12.1. Where the versions differ, organism counts, group structure, and available functions may have changed.

NOTE — a known cosmetic discrepancy. In V0.309 the subtitle line of the **Organism Taxonomy & Classification** panel reports the version as V0.308. This is a display artefact in that panel only; the organism and group counts it reports are computed live from the database and are correct. The authoritative version indicator is the print header of an exported record.

12.4 Manual revision history

Edition	Date	Software version	Summary
1.0	August 2026	V0.309	First released edition. Complete coverage of core and extended functionality, definitions, symbol guide, taxonomy, methodology reference, data model, troubleshooting, and appendices.

12.5 Feedback and corrections

Corrections to this manual, and proposed additions to the database, should be directed to GMExpression through the submission route described in Section 9.3. Reports of a suspected data error should identify the organism, the field, the value shown, the value believed correct, and the primary source supporting the correction.

Appendix A — Complete Organism Index

The index below lists all 455 organism profiles in software version V0.309, arranged by group and subgroup as they appear in the taxonomy browser. It was generated directly from the shipped database.

Column key

- **O₂** — oxygen requirement class: E extreme oxygen-sensitive · S strict anaerobe · M microaerophile · F facultative · A obligate aerobe · X variable or not applicable (Section 3.2)
- **Gram** — P Gram-positive · N Gram-negative · X variable or not applicable (Section 3.3)
- **BSL** — 0 non-pathogenic / GRAS · 1 BSL-1 · 2 BSL-2 · 3 BSL-3 · – not recorded (Section 3.5)

CRITICAL — The BSL column is an orientation aid only. It does not substitute for the institutional risk assessment required before any organism is handled (Section 11.4).

Group 1 — Gut Commensals & SCFA Producers

197 organisms in 9 subgroups.

Core Butyrate Producers (31)

Scientific name	O ₂	Gram	BSL
<i>Faecalibacterium prausnitzii</i>	E	P	0
<i>Faecalibacterium duncaniae</i>	E	P	0
<i>Roseburia intestinalis</i> / <i>Eubacterium rectale</i>	S	P	0
<i>Roseburia intestinalis</i>	S	P	0
<i>Roseburia faecis</i>	S	P	0
<i>Roseburia inulinivorans</i>	S	P	0
<i>Anaerotruncus colihominis</i>	S	P	1
<i>Butyricicoccus pullicaecorum</i>	S	P	0
<i>Eisenbergiella tayi</i>	S	P	0
<i>Marvinbryantia formatexigens</i>	S	P	0
<i>Eubacterium rectale</i>	S	P	0
<i>Eubacterium ventriosum</i>	S	P	0
<i>Eubacterium siraeum</i>	S	P	0
<i>Eubacterium cylindroides</i>	S	P	0
<i>Eubacterium dolichum</i>	S	P	0
<i>Coprococcus comes</i> / <i>C. eutactus</i>	S	P	0
<i>Blautia obeum</i>	S	P	0
<i>Megasphaera elsdenii</i>	S	N	0
<i>Subdoligranulum variabile</i>	S	P	0
<i>Butyrivibrio fibrisolvens</i>	S	P	0
<i>Butyrivibrio crossotus</i>	S	P	0
<i>Clostridium leptum</i>	S	P	0
<i>Intestinimonas butyriciproducens</i>	S	P	0

Scientific name	O ₂	Gram	BSL
<i>Pseudoflavonifractor capillosus</i>	S	P	0
<i>Lactonifractor longoviformis</i>	S	P	0
<i>Clostridium asparagiforme</i>	S	P	0
<i>Clostridium methylpentosum</i>	S	P	0
<i>Ruminococcus bicirculans</i>	S	P	1
<i>Agathobaculum butyriciproducens</i>	S	P	1
<i>Mediterraneibacter faecis</i>	S	P	1
<i>Gemmiger formicilis</i>	S	P	1

Acetate & Cross-Feeding Species (38)

Scientific name	O ₂	Gram	BSL
<i>Eubacterium limosum</i>	S	P	1
<i>Eubacterium bifforme</i>	S	P	0
<i>Anaerobutyricum hallii</i>	S	P	0
<i>Anaerostipes butyraticus</i>	S	P	0
<i>Anaerostipes rhamnosivorans</i>	S	P	0
<i>Bifidobacterium longum</i>	S	P	0
<i>Bifidobacterium longum subsp. longum</i>	S	P	0
<i>Bifidobacterium breve</i>	S	P	0
<i>Bifidobacterium adolescentis</i>	S	P	0
<i>Bifidobacterium catenulatum</i>	S	P	0
<i>Bifidobacterium angulatum</i>	S	P	0
<i>Bifidobacterium pseudolongum</i>	S	P	0
<i>Bifidobacterium minimum</i>	S	P	0
<i>Bifidobacterium subtile</i>	S	P	0
<i>Bifidobacterium stercoris</i>	S	P	0
<i>Bifidobacterium bifidum</i>	S	P	0
<i>Collinsella aerofaciens</i>	S	P	0
<i>Collinsella stercoris</i>	S	P	0
<i>Collinsella intestinalis</i>	S	P	0
<i>Eggerthella lenta</i>	S	P	2
<i>Blautia producta</i>	S	P	0
<i>Blautia wexlerae</i>	S	P	0
<i>Blautia hydrogenotrophica</i>	S	P	0
<i>Blautia hansenii</i>	S	P	0
<i>Blautia coccoides</i>	S	P	0
<i>Anaerostipes caccae</i>	S	P	0
<i>Anaerostipes hadrus</i>	S	P	0
<i>Dorea formicigenerans</i>	S	P	0
<i>Slackia equolifaciens</i>	S	P	0
<i>Slackia isoflavoniconvertens</i>	S	P	0
<i>Gordonibacter pamelaee</i>	S	P	0
<i>Gordonibacter urolithinfaciens</i>	S	P	0
<i>Senegalimassilia anaerobia</i>	S	P	0
<i>Ellagibacter isourolithinifaciens</i>	S	P	1
<i>Ruthenibacterium lactatiformans</i>	S	P	1
<i>Adlercreutzia equolifaciens</i>	S	P	0
<i>Flavonifractor plautii</i>	S	P	0
<i>Catenibacterium mitsuokai</i>	S	P	0

Mucosal & Polysaccharide Degradors (50)

Scientific name	O ₂	Gram	BSL
<i>Akkermansia muciniphila</i>	S	N	0
<i>Bacteroides thetaiotaomicron</i>	S	N	0
<i>Bacteroides ovatus</i>	S	N	0
<i>Bacteroides uniformis</i>	S	N	0
<i>Bacteroides stercoris</i>	S	N	0
<i>Bacteroides eggerthii</i>	S	N	0
<i>Bacteroides nordii</i>	S	N	0
<i>Bacteroides intestinalis</i>	S	N	0
<i>Bacteroides salyersiae</i>	S	N	0
<i>Bacteroides finegoldii</i>	S	N	0
<i>Bacteroides coprocola</i>	S	N	0
<i>Bacteroides clarus</i>	S	N	0
<i>Bacteroides fluxus</i>	S	N	0
<i>Bacteroides coprophilus</i>	S	N	0
<i>Bacteroides pyogenes</i>	S	N	2
<i>Ruminococcus bromii</i>	S	P	0
<i>Ruminococcus torques</i>	S	P	0
<i>Ruminococcus albus</i>	S	P	0
<i>Ruminococcus callidus</i>	S	P	0
<i>Ruminococcus champanellensis</i>	S	P	0
<i>Ruminococcus lactaris</i>	S	P	0
<i>Ruminococcus flavefaciens</i>	S	P	0
<i>Christensenella minuta</i>	E	N	0
<i>Prevotella copri</i>	S	N	1
<i>Prevotella bivia</i>	S	N	2
<i>Prevotella stercorea</i>	S	N	0
<i>Alistipes putredinis</i>	S	N	0
<i>Alistipes onderdonkii</i>	S	N	0
<i>Alistipes indistinctus</i>	S	N	0
<i>Alistipes senegalensis</i>	S	N	0
<i>Alistipes timonensis</i>	S	N	0
<i>Alistipes obesi</i>	S	N	0
<i>Phocaeicola vulgatus</i>	S	N	0
<i>Parabacteroides distasonis</i>	S	N	0
<i>Parabacteroides johnsonii</i>	S	N	0
<i>Odoribacter splanchnicus</i>	S	N	0
<i>Odoribacter laneus</i>	S	N	0
<i>Porphyromonas asaccharolytica</i>	S	N	2
<i>Dysgonomonas gadei</i>	F	N	1
<i>Lachnospira multipara</i>	S	P	0
<i>Eubacterium eligens</i>	S	P	0
<i>Victivallis vadensis</i>	S	N	0
<i>Alistipes ihumii</i>	S	N	1
<i>Butyricimonas virosa</i>	S	N	1
<i>Paraprevotella clara</i>	S	N	1
<i>Paraprevotella xylaniphila</i>	S	N	1
<i>Alloprevotella tannerae</i>	S	N	1
<i>Coproacter fastidiosus</i>	S	N	1
<i>Rikenella microfus</i>	S	N	1
<i>Bacteroides massiliensis senegalensis</i>	S	N	1

Colonic Commensals & Modulators (48)

Scientific name	O ₂	Gram	BSL
<i>Lactobacillus acidophilus</i>	F	P	0

Scientific name	O ₂	Gram	BSL
<i>Lactobacillus gasseri</i>	F	P	0
<i>Lactobacillus johnsonii</i>	F	P	0
<i>Fusicatenibacter saccharivorans</i>	S	P	0
<i>Limosilactobacillus reuteri</i>	F	P	1
<i>Lactobacillus delbrueckii</i>	F	P	0
<i>Ligilactobacillus ruminis</i>	F	P	0
<i>Lactobacillus rogosae</i>	F	P	0
<i>Limosilactobacillus mucosae</i>	F	P	0
<i>Ligilactobacillus salivarius</i>	F	P	0
<i>Lacticaseibacillus rhamnosus</i>	F	P	0
<i>Lactiplantibacillus plantarum</i>	F	P	0
<i>Streptococcus pleomorphus</i>	S	P	0
<i>Propionibacterium freudenreichii</i>	F	P	0
<i>Phascolarctobacterium faecium</i>	S	N	0
<i>Oscillibacter valericigenes</i>	S	X	0
<i>Mediterraneibacter gnavus</i> (formerly <i>Ruminococcus gnavus</i>)	S	P	1
<i>Clostridium scindens</i>	S	P	0
<i>Desulfovibrio piger</i>	S	N	1
<i>Desulfovibrio desulfuricans</i>	S	N	1
<i>Desulfitobacterium hafniense</i>	S	P	1
<i>Bilophila wadsworthensis</i>	S	N	0
<i>Oxalobacter formigenes</i>	S	N	0
<i>Barnesiella intestinihominis</i>	S	N	0
<i>Butyricimonas synergistica</i>	S	N	0
<i>Sutterella wadsworthensis</i>	S	N	1
<i>Clostridium bolteae</i>	S	P	1
<i>Clostridium nexile</i>	S	P	0
<i>Clostridium symbiosum</i>	S	P	0

Scientific name	O ₂	Gram	BSL
<i>Erysipelatoclostridium ramosum</i>	S	P	1
<i>Catabacter hongkongensis</i>	S	P	2
<i>Megamonas funiformis</i>	S	N	0
<i>Dialister succinatiphilus</i>	S	N	0
<i>Acidaminococcus intestini</i>	S	N	0
<i>Negativicoccus succinicivorans</i>	S	N	0
<i>Sutterella stercoricanis</i>	S	N	1
<i>Bilophila wadsworthia</i>	S	N	1
<i>Desulfovibrio fairfieldensis</i>	S	N	2
<i>Holdemanella biformis</i>	S	P	1
<i>Megamonas rupellensis</i>	S	N	1
<i>Holdemania massiliensis</i>	S	P	1
<i>Murdochiella asaccharolytica</i>	S	P	1
<i>Dialister massiliensis</i>	S	N	1
<i>Parasutterella excrementihominis</i>	M	N	0
<i>Turicibacter sanguinis</i>	S	P	0
<i>Coprobacillus cateniformis</i>	S	P	0
<i>Mitsuokella multacida</i>	S	N	0
<i>Succinatimonas hippei</i>	S	N	0

Spore-Forming Gut Colonisers (16)

Scientific name	O ₂	Gram	BSL
<i>Clostridium butyricum</i>	S	P	1
<i>Bacillus coagulans</i>	F	P	1
<i>Bacillus subtilis</i>	F	P	0
<i>Bacillus cereus</i>	F	P	2
<i>Christensenella massiliensis</i>	S	N	0
<i>Clostridium clostridioforme</i>	S	P	1
<i>Clostridium tertium</i>	F	P	2
<i>Clostridium baratii</i>	S	P	1
<i>Clostridium paraputrificum</i>	S	P	1
<i>Sarcina ventriculi</i>	S	P	2
<i>Clostridium hathewayi</i>	S	P	2
<i>Clostridium citroniae</i>	S	P	1
<i>Clostridium aldenense</i>	S	P	1
<i>Intestinibacter bartlettii</i>	S	P	1

Scientific name	O ₂	Gram	BSL
<i>Longibaculum muris</i>	S	P	1
<i>Romboutsia lituseburensis</i>	S	P	0

Archaea (Gut) (1)

Scientific name	O ₂	Gram	BSL
<i>Methanobrevibacter smithii</i>	S	X	0

Obligate Intracellular & Rare GI Pathogens (3)

Scientific name	O ₂	Gram	BSL
<i>Tropheryma whipplei</i>	F	P	2
<i>Mycoplasma hominis</i>	F	X	2
<i>Ureaplasma urealyticum</i>	F	X	2

Novel Phyla Representatives (Synergistota, Deinococcota) (9)

Scientific name	O ₂	Gram	BSL
<i>Synergistes jonesii</i>	S	N	0
<i>Deinococcus radiodurans</i>	A	P	1
<i>Enorma massiliensis</i>	S	P	1
<i>Dielma fastidiosa</i>	S	P	1
<i>Massiliomicrobiota timonensis</i>	S	P	1
<i>Anaerosalibacter massiliensis</i>	S	P	1
<i>Niameybacter massiliensis</i>	S	N	1
<i>Senegalia massiliensis</i>	S	P	1
<i>Cloacibacillus evryensis</i>	S	N	1

Candidate Phyla / Unculturable Dark Matter (1)

Scientific name	O ₂	Gram	BSL
Novel / Candidate Phyla ("Microbial Dark Matter")	S	X	0

Group 2 — Enteric & Foodborne Pathogens

49 organisms in 6 subgroups.

Enterobacteriaceae & Gram-Negative Enteropathogens (21)

Scientific name	O ₂	Gram	BSL
<i>Escherichia coli</i> — Pathogenic Pathotypes	F	N	2
<i>Salmonella enterica</i>	F	N	2
<i>Shigella</i> spp.	F	N	2
<i>Yersinia enterocolitica</i>	F	N	2
<i>Klebsiella pneumoniae</i>	F	N	2
<i>Klebsiella oxytoca</i>	F	N	2
<i>Enterobacter aerogenes</i>	F	N	2
<i>Morganella morganii</i>	F	N	2
<i>Cronobacter sakazakii</i>	F	N	2
<i>Citrobacter koseri</i>	F	N	2

Scientific name	O ₂	Gram	BSL
<i>Proteus vulgaris</i>	F	N	2
<i>Providencia rettgeri</i>	F	N	2
<i>Providencia stuartii</i>	F	N	2
<i>Serratia marcescens</i>	F	N	2
<i>Edwardsiella tarda</i>	F	N	2
<i>Shigella dysenteriae</i>	F	N	2
<i>Shigella sonnei</i>	F	N	2
<i>Proteus mirabilis</i>	F	N	2
<i>Shigella flexneri</i>	F	N	2
<i>Enterobacter cloacae</i>	F	N	2
<i>Citrobacter freundii</i>	F	N	2

Vibrio & Aeromonadaceae (5)

Scientific name	O ₂	Gram	BSL
<i>Vibrio cholerae</i>	F	N	2
<i>Vibrio vulnificus</i>	F	N	2
<i>Aeromonas hydrophila</i>	F	N	2
<i>Plesiomonas shigelloides</i>	F	N	2
<i>Vibrio parahaemolyticus</i>	F	N	2

Anaerobic GI Pathogens (9)

Scientific name	O ₂	Gram	BSL
<i>Clostridioides difficile</i>	S	P	2
<i>Clostridium perfringens</i>	S	P	2
<i>Paraclostridium sordellii</i>	S	P	2
<i>Bacteroides fragilis</i>	S	N	2
<i>Prevotella / Porphyromonas spp.</i>	S	N	1
<i>Fusobacterium nucleatum</i>	S	N	2
<i>Hungatella hathewayi</i>	S	P	2
<i>Clostridium spiroforme</i>	S	P	2
<i>Fusobacterium ulcerans</i>	S	N	2

Hospital-Acquired GI Pathogens (10)

Scientific name	O ₂	Gram	BSL
<i>Enterococcus faecium</i>	F	P	2
<i>Enterococcus gallinarum</i>	F	P	2
<i>Enterococcus durans</i>	F	P	1
<i>Enterococcus hirae</i>	F	P	2
<i>Enterococcus casseliflavus</i>	F	P	2
<i>Enterococcus avium</i>	F	P	2
<i>Streptococcus gallolyticus</i>	F	P	2
<i>Streptococcus bovis</i>	F	P	2
<i>Streptococcus infantarius</i>	F	P	2
<i>Streptococcus equinus</i>	F	P	2

Microaerophilic Enteric Pathogens (3)

Scientific name	O ₂	Gram	BSL
<i>Campylobacter jejuni</i>	M	N	2
<i>Campylobacter coli</i>	M	N	2
<i>Helicobacter pylori</i>	M	N	2

Foodborne Pathogens (Non-Spore) (1)

Scientific name	O ₂	Gram	BSL
<i>Listeria monocytogenes</i>	F	P	2

Group 3 — Respiratory, Wound & Soft Tissue Pathogens

29 organisms in 7 subgroups.

Anaerobic Wound & Soft-Tissue Pathogens (4)

Scientific name	O ₂	Gram	BSL
<i>Finegoldia magna</i>	S	P	1
<i>Cutibacterium acnes</i>	S	P	1
<i>Cutibacterium granulosum</i>	F	P	1
<i>Streptococcus anginosus</i> group (Milleri group)	F	P	2

Aerobic Gram-Positive Rods & Diphtheroids (Corynebacteriaceae) (2)

Scientific name	O ₂	Gram	BSL
<i>Corynebacterium diphtheriae</i>	A	P	2
<i>Corynebacterium amycolatum</i>	F	P	2

Pyogenic Cocci & Streptococci (8)

Scientific name	O ₂	Gram	BSL
<i>Staphylococcus aureus</i> — Deep Tissue / Abscess	F	P	2
<i>Staphylococcus epidermidis</i>	F	P	2
<i>Streptococcus pyogenes</i> (Group A Streptococcus)	F	P	2
<i>Streptococcus pneumoniae</i>	F	P	2
<i>Enterococcus faecalis</i>	F	P	2
<i>Streptococcus agalactiae</i>	F	P	2
<i>Staphylococcus saprophyticus</i>	F	P	2
<i>Staphylococcus lugdunensis</i>	F	P	2

Gram-Negative Respiratory & Wound (6)

Scientific name	O ₂	Gram	BSL
<i>Pseudomonas aeruginosa</i>	A	N	2
<i>Acinetobacter baumannii</i>	A	N	2
<i>Stenotrophomonas maltophilia</i>	A	N	2
<i>Burkholderia cepacia</i> complex	A	N	2
<i>Moraxella catarrhalis</i>	A	N	2
<i>Legionella pneumophila</i>	A	N	2

Non-Tuberculous Mycobacteria & Leprosy (7)

Scientific name	O ₂	Gram	BSL
<i>Mycobacterium chimaera</i>	A	P	2
<i>Nocardia asteroides complex</i>	A	P	2
<i>Mycobacterium leprae</i>	A	P	2
<i>Mycobacterium avium complex (MAC)</i>	A	P	2
<i>Mycobacterium abscessus</i>	A	P	2
<i>Mycobacterium kansasii</i>	A	P	2
<i>Mycobacterium marinum</i>	A	P	2

Mycobacterium tuberculosis Complex (1)

Scientific name	O ₂	Gram	BSL
<i>Mycobacterium tuberculosis</i>	A	P	3

Pathogenic Yeasts — Non-albicans Candida (1)

Scientific name	O ₂	Gram	BSL
<i>Pichia kudriavzevii</i> (<i>Candida krusei</i>) · <i>C. parapsilosis</i> · <i>C. glabrata</i> · <i>C. tropicalis</i> · <i>C. guilliermondii</i> · <i>C. rugosa</i>	F	X	1

Group 4 — Zoonotic, Vector-Borne & Systemic Pathogens

33 organisms in 6 subgroups.

BSL-3 & Select Agents (7)

Scientific name	O ₂	Gram	BSL
<i>Yersinia pestis</i>	F	N	3
<i>Francisella tularensis</i>	A	N	3
<i>Burkholderia pseudomallei</i>	A	N	3
<i>Brucella melitensis</i>	A	N	3
<i>Brucella abortus</i>	A	N	3
<i>Bacillus anthracis</i>	F	P	3
<i>Burkholderia mallei</i>	A	N	3

Spirochaetal Zoonoses (4)

Scientific name	O ₂	Gram	BSL
<i>Borrelia burgdorferi sensu lato</i>	M	N	2
<i>Leptospira interrogans</i>	A	N	2
<i>Borrelia recurrentis</i>	M	N	2
<i>Treponema pallidum</i>	X	N	2

Bite & Animal-Contact Zoonoses (6)

Scientific name	O ₂	Gram	BSL
<i>Capnocytophaga canimorsus</i>	F	N	2
<i>Streptobacillus moniliformis</i>	F	N	2
<i>Pasteurella multocida</i>	F	N	2
<i>Erysipelothrix rhusiopathiae</i>	F	P	2
<i>Bartonella henselae</i>	A	N	2
<i>Bartonella quintana</i>	A	N	2

Systemic & Meningeal Pathogens (4)

Scientific name	O ₂	Gram	BSL
<i>Neisseria meningitidis</i>	F	N	2
<i>Neisseria gonorrhoeae</i>	A	N	2
<i>Haemophilus influenzae</i>	F	N	2
<i>Bordetella pertussis</i>	A	N	2

Obligate Intracellular & Tick-Borne (Rickettsiales) (7)

Scientific name	O ₂	Gram	BSL
<i>Rickettsia rickettsii</i>	A	N	3
<i>Coxiella burnetii</i>	A	N	3
<i>Ehrlichia chaffeensis</i>	A	N	2
<i>Anaplasma phagocytophilum</i>	A	N	2
<i>Rickettsia prowazekii</i>	A	N	3
<i>Orientia tsutsugamushi</i>	X	N	3
<i>Rickettsia typhi</i>	A	N	2

Obligate Intracellular — Chlamydiales & Mycoplasmas (5)

Scientific name	O ₂	Gram	BSL
<i>Chlamydia trachomatis</i>	X	X	2
<i>Chlamydia pneumoniae</i>	X	X	2
<i>Chlamydia psittaci</i>	X	X	2
<i>Mycoplasma pneumoniae</i>	A	X	2
<i>Mycoplasma genitalium</i>	F	X	2

Group 5 — Oral Microbiome & Upper GI Tract

62 organisms in 7 subgroups.

Viridans Streptococci — Early Colonisers (6)

Scientific name	O ₂	Gram	BSL
<i>Streptococcus salivarius</i>	F	P	1
<i>Streptococcus sanguinis</i>	F	P	2
<i>Streptococcus gordonii</i>	F	P	2
<i>Streptococcus mitis</i>	F	P	2
<i>Streptococcus oralis</i>	F	P	2
<i>Streptococcus parasanguinis</i>	F	P	2

Cariogenic Organisms (2)

Scientific name	O ₂	Gram	BSL
<i>Streptococcus mutans</i>	F	P	2
<i>Streptococcus sobrinus</i>	F	P	2

Periodontal Pathogens — Red Complex (4)

Scientific name	O ₂	Gram	BSL
<i>Porphyromonas gingivalis</i>	S	N	2
<i>Treponema denticola</i>	E	N	2
<i>Tannerella forsythia</i>	S	N	2
<i>Treponema socranskii</i>	S	N	2

Periodontal Pathogens — Orange & Emerging (11)

Scientific name	O ₂	Gram	BSL
<i>Aggregatibacter actinomycetemcomitans</i>	F	N	2
<i>Prevotella intermedia</i>	S	N	2
<i>Porphyromonas endodontalis</i>	S	N	2
<i>Prevotella melaninogenica</i>	S	N	1
<i>Prevotella nigrescens</i>	S	N	2
<i>Prevotella denticola</i>	S	N	2
<i>Prevotella loeschii</i>	S	N	2
<i>Filifactor alocis</i>	S	P	2
<i>Parvimonas micra</i>	S	P	2
<i>Dialister invisus</i>	S	N	1
<i>Selenomonas sputigena</i>	S	N	1

Oral Microaerophiles (5)

Scientific name	O ₂	Gram	BSL
<i>Campylobacter concisus</i>	M	N	2
<i>Campylobacter rectus</i>	M	N	2
<i>Campylobacter showae</i>	M	N	2
<i>Campylobacter hominis</i>	M	N	1
<i>Campylobacter ureolyticus</i>	M	N	2

Oral Anaerobes & Commensals (24)

Scientific name	O ₂	Gram	BSL
<i>Veillonella parvula</i>	S	N	1
<i>Veillonella atypica</i>	S	N	0
<i>Rothia mucilaginosa</i>	F	P	2
<i>Rothia dentocariosa</i>	F	P	1
<i>Peptostreptococcus anaerobius</i>	S	P	2
<i>Peptostreptococcus stomatis</i>	S	P	0
<i>Mogibacterium diversum</i>	S	P	0
<i>Anaerococcus prevotii</i>	S	P	2
<i>Anaerococcus vaginalis</i>	S	P	2
<i>Peptococcus niger</i>	S	P	1
<i>Actinomyces naeslundii</i>	F	P	1
<i>Actinomyces odontolyticus</i>	F	P	1
<i>Actinomyces israelii</i>	S	P	2

Scientific name	O ₂	Gram	BSL
<i>Actinomyces graevenitzii</i>	F	P	2
<i>Bifidobacterium dentium</i>	S	P	2
<i>Atopobium parvulum</i>	S	P	1
<i>Leptotrichia buccalis</i>	S	N	2
<i>Fusobacterium periodonticum</i>	S	N	2
<i>Fusobacterium necrophorum</i>	S	N	2
<i>Fusobacterium gonidiaformans</i>	S	N	2
<i>Corynebacterium durum</i>	F	P	1
<i>Micrococcus luteus</i>	A	P	1
<i>Kocuria rhizophila</i>	A	P	1
<i>Brevibacterium casei</i>	F	P	1

Fastidious, CO₂-Requiring & NVS (10)

Scientific name	O ₂	Gram	BSL
<i>Granulicatella adiacens</i>	F	P	2
<i>Abiotrophia defectiva</i>	F	P	2
<i>Capnocytophaga ochracea</i>	F	N	2
<i>Eikenella corrodens</i>	F	N	2
<i>Haemophilus parainfluenzae</i>	F	N	2
<i>Gemella haemolysans</i>	F	P	2
<i>Neisseria subflava</i>	A	N	1
<i>Cardiobacterium hominis</i>	F	N	2
<i>Kingella kingae</i>	F	N	2
<i>Neisseria flavescens</i>	A	N	1

Group 6 — Biotechnology, Industrial & Research Models

16 organisms in 5 subgroups.

Research & Genetic Model Organisms (1)

Scientific name	O ₂	Gram	BSL
<i>Escherichia coli</i> K-12 (Research Reference Strain)	F	N	1

Fermentation & Organic Acid Producers (5)

Scientific name	O ₂	Gram	BSL
<i>Lactococcus lactis</i>	F	P	0
<i>Clostridium acetobutylicum</i>	S	P	1
<i>Zymomonas mobilis</i>	F	N	0
<i>Acetobacter aceti</i>	A	N	0
<i>Gluconobacter oxydans</i>	A	N	0

Industrial Biosynthesis (4)

Scientific name	O ₂	Gram	BSL
<i>Corynebacterium glutamicum</i>	F	P	0
<i>Streptomyces coelicolor</i>	A	P	1
<i>Cupriavidus necator</i> (R. eutropha)	F	N	1
<i>Pseudomonas putida</i>	A	N	1

Rhizosphere & Bioengineering (5)

Scientific name	O ₂	Gram	BSL
<i>Agrobacterium tumefaciens</i>	A	N	1
<i>Rhizobium leguminosarum</i>	A	N	0
<i>Methylobacterium extorquens</i>	A	N	1
<i>Bradyrhizobium japonicum</i>	A	N	0
<i>Paenibacillus polymyxa</i>	F	P	1

Methylotrophic Yeast Expression Hosts (1)

Scientific name	O ₂	Gram	BSL
<i>Komagataella phaffii</i> (syn. <i>K. pastoris</i> ; formerly <i>Pichia pastoris</i>)	F	X	0

Group 7 — Food Processing & Fermentation

20 organisms in 8 subgroups.

Dairy Starter Cultures — Yogurt & Cheese (2)

Scientific name	O ₂	Gram	BSL
<i>Lactobacillus delbrueckii subsp. bulgaricus</i>	M	P	0
<i>Streptococcus thermophilus</i>	M	P	0

Vegetable & Dough Fermentation LAB (3)

Scientific name	O ₂	Gram	BSL
<i>Leuconostoc mesenteroides</i>	M	P	0
<i>Lactiplantibacillus plantarum</i> (formerly <i>Lactobacillus plantarum</i>)	M	P	0
<i>Pediococcus acidilactici</i>	M	P	0

Probiotic & Meat Cultures (3)

Scientific name	O ₂	Gram	BSL
<i>Bifidobacterium animalis subsp. lactis</i>	S	P	0
<i>Staphylococcus carnosus</i>	F	P	0
<i>Carnobacterium maltaromaticum</i>	M	P	0

Specialty Sourdough & Dough LAB (2)

Scientific name	O ₂	Gram	BSL
<i>Fructilactobacillus sanfranciscensis</i>	M	P	0
<i>Weissella cibaria</i>	M	P	0

Cheese Rind & Smear Ripening (4)

Scientific name	O ₂	Gram	BSL
<i>Brachybacterium tyrofermentans</i>	A	P	0
<i>Hafnia alvei</i>	F	N	2
<i>Microbacterium gubbeenense</i>	A	P	0
<i>Geotrichum candidum</i> (syn. <i>Saprochaete candidum</i>)	A	X	0

Mould-Based Fermentation (2)

Scientific name	O ₂	Gram	BSL
<i>Penicillium roqueforti</i>	A	X	0
<i>Aspergillus oryzae</i> (Koji mould)	A	X	0

Food Fermentation Yeasts (1)

Scientific name	O ₂	Gram	BSL
<i>Kluyveromyces marxianus</i>	F	X	0

Rare & Artisan Food Fermenters (3)

Scientific name	O ₂	Gram	BSL
<i>Bacillus subtilis</i> var. <i>natto</i>	A	P	0
<i>Tatumella citrea</i>	F	N	1
<i>Haloanaerobium praevalens</i>	S	N	0

Group 8 — Soil, Environmental & Spore-Forming Organisms

5 organisms in 3 subgroups.

Spore-Forming Soil Pathogens (3)

Scientific name	O ₂	Gram	BSL
<i>Clostridium botulinum</i>	S	P	2
<i>Clostridium tetani</i>	S	P	2
<i>Clostridium sporogenes</i>	S	P	1

Actinomycetes & Mycobacteria — Soil Origin (1)

Scientific name	O ₂	Gram	BSL
<i>Mycobacterium smegmatis</i>	A	P	1

Environmental Fungi & Moulds (1)

Scientific name	O ₂	Gram	BSL
<i>Geotrichum spp. (incl. Saprochaete, Dipodascus spp.)</i>	A	X	1

Group 9 — Extremophiles

12 organisms in 5 subgroups.

Extreme & Moderate Halophiles (3)

Scientific name	O ₂	Gram	BSL
<i>Halobacterium salinarum</i>	A	X	0
<i>Haloarcula marismortui</i>	A	X	0
<i>Salinibacter ruber</i>	A	N	0

Alkaliphiles (2)

Scientific name	O ₂	Gram	BSL
<i>Natranaerobius thermophilus</i>	S	P	0
<i>Bacillus alcalophilus</i>	F	P	0

Moderate Thermophiles (55-80 °C) (2)

Scientific name	O ₂	Gram	BSL
<i>Thermus aquaticus</i>	A	N	0
<i>Geobacillus stearothermophilus</i>	F	P	0

Hyperthermophiles (>80 °C) (4)

Scientific name	O ₂	Gram	BSL
<i>Thermotoga maritima</i>	S	N	0
<i>Sulfolobus acidocaldarius</i>	A	X	0
<i>Pyrococcus furiosus</i>	S	X	0
<i>Aquifex aeolicus</i>	M	N	0

Acidophiles (1)

Scientific name	O ₂	Gram	BSL
<i>Acidithiobacillus thiooxidans</i>	A	N	1

Group 10 — Chemolithotrophs, Gas Metabolism & Photolithotrophs

10 organisms in 5 subgroups.

H₂-Oxidising Chemolithotrophs (1)

Scientific name	O ₂	Gram	BSL
<i>Hydrogenophaga pseudoflava</i>	F	N	0

Methanotrophs (CH₄ Oxidisers) (2)

Scientific name	O ₂	Gram	BSL
<i>Methylococcus capsulatus</i> Bath	A	N	0
<i>Methylosinus trichosporium</i> OB3b	A	N	0

Nitrifiers (NH₃ / NO₂⁻ Oxidisers) (4)

Scientific name	O ₂	Gram	BSL
<i>Nitrosomonas europaea</i>	A	N	1
<i>Nitrobacter winogradskyi</i>	A	N	0
<i>Candidatus Nitrososphaera viennensis</i>	A	X	0
<i>Candidatus Nitrospira inopinata</i>	A	N	0

Sulphur & Denitrifying Chemolithotrophs (1)

Scientific name	O ₂	Gram	BSL
<i>Thiobacillus denitrificans</i>	S	N	0

Photolithotrophs (2)

Scientific name	O ₂	Gram	BSL
<i>Chlorobaculum tepidum</i>	S	N	0
<i>Synechocystis</i> sp. PCC 6803	A	N	0

Group 11 — Pathogenic Fungi (Eukaryota)

22 organisms in 6 subgroups.

Pathogenic Yeasts — *Candida* spp. (5)

Scientific name	O ₂	Gram	BSL
<i>Candida albicans</i>	F	X	2
<i>Candida auris</i>	A	X	2
<i>Candida glabrata</i> (<i>Nakaseomyces glabrata</i>)	A	X	2
<i>Candida tropicalis</i>	F	X	2
<i>Candida parapsilosis</i>	F	X	2

Aspergillus & Moulds (3)

Scientific name	O ₂	Gram	BSL
<i>Aspergillus fumigatus</i>	A	X	2
<i>Aspergillus niger</i>	A	X	2
<i>Aspergillus flavus</i>	A	X	2

Encapsulated Yeasts (2)

Scientific name	O ₂	Gram	BSL
<i>Cryptococcus neoformans</i>	A	X	2
<i>Cryptococcus gattii</i>	A	X	2

Dimorphic Systemic Fungi (6)

Scientific name	O ₂	Gram	BSL
<i>Histoplasma capsulatum</i>	A	X	3
<i>Blastomyces dermatitidis</i>	A	X	2
<i>Coccidioides immitis</i>	A	X	3
<i>Paracoccidioides brasiliensis</i>	A	X	2
<i>Talaromyces marneffe</i>	A	X	2
<i>Sporothrix schenckii</i>	A	X	2

Pneumocystis & Mucorales (2)

Scientific name	O ₂	Gram	BSL
<i>Pneumocystis jirovecii</i>	X	X	2
<i>Rhizopus oryzae</i> (Mucorales)	A	X	2

Dermatophytes (4)

Scientific name	O ₂	Gram	BSL
<i>Trichophyton rubrum</i>	A	X	2
<i>Trichophyton mentagrophytes</i>	A	X	2
<i>Microsporum canis</i>	A	X	2
<i>Epidermophyton floccosum</i>	A	X	2

Appendix B — Shared Media Index

The 53 media below are each associated with three or more organisms in the database. They represent the highest-value stock items for a laboratory working across this organism set, and are the natural starting point for the media-rationalisation workflow described in Section 5.5.3.

Counts are the number of organism records citing the medium in any of the three roles — primary, selective, or enrichment. Names are shown as indexed, after normalisation (Section 4.5).

Medium (as indexed)	Organisms
YCFA Agar (Yeast-Casitone-Fatty Acid)	72
PRAS BHI Broth	52
Non-Selective BHIS Agar	23
BBE Agar (Bacteroides Bile Esculin)	20
Blood Agar (5% Sheep Blood)	18
MRS Agar (de Man-Rogosa-Sharpe)	16
BHI Broth (Aerobic or CO ₂ -Supplemented)	16
MacConkey Agar (Standard Diagnostic)	14
MRS Broth	12
BHIS Agar	10
CMGB Broth	8
mGAM Agar (Modified Gifu Anaerobic Medium)	8
Wilkins-Chalgren Anaerobe Agar (WCA)	7
YCFA Broth (Pre-Reduced Liquid Enrichment)	7
BHIS Anaerobic Agar (Brain Heart Infusion + Supplements)	7
Mitis-Salivarius Agar (MS)	6
Real-Time PCR (16S rRNA / p28-1 gene) — Primary Diagnostic	6
Columbia Blood Agar (DSMZ Medium 28)	5
Todd-Hewitt Broth (THB)	5
Columbia Blood Agar (CBA) — 5% Sheep Blood	5
CVE Agar (Crystal Violet Erythromycin — Fusobacterium Selective)	5
BHIS Broth (Brain Heart Infusion Supplemented)	5
Neomycin Blood Agar (NBA)	4
Chocolate Agar (DSMZ Medium 397)	4
Sabouraud Dextrose Agar (SDA)	4
KVLB Agar (Kanamycin-Vancomycin Laked Blood)	4
BSM Agar (Bifidobacterium Selective Agar — modified MRS)	4
BEA Agar	4
MRS + Mupirocin Agar	4
Tinsdale Agar	4
Middlebrook 7H10/7H11 Agar	4
Brucella Blood Agar (BBA) + Haemin/Vit K ₁	3
Brucella Blood Agar (BBA)	3
Todd-Hewitt Broth + 5% CO ₂	3
Brain Heart Infusion Broth (BHIB)	3

Medium (as indexed)	Organisms
Supplemented Brucella Blood Agar (Anaerobic)	3
Enriched Thioglycollate + Haemin + VK1	3
Columbia Blood Agar + 5% CO ₂	3
Modified Thayer-Martin (MTM) Agar	3
Chopped Meat Glucose (CMG) Broth	3
BHIS Broth Anaerobic	3
PRAS BHIS Broth (Pre-Reduced Anaerobically Sterilised)	3
LKV Agar (Laked Kanamycin-Vancomycin Blood Agar)	3
Laked Kanamycin-Vancomycin (LKV) Blood Agar	3
Blood Agar (5% Sheep) + 5% CO ₂	3
KVLB Blood Agar (Kanamycin-Vancomycin Laked Blood)	3
Thioglycolate Broth	3
BHIS + Ethanol Spore Selection	3
Rogosa SL Agar	3
Enterococcus Enrichment Broth	3
Fastidious Anaerobe Agar (FAA)	3
CLED Agar (Cystine Lactose Electrolyte-Deficient)	3
GAM Agar (Gifu Anaerobic Medium) — Strict Anaerobic 37°C	3

The database contains 943 distinct normalised medium names in total. The 890 not listed above are associated with one or two organisms each, and are typically bespoke or organism-specific formulations.

Appendix C — Metabolite Ontology Reference

The symbiosis engine (Section 5.1) recognises the metabolite tags below. The weight determines the contribution a matched exchange makes to the pairing score: higher weights reflect greater ecological significance in the systems the database principally covers.

Tag	Metabolite	Class	Weight
butyrate	Butyrate	SCFA	10
H ₂	Molecular Hydrogen (H ₂)	gas	9
acetate	Acetate	SCFA	8
lactate	Lactate	organic-acid	7
mucin-sugars	Mucin-derived Sugars	sugar	6
SCFAs	Short-Chain Fatty Acids (general)	SCFA	6
HMOs	Human Milk Oligosaccharides	sugar	5
propionate	Propionate	SCFA	5
oligosaccharides	Oligosaccharides	sugar	4
organic-carbon	Organic Carbon (from CO ₂ fixation)	carbon	4
vitamin-B12	Cobalamin (B ₁₂)	vitamin	4
BCFAs	Branched-Chain Fatty Acids	fatty-acid	3
exogenous-vitamins	Exogenous Vitamins	vitamin	3
succinate	Succinate	organic-acid	3
vitamin-K	Menaquinone (K ₂)	vitamin	3
ammonia	Ammonia (NH ₃)	gas	2
CH ₄	Methane (CH ₄)	gas	2
formate	Formate	organic-acid	2
H ₂ S	Hydrogen Sulfide (H ₂ S)	gas	2
methanol	Methanol	alcohol	2
CO ₂	Carbon Dioxide (CO ₂)	gas	1
ethanol	Ethanol	alcohol	1
sulfate	Sulfate	inorganic	1

Reading the weights. Butyrate carries the highest weight because of its central role as the colonocyte energy substrate and as the functional endpoint of gut fibre fermentation. Molecular hydrogen ranks next, reflecting the thermodynamic importance of interspecies hydrogen transfer in anaerobic communities. Acetate ranks third as the principal cross-feeding currency between primary fermenters and butyrogens. Ubiquitous or minor metabolites such as CO₂ and sulfate carry the lowest weights so that they cannot dominate a score on their own.

Three further tags — secondary-bile-acids, equol, and phenolic-metabolites — are emitted by the trait rules for bile acid, phytoestrogen, and polyphenol metabolism respectively. They have no entry in the weight table above and therefore contribute the default weight of 1 when matched.

Appendix D — Oxygen Compatibility Matrix

The matrix below is applied as the oxygen-compatibility term of the symbiosis score (Section 5.1.3). It expresses whether two organisms can share a single atmosphere.

Target ↓ / Candidate →	E	S	M	F	A	X
E	+5	+4	-2	-5	-10	0
S	+4	+5	0	-3	-10	0
M	-2	0	+5	+3	-5	+1
F	-5	-3	+3	+5	+3	+2
A	-10	-10	-5	+3	+5	0
X	0	0	+1	+2	0	+3

Interpretation

- **+5** — identical oxygen class; a single atmosphere serves both optimally.
- **+3 to +4** — adjacent classes; a compromise atmosphere is achievable.
- **0 to +2** — neutral or weakly compatible; feasible with care.
- **-2 to -5** — poorly compatible; a shared atmosphere will disadvantage one partner.
- **-10** — incompatible. Applied between anaerobes (E, S) and obligate aerobes (A). In practice this term alone removes the pair from the ranked list regardless of metabolic complementarity, correctly encoding the physical impossibility of a single-atmosphere co-culture.

The matrix is **symmetric**: the score for a target of class E against a candidate of class F is the same as for F against E. Oxygen compatibility is therefore a property of the pair rather than of the direction of enquiry, and it contributes equally however the two organisms are ordered. This is a deliberate simplification. It does not capture the biological asymmetry that an aerobe generally tolerates a reduced-oxygen environment better than an anaerobe tolerates oxygen, so a pairing such as F with S may in practice be more workable than its symmetric score suggests — the facultative partner can usually be cultured anaerobically.

Appendix E — Authoritative Sources and Standards

The sources below are those on which the database and this manual depend.

Biosafety

Source	Reference
CDC / NIH	<i>Biosafety in Microbiological and Biomedical Laboratories</i> (BMBL), 6th Edition, revised June 2020. U.S. Department of Health and Human Services.
World Health Organization	<i>Laboratory Biosafety Manual</i> , 4th Edition, 2020.
U.S. Federal Select Agent Program	42 CFR Part 73 (human pathogens); 9 CFR Part 121 (animal and plant pathogens).

Culture collections and media

Source	Role
DSMZ — Deutsche Sammlung von Mikroorganismen und Zellkulturen	Type strains and numbered medium formulations
ATCC — American Type Culture Collection	Reference strains and validated culture conditions
JCM — Japan Collection of Microorganisms (RIKEN)	Type strains with DSMZ cross-accessions

Nomenclature and taxonomy

Source	Role
LPSN — List of Prokaryotic Names with Standing in Nomenclature	Authoritative registry of validly published names
IJSEM — <i>International Journal of Systematic and Evolutionary Microbiology</i>	Journal of record for new species descriptions
NCBI Taxonomy	Working taxonomic hierarchy and sequence linkage
International Code of Nomenclature of Prokaryotes	Governing nomenclatural code

Sequence and literature databases

Source	Role
NCBI GenBank	Nucleotide sequence records
NCBI PubMed	Peer-reviewed literature index

Clinical and methodological standards

Source	Role
CLSI — Clinical and Laboratory Standards Institute	United States reference methods and breakpoints
EUCAST — European Committee on Antimicrobial Susceptibility Testing	European breakpoints and epidemiological cut-off values
ISO — International Organization for Standardization	Standardised microbiological methods

Foundational methods cited within the database

The medium formulations in the database cite their originating publications individually in the **Authorised References & Database Sources** block of each result. Methods recurring across many records include the pre-reduced anaerobically sterilised technique of Dowell and Hawkins (1977), the VPI anaerobe laboratory manual of Holdeman and colleagues (1977), the de Man, Rogosa and Sharpe medium (1960), the Middlebrook mycobacterial media (Middlebrook and Cohn, 1958), the Löwenstein-Jensen medium (Löwenstein, 1931), the Thayer-Martin selective medium (Thayer and Martin, 1966), the kanamycin-vancomycin laked blood agar of Sutter and colleagues (1972), and the buffered charcoal yeast extract medium of Feeley and colleagues (1979).

Disclaimer

This manual is provided for informational, instructional, and advisory purposes. It does not constitute medical advice, clinical guidance, professional engineering advice, or formal peer review.

The Culturomics & Media Navigator is **For Research Use Only** and is **not a medical device**. It is not intended for clinical diagnosis, patient management, or therapeutic decision-making, and it has not been evaluated or cleared by any regulatory authority for diagnostic use.

All formulations, growth parameters, biosafety classifications, detection methods, and predicted metabolic interactions must be independently verified against the cited primary sources and validated experimentally before laboratory adoption. Users remain solely responsible for compliance with the biosafety, biosecurity, regulatory, and quality management requirements applicable in their own jurisdiction and institution.

Where this manual and the application disagree, the application is authoritative for interface behaviour and data content; this manual is authoritative for procedure and interpretation.

Culturomics & Media Navigator — User Manual · Edition 1.0 · August 2026 · Applies to software version V0.309

© 2026 GMEExpression. Data derived from authorised research publications and databases (NCBI/NIH, DSMZ, IJSEM, CLSI, ISO, WHO).