

Package: glyhub (via r-universe)

October 18, 2026

Title Curated Glycomics and Glycoproteomics Data Resources

Version 0.1.0

Description Provides access to curated public glycomics and glycoproteomics datasets from GlycoPOST, CPTAC, and published studies as 'glyexp' 'GlycomicSE' and 'GlycoproteomicSE' objects. Datasets preserve source molecular annotations, measurement provenance, and explicit processing records. A catalog and shared loader retrieve data from versioned GitHub Releases, verify file integrity with SHA-256 checksums, and cache downloads for offline reuse.

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Depends R (>= 4.1)

Imports digest, methods, glyexp (>= 0.17.0), tibble

Suggests glyrepr, jsonlite, readxl, S4Vectors, SummarizedExperiment, testthat (>= 3.0.0)

Config/testthat/edition 3

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URL <https://glycoverse.github.io/glyhub/>,
<https://github.com/glycoverse/glyhub>

BugReports <https://github.com/glycoverse/glyhub/issues>

Additional_repositories <https://glycoverse.r-universe.dev>

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glyhub_catalog	<i>List available glyhub datasets</i>
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Description

List released and locally staged datasets without downloading any files. Data assets are excluded from the package. A staged entry has no download URL and requires the maintainer's verified local cache.

Usage

```
glyhub_catalog(kind = c("curated", "raw", "all"))
```

Arguments

kind	List "curated" datasets (default), "raw" source archives, or "all" resources. Raw archives are currently available for CPTAC only.
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Value

A tibble containing dataset identifiers, source, file format, storage, compressed bytes, SHA-256, version, URL and dimensions. Additional metadata columns are:

- exp_type: "glycomics" or "glycoproteomics".
- glycan_type: Glycan type recorded in the curated object.
- has_glycan_structures: Whether at least one non-missing typed glycan structure is available, rather than compositions alone.
- quant_method: Source-recorded quantification description, falling back to the assay scale or unit when no explicit method is recorded. This is descriptive text, not a controlled classification of instruments.

Raw archives inherit experiment and glycan types from their curated dataset; structure availability and quantification descriptions are NA for raw archives. Unavailable or outdated object metadata is also returned as NA.

Examples

```
glyhub_catalog()[, c("dataset", "storage", "bytes")]
```

glyhub_CPTAC_CCRCC	<i>Clear cell renal cell carcinoma: CPTAC N-glycoproteome</i>
--------------------	---

Description

Load the supplied JHU GENCODEv34 median-normalized glycoform-peptide abundance matrix as a [glyexp::GlycoproteomicSE](#). Downloads are cached.

Usage

```
glyhub_CPTAC_CCRCC(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Details

The assay is $2^{\text{source_value}}$, a linearized normalized abundance. Source log2 values, including zeros, are retained in `metadata(x)$raw_abundance`. Source None entries become NA; no filtering, imputation, aggregation or further normalization is performed. These data are an exception to the zero-to-NA convention used for GlycoPOST datasets.

Reference and QC columns remain present, with source-label-derived roles in `colData`. Unresolved roles remain unresolved. Repeated measurements are not independent patients. `Intensity.Reference` is retained in `rowData(x)$intensity_reference_log2`, not treated as a sample. Source peptide, gene and composition annotations are retained. N/H/F/S/G denotes HexNAc/Hex/Fuc/Neu5Ac/Neu5Gc. No structures are inferred. Protein accessions and absolute sites are unknown (NA); source gene annotations must not be treated as protein accessions.

Provenance records the supplied file hash and upstream checksum status. COAD and PDAC match upstream CRC and PDA after reversing column-prefix renaming; HGSC has not been matched to the supplied upstream MD5 list. The HGSC fractionation identity therefore remains unverified. See [glyhub_catalog\(\)](#) for dimensions, sizes and download URLs.

Access

Use `glyhub_load("glyhub_CPTAC_CCRCC")` to load this dataset.

Source

<https://pdc.cancer.gov/pdc/cptac-pancancer> Data use and attribution: <https://pdc.cancer.gov/pdc/data-use-guidelines>. The source data are not licensed under the package’s MIT code license.

See Also

[glyhub_load\(\)](#) to retrieve the original TSV archive.

glyhub_CPTAC_COAD	<i>Colon adenocarcinoma: CPTAC N-glycoproteome</i>
-------------------	--

Description

Load the supplied JHU GENCODEv34 median-normalized glycoform-peptide abundance matrix as a [glyexp::GlycoproteomicSE](#). Downloads are cached.

Usage

```
glyhub_CPTAC_COAD(  
  kind = c("curated", "raw"),  
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),  
  refresh = FALSE,  
  offline = FALSE  
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Details

The assay is $2^{\text{source_value}}$, a linearized normalized abundance. Source log2 values, including zeros, are retained in `metadata(x)$raw_abundance`. Source None entries become NA; no filtering, imputation, aggregation or further normalization is performed. These data are an exception to the zero-to-NA convention used for GlycoPOST datasets.

Reference and QC columns remain present, with source-label-derived roles in `colData`. Unresolved roles remain unresolved. Repeated measurements are not independent patients. Intensity.Reference is retained in `rowData(x)$intensity_reference_log2`, not treated as a sample. Source peptide, gene and composition annotations are retained. N/H/F/S/G denotes HexNAc/Hex/Fuc/Neu5Ac/Neu5Gc.

No structures are inferred. Protein accessions and absolute sites are unknown (NA); source gene annotations must not be treated as protein accessions.

Provenance records the supplied file hash and upstream checksum status. COAD and PDAC match upstream CRC and PDA after reversing column-prefix renaming; HGSC has not been matched to the supplied upstream MD5 list. The HGSC fractionation identity therefore remains unverified. See [glyhub_catalog\(\)](#) for dimensions, sizes and download URLs.

Access

Use `glyhub_load("glyhub_CPTAC_COAD")` to load this dataset.

Source

<https://pdc.cancer.gov/pdc/cptac-pancancer> Data use and attribution: <https://pdc.cancer.gov/pdc/data-use-guidelines>. The source data are not licensed under the package's MIT code license.

See Also

[glyhub_load\(\)](#) to retrieve the original TSV archive.

glyhub_CPTAC_HGSC	<i>High-grade serous ovarian carcinoma: CPTAC N-glycoproteome</i>
-------------------	---

Description

Load the supplied JHU GENCODEv34 median-normalized glycoform-peptide abundance matrix as a [glyexp::GlycoproteomicSE](#). Downloads are cached.

Usage

```
glyhub_CPTAC_HGSC(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Details

The assay is $2^{\text{source_value}}$, a linearized normalized abundance. Source log2 values, including zeros, are retained in `metadata(x)$raw_abundance`. Source None entries become NA; no filtering, imputation, aggregation or further normalization is performed. These data are an exception to the zero-to-NA convention used for GlycoPOST datasets.

Reference and QC columns remain present, with source-label-derived roles in `colData`. Unresolved roles remain unresolved. Repeated measurements are not independent patients. `Intensity.Reference` is retained in `rowData(x)$intensity_reference_log2`, not treated as a sample. Source peptide, gene and composition annotations are retained. N/H/F/S/G denotes HexNAc/Hex/Fuc/Neu5Ac/Neu5Gc. No structures are inferred. Protein accessions and absolute sites are unknown (NA); source gene annotations must not be treated as protein accessions.

Provenance records the supplied file hash and upstream checksum status. COAD and PDAC match upstream CRC and PDA after reversing column-prefix renaming; HGSC has not been matched to the supplied upstream MD5 list. The HGSC fractionation identity therefore remains unverified. See [glyhub_catalog\(\)](#) for dimensions, sizes and download URLs.

Access

Use `glyhub_load("glyhub_CPTAC_HGSC")` to load this dataset.

Source

<https://pdc.cancer.gov/pdc/cptac-pancancer> Data use and attribution: <https://pdc.cancer.gov/pdc/data-use-guidelines>. The source data are not licensed under the package's MIT code license.

See Also

[glyhub_load\(\)](#) to retrieve the original TSV archive.

glyhub_CPTAC_HNSCC	<i>Head and neck squamous cell carcinoma: CPTAC N-glycoproteome</i>
--------------------	---

Description

Load the supplied JHU GENCODEv34 median-normalized glycoform-peptide abundance matrix as a [glyexp::GlycoproteomicSE](#). Downloads are cached.

Usage

```
glyhub_CPTAC_HNSCC(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Details

The assay is $2^{\text{source_value}}$, a linearized normalized abundance. Source log2 values, including zeros, are retained in `metadata(x)$raw_abundance`. Source None entries become NA; no filtering, imputation, aggregation or further normalization is performed. These data are an exception to the zero-to-NA convention used for GlycoPOST datasets.

Reference and QC columns remain present, with source-label-derived roles in `colData`. Unresolved roles remain unresolved. Repeated measurements are not independent patients. `Intensity.Reference` is retained in `rowData(x)$intensity_reference_log2`, not treated as a sample. Source peptide, gene and composition annotations are retained. N/H/F/S/G denotes HexNAc/Hex/Fuc/Neu5Ac/Neu5Gc. No structures are inferred. Protein accessions and absolute sites are unknown (NA); source gene annotations must not be treated as protein accessions.

Provenance records the supplied file hash and upstream checksum status. COAD and PDAC match upstream CRC and PDA after reversing column-prefix renaming; HGSC has not been matched to the supplied upstream MD5 list. The HGSC fractionation identity therefore remains unverified. See [glyhub_catalog\(\)](#) for dimensions, sizes and download URLs.

Access

Use `glyhub_load("glyhub_CPTAC_HNSCC")` to load this dataset.

Source

<https://pdc.cancer.gov/pdc/cptac-pancancer> Data use and attribution: <https://pdc.cancer.gov/pdc/data-use-guidelines>. The source data are not licensed under the package's MIT code license.

See Also

[glyhub_load\(\)](#) to retrieve the original TSV archive.

glyhub_CPTAC_LSCC

*Lung squamous cell carcinoma: CPTAC N-glycoproteome***Description**

Load the supplied JHU GENCODEv34 median-normalized glycoform-peptide abundance matrix as a [glyexp::GlycoproteomicSE](#). Downloads are cached.

Usage

```
glyhub_CPTAC_LSCC(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Details

The assay is $2^{\text{source_value}}$, a linearized normalized abundance. Source log2 values, including zeros, are retained in `metadata(x)$raw_abundance`. Source None entries become NA; no filtering, imputation, aggregation or further normalization is performed. These data are an exception to the zero-to-NA convention used for GlycoPOST datasets.

Reference and QC columns remain present, with source-label-derived roles in `colData`. Unresolved roles remain unresolved. Repeated measurements are not independent patients. `Intensity.Reference` is retained in `rowData(x)$intensity_reference_log2`, not treated as a sample. Source peptide, gene and composition annotations are retained. N/H/F/S/G denotes HexNAc/Hex/Fuc/Neu5Ac/Neu5Gc. No structures are inferred. Protein accessions and absolute sites are unknown (NA); source gene annotations must not be treated as protein accessions.

Provenance records the supplied file hash and upstream checksum status. COAD and PDAC match upstream CRC and PDA after reversing column-prefix renaming; HGSC has not been matched to the supplied upstream MD5 list. The HGSC fractionation identity therefore remains unverified. See [glyhub_catalog\(\)](#) for dimensions, sizes and download URLs.

Access

Use `glyhub_load("glyhub_CPTAC_LSCC")` to load this dataset.

Source

<https://pdc.cancer.gov/pdc/cptac-pancancer> Data use and attribution: <https://pdc.cancer.gov/pdc/data-use-guidelines>. The source data are not licensed under the package's MIT code license.

See Also

[glyhub_load\(\)](#) to retrieve the original TSV archive.

glyhub_CPTAC_LUAD	<i>Lung adenocarcinoma: CPTAC N-glycoproteome</i>
-------------------	---

Description

Load the supplied JHU GENCODEv34 median-normalized glycoform-peptide abundance matrix as a [glyexp::GlycoproteomicSE](#). Downloads are cached.

Usage

```
glyhub_CPTAC_LUAD(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Details

The assay is $2^{\text{source_value}}$, a linearized normalized abundance. Source log2 values, including zeros, are retained in `metadata(x)$raw_abundance`. Source None entries become NA; no filtering, imputation, aggregation or further normalization is performed. These data are an exception to the zero-to-NA convention used for GlycoPOST datasets.

Reference and QC columns remain present, with source-label-derived roles in `colData`. Unresolved roles remain unresolved. Repeated measurements are not independent patients. Intensity.Reference is retained in `rowData(x)$intensity_reference_log2`, not treated as a sample. Source peptide, gene and composition annotations are retained. N/H/F/S/G denotes HexNAc/Hex/Fuc/Neu5Ac/Neu5Gc.

No structures are inferred. Protein accessions and absolute sites are unknown (NA); source gene annotations must not be treated as protein accessions.

Provenance records the supplied file hash and upstream checksum status. COAD and PDAC match upstream CRC and PDA after reversing column-prefix renaming; HGSC has not been matched to the supplied upstream MD5 list. The HGSC fractionation identity therefore remains unverified. See [glyhub_catalog\(\)](#) for dimensions, sizes and download URLs.

Access

Use `glyhub_load("glyhub_CPTAC_LUAD")` to load this dataset.

Source

<https://pdc.cancer.gov/pdc/cptac-pancancer> Data use and attribution: <https://pdc.cancer.gov/pdc/data-use-guidelines>. The source data are not licensed under the package's MIT code license.

See Also

[glyhub_load\(\)](#) to retrieve the original TSV archive.

glyhub_CPTAC_PDAC	<i>Pancreatic ductal adenocarcinoma: CPTAC N-glycoproteome</i>
-------------------	--

Description

Load the supplied JHU GENCODEv34 median-normalized glycoform-peptide abundance matrix as a [glyexp::GlycoproteomicSE](#). Downloads are cached.

Usage

```
glyhub_CPTAC_PDAC(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Details

The assay is $2^{\text{source_value}}$, a linearized normalized abundance. Source log2 values, including zeros, are retained in `metadata(x)$raw_abundance`. Source None entries become NA; no filtering, imputation, aggregation or further normalization is performed. These data are an exception to the zero-to-NA convention used for GlycoPOST datasets.

Reference and QC columns remain present, with source-label-derived roles in `colData`. Unresolved roles remain unresolved. Repeated measurements are not independent patients. `Intensity.Reference` is retained in `rowData(x)$intensity_reference_log2`, not treated as a sample. Source peptide, gene and composition annotations are retained. N/H/F/S/G denotes HexNAc/Hex/Fuc/Neu5Ac/Neu5Gc. No structures are inferred. Protein accessions and absolute sites are unknown (NA); source gene annotations must not be treated as protein accessions.

Provenance records the supplied file hash and upstream checksum status. COAD and PDAC match upstream CRC and PDA after reversing column-prefix renaming; HGSC has not been matched to the supplied upstream MD5 list. The HGSC fractionation identity therefore remains unverified. See [glyhub_catalog\(\)](#) for dimensions, sizes and download URLs.

Access

Use `glyhub_load("glyhub_CPTAC_PDAC")` to load this dataset.

Source

<https://pdc.cancer.gov/pdc/cptac-pancancer> Data use and attribution: <https://pdc.cancer.gov/pdc/data-use-guidelines>. The source data are not licensed under the package's MIT code license.

See Also

[glyhub_load\(\)](#) to retrieve the original TSV archive.

glyhub_CPTAC_UCEC

Uterine corpus endometrial carcinoma: CPTAC N-glycoproteome

Description

Load the supplied JHU GENCODEv34 median-normalized glycoform-peptide abundance matrix as a [glyexp::GlycoproteomicSE](#). Downloads are cached.

Usage

```
glyhub_CPTAC_UCEC(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Details

The assay is $2^{\text{source_value}}$, a linearized normalized abundance. Source log2 values, including zeros, are retained in `metadata(x)$raw_abundance`. Source None entries become NA; no filtering, imputation, aggregation or further normalization is performed. These data are an exception to the zero-to-NA convention used for GlycoPOST datasets.

Reference and QC columns remain present, with source-label-derived roles in `colData`. Unresolved roles remain unresolved. Repeated measurements are not independent patients. `Intensity.Reference` is retained in `rowData(x)$intensity_reference_log2`, not treated as a sample. Source peptide, gene and composition annotations are retained. N/H/F/S/G denotes HexNAc/Hex/Fuc/Neu5Ac/Neu5Gc. No structures are inferred. Protein accessions and absolute sites are unknown (NA); source gene annotations must not be treated as protein accessions.

Provenance records the supplied file hash and upstream checksum status. COAD and PDAC match upstream CRC and PDA after reversing column-prefix renaming; HGSC has not been matched to the supplied upstream MD5 list. The HGSC fractionation identity therefore remains unverified. See [glyhub_catalog\(\)](#) for dimensions, sizes and download URLs.

Access

Use `glyhub_load("glyhub_CPTAC_UCEC")` to load this dataset.

Source

<https://pdc.cancer.gov/pdc/cptac-pancancer> Data use and attribution: <https://pdc.cancer.gov/pdc/data-use-guidelines>. The source data are not licensed under the package's MIT code license.

See Also

[glyhub_load\(\)](#) to retrieve the original TSV archive.

`glyhub_data_conventions`*Measurement and annotation conventions for glyhub datasets*

Description

Shared conventions for reading glyhub abundance matrices, molecular annotations and source provenance. Each dataset's help page describes its experimental design, units and specific limitations.

Details

These zero-handling and processing-ledger conventions apply to the curated GlycoPOST datasets. CPTAC loaders retain source log2 values in metadata and use $2^{\text{source_value}}$ in the assay; source zeros become 1. See [glyhub_CPTAC_CCRCC](#) and [glyhub_catalog\(\)](#). Locally staged non-CPTAC datasets retain source numeric values and zeros without added normalization, imputation or inverse transformation. Prefer original intensities where available; processed-only matrices explicitly document their source scale. `raw_abundance` means the source numeric matrix, not a guarantee that authors supplied unprocessed intensities. See each dataset's help and metadata.

Zero-valued abundances are represented as NA in the distributed abundance assay. This representation differs from the original source tables, which remain available in metadata. Missing values are not imputed, and abundances are not renormalized after this conversion. Zero-valued times and categorical annotations are unchanged.

For GPST000738, measurements with unresolved source-table conflicts are also NA. `metadata(x)$processing_masks` distinguishes original missing entries, source not-detected entries, conflicts and zero conversions. Masks may overlap. For GPST000643, not-detected retention-time entries are recorded separately from zero-valued quantitative measurements.

`metadata(x)$raw_abundance` preserves the original numerical matrix. `raw_text`, source tables and `processing_ledger` retain source notation, cell coordinates and the explanation for each processed value. Original AUCs and retention times are available for GPST000643. These provenance matrices are not additional abundance assays and may use different units.

`rowData(x)` retains source feature labels, typed glyrepr compositions and structures where supported. A `glycan_structure` column is present only when at least one feature has a valid structural annotation; unannotated features in that column remain NA. If none has a structural annotation, the column is absent. Putative assignments remain putative; ambiguous linkages are not completed. Unconverted notation and annotation disagreements are retained explicitly. Source mass/isomer labels are not universal IDs. Consult individual feature annotations when an experiment includes more than one glycan class.

`colData(x)` contains source conditions and observation labels. Common numeric and logical source types are preserved when combining panels, with typed missing values for absent or conflicting observations. Genuinely mixed source types retain their original text rather than being guessed or coerced to numbers. A source label such as Sample 1 or Replicate 1 does not by itself establish biological replication, independence or pairing across tables. Each object's source, doi and license metadata identify its references and source-data license. Source-data licenses are separate from the package code license.

glyhub_GPST000009_O *Atlantic salmon epithelial mucin O-glycans*

Description

O-glycan relative abundances from Atlantic salmon skin, pyloric caeca and distal-intestinal mucins across six geographic and husbandry cohorts from Tasmania, Sweden and Norway.

Usage

```
glyhub_GPST000009_O(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 169 features and 57 observations. The abundance assay is in relative abundance (%). `rowData` includes a typed `glycan_structure` column; features without a supported structure are NA.

Details

All compatible tissue and cohort measurements are retained in one matrix. Original retention times, peak areas, suggested structures and per-sample MS1-only asterisks remain available in source annotations. Relative abundance is preserved as reported; ionisation differences limit interpretation across different glycan species. Typed structures describe native residue topology with analytical reducing-end reduction documented separately. Unresolved linkages remain unknown; malformed or sulfated structure strings remain as source annotations pending unambiguous representation.

Source-derived compositions and original labels are retained. 152 source-supported structures are typed; unspecified bonds remain unknown. Unresolved or conflicting structures remain missing with source provenance.

Access

Use `glyhub_load("glyhub_GPST000009_O")` to load this dataset.

Source

GlycoPOST GPST000009. Sheet1. Study: <https://doi.org/10.1074/mcp.ra119.001319>. Repository: <https://glycopost.glycosmos.org/entry/GPST000009>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000027_031_N

Mgat3 mouse brain and kidney N-glycan source profiles

Description

Source-preserving study-level N-glycan resource from *Mgat3* wild-type and knockout mouse brain and kidney. It contains the complete published 51-feature brain table and 287-feature kidney workbook as distinct source panels.

Usage

```
glyhub_GPST000027_031_N(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

<code>kind</code>	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
<code>cache_dir</code>	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
<code>refresh</code>	Download the pinned resource again, even if cached.
<code>offline</code>	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 338 features and 6 observations. The abundance assay is in source EIC peak intensity (panel-specific instrument units). `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

The object is a disjoint union of 338 source-specific chromatographic features across six source observations: two genotype-labelled brain profiles and four kidney sample/run columns. Of the 2,028 storage cells, 1,250 are measured source cells and 778 cross-panel combinations are unmeasured; `source_coverage` and `processing_masks` distinguish these from the 324 source zeros represented as NA. The original brain and kidney matrices, annotations, sample metadata and exact maps remain in `metadata(x)$panels`, `panel_row_data`, `panel_col_data` and `panel_maps`. No rows are aligned across tissues using composition, mass or author numbering.

The one abundance assay retains EIC peak intensities in panel-specific instrument units. Brain uses `aminoxylTMT6` whereas kidney uses `aminoxylTMT0`; combining storage does not establish calibrated numerical comparability across tissues or protocols. Original percentages remain `metadata(x)$source_relative_abundance`, not a second assay. Both source percentage blocks use high-mannose intensity sums as denominators rather than total glycome. Brain values retain the published one-decimal precision; kidney values retain Excel precision. No averaging, imputation or normalization is added.

Kidney workbook run IDs exactly match four GPST000031 raw filenames. Brain S2C supplies no run or replicate IDs; its raw-file links are explicitly marked genotype-and-filename-based candidates in GPST000027. Although the article reports three independent brain WT/KO pairs, only two genotype columns are published in S2C; these are not expanded or labelled as independent individual mice. Biological replication, pairing, age and sex are not inferred. This object represents the complete published tables, not every raw detected peak or every experiment in the paper.

306 features have a single source composition, retaining generic residues plus the explicitly stated `Man3GlcNAc2` core. For 32 ambiguous kidney features, typed composition is NA while every original candidate string/count and all quantitative cells remain. Chromatographic subpeaks stay distinct even when composition and mass match. Diagnostic MS/MS scan identifiers do not establish complete topology; no `glycan_structure` column is present. Source file attribution and article-version CC BY 4.0 license evidence are retained separately from the package code license; no supplement-specific license declaration was independently verified.

Access

Use `glyhub_load("glyhub_GPST000027_031_N")` to load this dataset.

Source

GlycoPOST GPST000027 and GPST000031. Supplementary Figure S2C (PDF page 4) and Supplemental Table S2 (WT&Mgat3KO sheet). Study: <https://doi.org/10.1074/mcp.RA119.001534>. Repository: <https://glycopost.glycosmos.org/entry/GPST000027> and <https://glycopost.glycosmos.org/entry/GPST000031>. Quantitative source: <https://pmc.ncbi.nlm.nih.gov/articles/PMC6773561/>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000035_O *O-glycan profile of Fetuin_standard and related study experiments*

Description

Complete O-glycan peak-area profile from source panel S2 Fetuin_standard, in the study of cell-line-specific O-glycosylation. All 3 source quantitative features and 3 replicate observations are retained. Combined O-glycan quantitative profiles from GPST000035. 231 union features and 66 source observations are represented.

Usage

```
glyhub_GPST000035_O(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 231 features and 66 observations. The abundance assay is in peak_area. rowData has no glycan_structure column because no feature has a supported structural annotation.

Details

Source experiments are identified in colData and original panel-specific metadata, annotations and measurements are retained in metadata. Feature identities are aligned only when supported by author identifiers or explicit molecular structures; other features retain source-specific identities. The source_coverage matrix distinguishes unmeasured combinations from measured missing values. Units: peak_area.

O-glycan profile of Fetuin_standard: The 3 observations are source-labelled technical replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed

composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of C10: The 2 observations are source-labelled technical replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of COLO205 : The 2 observations are source-labelled technical replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of HT29: The 3 observations are source-labelled biological replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of HT29_Vumc : The 2 observations are source-labelled technical replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of WiDr: The 2 observations are source-labelled technical replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of KM12: The 2 observations are source-labelled technical replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of T84 : The 2 observations are source-labelled unspecified replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source

retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of LS174T: The 2 observations are source-labelled technical replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of LS180: The 2 observations are source-labelled unspecified replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of SW1116: The 2 observations are source-labelled technical replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of SW1463: The 2 observations are source-labelled technical replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of SW948: The 2 observations are source-labelled technical replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of SW1398: The 2 observations are source-labelled technical replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of SW48: The 2 observations are source-labelled technical replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of SW480: The 3 observations are source-labelled biological replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of SW480_Vumc : The 2 observations are source-labelled technical replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of SW620: The 3 observations are source-labelled biological replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of SW837: The 2 observations are source-labelled technical replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of CaCo-2: The 2 observations are source-labelled technical replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of Co115 : The 2 observations are source-labelled technical replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition,

while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of Colo320: The 2 observations are source-labelled technical replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of DLD-1: The 2 observations are source-labelled technical replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of HCT116: The 3 observations are source-labelled biological replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of HCT116 Vumc: The 2 observations are source-labelled technical replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of HCT 15: The 2 observations are source-labelled technical replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of HCT 8 : The 3 observations are source-labelled biological replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of LOVO: The 2 observations are source-labelled technical replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source

retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of LS411N: The 2 observations are source-labelled technical replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

O-glycan profile of RKO : The 2 observations are source-labelled technical replicates in this panel. Source biological and technical replicate designations are retained in colData where stated. Source retention-time isomers retain distinct feature identities unless the author global identifier, composition, retention time and relative area establish a match. Fetuin is a quality-control standard rather than a cell line. Source monosaccharide-count conflicts produce unknown typed composition, while the original label, counts and quantitative matrix are preserved. Sulfation is encoded as a substituent where supported.

Molecular annotations retain source precision. Unresolved compositions or structures are NA; original annotations are retained in rowData. All quantitative source features are preserved.

Access

Use `glyhub_load("glyhub_GPST000035_0")` to load this dataset.

Source

GlycoPOST GPST000035. S2 Fetuin_standard. Study: <https://doi.org/10.1007/s00018-020-03504-z>.
Repository: <https://glycopost.glycosmos.org/entry/GPST000035>. Quantitative source: https://media.springernature.com/original/springer-static/esm/art%3A10.1007%2Fs00018-020-03504-z/MediaObjects/18_2020_3504_MOESM4_ESM.xlsx.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000079_N *Postnatal mouse skeletal-muscle N-glycome*

Description

Released N-glycans from skeletal muscle at postnatal days 1, 7, 14 and 21, with three source observations at each age.

Usage

```
glyhub_GPST000079_N(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 104 features and 12 observations. The abundance assay is in relative abundance (fraction). rowData has no glycan_structure column because no feature has a supported structural annotation.

Details

Supplementary Table S5 individual abundance columns are used; derived fold changes, SEMs and group averages are not treated as additional samples. The source isomer identifiers and partial linkage annotations are retained. This matrix supports the study of the digalactose-to-sialic-acid switch during muscle development.

Source-derived compositions and original annotation fields are preserved; unknown linkages are not inferred.

Access

Use `glyhub_load("glyhub_GPST000079_N")` to load this dataset.

Source

GlycoPOST GPST000079. BP_muscles_rawdata_251017_Perse. Study: <https://doi.org/10.1074/mcp.ra120.002166>. Repository: <https://glycopost.glycosmos.org/entry/GPST000079>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000120_O_Spike_ACE2

Released O-glycans of recombinant SARS-CoV-2 Spike and ACE2

Description

The study characterizes the glycosylation of recombinant Spike and soluble human ACE2. This complete source O-glycan table reports percent of total profile for 16 glycan features in each protein preparation. Columns are protein-level profiles, not biological replicates.

Usage

```
glyhub_GPST000120_O_Spike_ACE2(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 16 features and 2 observations. The abundance assay is in percent of total O-glycan profile. rowData includes a typed glycan_structure column; features without a supported structure are NA.

Details

The entire 16-feature source O-glycan table is retained. The two columns are protein-level profiles for recombinant Spike and soluble human ACE2, with no biological replicate identity inferred. Original nd/nd* markers and measurements are retained; abundance zeros and not-detected entries are represented as NA without renormalization.

All 16 source GlyTouCan accessions were resolved to WURCS records from the official GlyTouCan SPARQL service. The registered structures were converted with glyparse 0.8.1, reparsed and validated with glyrepr 1.1.0, and compositions derived from those structures. This preserves the source accession assignments and does not infer structures from mass or infer new experimental linkage evidence.

Access

Use `glyhub_load("glyhub_GPST000120_O_Spike_ACE2")` to load this dataset.

Source

GlycoPOST GPST000120. Sheet1. Study: <https://doi.org/10.1016/j.chom.2020.08.004>.
 Repository: <https://glycopost.glycosmos.org/entry/GPST000120>. Quantitative source: <https://glycopost.glycosmos.org/data/GPST000120.0/olinked3.xlsx>. Annotation evidence: <https://ts.glytoucan.org/sparql>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000125_GSL_HEK293

Glycosphingolipid glycan profiles in HEK293 glycosylation-knockout cells

Description

Complete Table S4_1 glycosphingolipid glycan relative-abundance block from Global mapping of glycosylation pathways in human-derived cells, comparing wild-type HEK293 with seven glycosylation knockout conditions.

Usage

```
glyhub_GPST000125_GSL_HEK293(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

<code>kind</code>	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
<code>cache_dir</code>	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
<code>refresh</code>	Download the pinned resource again, even if cached.
<code>offline</code>	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 12 features and 16 observations. The abundance assay is in percent relative abundance. rowData includes a typed glycan_structure column; features without a supported structure are NA.

Details

All source-numbered features and both experiment columns for all eight conditions are retained. The article methods explicitly call these two biological replicates. Average/error columns are retained only in source cell records and are not sample observations. Quantitative zeros become NA without renormalization; original numeric measurements remain in raw_matrix. Same-composition source rows are not collapsed. Five conflicting source compositions are supported by the original name and diagram; one unresolved row remains NA. All conflicting registry IDs and quantitative rows are preserved.

Composition counts are from source Component IDs resolved through the official GlyTouCan WURCS registry. Generic base-composition residues are counted directly from explicit WURCS residue indices; full structures are parsed with glyparse 0.8.1 and glyrepr 1.1.0. A single, non-conflicting source Structure ID is eligible for typed structure. Candidate lists remain lists; no representative is chosen from a mixture. Five previously conflicting compositions are supported by original names and native-vector diagrams; N feature 17 remains unresolved because its source drawing also disagrees. Registry identifiers and all conflicting evidence remain intact. No mass-derived structure or sample identity is inferred.

Access

Use `glyhub_load("glyhub_GPST000125_GSL_HEK293")` to load this dataset.

Source

GlycoPOST GPST000125. Table S4_1, GSL block. Study: <https://doi.org/10.1016/j.devcel.2021.02.023>. Repository: <https://glycopost.glycosmos.org/entry/GPST000125>. Quantitative source: <https://pmc.ncbi.nlm.nih.gov/articles/instance/8086148/bin/NIHMS1683936-supplement-5.xlsx>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000125_N_HEK293

N-glycan profiles in HEK293 glycosylation-knockout cells

Description

Complete Table S4_1 N-glycan relative-abundance block from Global mapping of glycosylation pathways in human-derived cells, comparing wild-type HEK293 with seven glycosylation knockout conditions.

Usage

```
glyhub_GPST000125_N_HEK293(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 41 features and 16 observations. The abundance assay is in percent relative abundance. `rowData` includes a typed `glycan_structure` column; features without a supported structure are NA.

Details

All source-numbered features and both experiment columns for all eight conditions are retained. The article methods explicitly call these two biological replicates. Average/error columns are retained only in source cell records and are not sample observations. Quantitative zeros become NA without renormalization; original numeric measurements remain in `raw_matrix`. Same-composition source rows are not collapsed. Five conflicting source compositions are supported by the original name and diagram; one unresolved row remains NA. All conflicting registry IDs and quantitative rows are preserved.

Composition counts are from source Component IDs resolved through the official GlyTouCan WURCS registry. Generic base-composition residues are counted directly from explicit WURCS residue indices; full structures are parsed with `glyparse` 0.8.1 and `glyrepr` 1.1.0. A single, non-conflicting source Structure ID is eligible for typed structure. Candidate lists remain lists; no representative is chosen from a mixture. Five previously conflicting compositions are supported by original names and native-vector diagrams; N feature 17 remains unresolved because its source drawing also disagrees. Registry identifiers and all conflicting evidence remain intact. No mass-derived structure or sample identity is inferred.

Access

Use `glyhub_load("glyhub_GPST000125_N_HEK293")` to load this dataset.

Source

GlycoPOST GPST000125. Table S4_1, N block. Study: <https://doi.org/10.1016/j.devcel.2021.02.023>. Repository: <https://glycopost.glycosmos.org/entry/GPST000125>. Quantitative source: <https://pmc.ncbi.nlm.nih.gov/articles/instance/8086148/bin/NIHMS1683936-supplement-5.xlsx>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000125_O_HEK293

O-glycan profiles in HEK293 glycosylation-knockout cells

Description

Complete Table S4_1 O-glycan relative-abundance block from Global mapping of glycosylation pathways in human-derived cells, comparing wild-type HEK293 with seven glycosylation knockout conditions.

Usage

```
glyhub_GPST000125_O_HEK293(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 14 features and 16 observations. The abundance assay is in percent relative abundance. `rowData` includes a typed `glycan_structure` column; features without a supported structure are NA.

Details

All source-numbered features and both experiment columns for all eight conditions are retained. The article methods explicitly call these two biological replicates. Average/error columns are retained only in source cell records and are not sample observations. Quantitative zeros become NA without renormalization; original numeric measurements remain in `raw_matrix`. Same-composition source rows are not collapsed. Five conflicting source compositions are supported by the original name and diagram; one unresolved row remains NA. All conflicting registry IDs and quantitative rows are preserved.

Composition counts are from source Component IDs resolved through the official GlyTouCan WURCS registry. Generic base-composition residues are counted directly from explicit WURCS residue indices; full structures are parsed with `glyparse 0.8.1` and `glyrepr 1.1.0`. A single, non-conflicting source Structure ID is eligible for typed structure. Candidate lists remain lists; no representative is chosen from a mixture. Five previously conflicting compositions are supported by original names and native-vector diagrams; N feature 17 remains unresolved because its source drawing also disagrees. Registry identifiers and all conflicting evidence remain intact. No mass-derived structure or sample identity is inferred.

Access

Use `glyhub_load("glyhub_GPST000125_O_HEK293")` to load this dataset.

Source

GlycoPOST GPST000125. Table S4_1, O block. Study: <https://doi.org/10.1016/j.devcel.2021.02.023>. Repository: <https://glycopost.glycosmos.org/entry/GPST000125>. Quantitative source: <https://pmc.ncbi.nlm.nih.gov/articles/instance/8086148/bin/NIHMS1683936-supplement-5.xlsx>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

`glyhub_GPST000128_n_precursor`*Red-blood-cell N-glycan precursor quantification*

Description

Complete public Panorama precursor-by-sample TotalArea export; all source precursors including explicitly marked glucose QC/normalization standards retained.

Usage

```
glyhub_GPST000128_n_precursor(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 128 features and 6 observations. The abundance assay is in peak_area. rowData has no glycan_structure column because no feature has a supported structural annotation.

Details

Six source sample identifiers 07,08,13,39,55,56 retained. Clinical group mapping not verified, group=NA. Multiple precursors per glycan remain separate by source precursor ID; no arbitrary charge merging. This is an already integrated processed quantity export, no raw-MS reprocessing.

Molecular annotations retain source precision. Unresolved compositions or structures are NA; original annotations are retained in rowData. All quantitative source features are preserved.

Access

Use glyhub_load("glyhub_GPST000128_n_precursor") to load this dataset.

Source

GlycoPOST GPST000128. Panorama PrecursorChromInfo. Study: <https://doi.org/10.1182/bloodadvances.2020003376>. Repository: <https://glycopost.glycosmos.org/entry/GPST000128>. Quantitative source: <https://panoramaweb.org/Panorama%20Public/2020/U%20of%20Nebraska%20Medical%20Center%20Gundry%20Lab%20-%20Sickle%20Cell%20Manuscript/query-selectRows.api?schemaName=targetedms&query.queryName=PrecursorChromInfo&query.maxRows=2000>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000128_o_precursor

Red-blood-cell O-glycan precursor quantification

Description

Complete public Panorama precursor-by-sample TotalArea export; all source precursors including explicitly marked glucose QC/normalization standards retained.

Usage

```
glyhub_GPST000128_o_precursor(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 35 features and 6 observations. The abundance assay is in peak_area. rowData has no glycan_structure column because no feature has a supported structural annotation.

Details

Six source sample identifiers 07,08,13,39,55,56 retained. Clinical group mapping not verified, group=NA. Multiple precursors per glycan remain separate by source precursor ID; no arbitrary charge merging. This is an already integrated processed quantity export, no raw-MS reprocessing.

Molecular annotations retain source precision. Unresolved compositions or structures are NA; original annotations are retained in rowData. All quantitative source features are preserved.

Access

Use glyhub_load("glyhub_GPST000128_o_precursor") to load this dataset.

Source

GlycoPOST GPST000128. Panorama PrecursorChromInfo. Study: <https://doi.org/10.1182/bloodadvances.2020003376>. Repository: <https://glycopost.glycosmos.org/entry/GPST000128>. Quantitative source: <https://panoramaweb.org/Panorama%20Public/2020/U%20of%20Nebraska%20Medical%20Center%20Gundry%20Lab%20-%20Sickle%20Cell%20Manuscript/query-selectRows.api?schemaName=targetedms&query.queryName=PrecursorChromInfo&query.maxRows=2000>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000170_N *Ion-source dopant effects on N-glycan signal*

Description

Targeted peak areas for 15 selected N-glycan features measured in technical injection replicates under six ion-source gas/dopant conditions.

Usage

```
glyhub_GPST000170_N(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 15 features and 18 observations. The abundance assay is in peak area. `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

The panel compares AIR, nitrogen and solvent-enriched nitrogen conditions using three injections per condition. This is the complete author-defined 15-feature targeted panel, not an unbiased whole-glycome survey. Isomer suffixes remain separate; Sg denotes Neu5Gc. Relative area summaries and signal-to-noise statistics are not mistaken for extra samples. The N-glycan sample is a 1:1 mixture released from human IgG and bovine fetuin; the O-glycan sample derives from bovine submaxillary mucin. Each run injected 1 microlitre.

Source molecular compositions retained without inferring glycosidic linkages.

Access

Use `glyhub_load("glyhub_GPST000170_N")` to load this dataset.

Source

GlycoPOST GPST000170. S1. Study: <https://doi.org/10.1021/acs.analchem.1c00023>.
Repository: <https://glycopost.glycosmos.org/entry/GPST000170>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000170_O *Ion-source dopant effects on O-glycan signal*

Description

Targeted peak areas for 15 selected O-glycan features measured in technical injection replicates under six ion-source gas/dopant conditions.

Usage

```
glyhub_GPST000170_O(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

<code>kind</code>	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
<code>cache_dir</code>	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
<code>refresh</code>	Download the pinned resource again, even if cached.
<code>offline</code>	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 15 features and 18 observations. The abundance assay is in peak area. rowData has no glycan_structure column because no feature has a supported structural annotation.

Details

The panel compares AIR, nitrogen and solvent-enriched nitrogen conditions using three injections per condition. This is the complete author-defined 15-feature targeted panel, not an unbiased whole-glycome survey. Isomer suffixes remain separate; Sg denotes Neu5Gc. Relative area summaries and signal-to-noise statistics are not mistaken for extra samples. The N-glycan sample is a 1:1 mixture released from human IgG and bovine fetuin; the O-glycan sample derives from bovine submaxillary mucin. Each run injected 1 microlitre.

Source molecular compositions retained without inferring glycosidic linkages.

Access

Use `glyhub_load("glyhub_GPST000170_0")` to load this dataset.

Source

GlycoPOST GPST000170. S1. Study: <https://doi.org/10.1021/acs.analchem.1c00023>.
Repository: <https://glycopost.glycosmos.org/entry/GPST000170>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000183_n	<i>MLL-rearranged B-cell precursor ALL N-glycome</i>
---------------------	--

Description

Complete source abundance matrix; O-table merged glycan identity spans alternative charge rows, with quantities taken from the sole nonempty quantitative row.

Usage

```
glyhub_GPST000183_n(  
  kind = c("curated", "raw"),  
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),  
  refresh = FALSE,  
  offline = FALSE  
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A `glyexp::GlycomicSE` with 101 features and 7 observations. The abundance assay is in `relative_abundance_percent`. `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

All published features and samples retained, including N-table BM41/R7B11 that paper later excluded from final preparations due to low yield; flag rather than silently discard. GlyTouCan IDs retained as identifiers, not invented full structures. N table is seven per-donor relative abundance profiles; O suffixes 1-4 are technical replicates per paper figure caption.

Molecular annotations retain source precision. Unresolved compositions or structures are NA; original annotations are retained in `rowData`. All quantitative source features are preserved.

Access

Use `glyhub_load("glyhub_GPST000183_n")` to load this dataset.

Source

GlycoPOST GPST000183. N-glycans. Study: <https://doi.org/10.7150/thno.65398>. Repository: <https://glycopost.glycosmos.org/entry/GPST000183>. Quantitative source: <https://glycopost.glycosmos.org/data/GPST000183.0/Sup%20Table%205%20-%20N-glycomics%20Results.xlsx>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000183_o *MLL-rearranged B-cell precursor ALL O-glycome*

Description

Complete source abundance matrix; O-table merged glycan identity spans alternative charge rows, with quantities taken from the sole nonempty quantitative row.

Usage

```
glyhub_GPST000183_o(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A `glyexp::GlycomicSE` with 21 features and 20 observations. The abundance assay is in `relative_abundance_percent`. `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

All published features and samples retained, including N-table BM41/R7B11 that paper later excluded from final preparations due to low yield; flag rather than silently discard. GlyTouCan IDs retained as identifiers, not invented full structures. N table is seven per-donor relative abundance profiles; O suffixes 1-4 are technical replicates per paper figure caption.

Molecular annotations retain source precision. Unresolved compositions or structures are NA; original annotations are retained in `rowData`. All quantitative source features are preserved.

Access

Use `glyhub_load("glyhub_GPST000183_o")` to load this dataset.

Source

GlycoPOST GPST000183. Glycomics Reporting. Study: <https://doi.org/10.7150/thno.65398>. Repository: <https://glycopost.glycosmos.org/entry/GPST000183>. Quantitative source: <https://glycopost.glycosmos.org/data/GPST000183.0/Sup%20Table%204%20-%20glycomics%20Results.xlsx>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000190_N *Linkage-specific sialic-acid derivatization of plasma N-glycans*

Description

Background-subtracted extracted-ion intensities of procainamide-labelled plasma N-glycans after linkage-specific sialic-acid derivatization.

Usage

```
glyhub_GPST000190_N(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicsSE](#) with 78 features and 54 observations. The abundance assay is in background-subtracted extracted-ion intensity. `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

The deposited complete extraction table contains 39 composition/retention features in two charge states across 54 LC-MS runs, including explicitly labelled blanks. Charge states remain separate measurement features rather than being summed without an author-defined rule. Am and E denote the source derivatization products used to distinguish alpha2,3- and alpha2,6-linked sialic acids; their counts are retained alongside the underlying Neu5Ac composition. Unmeasured charge states and reported zeros are missing in the curated assay. Run identifiers retain the original experimental batches; they are not interpreted as independent biological donors.

Composition-level glycans with source charge, retention time, procainamide label, and linkage-specific sialic-acid derivative counts; no full topology inferred.

Access

Use `glyhub_load("glyhub_GPST000190_N")` to load this dataset.

Source

GlycoPOST GPST000190. Table S-3. Study: <https://doi.org/10.1021/acs.analchem.1c02610>.
Repository: <https://glycopost.glycosmos.org/entry/GPST000190>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000211_O	<i>O-glycans released by thrombin-activated human platelets</i>
---------------------	---

Description

Released O-glycan peak areas from platelet releasates of five human donors following thrombin stimulation.

Usage

```
glyhub_GPST000211_O(  
  kind = c("curated", "raw"),  
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),  
  refresh = FALSE,  
  offline = FALSE  
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A `glyexp::GlycomicSE` with 11 features and 5 observations. The abundance assay is in peak area. `rowData` includes a typed `glycan_structure` column; features without a supported structure are NA.

Details

The published total-AUC columns combine the author-measured charge states for each of eleven glycan features. Isomer-resolved features remain distinct. Glycans below 300 Da were outside the reported detection range. Proposed source structures and their known linkages are retained where explicitly represented; the trisialylated feature has unresolved sialic-acid attachment topology and retains composition-level annotation.

Source composition counts and proposed structures cross-checked against the source table images and deposited GlycoWorkbench workspace; unresolved topology remains missing.

Access

Use `glyhub_load("glyhub_GPST000211_0")` to load this dataset.

Source

GlycoPOST GPST000211. Table S3. Study: <https://doi.org/10.1016/j.mcpro.2024.100717>. Repository: <https://glycopost.glycosmos.org/entry/GPST000211>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000213_N	<i>Mouse CTX (M) N-glycan source peak profiles and related study experiments</i>
---------------------	--

Description

Complete source-defined N-glycan peak-intensity matrix for mouse CTX (M). The repository includes wild-type and `Slc39a8 A391T` mutant observations; specimen labels and source genotypes are retained where given. Combined N-glycan quantitative profiles from GPST000213. 679 union features and 86 source observations are represented.

Usage

```
glyhub_GPST000213_N(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 679 features and 86 observations. The abundance assay is in source peak intensity. `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

Source experiments are identified in `colData` and original panel-specific metadata, annotations and measurements are retained in metadata. Feature identities are aligned only when supported by author identifiers or explicit molecular structures; other features retain source-specific identities. The `source_coverage` matrix distinguishes unmeasured combinations from measured missing values. Units: source peak intensity.

Mouse CTX (M) N-glycan source peak profiles: 130 quantified source peaks are retained, including peaks without resolved molecular annotation. This is the complete raw-intensity block of the processed workbook, not raw MS reprocessing. Peaks are indexed within the source sheet; no mass-tolerance matching or inter-tissue alignment is imposed. Published normalized and signal-to-noise tables remain in the original workbook; they are not substituted for the intensity assay. Sex and specimen labels are source-defined. Glycan composition is unknown for these peak-level features because the separate rounded-mass annotation list has no exact source feature key. Source QC: the full 130-value raw-intensity vectors for M480 (WT, source G) and M11 (MUT, source I) are identical, as are M10 (MUT, source H) and M444 (MUT, source K). All four source columns are preserved, but their analysis assay values are masked as NA because source sample provenance cannot be resolved. No member of either pair is guessed to be correct. The repository combines wild-type profiling with Slc39a8 A391T data discussed in the related study (DOI: 10.1038/s41380-022-01490-1); the linked Nature Communications data-availability statement explicitly identifies this shared accession.

Mouse HIP (M) N-glycan source peak profiles: 130 quantified source peaks are retained, including peaks without resolved molecular annotation. This is the complete raw-intensity block of the

processed workbook, not raw MS reprocessing. Peaks are indexed within the source sheet; no mass-tolerance matching or inter-tissue alignment is imposed. Published normalized and signal-to-noise tables remain in the original workbook; they are not substituted for the intensity assay. Sex and specimen labels are source-defined. Glycan composition is unknown for these peak-level features because the separate rounded-mass annotation list has no exact source feature key. The repository combines wild-type profiling with Slc39a8 A391T data discussed in the related study (DOI: 10.1038/s41380-022-01490-1); the linked Nature Communications data-availability statement explicitly identifies this shared accession.

Mouse STR (M) N-glycan source peak profiles: 130 quantified source peaks are retained, including peaks without resolved molecular annotation. This is the complete raw-intensity block of the processed workbook, not raw MS reprocessing. Peaks are indexed within the source sheet; no mass-tolerance matching or inter-tissue alignment is imposed. Published normalized and signal-to-noise tables remain in the original workbook; they are not substituted for the intensity assay. Sex and specimen labels are source-defined. Glycan composition is unknown for these peak-level features because the separate rounded-mass annotation list has no exact source feature key. The repository combines wild-type profiling with Slc39a8 A391T data discussed in the related study (DOI: 10.1038/s41380-022-01490-1); the linked Nature Communications data-availability statement explicitly identifies this shared accession.

Mouse CBLM (M) N-glycan source peak profiles: 130 quantified source peaks are retained, including peaks without resolved molecular annotation. This is the complete raw-intensity block of the processed workbook, not raw MS reprocessing. Peaks are indexed within the source sheet; no mass-tolerance matching or inter-tissue alignment is imposed. Published normalized and signal-to-noise tables remain in the original workbook; they are not substituted for the intensity assay. Sex and specimen labels are source-defined. Glycan composition is unknown for these peak-level features because the separate rounded-mass annotation list has no exact source feature key. The repository combines wild-type profiling with Slc39a8 A391T data discussed in the related study (DOI: 10.1038/s41380-022-01490-1); the linked Nature Communications data-availability statement explicitly identifies this shared accession.

Mouse CTX (F) N-glycan source peak profiles: 130 quantified source peaks are retained, including peaks without resolved molecular annotation. This is the complete raw-intensity block of the processed workbook, not raw MS reprocessing. Peaks are indexed within the source sheet; no mass-tolerance matching or inter-tissue alignment is imposed. Published normalized and signal-to-noise tables remain in the original workbook; they are not substituted for the intensity assay. Sex and specimen labels are source-defined. Glycan composition is unknown for these peak-level features because the separate rounded-mass annotation list has no exact source feature key. The repository combines wild-type profiling with Slc39a8 A391T data discussed in the related study (DOI: 10.1038/s41380-022-01490-1); the linked Nature Communications data-availability statement explicitly identifies this shared accession.

Mouse CBLM (F) N-glycan source peak profiles: 130 quantified source peaks are retained, including peaks without resolved molecular annotation. This is the complete raw-intensity block of the processed workbook, not raw MS reprocessing. Peaks are indexed within the source sheet; no mass-tolerance matching or inter-tissue alignment is imposed. Published normalized and signal-to-noise tables remain in the original workbook; they are not substituted for the intensity assay. Sex and specimen labels are source-defined. Glycan composition is unknown for these peak-level features because the separate rounded-mass annotation list has no exact source feature key. The repository combines wild-type profiling with Slc39a8 A391T data discussed in the related study (DOI: 10.1038/s41380-022-01490-1); the linked Nature Communications data-availability statement ex-

plicitly identifies this shared accession.

Mouse Plasma (M F) N-glycan source peak profiles: 29 quantified source peaks are retained, including peaks without resolved molecular annotation. This is the complete raw-intensity block of the processed workbook, not raw MS reprocessing. Peaks are indexed within the source sheet; no mass-tolerance matching or inter-tissue alignment is imposed. Published normalized and signal-to-noise tables remain in the original workbook; they are not substituted for the intensity assay. Sex and specimen labels are source-defined. Glycan composition is unknown for these peak-level features because the separate rounded-mass annotation list has no exact source feature key. The repository combines wild-type profiling with Slc39a8 A391T data discussed in the related study (DOI: 10.1038/s41380-022-01490-1); the linked Nature Communications data-availability statement explicitly identifies this shared accession.

No molecular annotation is inferred from mass alone; source m/z labels remain available.

Access

Use `glyhub_load("glyhub_GPST000213_N")` to load this dataset.

Source

GlycoPOST GPST000213. CTX (M). Study: <https://doi.org/10.1038/s41467-021-27781-9>. Repository: <https://glycopost.glycosmos.org/entry/GPST000213>. Quantitative source: <https://glycopost.glycosmos.org/data/GPST000213.0/Source%20Data%20N-Glycans.xlsx>. Related study: <https://doi.org/10.1038/s41380-022-01490-1>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000213_O	<i>Mouse CTX (M) O-glycan source peak profiles and related study experiments</i>
---------------------	--

Description

Complete source-defined O-glycan peak-intensity matrix for mouse CTX (M). The repository includes wild-type and Slc39a8 A391T mutant observations; specimen labels and source genotypes are retained where given. Combined O-glycan quantitative profiles from GPST000213. 148 union features and 39 source observations are represented.

Usage

```
glyhub_GPST000213_O(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A `glyexp::GlycomicSE` with 148 features and 39 observations. The abundance assay is in source peak intensity. `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

Source experiments are identified in `colData` and original panel-specific metadata, annotations and measurements are retained in metadata. Feature identities are aligned only when supported by author identifiers or explicit molecular structures; other features retain source-specific identities. The `source_coverage` matrix distinguishes unmeasured combinations from measured missing values. Units: source peak intensity.

Mouse CTX (M) O-glycan source peak profiles: 30 quantified source peaks are retained, including peaks without resolved molecular annotation. This is the complete raw-intensity block of the processed workbook, not raw MS reprocessing. Peaks are indexed within the source sheet; no mass-tolerance matching or inter-tissue alignment is imposed. Published normalized and signal-to-noise tables remain in the original workbook; they are not substituted for the intensity assay. Sex and specimen labels are source-defined. Glycan composition is unknown for these peak-level features because the separate rounded-mass annotation list has no exact source feature key. The repository combines wild-type profiling with Slc39a8 A391T data discussed in the related study (DOI: 10.1038/s41380-022-01490-1); the linked Nature Communications data-availability statement explicitly identifies this shared accession.

Mouse HIP (M) O-glycan source peak profiles: 30 quantified source peaks are retained, including peaks without resolved molecular annotation. This is the complete raw-intensity block of the processed workbook, not raw MS reprocessing. Peaks are indexed within the source sheet; no mass-tolerance matching or inter-tissue alignment is imposed. Published normalized and signal-to-noise tables remain in the original workbook; they are not substituted for the intensity assay. Sex and specimen labels are source-defined. Glycan composition is unknown for these peak-level features because the separate rounded-mass annotation list has no exact source feature key. The repository combines wild-type profiling with Slc39a8 A391T data discussed in the related study (DOI: 10.1038/s41380-022-01490-1); the linked Nature Communications data-availability statement explicitly identifies this shared accession.

Mouse STR (M) O-glycan source peak profiles: 30 quantified source peaks are retained, including peaks without resolved molecular annotation. This is the complete raw-intensity block of the processed workbook, not raw MS reprocessing. Peaks are indexed within the source sheet; no mass-tolerance matching or inter-tissue alignment is imposed. Published normalized and signal-to-noise tables remain in the original workbook; they are not substituted for the intensity assay. Sex and specimen labels are source-defined. Glycan composition is unknown for these peak-level features

because the separate rounded-mass annotation list has no exact source feature key. The repository combines wild-type profiling with Slc39a8 A391T data discussed in the related study (DOI: 10.1038/s41380-022-01490-1); the linked Nature Communications data-availability statement explicitly identifies this shared accession.

Mouse CBLM (M) O-glycan source peak profiles: 30 quantified source peaks are retained, including peaks without resolved molecular annotation. This is the complete raw-intensity block of the processed workbook, not raw MS reprocessing. Peaks are indexed within the source sheet; no mass-tolerance matching or inter-tissue alignment is imposed. Published normalized and signal-to-noise tables remain in the original workbook; they are not substituted for the intensity assay. Sex and specimen labels are source-defined. Glycan composition is unknown for these peak-level features because the separate rounded-mass annotation list has no exact source feature key. The repository combines wild-type profiling with Slc39a8 A391T data discussed in the related study (DOI: 10.1038/s41380-022-01490-1); the linked Nature Communications data-availability statement explicitly identifies this shared accession.

Mouse CTX (Female) O-glycan source peak profiles: 28 quantified source peaks are retained, including peaks without resolved molecular annotation. This is the complete raw-intensity block of the processed workbook, not raw MS reprocessing. Peaks are indexed within the source sheet; no mass-tolerance matching or inter-tissue alignment is imposed. Published normalized and signal-to-noise tables remain in the original workbook; they are not substituted for the intensity assay. Sex and specimen labels are source-defined. Glycan composition is unknown for these peak-level features because the separate rounded-mass annotation list has no exact source feature key. The repository combines wild-type profiling with Slc39a8 A391T data discussed in the related study (DOI: 10.1038/s41380-022-01490-1); the linked Nature Communications data-availability statement explicitly identifies this shared accession.

No molecular annotation is inferred from mass alone; source m/z labels remain available.

Access

Use `glyhub_load("glyhub_GPST000213_O")` to load this dataset.

Source

GlycoPOST GPST000213. CTX (M). Study: <https://doi.org/10.1038/s41467-021-27781-9>. Repository: <https://glycopost.glycosmos.org/entry/GPST000213>. Quantitative source: <https://glycopost.glycosmos.org/data/GPST000213.0/Source%20Data%20-Glycans.xlsx>. Related study: <https://doi.org/10.1038/s41380-022-01490-1>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000214_N_AML_CellLines

N-glycan profiles of 21 acute myeloid leukemia cell lines

Description

Complete 68-feature released N-glycan fractional-abundance matrix in 21 AML cell lines from Integrated N- and O-Glycomics of Acute Myeloid Leukemia (AML) Cell Lines.

Usage

```
glyhub_GPST000214_N_AML_CellLines(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 68 features and 21 observations. The abundance assay is in percent fractional abundance. rowData has no glycan_structure column because no feature has a supported structural annotation.

Details

Source assay is the complete individual-glycan block only; following glycan-feature/derived-trait rows are not molecular features. Author-imputed values of 0.01 replacing zeros are preserved exactly as published; this curation does not reverse or add imputation. Only actual quantitative zero values become NA. No renormalization is applied. One source profile column represents each cell line; biological/technical replicate status of the main table is not specified by its headers and is left unknown. The RSD_MOLM-14 sheet is retained as auxiliary variability data rather than appended: biological rep1 overlaps technical replicates, and N-glycan technical and biological panels have different feature denominators. Isomer suffixes are preserved without collapsing rows.

Counts follow the author legend: H=Hex, N=HexNAc, F=Fuc, S=NeuAc, P=phosphate, Su=sulfate. In typed composition, sulfate uses S and sialic acid uses NeuAc. Structures are not inferred from composition, retention order or mass.

Access

Use `glyhub_load("glyhub_GPST000214_N_AML_CellLines")` to load this dataset.

Source

GlycoPOST GPST000214. . Study: <https://doi.org/10.3390/cells10113058>. Repository: <https://glycopost.glycosmos.org/entry/GPST000214>. Quantitative source: <https://www.ebi.ac.uk/europepmc/webservices/rest/PMC8616353/supplementaryFiles>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000214_O_AML_CellLines

O-glycan profiles of 21 acute myeloid leukemia cell lines

Description

Complete 23-feature released O-glycan fractional-abundance matrix in 21 AML cell lines from Integrated N- and O-Glycomics of Acute Myeloid Leukemia (AML) Cell Lines.

Usage

```
glyhub_GPST000214_O_AML_CellLines(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

<code>kind</code>	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
<code>cache_dir</code>	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
<code>refresh</code>	Download the pinned resource again, even if cached.
<code>offline</code>	Prohibit downloads; require a verified local resource.

Format

A `glyexp::GlycomicSE` with 23 features and 21 observations. The abundance assay is in percent fractional abundance. `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

Source assay is the complete individual-glycan block only; following glycan-feature/derived-trait rows are not molecular features. Author-imputed values of 0.01 replacing zeros are preserved exactly as published; this curation does not reverse or add imputation. Only actual quantitative zero values become NA. No renormalization is applied. One source profile column represents each cell line; biological/technical replicate status of the main table is not specified by its headers and is left unknown. The RSD_MOLM-14 sheet is retained as auxiliary variability data rather than appended: biological rep1 overlaps technical replicates, and N-glycan technical and biological panels have different feature denominators. Isomer suffixes are preserved without collapsing rows.

Counts follow the author legend: H=Hex, N=HexNAc, F=Fuc, S=NeuAc, P=phosphate, Su=sulfate. In typed composition, sulfate uses S and sialic acid uses NeuAc. Structures are not inferred from composition, retention order or mass.

Access

Use `glyhub_load("glyhub_GPST000214_O_AML_CellLines")` to load this dataset.

Source

GlycoPOST GPST000214. . Study: <https://doi.org/10.3390/cells10113058>. Repository: <https://glycopost.glycosmos.org/entry/GPST000214>. Quantitative source: <https://www.ebi.ac.uk/europepmc/webservices/rest/PMC8616353/supplementaryFiles>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000239_GSL *Colorectal-cancer cell-line glycosphingolipid glycans*

Description

Relative glycosphingolipid-glycan abundances across 22 human colorectal-cancer cell lines spanning unassigned, undifferentiated and colon-like transcriptional subtypes.

Usage

```
glyhub_GPST000239_GSL(  
  kind = c("curated", "raw"),  
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),  
  refresh = FALSE,  
  offline = FALSE  
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A `glyexp::GlycomicSE` with 94 features and 22 observations. The abundance assay is in relative abundance (%). `rowData` includes a typed `glycan_structure` column; features without a supported structure are NA.

Details

Supplementary Table S5 supplies 94 chromatographically distinguished glycan features and cell-line aggregate abundance values. Cell-line origin, tumour stage, differentiation and microsatellite status are joined from Table S1 when the source identifier matches exactly. Original antigen, glycan-family and linkage annotations are retained. Typed structures are transcribed from the same-row SNFG diagrams with all unspecified linkages left unknown; repeated compositions remain separate isomer features. Values are cell-line summaries, not individual biological-replicate measurements.

Source-derived compositions and original labels are retained. 94 source-supported structures are typed; unspecified bonds remain unknown. Unresolved or conflicting structures remain missing with source provenance.

Access

Use `glyhub_load("glyhub_GPST000239_GSL")` to load this dataset.

Source

GlycoPOST GPST000239. S-5. Study: <https://doi.org/10.1016/j.mcpro.2022.100239>. Repository: <https://glycopost.glycosmos.org/entry/GPST000239>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000240_GSL *Brugia malayi* glycosphingolipid glycans across life stages

Description

MALDI-TOF MS peak-area profiles of released glycans from mixed-sex adult worms, microfilariae, adult females and adult males.

Usage

```
glyhub_GPST000240_GSL(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 47 features and 8 observations. The abundance assay is in MALDI-TOF MS integrated peak area (arbitrary units). rowData includes a typed glycan_structure column; features without a supported structure are NA.

Details

Forty-seven source-assigned molecular features are retained, including features without a quantified assignment in a particular spectrum. Mixed-sex adult and microfilarial material each have an original spectrum and two explicitly labelled biological replicates. Sex-separated adults have one profile each. Areas are preserved on the source instrumental scale. Unassigned or undetected features remain missing; no zero filling or normalization is applied. Source phosphorylcholine and glucuronic-acid composition components are represented explicitly. Proposed structural diagrams are transcribed and composition-checked against the same source feature rows. Unlabelled bonds are unknown; source ambiguity braces are represented as floating groups without selecting a particular attachment. GSL-GP34 has H2N6PC1A1 in the source composition but H2N4PC1A1 in its proposed diagram; both typed composition and structure are missing for this feature, while the conflicting evidence and peak areas remain available.

46 proposed source structures are encoded with unspecified linkages and floating groups kept uncertain. Source compositions preserve Hex, HexNAc, Fuc, GlcA and phosphorylcholine; analytical anthranilic-acid labeling is recorded separately.

Access

Use `glyhub_load("glyhub_GPST000240_GSL")` to load this dataset.

Source

GlycoPOST GPST000240. Supplementary Table S4, B - MALDI Raw Data. Study: <https://doi.org/10.1016/j.mcpro.2022.100201>. Repository: <https://glycopost.glycosmos.org/entry/GPST000240>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000240_N	<i>Brugia malayi</i> N-glycans across life stages
---------------------	---

Description

MALDI-TOF MS peak-area profiles of released glycans from mixed-sex adult worms, microfilariae, adult females and adult males, and L3 larvae.

Usage

```
glyhub_GPST000240_N(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 47 features and 9 observations. The abundance assay is in MALDI-TOF MS integrated peak area (arbitrary units). rowData includes a typed glycan_structure column; features without a supported structure are NA.

Details

Forty-seven source-assigned molecular features are retained, including features without a quantified assignment in a particular spectrum. Mixed-sex adult and microfilarial material each have an original spectrum and two explicitly labelled biological replicates. Sex-separated adults and L3 larvae have one profile each. Areas are preserved on the source instrumental scale. Unassigned or undetected features remain missing; no zero filling or normalization is applied. Source phosphorylcholine and glucuronic-acid composition components are represented explicitly. Proposed structural diagrams are transcribed and composition-checked against the same source feature rows. Unlabelled bonds are unknown; source ambiguity braces are represented as floating groups without selecting a particular attachment.

47 proposed source structures are encoded with unspecified linkages and floating groups kept uncertain. Source compositions preserve Hex, HexNAc, Fuc, GlcA and phosphorylcholine; analytical anthranilic-acid labeling is recorded separately.

Access

Use `glyhub_load("glyhub_GPST000240_N")` to load this dataset.

Source

GlycoPOST GPST000240. Supplementary Table S3, B - MALDI Raw Data. Study: <https://doi.org/10.1016/j.mcpro.2022.100201>. Repository: <https://glycopost.glycosmos.org/entry/GPST000240>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000271_N_CAL51

N-glycan profiles in CAL51 Golgi knockout cells

Description

Complete N-glycan relative-abundance profiles from CAL51 control, GOLGA5 knockout and GOLGA8M knockout cells, investigating organelle-biogenesis interactions.

Usage

```
glyhub_GPST000271_N_CAL51(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 69 features and 15 observations. The abundance assay is in percent relative abundance. rowData has no glycan_structure column because no feature has a supported structural annotation.

Details

Five source-numbered observations are provided for each of the three cell conditions. The source table does not explicitly establish biological versus technical replicate status. Chromatographic features with equal compositions remain separate; no cross-isomer collapse is performed. Source mass and monosaccharide-count annotations remain available. No glycan topology is inferred from composition.

Composition and retention-time-resolved feature labels are preserved; structure is not assigned.

Access

Use `glyhub_load("glyhub_GPST000271_N_CAL51")` to load this dataset.

Source

GlycoPOST GPST000271. Summary - N_glycans. Study: <https://doi.org/10.1038/s41556-023-01297-4>. Repository: <https://glycopost.glycosmos.org/entry/GPST000271>. Quantitative source: https://glycopost.glycosmos.org/data/GPST000271.1/Glycan_supplementary_table_N_0_glycan.xlsx.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000271_O_CAL51

O-glycan profiles in CAL51 Golgi knockout cells

Description

Complete O-glycan relative-abundance profiles from CAL51 control, GOLGA5 knockout and GOLGA8M knockout cells, investigating organelle-biogenesis interactions.

Usage

```
glyhub_GPST000271_O_CAL51(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 7 features and 15 observations. The abundance assay is in percent relative abundance. rowData has no glycan_structure column because no feature has a supported structural annotation.

Details

Five source-numbered observations are provided for each of the three cell conditions. The source table does not explicitly establish biological versus technical replicate status. Chromatographic features with equal compositions remain separate; no cross-isomer collapse is performed. Source mass and monosaccharide-count annotations remain available. No glycan topology is inferred from composition.

Composition and retention-time-resolved feature labels are preserved; structure is not assigned.

Access

Use glyhub_load("glyhub_GPST000271_O_CAL51") to load this dataset.

Source

GlycoPOST GPST000271. Summary - O_glycans. Study: <https://doi.org/10.1038/s41556-023-01297-4>.
 Repository: <https://glycopost.glycosmos.org/entry/GPST000271>. Quantitative source: https://glycopost.glycosmos.org/data/GPST000271.1/Glycan_supplementary_table_N_0_glycan.xlsx.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000294_N_Celegans_L4

Caenorhabditis elegans L4 N-glycans across culture and release fractions

Description

All 202 molecular-feature rows of Supplementary Table S1, with relative percentages reported for four L4 culture and glycan-release fraction profiles.

Usage

```
glyhub_GPST000294_N_Celegans_L4(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 202 features and 4 observations. The abundance assay is in reported relative percentage. rowData includes a typed glycan_structure column; features without a supported structure are NA.

Details

L4 larvae were grown in liquid or on plates. PNGase F and the subsequent Ar release fractions are separate analytical fractions of these preparations, not four independent biological replicates. The table reports percentages for the second L4 preparations together with retention times from eleven preparations. Only the percentage tokens are used in the abundance assay; embryo and first-preparation retention times are preserved as source annotations. All 202 source rows remain, including 14 with no percentage in any profile. There are 147 exact percentage measurements and 150 source values explicitly reported as >0.1%; censored values have missing numeric abundance and retain their literal inequalities. Unreported percentages remain missing. No threshold substitution or renormalization is performed.

Each source diagram is transcribed with its displayed topology and residue identity. Unlabelled glycosidic configurations and acceptor positions remain unknown. Explicit author GlyTouCan accessions refine bond information only after residue-labelled topology is verified. PC and methyl substituents retain their source placement uncertainty, including a PC restricted to two candidate GlcNAc residues. Source composition/mass, original table cells, diagram row and review evidence remain available. All 202 rows have parsed, source-backed structures; broad source H/N/F/substituent totals match where a printed composition exists (201 rows). The one row without printed composition is assigned from its diagram. Twelve explicit GlyTouCan identifiers have residue-labelled topology verification. Row 196 uses the article Results identification of Figure 4I as a branched Man-HexNAc motif to constrain both fragments to the upper-arm Man; row 197 retains uncertain arm placement of long and short chains.

Access

Use `glyhub_load("glyhub_GPST000294_N_Celegans_L4")` to load this dataset.

Source

GlycoPOST GPST000294. Supplementary Table S1, PDF pages 4–17. Study: <https://doi.org/10.1016/j.mcpro.2023.100505>. Repository: <https://glycopost.glycosmos.org/entry/GPST000294>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000294_O_Celegans_Development

Caenorhabditis elegans developmental O-glycan profiles

Description

Complete Supplementary Table S2 of Increasing Complexity of the N-Glycome During *Caenorhabditis* Development: 20 O-glycan features quantified across six source culture profiles.

Usage

```
glyhub_GPST000294_O_Celegans_Development(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 20 features and 6 observations. The abundance assay is in percent occurrence. rowData has no glycan_structure column because no feature has a supported structural annotation.

Details

O-glycans were released by reductive beta-elimination from peptic glycopeptides remaining after PNGase A/F digestion and analyzed without further derivatization by LC-ESI-MS. Source PDF page 18 has calculated m/z, RT, composition and paired observed-m/z/percentage columns for six samples. Only percentage occurrence is quantitative abundance; observed m/z, nd and fragmentation asterisks are annotations. All 20 rows are retained, including same-composition isomers. Quantitative zeros become NA without imputation or renormalization; raw zeros are preserved. Source columns are culture profiles, not six biological replicates of a common condition. Replication for individual S2 profiles is not explicit and remains unknown. The separately distributed N-glycan Table S1 object extracts the reported percentages from mixed retention-time/percentage cells, preserving censored inequalities and unreported values explicitly.

Explicit author composition tokens provide Hex, HexNAc, dHex, HexA and PC/Me substituent counts. The source Hex3HexNAc1 Hex1Me has four Hex residues and one Me substituent. No Fuc identity is assigned to generic dHex. Linear/branched qualifiers and source isomers remain annotations; no full structure is inferred.

Access

Use `glyhub_load("glyhub_GPST000294_O_Celegans_Development")` to load this dataset.

Source

GlycoPOST GPST000294. . Study: <https://doi.org/10.1016/j.mcpro.2023.100505>. Repository: <https://glycopost.glycosmos.org/entry/GPST000294>. Quantitative source: <https://www.ebi.ac.uk/europepmc/webservices/rest/PMC7614267/supplementaryFiles>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000296_N *Oral tumor N-glycans associated with lymph node metastasis*

Description

Relative abundances of 83 isomer-resolved N-glycan features from 31 oral squamous cell carcinoma tumors with or without lymph node metastasis.

Usage

```
glyhub_GPST000296_N(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A `glyexp::GlycomicSE` with 83 features and 31 observations. The abundance assay is in relative abundance fraction. `rowData` includes a typed `glycan_structure` column; features without a supported structure are NA.

Details

The complete source matrix contains 12 N0 and 19 N+ tumor samples. Glycan isomers remain distinct and source MS/MS confirmation, retention time, core fucosylation, bisecting GlcNAc and sialic-acid diagnostics are retained. Eighty-two partial structures combine the source spectral atlas with explicit sialic-acid linkage information from Table S3; unnumbered linkages and unresolved arms remain unknown. Feature 9b has no MS/MS-confirmed topology and retains composition only. Analytes were reduced glycans; this preparation is recorded separately from monosaccharide identity.

Source spectral-atlas topologies with TS3-supported sialic linkages; unnumbered linkages and uncertain arms retained as unknown. Composition-only annotation for 9b.

Access

Use `glyhub_load("glyhub_GPST000296_N")` to load this dataset.

Source

GlycoPOST GPST000296. Deposited Glycan_results.xlsx, TS3; published supplementary spectral atlas. Study: <https://doi.org/10.1016/j.mcpro.2023.100586>. Repository: <https://glycopost.glycosmos.org/entry/GPST000296>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000296_N_Glycoproteomics

Site-specific N-glycoproteome of oral squamous-cell carcinoma tissues

Description

Quantitative N-glycopeptide profiles of 30 oral squamous-cell carcinoma tumour tissues, comprising 12 node-negative and 18 node-positive samples.

Usage

```
glyhub_GPST000296_N_Glycoproteomics(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

<code>kind</code>	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
<code>cache_dir</code>	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
<code>refresh</code>	Download the pinned resource again, even if cached.
<code>offline</code>	Prohibit downloads; require a verified local resource.

Format

A `glyexp::GlycomicSE` with 3117 features and 30 observations. The abundance assay is in pooled-reference-normalized and channel-total-normalized reporter-ion abundance (fraction). `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

The 3,117 author-grouped UniProt, protein-site and glycan-composition features are retained. Reporter ion intensities were divided by the pooled reference channel within each TMT experiment and normalized to each channel total. Source NaN values remain missing; numerical zeros become NA. No reaggregation or imputation is applied. The companion released-glycan dataset has a different molecular observation unit and is retained separately.

Compositions are transcribed directly from the Glycan field. Protein positions come from the author glycopeptide identifier and agree with every reported Glycosite entry. Peptide-relative positions and peptide starts are retained separately; all reported start plus relative-position coordinates agree with the protein absolute position. Representative peptide sequences cannot consistently validate every PSM-relative position, so original fields and a residue-consistency flag are retained without changing the author site. No site-specific glycan topology is inferred from companion released-glycan diagrams.

Access

Use `glyhub_load("glyhub_GPST000296_N_Glycoproteomics")` to load this dataset.

Source

GlycoPOST GPST000296. . Study: <https://doi.org/10.1016/j.mcpro.2023.100586>. Repository: <https://glycopost.glycosmos.org/entry/GPST000296>. Quantitative source: <https://www.ebi.ac.uk/europepmc/webservices/rest/PMC10336694/supplementaryFiles>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000297_N *Cornu aspersum mucus N-glycan profiles*

Description

Released glycans from adhesive, lubricating and protective snail mucus, measured by glycomic mass spectrometry after per-deuterio-methylation.

Usage

```
glyhub_GPST000297_N(  
  kind = c("curated", "raw"),  
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),  
  refresh = FALSE,  
  offline = FALSE  
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A `glyexp::GlycomicSE` with 24 features and 3 observations. The abundance assay is in relative glycan peak-area percentage. `rowData` includes a typed `glycan_structure` column; features without a supported structure are NA.

Details

All 25 reported rows of Supplementary Table 10 are retained across three source mucus profiles. Values are the published glycan-peak area percentages. Identical source mass/composition/topology assignments are aligned across samples; conflicting masses or proposed isomers remain distinct. Unreported combinations are missing and no renormalization is applied. Each of the three reported N-glycan profiles totals 100%. Native methyl substituents are preserved separately from analytical derivatization. In Table 10 row 10, the diagram adds an outlined diamond absent from the stated composition; row 11 draws two fucoses while its composition states one. Typed composition and structure remain missing for these two features without removing their quantitative observations.

22 proposed source structures retain unspecified linkages and floating-group uncertainty. Native methyl groups remain explicit. Source composition and structure are missing for conflicting N-glycan assignments rather than selected by assumption.

Access

Use `glyhub_load("glyhub_GPST000297_N")` to load this dataset.

Source

GlycoPOST GPST000297. Supplementary Table 10 (PDF S47). Study: <https://doi.org/10.1038/s41467-023-41094-z>. Repository: <https://glycopost.glycosmos.org/entry/GPST000297>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000297_O *Cornu aspersum mucus O-glycan profiles*

Description

Released glycans from adhesive, lubricating and protective snail mucus, measured by glycomic mass spectrometry after per-deuter-O-methylation.

Usage

```
glyhub_GPST000297_O(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 13 features and 3 observations. The abundance assay is in relative glycan peak-area percentage. rowData includes a typed glycan_structure column; features without a supported structure are NA.

Details

All 14 reported rows of Supplementary Table 9 are retained across three source mucus profiles. Values are the published glycan-peak area percentages. Identical source mass/composition/topology assignments are aligned across samples; conflicting masses or proposed isomers remain distinct. Unreported combinations are missing and no renormalization is applied. O-glycan lubricating and protective reported totals are 25.16% and 99%, respectively, retained as published. Native methyl substituents are preserved separately from analytical derivatization.

All 13 proposed O-glycan structures are encoded with unknown linkages and source floating-group ambiguity. Native methyl substituents remain explicit.

Access

Use glyhub_load("glyhub_GPST000297_O") to load this dataset.

Source

GlycoPOST GPST000297. Supplementary Table 9 (PDF S46). Study: <https://doi.org/10.1038/s41467-023-41094-z>. Repository: <https://glycopost.glycosmos.org/entry/GPST000297>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000299_GSL *Onchocerca volvulus* adult-female GSL glycan profile

Description

A complete published MALDI peak-area profile from adult female *Onchocerca volvulus*, used to investigate shared antigenic glycans across filarial nematodes.

Usage

```
glyhub_GPST000299_GSL(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 41 features and 1 observations. The abundance assay is in unnormalized MALDI peak area. `rowData` includes a typed `glycan_structure` column; features without a supported structure are NA.

Details

Table S4 supplies one profile per glycan class without biological-replicate columns. All measured peaks with numerical areas are retained, including unassigned peaks with missing molecular annotation. Areas are preserved without normalization and cannot support replicate-based statistical inference. Same-row SNFG topology is transcribed where unambiguous; unspecified glycosidic bonds and phosphocholine positions remain unknown. Ambiguous antenna attachment, alternative isomers or missing modification placement are retained in the source workbook rather than resolved by assumption. Analytical 2-AA is excluded from the native glycan annotation and recorded separately.

Source-derived compositions and original labels are retained. 18 source-supported structures are typed; unspecified bonds remain unknown. Unresolved or conflicting structures remain missing with source provenance.

Access

Use `glyhub_load("glyhub_GPST000299_GSL")` to load this dataset.

Source

GlycoPOST GPST000299. GSL glycans. Study: <https://doi.org/10.3389/fimmu.2023.1102344>.
Repository: <https://glycopost.glycosmos.org/entry/GPST000299>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000299_N	<i>Onchocerca volvulus</i> adult-female N glycan profile
---------------------	--

Description

A complete published MALDI peak-area profile from adult female *Onchocerca volvulus*, used to investigate shared antigenic glycans across filarial nematodes.

Usage

```
glyhub_GPST000299_N(  
  kind = c("curated", "raw"),  
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),  
  refresh = FALSE,  
  offline = FALSE  
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A `glyexp::GlycomicSE` with 48 features and 1 observations. The abundance assay is in unnormalized MALDI peak area. `rowData` includes a typed `glycan_structure` column; features without a supported structure are NA.

Details

Table S4 supplies one profile per glycan class without biological-replicate columns. All measured peaks with numerical areas are retained, including unassigned peaks with missing molecular annotation. Areas are preserved without normalization and cannot support replicate-based statistical inference. Same-row SNFG topology is transcribed where unambiguous; unspecified glycosidic bonds and phosphocholine positions remain unknown. Ambiguous antenna attachment, alternative isomers or missing modification placement are retained in the source workbook rather than resolved by assumption. Analytical 2-AA is excluded from the native glycan annotation and recorded separately.

Source-derived compositions and original labels are retained. 19 source-supported structures are typed; unspecified bonds remain unknown. Unresolved or conflicting structures remain missing with source provenance.

Access

Use `glyhub_load("glyhub_GPST000299_N")` to load this dataset.

Source

GlycoPOST GPST000299. N-glycans. Study: <https://doi.org/10.3389/fimmu.2023.1102344>.
Repository: <https://glycopost.glycosmos.org/entry/GPST000299>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000351_N	<i>Plasma N-glycomes of ASGR1- and MRC1-deficient mice under dietary challenge</i>
---------------------	--

Description

Seventy-two sialic-linkage-resolved plasma N-glycan features across 46 MALDI-TOF-MS observations from a study of hepatic and macrophage glycan-receptor deficiency. Observations include experimental animals and pooled controls.

Usage

```
glyhub_GPST000351_N(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 72 features and 46 observations. The abundance assay is in relative abundance fraction. `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

The complete author-renormalized matrix is retained as fractions, with its individual acquisition filenames as observation identifiers. Genotype, diet, sex, sample ID and source group are joined by exact acquisition filename. Pooled controls remain explicitly identified; the source metadata are not reinterpreted as independent animals. Neu5Ac/Neu5Gc linkage-specific derivatization and O-acetylated species are preserved. No additional normalization or imputation is performed.

H and N encode Hex and HexNAc; F encodes Fuc. Ge/Gl encode alpha2,6/alpha2,3-linked Neu5Gc, E/L encode the corresponding Neu5Ac linkages, and Ac denotes an acetyl substituent. Linkage counts remain in source annotations; composition does not imply a full structure.

Access

Use `glyhub_load("glyhub_GPST000351_N")` to load this dataset.

Source

GlycoPOST GPST000351. . Study: <https://doi.org/10.1016/j.mcpro.2023.100615>. Repository: <https://glycopost.glycosmos.org/entry/GPST000351>. Quantitative source: <https://glycopost.glycosmos.org/data/GPST000351.0/TPNG%20curated%20data%20MALDI.xlsx>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000374_O	<i>SSSMuG: Same Sample Sequential Multi-Glycomics. and related study experiments</i>
---------------------	--

Description

Sequential release versus single-class control from mouse brain lysate. Author structural assignments retained with uncertainty; no inferred cross-class subject pairing. O subclasses are separately normalized in source and therefore separate objects. Combined O-glycan quantitative profiles from GPST000374. 15 union features and 7 source observations are represented.

Usage

```
glyhub_GPST000374_O(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A `glyexp::GlycomicSE` with 15 features and 7 observations. The abundance assay is in LC-MS peak area. `rowData` includes a typed `glycan_structure` column; features without a supported structure are NA.

Details

Source experiments are identified in colData and original panel-specific metadata, annotations and measurements are retained in metadata. Feature identities are aligned only when supported by author identifiers or explicit molecular structures; other features retain source-specific identities. The source_coverage matrix distinguishes unmeasured combinations from measured missing values. Units: LC-MS peak area.

SSSMuG: Same Sample Sequential Multi-Glycomics.: Sequential release versus single-class control from mouse brain lysate. Author structural assignments retained with uncertainty; no inferred cross-class subject pairing. O subclasses are separately normalized in source and therefore separate objects.

SSSMuG: Same Sample Sequential Multi-Glycomics.: Sequential release versus single-class control from mouse brain lysate. Author structural assignments retained with uncertainty; no inferred cross-class subject pairing. O subclasses are separately normalized in source and therefore separate objects.

SSSMuG: Same Sample Sequential Multi-Glycomics.: Sequential release versus single-class control from mouse brain lysate. Author structural assignments retained with uncertainty; no inferred cross-class subject pairing. O subclasses are separately normalized in source and therefore separate objects.

Molecular annotations retain source precision. Unresolved compositions or structures are NA; original annotations are retained in rowData. All quantitative source features are preserved.

Access

Use `glyhub_load("glyhub_GPST000374_0")` to load this dataset.

Source

GlycoPOST GPST000374. Table S3 - O-glycans. Study: <https://doi.org/10.1021/acs.analchem.3c04928>. Repository: <https://glycopost.glycosmos.org/entry/GPST000374>. Quantitative source: <https://glycopost.glycosmos.org/data/GPST000374.0/Glycopost%20result%20file.xlsx>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000374_sssmug_gsl

SSSMuG: Same Sample Sequential Multi-Glycomics.

Description

Sequential release versus single-class control from mouse brain lysate. Author structural assignments retained with uncertainty; no inferred cross-class subject pairing. O subclasses are separately normalized in source and therefore separate objects.

Usage

```
glyhub_GPST000374_sssmug_gsl(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 13 features and 10 observations. The abundance assay is in LC-MS peak area. rowData includes a typed glycan_structure column; features without a supported structure are NA.

Details

Sequential release versus single-class control from mouse brain lysate. Author structural assignments retained with uncertainty; no inferred cross-class subject pairing. O subclasses are separately normalized in source and therefore separate objects.

Molecular annotations retain source precision. Unresolved compositions or structures are NA; original annotations are retained in rowData. All quantitative source features are preserved.

Access

Use `glyhub_load("glyhub_GPST000374_sssmug_gsl")` to load this dataset.

Source

GlycoPOST GPST000374. Table S1 - GSL glycans. Study: <https://doi.org/10.1021/acs.analchem.3c04928>. Repository: <https://glycopost.glycosmos.org/entry/GPST000374>. Quantitative source: <https://glycopost.glycosmos.org/data/GPST000374.0/Glycopost%20result%20file.xlsx>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000374_sssmug_n*SSSMuG: Same Sample Sequential Multi-Glycomics.*

Description

Sequential release versus single-class control from mouse brain lysate. Author structural assignments retained with uncertainty; no inferred cross-class subject pairing. O subclasses are separately normalized in source and therefore separate objects.

Usage

```
glyhub_GPST000374_sssmug_n(  
  kind = c("curated", "raw"),  
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),  
  refresh = FALSE,  
  offline = FALSE  
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 218 features and 10 observations. The abundance assay is in LC-MS peak area. `rowData` includes a typed `glycan_structure` column; features without a supported structure are NA.

Details

Sequential release versus single-class control from mouse brain lysate. Author structural assignments retained with uncertainty; no inferred cross-class subject pairing. O subclasses are separately normalized in source and therefore separate objects.

Molecular annotations retain source precision. Unresolved compositions or structures are NA; original annotations are retained in `rowData`. All quantitative source features are preserved.

Access

Use `glyhub_load("glyhub_GPST000374_sssmug_n")` to load this dataset.

Source

GlycoPOST GPST000374. Table S2 - N-glycans. Study: <https://doi.org/10.1021/acs.analchem.3c04928>. Repository: <https://glycopost.glycosmos.org/entry/GPST000374>. Quantitative source: <https://glycopost.glycosmos.org/data/GPST000374.0/Glycopost%20result%20file.xlsx>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000381_N_Prosaposin

Released N-glycans of pSAP65 and pSAP75 prosaposin forms

Description

Relative N-glycan profiles of two prosaposin forms in a study of hyperglycosylation and tumor dendritic-cell immune escape. The author-aligned expression table contains 36 features and two profile observations.

Usage

```
glyhub_GPST000381_N_Prosaposin(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A `glyexp::GlycomicSE` with 36 features and 2 observations. The abundance assay is in fraction of the source profile total intensity. `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

The quantitative assay is the complete Relative expression block (I:J), using its pSAP65 and pSAP75 column labels. The separate intensity blocks B and E carry contradictory pSAP labels: their relative values match expression columns J and I, respectively. The expression-block labels are adopted for this dataset; this is a curation choice, not an author-issued correction. The complete workbook and original labels remain available. Source expression values are fractions that sum to one per observed profile; they are not multiplied by 100. Blank cells remain missing. The source does not identify biological or technical replication for these two profiles, so replicate type is unknown.

Composition counts are directly transcribed from the author Sugar Composition block; NeuAc and NeuGc are distinguished. No glycan structure is inferred from composition or mass.

Access

Use `glyhub_load("glyhub_GPST000381_N_Prosaposin")` to load this dataset.

Source

GlycoPOST GPST000381. Sheet1. Study: <https://doi.org/10.1126/science.adg1955>. Repository: <https://glycopost.glycosmos.org/entry/GPST000381>. Quantitative source: <https://glycopost.glycosmos.org/data/GPST000381.0/Analyzed%20data.xlsx>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000403_N	<i>Rat serum N-glycans after chronic herbicide exposure</i>
---------------------	---

Description

Serum N-glycan profiles from control and glyphosate-based-herbicide-exposed rats, comprising six control males, six control females, five exposed males and seven exposed females.

Usage

```
glyhub_GPST000403_N(  
  kind = c("curated", "raw"),  
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),  
  refresh = FALSE,  
  offline = FALSE  
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A `glyexp::GlycomicSE` with 113 features and 24 observations. The abundance assay is in relative abundance (%). `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

The 113-feature matrix is the final percentage matrix on Sheet 1, corroborated by published Supplementary Tables S1 and S2. Sheet 2 contains a differently normalised intermediate for the same samples and is not duplicated as independent observations. Five-digit glycan codes follow the paper order HexNAc, Hex, Fuc, NeuAc and NeuGc. Compositions are retained; structural isomers are unresolved.

Source-derived composition annotations; linkage information is retained as source annotation without inferring a full topology. No complete unambiguous structures are asserted.

Access

Use `glyhub_load("glyhub_GPST000403_N")` to load this dataset.

Source

GlycoPOST GPST000403. Sheet1. Study: <https://doi.org/10.3390/biom14091077>. Repository: <https://glycopost.glycosmos.org/entry/GPST000403>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000431_N	<i>Swift Universal Glycan Acquisition (SUGA) Enables Quantitative Glycan Profiling across Diverse Sample Types. and related study experiments</i>
---------------------	---

Description

Native unreduced released N-glycan composition quantification. Drug treatment/time is column metadata; includes three identified blanks. Combined N-glycan quantitative profiles from GPST000431. 70 union features and 62 source observations are represented.

Usage

```
glyhub_GPST000431_N(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 70 features and 62 observations. The abundance assay is in MS1 integrated area. rowData has no glycan_structure column because no feature has a supported structural annotation.

Details

Source experiments are identified in colData and original panel-specific metadata, annotations and measurements are retained in metadata. Feature identities are aligned only when supported by author identifiers or explicit molecular structures; other features retain source-specific identities. The source_coverage matrix distinguishes unmeasured combinations from measured missing values. Units: MS1 integrated area.

Swift Universal Glycan Acquisition (SUGA) Enables Quantitative Glycan Profiling across Diverse Sample Types.: Native unreduced released N-glycan composition quantification. Drug treatment/time is column metadata; includes three identified blanks.

Swift Universal Glycan Acquisition (SUGA) Enables Quantitative Glycan Profiling across Diverse Sample Types.: Native unreduced released N-glycan composition quantification. Independent method benchmark; distinct experiments are retained in column metadata.

Swift Universal Glycan Acquisition (SUGA) Enables Quantitative Glycan Profiling across Diverse Sample Types.: Native unreduced released N-glycan composition quantification. Independent method benchmark; distinct experiments are retained in column metadata.

Molecular annotations retain source precision. Unresolved compositions or structures are NA; original annotations are retained in rowData. All quantitative source features are preserved.

Access

Use `glyhub_load("glyhub_GPST000431_N")` to load this dataset.

Source

GlycoPOST GPST000431. SUGA_DrugTreatments_GlycanQuant. Study: <https://doi.org/10.1021/acs.jproteome.4c00657>. Repository: <https://glycopost.glycosmos.org/entry/GPST000431>. Quantitative source: https://glycopost.glycosmos.org/data/GPST000431.1/SUGA_DrugTreatments_GlycanQuant_treatmentkey.xlsx.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000460_N	<i>Cardiac N-glycomes in fatal COVID-19</i>
---------------------	---

Description

N-glycan MS1 peak areas from cardiac tissue and isolated cardiomyocytes of COVID-positive and COVID-negative donors.

Usage

```
glyhub_GPST000460_N(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

<code>kind</code>	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
<code>cache_dir</code>	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
<code>refresh</code>	Download the pinned resource again, even if cached.
<code>offline</code>	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 162 features and 43 observations. The abundance assay is in peak area. `rowData` includes a typed `glycan_structure` column; features without a supported structure are NA.

Details

Four source tables are combined by exact composition-plus-retention labels, normalizing only GU/RRT notation and spacing. The sample metadata distinguishes FFPE tissue from isolated cardiomyocytes and COVID status. Features absent from a source table remain missing rather than zero. Maltodextrin calibration ladders and class summaries are excluded. Published GlyTouCan structures are linked only when composition and retention position identify a unique annotation; inconsistent registry assignments remain unresolved. Clinical metadata uses exact published patient identifiers; abbreviated ambiguous cardiomyocyte IDs are not guessed.

Author glycan labels, additive monosaccharide counts, and uniquely matched registry structures. Source/registry annotation conflicts are preserved for review.

Access

Use `glyhub_load("glyhub_GPST000460_N")` to load this dataset.

Source

GlycoPOST GPST000460. Tables S5-S8. Study: <https://doi.org/10.1021/acs.analchem.3c03649>. Repository: <https://glycopost.glycosmos.org/entry/GPST000460>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000473_N	<i>N-glycan remodeling after TANGO2 loss</i>
---------------------	--

Description

Relative abundances of 82 released N-glycan features in TANGO2 knockout and control cells, with three quantitative columns per genotype.

Usage

```
glyhub_GPST000473_N(  
  kind = c("curated", "raw"),  
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),  
  refresh = FALSE,  
  offline = FALSE  
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A `glyexp::GlycomicSE` with 82 features and 6 observations. The abundance assay is in relative abundance fraction. `rowData` includes a typed `glycan_structure` column; features without a supported structure are NA.

Details

PGC-LC-MS profiling of PNGase F-released, reduced N-glycans examines cellular glycosylation changes associated with TANGO2 loss and altered cytoskeletal organization. The six individual source columns are retained; the figure caption reports five biological replicates for a broader panel but this table contains three per genotype. Likely source topologies are retained with unmarked linkages and bracketed attachments unresolved. The FA3 feature has conflicting shorthand and diagram annotations and therefore lacks typed glycan annotations.

Likely SNFG topologies transcribed from the source diagrams; uncertain linkages and bracketed terminal parents remain ambiguous. Source row 38 has a label/diagram conflict.

Access

Use `glyhub_load("glyhub_GPST000473_N")` to load this dataset.

Source

GlycoPOST GPST000473. Supplementary Data 3, glycomics. Study: <https://doi.org/10.1038/s41467-025-60563-1>. Repository: <https://glycopost.glycosmos.org/entry/GPST000473>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000533_N_Glycopeptides

Desialylated haptoglobin glycopeptides in sepsis serum

Description

Haptoglobin purified from healthy-control and sepsis serum was analyzed by LC-ESI MS after desialylation. The complete six-panel source table contains three HC0, three SG1 and three SG2 observations.

Usage

```
glyhub_GPST000533_N_Glycopeptides(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycoproteomicSE](#) with 54 features and 9 observations. The abundance assay is in LC-MS extracted-ion peak intensity. rowData includes a typed glycan_structure column; features without a supported structure are NA.

Details

The source protein is UniProt P00738. All six quantitative panels in the selected author sheet are retained: Site 3 (3+), Site 4 (4+ and 3+), Site 2 (3+ and 2+), and oxidized Site 1 (3+). Charge states are distinct features, not independent samples, and are not summed. All panels have matching sample and raw-data identifiers. Source Site 1 binding position 84 conflicts with the listed peptide interval 179-194, so typed protein_site is NA for that panel. Other site positions are retained directly. Source intensity is the assay; author percentages are preserved separately. No normalization, replicate pooling or composition-from-mass reconstruction is applied. Antennarity and fucosylation labels are source annotations. Compositions and supported structures are transcribed from directly reviewed Supplementary Figures 1d/e and 2a; unresolved fucose positions remain structurally unsigned.

Composition counts are transcribed from the author-labelled SNFG structures in Supplementary Figures 1d/e and 2a. Typed structures preserve unknown linkages; terminal or otherwise unlocalized fucose is left structurally unassigned. Original labels and figure evidence are retained.

Access

Use `glyhub_load("glyhub_GPST000533_N_Glycopeptides")` to load this dataset.

Source

GlycoPOST GPST000533. results of 231111_Hpt. Study: <https://doi.org/10.1038/s41467-025-56524-3>. Repository: <https://glycopost.glycosmos.org/entry/GPST000533>. Quantitative source: https://glycopost.glycosmos.org/data/GPST000533.0/Result%20file%20of%20231111_Hpt_glycopeptides%20for%20Fig%20and%20GlycoPOST.xlsx. Annotation evidence: https://media.springernature.com/original/springer-static/esm/art%3A10.1038%2Fs41467-025-56524-3/MediaObjects/41467_2025_56524_MOESM1_ESM.pdf.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000533_N_Released

Desialylated haptoglobin released N-glycans in sepsis serum

Description

Haptoglobin purified from healthy-control and sepsis serum was analyzed by LC-ESI MS after desialylation. The complete source feature matrix contains three HC0, three SG1 and three SG2 observations.

Usage

```
glyhub_GPST000533_N_Released(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

<code>kind</code>	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
<code>cache_dir</code>	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
<code>refresh</code>	Download the pinned resource again, even if cached.
<code>offline</code>	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 13 features and 9 observations. The abundance assay is in LC-MS extracted-ion peak intensity. rowData includes a typed glycan_structure column; features without a supported structure are NA.

Details

PNGase F-released glycans were labeled with aminoxy tandem mass tag (aTMT6); distinct core- and Lewis-fucosylated chromatographic labels remain separate. Source intensity is the assay; author percentages are preserved separately. No normalization, replicate pooling or composition-from-mass reconstruction is applied. Antennarity and fucosylation labels are mapped to the explicit source SNFG residue counts.

Composition counts are transcribed from the author-labelled SNFG structures in Supplementary Figures 1d/e and 2a. Typed structures preserve unknown linkages; terminal or otherwise unlocalized fucose is left structurally unassigned. Original labels and figure evidence are retained.

Access

Use `glyhub_load("glyhub_GPST000533_N_Released")` to load this dataset.

Source

GlycoPOST GPST000533. results of 231208_Hpt_glycans. Study: <https://doi.org/10.1038/s41467-025-56524-3>. Repository: <https://glycopost.glycosmos.org/entry/GPST000533>. Quantitative source: https://glycopost.glycosmos.org/data/GPST000533.0/Result%20file%20of%20231208_Hpt_aTMT6glycans%20for%20Fig%20and%20GlycoPOST.xlsx. Annotation evidence: https://media.springernature.com/original/springer-static/esm/art%3A10.1038%2Fs41467-025-56524-3/MediaObjects/41467_2025_56524_M0ESM1_ESM.pdf.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000534_N	<i>N-glycan profiles of two tardigrade species</i>
---------------------	--

Description

Published relative molar abundances of N-glycans isolated from *Ramazzottius varieornatus* and *Hypsibius exemplaris*.

Usage

```
glyhub_GPST000534_N(  
  kind = c("curated", "raw"),  
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),  
  refresh = FALSE,  
  offline = FALSE  
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 25 features and 2 observations. The abundance assay is in relative quantity mol %. rowData includes a typed glycan_structure column; features without a supported structure are NA.

Details

The author table reports 24 identified glycan structures and an unresolved Others fraction for two species-level profiles. PA-labeled glycans were separated chromatographically; analytes sharing an LC peak remain separate by observed mass, using the author-reported MALDI intensity-based proportions. The source does not provide individual biological replicate columns, so these profiles cannot estimate within-species variation. Linkages explicitly drawn in the source are preserved; the unresolved aggregate has no typed glycan annotation.

Twenty-four source linkage diagrams independently checked against the rendered deposited table; Others retains missing composition and structure.

Access

Use `glyhub_load("glyhub_GPST000534_N")` to load this dataset.

Source

GlycoPOST GPST000534. Deposited Table.docx, N-Glycans derived from *R. varieornatus* and *H. exemplaris*. Study: <https://doi.org/10.1016/j.mcpro.2025.100979>. Repository: <https://glycopost.glycosmos.org/entry/GPST000534>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000562_CS_DS

CS/DS disaccharide amounts in A549 and BEAS-2B small extracellular vesicles

Description

Four chondroitin/dermatan sulfate disaccharides quantified as fmol in five A549 and six BEAS-2B small-extracellular-vesicle preparations.

Usage

```
glyhub_GPST000562_CS_DS(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 4 features and 11 observations. The abundance assay is in fmol. row-Data has no glycan_structure column because no feature has a supported structural annotation.

Details

Amounts derive from enzymatic CS/DS depolymerization and LC-MS/MS integration. D0a4 and D0a6 were distinguished by diagnostic fragments; the original 11 quantitative observations are preserved. The publication reports six preparations per cell line but excludes one A549 CS/DS preparation after a presumed preparation failure; the absent A5 observation is not manufactured. The N-glycan profiles from the same paper are stored under GPST000667.

Author CS/DS disaccharide codes and sulfate positions are retained. The measured lyase products contain an unsaturated uronic acid that the installed glyrepr vocabulary cannot represent faithfully; typed compositions therefore remain missing rather than substituting saturated HexA. D0a0, D0a4, D0a6 and D0a10 denote zero, 4-O, 6-O and 4,6-di-O-sulfation, respectively.

Access

Use `glyhub_load("glyhub_GPST000562_CS_DS")` to load this dataset.

Source

GlycoPOST GPST000562. . Study: <https://doi.org/10.1016/j.mcpro.2026.101524>. Repository: <https://glycopost.glycosmos.org/entry/GPST000562>. Quantitative source: https://glycopost.glycosmos.org/data/GPST000562.0/identification_quantification_table.xlsx.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000578_N_Fetuin_TwoSites

Fetuin N-glycan peak areas across two instrument sites

Description

Complete 14-feature two-site fetuin source peak-area block. Site 1 and Site 2 remain distinct observations. Their sample identity/pairing is not inferred; accompanying dotp values are retained as quality annotations, not quantitative abundance.

Usage

```
glyhub_GPST000578_N_Fetuin_TwoSites(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

<code>kind</code>	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
<code>cache_dir</code>	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
<code>refresh</code>	Download the pinned resource again, even if cached.
<code>offline</code>	Prohibit downloads; require a verified local resource.

Format

A `glyexp::GlycomicSE` with 14 features and 2 observations. The abundance assay is in peak area. `rowData` includes a typed `glycan_structure` column; features without a supported structure are NA.

Details

Complete 14-feature two-site fetuin source peak-area block. Site 1 and Site 2 remain distinct observations. Their sample identity/pairing is not inferred; accompanying dotp values are retained as quality annotations, not quantitative abundance. Quantitative zeros are represented as NA without imputation or renormalization; original measurements are retained. GlyTouCan identifiers remain the source assignments. Sites refer to laboratories/instruments, not protein glycosylation sites. Figure 4c names Site A (Altis Plus) and Site B (Altis); the workbook labels Site 1 and Site 2 are retained without inferring additional correspondence.

All source GlyTouCan identifiers resolve to WURCS through the official GlyTouCan SPARQL service. Structures are converted with glyparse 0.8.1 and validated with glyrepr 1.1.0, and compositions are derived from the validated structures. No mass-based assignments or new experimental linkage evidence are inferred.

Access

Use `glyhub_load("glyhub_GPST000578_N_Fetuin_TwoSites")` to load this dataset.

Source

GlycoPOST GPST000578. Figure 4e. Study: <https://doi.org/10.1038/s41467-026-73091-3>. Repository: <https://glycopost.glycosmos.org/entry/GPST000578>. Quantitative source: https://media.springernature.com/original/springer-static/esm/art%3A10.1038%2Fs41467-026-73091-3/MediaObjects/41467_2026_73091_M0ESM4_ESM.xls.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000578_N_source_repeatability_intensity

Ovalbumin N-glycan repeatability profiles and related study experiments

Description

Complete Ovalbumin source feature block from the Figure 4b sample-preparation repeatability assay. Three technical preparations are retained separately; average, standard deviation and CV are not samples. This panel is distinct from similarly named immunoglobulin application samples in Figure 5bc. Combined N-glycan quantitative profiles from GPST000578. 41 union features and 12 source observations are represented.

Usage

```
glyhub_GPST000578_N_source_repeatability_intensity(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

<code>kind</code>	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
<code>cache_dir</code>	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
<code>refresh</code>	Download the pinned resource again, even if cached.
<code>offline</code>	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 41 features and 12 observations. The abundance assay is in glycan intensity (source values). `rowData` includes a typed `glycan_structure` column; features without a supported structure are NA.

Details

Source experiments are identified in `colData` and original panel-specific metadata, annotations and measurements are retained in metadata. Feature identities are aligned only when supported by author identifiers or explicit molecular structures; other features retain source-specific identities. The `source_coverage` matrix distinguishes unmeasured combinations from measured missing values. Units: glycan intensity (source values).

Ovalbumin N-glycan repeatability profiles: Complete Ovalbumin source feature block from the Figure 4b sample-preparation repeatability assay. Three technical preparations are retained separately; average, standard deviation and CV are not samples. This panel is distinct from similarly named immunoglobulin application samples in Figure 5bc. Quantitative zeros are represented as NA without imputation or renormalization; original measurements are retained. GlyTouCan identifiers remain the source assignments. The `readxl` 1.5.0.1 reader substitutes embedded chart cache values into ten worksheet cells C3:C12. The original XLS is unchanged; all 1516 selected measurements agree exactly with independently decoded worksheet records. This is a reader issue, not an author-data conflict.

Xolair N-glycan repeatability profiles: Complete Xolair source feature block from the Figure 4b sample-preparation repeatability assay. Three technical preparations are retained separately; average, standard deviation and CV are not samples. This panel is distinct from similarly named immunoglobulin application samples in Figure 5bc. Quantitative zeros are represented as NA without imputation or renormalization; original measurements are retained. GlyTouCan identifiers remain the source assignments. The `readxl` 1.5.0.1 reader substitutes embedded chart cache values into ten worksheet cells C3:C12. The original XLS is unchanged; all 1516 selected measurements agree

exactly with independently decoded worksheet records. This is a reader issue, not an author-data conflict.

Fetuin N-glycan repeatability profiles: Complete Fetuin source feature block from the Figure 4b sample-preparation repeatability assay. Three technical preparations are retained separately; average, standard deviation and CV are not samples. This panel is distinct from similarly named immunoglobulin application samples in Figure 5bc. Quantitative zeros are represented as NA without imputation or renormalization; original measurements are retained. GlyTouCan identifiers remain the source assignments. The readxl 1.5.0.1 reader substitutes embedded chart cache values into ten worksheet cells C3:C12. The original XLS is unchanged; all 1516 selected measurements agree exactly with independently decoded worksheet records. This is a reader issue, not an author-data conflict.

hIgG N-glycan repeatability profiles: Complete hIgG source feature block from the Figure 4b sample-preparation repeatability assay. Three technical preparations are retained separately; average, standard deviation and CV are not samples. This panel is distinct from similarly named immunoglobulin application samples in Figure 5bc. Quantitative zeros are represented as NA without imputation or renormalization; original measurements are retained. GlyTouCan identifiers remain the source assignments. The readxl 1.5.0.1 reader substitutes embedded chart cache values into ten worksheet cells C3:C12. The original XLS is unchanged; all 1516 selected measurements agree exactly with independently decoded worksheet records. This is a reader issue, not an author-data conflict.

All source GlyTouCan identifiers resolve to WURCS through the official GlyTouCan SPARQL service. Structures are converted with glyparse 0.8.1 and validated with glyrepr 1.1.0, and compositions are derived from the validated structures. No mass-based assignments or new experimental linkage evidence are inferred.

Access

Use `glyhub_load("glyhub_GPST000578_N_source_repeatability_intensity")` to load this dataset.

Source

GlycoPOST GPST000578. Figure 4b. Study: <https://doi.org/10.1038/s41467-026-73091-3>. Repository: <https://glycopost.glycosmos.org/entry/GPST000578>. Quantitative source: https://media.springernature.com/original/springer-static/esm/art%3A10.1038%2Fs41467-026-73091-3/MediaObjects/41467_2026_73091_MOESM4_ESM.xls.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000578_N_total_peak_area

Immunoglobulins N-glycan total peak areas and related study experiments

Description

N-glycopedia applies structure-specific SRM profiling to purified human immunoglobulins. All 35 rows of the source IgA/IgG/IgM table and nine technical preparation/LC-MS replicate measurements are retained as raw total peak areas; normalized abundances and statistical summaries remain in the source workbook. Combined N-glycan quantitative profiles from GPST000578. 75 union features and 27 source observations are represented.

Usage

```
glyhub_GPST000578_N_total_peak_area(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 75 features and 27 observations. The abundance assay is in total peak area. rowData includes a typed glycan_structure column; features without a supported structure are NA.

Details

Source experiments are identified in colData and original panel-specific metadata, annotations and measurements are retained in metadata. Feature identities are aligned only when supported by author identifiers or explicit molecular structures; other features retain source-specific identities. The source_coverage matrix distinguishes unmeasured combinations from measured missing values. Units: total peak area.

Immunoglobulins N-glycan total peak areas: Entire source feature block retained. Zero-valued abundance is to be converted to NA with original values retained; no sample pairing inferred. GlyTouCan IDs are source annotations; sequence/composition mapping is pending verification. Quantitative zeros are represented as NA without imputation or renormalization; original measurements are retained. GlyTouCan identifiers remain the source assignments.

CHO Perturbation N-glycan total peak areas: Entire source feature block retained. Zero-valued abundance is to be converted to NA with original values retained; no sample pairing inferred. GlyTouCan IDs are source annotations; sequence/composition mapping is pending verification. Quantitative zeros are represented as NA without imputation or renormalization; original measurements are retained. GlyTouCan identifiers remain the source assignments.

Recombinant Spike N-glycans from SF9 and CHO expression: Complete 61-feature raw total-area block from Figure 5a. The later 9-feature SF9 and 51-feature CHO presentation blocks repeat measurements from this block; these filtered presentations are retained as source context and not counted as additional observations. Quantitative zeros are represented as NA without imputation or renormalization; original measurements are retained. GlyTouCan identifiers remain the source assignments.

Recombinant Spike N-glycans from HEK293 expression: Complete 34-feature HEK293 source block from Figure 5a, retaining raw total peak areas for the three technical preparations. Source per-glycan class and summary relative values are contextual annotations, not additional samples. Quantitative zeros are represented as NA without imputation or renormalization; original measurements are retained. GlyTouCan identifiers remain the source assignments.

All source GlyTouCan identifiers resolve to WURCS through the official GlyTouCan SPARQL service. Structures are converted with glyparse 0.8.1 and validated with glyrepr 1.1.0, and compositions are derived from the validated structures. No mass-based assignments or new experimental linkage evidence are inferred.

Access

Use `glyhub_load("glyhub_GPST000578_N_total_peak_area")` to load this dataset.

Source

GlycoPOST GPST000578. Figure 5bc. Study: <https://doi.org/10.1038/s41467-026-73091-3>.
Repository: <https://glycopost.glycosmos.org/entry/GPST000578>. Quantitative source: https://media.springernature.com/original/springer-static/esm/art%3A10.1038%2Fs41467-026-73091-3/MediaObjects/41467_2026_73091_M0ESM4_ESM.xls.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000584_N *Serum N-glycan profiles across hepatocellular carcinoma progression*

Description

MALDI-TOF serum N-glycomics from the hepatocellular carcinoma study, retaining the complete published pre-processing abundance table.

Usage

```
glyhub_GPST000584_N(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 201 features and 743 observations. The abundance assay is in peak area. rowData has no glycan_structure column because no feature has a supported structural annotation.

Details

The raw sheet of Supplementary Data 2 contains 201 composition features and 743 source observations. The separate processed sheet is a filtered, normalized subset and is not appended as independent samples. Published clinical fields from Supplementary Data 8 are joined by exact sample ID; unmatched samples retain missing clinical metadata. The assay contains original peak-area measurements, with source zeros represented as missing and no new imputation or normalization. Composition-level measurements do not establish glycan topology or linkage isomers. Disease groups are joined from explicit sample/group columns in the source-data workbook, without inferring groups from sample numbering.

Source molecular compositions retained without inferring glycosidic linkages.

Access

Use `glyhub_load("glyhub_GPST000584_N")` to load this dataset.

Source

GlycoPOST GPST000584. raw. Study: <https://doi.org/10.1038/s41467-026-68579-x>. Repository: <https://glycopost.glycosmos.org/entry/GPST000584>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000585_N *Bladder-tissue N-glycans across cancer stages*

Description

N-glycan profiles from healthy bladder, cystitis and Ta, T1 and muscle-invasive bladder tumours. The table contains five observations in each of the first four groups and eight in the muscle-invasive group.

Usage

```
glyhub_GPST000585_N(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A `glyexp::GlycomicSE` with 23 features and 28 observations. The abundance assay is in source-labelled relative abundance (%). `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

PNGase F-released, reduced and permethylated N-glycans were quantified by mass spectrometry. Source Table S1 relative-abundance values are preserved without rescaling; paired peak areas are retained in row annotations rather than duplicating the dataset. n.d. cells are missing. Composition identities and source glycan classes are preserved without converting class labels into asserted structures.

Source-derived composition annotations; linkage information is retained as source annotation without inferring a full topology. No complete unambiguous structures are asserted.

Access

Use `glyhub_load("glyhub_GPST000585_N")` to load this dataset.

Source

GlycoPOST GPST000585. Table S1. Study: <https://doi.org/10.3390/ijms26104891>. Repository: <https://glycopost.glycosmos.org/entry/GPST000585>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000596_N	<i>Platelet N-glycan isomer profiles in control and FUT8-knockout mice</i>
---------------------	--

Description

Fifty N-glycan chromatographic features quantified in platelet lysates from three control and three FUT8-knockout mouse observations, supporting a study of platelet activation and thrombosis.

Usage

```
glyhub_GPST000596_N(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 50 features and 6 observations. The abundance assay is in area under chromatographic curve. `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

The assay contains the six original area-under-curve columns C1–C3 and K1–K3. Isomer labels, retention times, precursor charge and mass, glycan class and author-assigned fucosyl linkage are retained. The separate normalized block in the source workbook contains fractions despite its percent heading; it is not duplicated as an independent dataset. Replicate biology beyond the author condition labels is not inferred.

Explicit total Hex, HexNAc, Fuc, NeuGc and NeuAc counts are used. Distinct chromatographic isomers remain distinct features. Core/outer-arm linkage information is retained as an author annotation and is not expanded into an unsupported complete glycan topology.

Access

Use `glyhub_load("glyhub_GPST000596_N")` to load this dataset.

Source

GlycoPOST GPST000596. . Study: <https://doi.org/10.1161/atvbaha.126.324757>. Repository: <https://glycopost.glycosmos.org/entry/GPST000596>. Quantitative source: https://glycopost.glycosmos.org/data/GPST000596.0/FUT8-K0_Manuscript_SupplementaryTable_Final.xlsx.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000599_serum_n

Septic shock longitudinal serum N-glycome

Description

Complete published glycan-by-sample peak-area matrix, 45 source glycan features and 134 samples; paired fractional abundance block preserved.

Usage

```
glyhub_GPST000599_serum_n(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A `glyexp::GlycomicSE` with 45 features and 134 observations. The abundance assay is in `peak_area`. `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

Complete 45-feature by 134-sample glycan peak areas exactly match publisher SI Table S3. Relative abundance verified raw/column sum. Patient-ICU day naming is explicit in publisher SI; all 134 samples mapped without ambiguity to 37 subjects and actual sampling dates in S1. Clinical missing values N/A/Unknown remain null. Other SI tables are identification PSMs, narrow Lex subsets or peptide LFQ and are not imported as glycan matrices.

Molecular annotations retain source precision. Unresolved compositions or structures are NA; original annotations are retained in `rowData`. All quantitative source features are preserved.

Access

Use `glyhub_load("glyhub_GPST000599_serum_n")` to load this dataset.

Source

GlycoPOST GPST000599. Table S2. Study: <https://doi.org/10.1016/j.mcpro.2025.101470>. Repository: <https://glycopost.glycosmos.org/entry/GPST000599>. Quantitative source: <https://glycopost.glycosmos.org/data/GPST000599.0/Supplementary%20Table.xlsx>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000601_N *Longitudinal rat-serum released N-glycans*

Description

Released serum N-glycan amounts from four female and four male rats sampled over five days, measured in 139 explicitly named technical MALDI acquisitions.

Usage

```
glyhub_GPST000601_N(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 14 features and 139 observations. The abundance assay is in pmol (source export). rowData includes a typed glycan_structure column; features without a supported structure are NA.

Details

The complete quantitative-only (combine) export contains 14 features and 139 acquisition columns; repeated acquisitions are technical observations and must not be treated as independent animals. Source spot and run identifiers are retained, including the anomalous F1D4 E21 spot label. Assignment.pdf corroborates that complex-glycan codes omit the Man 3GlcNAc 2 core, whereas H5N2/H6N2 are full compositions. The final three source codes contain F1 but the diagram lacks fucose; their typed molecular annotation is missing while source labels and amounts remain intact. Unlocalized O-acetylation is represented at composition level only. Quantitative values are preserved in the reported pmol scale.

Source-derived compositions and original labels are retained. 6 source-supported structures are typed; unspecified bonds remain unknown. Unresolved or conflicting structures remain missing with source provenance.

Access

Use `glyhub_load("glyhub_GPST000601_N")` to load this dataset.

Source

GlycoPOST GPST000601. quantitative-only (combine). Study: <https://doi.org/10.3390/ijms26157266>. Repository: <https://glycopost.glycosmos.org/entry/GPST000601>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000601_N_glycopeptides

Rat serum N-glycopeptides across repeated sampling

Description

Glycopeptide-level grouped abundances from albumin/IgG-depleted rat serum, sampled on five days in three female rats and one male rat.

Usage

```
glyhub_GPST000601_N_glycopeptides(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

<code>kind</code>	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
<code>cache_dir</code>	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
<code>refresh</code>	Download the pinned resource again, even if cached.
<code>offline</code>	Prohibit downloads; require a verified local resource.

Format

A `glyexp::GlycomicSE` with 1256 features and 20 observations. The abundance assay is in source grouped abundance (relative scale). `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

Supplementary Table S2 provides 1256 quantified peptide-glycan feature rows. Grouped abundance columns are preserved on the published scale. Individual acquisition columns have mixed normalization labels and are retained only in the source workbook. Glycan acetyl counts are represented explicitly. A single protein site is assigned only when one protein position and one localized N-glycosylation site are unambiguous; all original peptide and protein mappings are retained.

Source-derived compositions and original annotation fields are preserved; unknown linkages are not inferred.

Access

Use `glyhub_load("glyhub_GPST000601_N_glycopeptides")` to load this dataset.

Source

GlycoPOST GPST000601. Table S2. Study: <https://doi.org/10.3390/ijms26157266>. Repository: <https://glycopost.glycosmos.org/entry/GPST000601>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000602_Sh_GSL

Major human schistosome species express different glycans with immunological and diagnostic implications

Description

Annotated *Schistosoma haematobium* GSL-glycan MALDI-TOF-MS peak-intensity records from Supplementary Data 1, sheet (A) Sh GSL glycans; 566 source-specific peak records across 11 spectra.

Usage

```
glyhub_GPST000602_Sh_GSL(  
  kind = c("curated", "raw"),  
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),  
  refresh = FALSE,  
  offline = FALSE  
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 566 features and 11 observations. The abundance assay is in MALDI-TOF-MS peak intensity (source instrument units; arbitrary units). `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

Each retained source peak is a separate feature identified by sheet, spectrum block and row. The sparse matrix organizes spectrum-specific measurements without asserting cross-spectrum molecular identity. Off-spectrum entries have `source_coverage=FALSE` and are not measured missing values or biological absence. The object scope is one object per source worksheet across the five source worksheets. This object is not a ready-to-use cross-sample aligned feature matrix; cross-spectrum comparisons require an independently justified feature alignment. Only rows with a non-null author composition annotation are retained. Raw workbook bytes and complete retained/dropped cell-level ledgers preserve source evidence. No averaging, summation, normalization, imputation, mass filtering, peak selection by intensity, or raw-MS processing is performed. All retained numeric assay zeros become NA; nonzero values are unchanged. Putative compositions do not establish exact structures or distinguish isomers. AA and redEnd labels are stored separately from monosaccharide counts.

All retained features have source putative composition annotations parsed to typed monosaccharide counts; exact glycan structures remain NA. Original labels, m/z values, all source block values and source formulas are preserved.

Access

Use `glyhub_load("glyhub_GPST000602_Sh_GSL")` to load this dataset.

Source

GlycoPOST GPST000602. Supplementary Data 1 / Table S1 - Raw MALDI-TOF-MS data. Study: <https://doi.org/10.1038/s41467-026-70850-0>. Repository: <https://glycopost.glycosmos.org/entry/GPST000602>. Quantitative source: https://media.springernature.com/original/springer-static/esm/art%3A10.1038%2Fs41467-026-70850-0/MediaObjects/41467_2026_70850_MOESM3_ESM.xlsx.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000602_Sh_N

Major human schistosome species express different glycans with immunological and diagnostic implications

Description

Annotated *Schistosoma haematobium* N-glycan MALDI-TOF-MS peak-intensity records from Supplementary Data 1, sheet (C) Sh N-glycans; 489 source-specific peak records across 10 spectra.

Usage

```
glyhub_GPST000602_Sh_N(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 489 features and 10 observations. The abundance assay is in MALDI-TOF-MS peak intensity (source instrument units; arbitrary units). `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

Each retained source peak is a separate feature identified by sheet, spectrum block and row. The sparse matrix organizes spectrum-specific measurements without asserting cross-spectrum molecular identity. Off-spectrum entries have `source_coverage=FALSE` and are not measured missing values or biological absence. The object scope is one object per source worksheet across the five source worksheets. This object is not a ready-to-use cross-sample aligned feature matrix; cross-spectrum comparisons require an independently justified feature alignment. Only rows with a non-null author composition annotation are retained. Raw workbook bytes and complete retained/dropped cell-level ledgers preserve source evidence. No averaging, summation, normalization, imputation, mass filtering, peak selection by intensity, or raw-MS processing is performed. All retained numeric assay zeros become NA; nonzero values are unchanged. Putative compositions do not establish exact

structures or distinguish isomers. AA and redEnd labels are stored separately from monosaccharide counts.

All retained features have source putative composition annotations parsed to typed monosaccharide counts; exact glycan structures remain NA. Original labels, m/z values, all source block values and source formulas are preserved.

Access

Use `glyhub_load("glyhub_GPST000602_Sh_N")` to load this dataset.

Source

GlycoPOST GPST000602. Supplementary Data 1 / Table S1 - Raw MALDI-TOF-MS data. Study: <https://doi.org/10.1038/s41467-026-70850-0>. Repository: <https://glycopost.glycosmos.org/entry/GPST000602>. Quantitative source: https://media.springernature.com/original/springer-static/esm/art%3A10.1038%2Fs41467-026-70850-0/MediaObjects/41467_2026_70850_MOESM3_ESM.xlsx.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000602_Sh_O

Major human schistosome species express different glycans with immunological and diagnostic implications

Description

Annotated *Schistosoma haematobium* O-glycan MALDI-TOF-MS peak-intensity records from Supplementary Data 1, sheet (E) Sh O-glycans; 122 source-specific peak records across 4 spectra.

Usage

```
glyhub_GPST000602_Sh_O(  
  kind = c("curated", "raw"),  
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),  
  refresh = FALSE,  
  offline = FALSE  
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 122 features and 4 observations. The abundance assay is in MALDI-TOF-MS peak intensity (source instrument units; arbitrary units). `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

Each retained source peak is a separate feature identified by sheet, spectrum block and row. The sparse matrix organizes spectrum-specific measurements without asserting cross-spectrum molecular identity. Off-spectrum entries have `source_coverage=FALSE` and are not measured missing values or biological absence. The object scope is one object per source worksheet across the five source worksheets. This object is not a ready-to-use cross-sample aligned feature matrix; cross-spectrum comparisons require an independently justified feature alignment. Only rows with a non-null author composition annotation are retained. Raw workbook bytes and complete retained/dropped cell-level ledgers preserve source evidence. No averaging, summation, normalization, imputation, mass filtering, peak selection by intensity, or raw-MS processing is performed. All retained numeric assay zeros become NA; nonzero values are unchanged. Putative compositions do not establish exact structures or distinguish isomers. AA and redEnd labels are stored separately from monosaccharide counts.

All retained features have source putative composition annotations parsed to typed monosaccharide counts; exact glycan structures remain NA. Original labels, m/z values, all source block values and source formulas are preserved.

Access

Use `glyhub_load("glyhub_GPST000602_Sh_O")` to load this dataset.

Source

GlycoPOST GPST000602. Supplementary Data 1 / Table S1 - Raw MALDI-TOF-MS data. Study: <https://doi.org/10.1038/s41467-026-70850-0>. Repository: <https://glycopost.glycosmos.org/entry/GPST000602>. Quantitative source: https://media.springernature.com/original/springer-static/esm/art%3A10.1038%2Fs41467-026-70850-0/MediaObjects/41467_2026_70850_MOESM3_ESM.xlsx.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000602_Sm_GSL

Major human schistosome species express different glycans with immunological and diagnostic implications

Description

Annotated *Schistosoma mansoni* GSL-glycan MALDI-TOF-MS peak-intensity records from Supplementary Data 1, sheet (B) Sm GSL glycans; 183 source-specific peak records across 3 spectra.

Usage

```
glyhub_GPST000602_Sm_GSL(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 183 features and 3 observations. The abundance assay is in MALDI-TOF-MS peak intensity (source instrument units; arbitrary units). `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

Each retained source peak is a separate feature identified by sheet, spectrum block and row. The sparse matrix organizes spectrum-specific measurements without asserting cross-spectrum molecular identity. Off-spectrum entries have `source_coverage=FALSE` and are not measured missing values or biological absence. The object scope is one object per source worksheet across the five source worksheets. This object is not a ready-to-use cross-sample aligned feature matrix; cross-spectrum comparisons require an independently justified feature alignment. Only rows with a non-null author composition annotation are retained. Raw workbook bytes and complete retained/dropped cell-level ledgers preserve source evidence. No averaging, summation, normalization, imputation, mass filtering, peak selection by intensity, or raw-MS processing is performed. All retained numeric assay zeros become NA; nonzero values are unchanged. Putative compositions do not establish exact

structures or distinguish isomers. AA and redEnd labels are stored separately from monosaccharide counts.

All retained features have source putative composition annotations parsed to typed monosaccharide counts; exact glycan structures remain NA. Original labels, m/z values, all source block values and source formulas are preserved.

Access

Use `glyhub_load("glyhub_GPST000602_Sm_GSL")` to load this dataset.

Source

GlycoPOST GPST000602. Supplementary Data 1 / Table S1 - Raw MALDI-TOF-MS data. Study: <https://doi.org/10.1038/s41467-026-70850-0>. Repository: <https://glycopost.glycosmos.org/entry/GPST000602>. Quantitative source: https://media.springernature.com/original/springer-static/esm/art%3A10.1038%2Fs41467-026-70850-0/MediaObjects/41467_2026_70850_MOESM3_ESM.xlsx.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000602_Sm_N

Major human schistosome species express different glycans with immunological and diagnostic implications

Description

Annotated *Schistosoma mansoni* N-glycan MALDI-TOF-MS peak-intensity records from Supplementary Data 1, sheet (D) Sm N-glycans; 247 source-specific peak records across 4 spectra.

Usage

```
glyhub_GPST000602_Sm_N(  
  kind = c("curated", "raw"),  
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),  
  refresh = FALSE,  
  offline = FALSE  
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 247 features and 4 observations. The abundance assay is in MALDI-TOF-MS peak intensity (source instrument units; arbitrary units). `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

Each retained source peak is a separate feature identified by sheet, spectrum block and row. The sparse matrix organizes spectrum-specific measurements without asserting cross-spectrum molecular identity. Off-spectrum entries have `source_coverage=FALSE` and are not measured missing values or biological absence. The object scope is one object per source worksheet across the five source worksheets. This object is not a ready-to-use cross-sample aligned feature matrix; cross-spectrum comparisons require an independently justified feature alignment. Only rows with a non-null author composition annotation are retained. Raw workbook bytes and complete retained/dropped cell-level ledgers preserve source evidence. No averaging, summation, normalization, imputation, mass filtering, peak selection by intensity, or raw-MS processing is performed. All retained numeric assay zeros become NA; nonzero values are unchanged. Putative compositions do not establish exact structures or distinguish isomers. AA and redEnd labels are stored separately from monosaccharide counts.

All retained features have source putative composition annotations parsed to typed monosaccharide counts; exact glycan structures remain NA. Original labels, m/z values, all source block values and source formulas are preserved.

Access

Use `glyhub_load("glyhub_GPST000602_Sm_N")` to load this dataset.

Source

GlycoPOST GPST000602. Supplementary Data 1 / Table S1 - Raw MALDI-TOF-MS data. Study: <https://doi.org/10.1038/s41467-026-70850-0>. Repository: <https://glycopost.glycosmos.org/entry/GPST000602>. Quantitative source: https://media.springernature.com/original/springer-static/esm/art%3A10.1038%2Fs41467-026-70850-0/MediaObjects/41467_2026_70850_MOESM3_ESM.xlsx.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000604_CS_DS*Chondroitin/dermatan sulfate disaccharide profiles measured by
HILIC-Q-TOF-MS*

Description

Lyase-derived disaccharides from commercial glycosaminoglycans, cultured human cells, murine tissues, and human urine measured after reductive isotopic aniline labeling.

Usage

```
glyhub_GPST000604_CS_DS(  
  kind = c("curated", "raw"),  
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),  
  refresh = FALSE,  
  offline = FALSE  
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 7 features and 18 observations. The abundance assay is in summed sample 12C XIC peak area, arbitrary units. `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

Sample 12C XIC peak areas are summed across observed sodium adducts. Matched 13C internal-standard areas and source-cell provenance are retained in metadata. These are unnormalized instrumental areas, not published absolute amounts. Source zero totals are represented as missing assay values. Source chemistry preserves the 4,5-unsaturated uronic acid and positional sulfation assignments from Supplemental Table S1. Typed composition and structure are missing because the current glyrepr vocabulary does not represent the unsaturated residue; exact source chemistry remains available in `rowData`.

Exact source structures and modification counts retained; typed composition missing because DeltaUA is unsupported. No saturated-residue substitution.

Access

Use `glyhub_load("glyhub_GPST000604_CS_DS")` to load this dataset.

Source

GlycoPOST GPST000604. ac5c02338_si_002.xlsx. Study: <https://doi.org/10.1021/acs.analchem.5c02338>. Repository: <https://glycopost.glycosmos.org/entry/GPST000604>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000604_HS *Heparan sulfate disaccharide profiles measured by HILIC-Q-TOF-MS*

Description

Lyase-derived disaccharides from commercial glycosaminoglycans, cultured human cells, murine tissues, and human urine measured after reductive isotopic aniline labeling.

Usage

```
glyhub_GPST000604_HS(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

<code>kind</code>	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
<code>cache_dir</code>	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
<code>refresh</code>	Download the pinned resource again, even if cached.
<code>offline</code>	Prohibit downloads; require a verified local resource.

Format

A `glyexp::GlycomicSE` with 8 features and 21 observations. The abundance assay is in summed sample 12C XIC peak area, arbitrary units. `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

Sample 12C XIC peak areas are summed across observed sodium adducts. Matched 13C internal-standard areas and source-cell provenance are retained in metadata. These are unnormalized instrumental areas, not published absolute amounts. Source zero totals are represented as missing assay values. Source chemistry preserves the 4,5-unsaturated uronic acid and positional sulfation assignments from Supplemental Table S1. Typed composition and structure are missing because the current glyrepr vocabulary does not represent the unsaturated residue; exact source chemistry remains available in rowData.

Exact source structures and modification counts retained; typed composition missing because DeltaUA is unsupported. No saturated-residue substitution.

Access

Use `glyhub_load("glyhub_GPST000604_HS")` to load this dataset.

Source

GlycoPOST GPST000604. ac5c02338_si_002.xlsx. Study: <https://doi.org/10.1021/acs.analchem.5c02338>. Repository: <https://glycopost.glycosmos.org/entry/GPST000604>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000625_N	<i>Human intervertebral-disc N-glycan chromatographic profiles</i>
---------------------	--

Description

Thirty-two shared HILIC-UPLC N-glycan peaks quantified in six biological replicates each of healthy and degenerated annulus fibrosus and nucleus pulposus tissue.

Usage

```
glyhub_GPST000625_N(  
  kind = c("curated", "raw"),  
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),  
  refresh = FALSE,  
  offline = FALSE  
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A `glyexp::GlycomicSE` with 32 features and 24 observations. The abundance assay is in relative peak area (%). `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

Dataset S2 contains the full individual-replicate percentage-area matrix. Glycan peaks may contain coeluting species, so peak identities are retained without assigning a single composition or structure. The separate 48-peak pooled-sample structural-deconvolution analysis is retained in the source workbook and is not equated to the 32-peak individual-replicate feature space. No glycan identities are inferred from peak numbers.

UPLC peak-level quantitative features; 32 individual-sample peaks cannot be uniquely matched to 48 pooled structural fractions. Composition and structure are intentionally missing; source peak identities are retained.

Access

Use `glyhub_load("glyhub_GPST000625_N")` to load this dataset.

Source

GlycoPOST GPST000625. UPLC_covariance_bio replicates. Study: <https://doi.org/10.1002/adv.202506669>. Repository: <https://glycopost.glycosmos.org/entry/GPST000625>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000643_N	<i>GH20 activity on N-glycans from pretreated PSGL-1 and related study experiments</i>
---------------------	--

Description

The N-glycan fraction reported alongside the PSGL-1 GH20 enzyme screen. These measurements describe three N-glycan features with exposed N-acetylglucosamine in the pretreated glycoprotein preparation, permitting inspection of enzyme responses outside the O-glycan core panel. Supplementary Table S10B reports the three features across eight conditions. Combined N-glycan quantitative profiles from GPST000643. 3 union features and 23 source observations are represented.

Usage

```
glyhub_GPST000643_N(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 3 features and 23 observations. The abundance assay is in percentage of source total glycan AUC. rowData includes a typed glycan_structure column; features without a supported structure are NA.

Details

Source experiments are identified in colData and original panel-specific metadata, annotations and measurements are retained in metadata. Feature identities are aligned only when supported by author identifiers or explicit molecular structures; other features retain source-specific identities. The source_coverage matrix distinguishes unmeasured combinations from measured missing values. Units: source-reported percentage of total glycan AUC.

GH20 activity on N-glycans from pretreated PSGL-1: The protein substrate was pretreated with BT0455 sialidase and the galactosidases BT1626 and BT4241 to expose terminal N-acetylglucosamine. The eight conditions are control, BT1621, BT1627, BT3178, BT3598, BT3868, BT4394 and BT4681.

There is one source column per condition; biological replicate type and expression-system species are not established by these table columns.

This object follows the workbook's explicit N-glycan classification rather than combining these features with its O-glycan section. It is not a separate set of eight biological samples inferred from that split. The source percentages are preserved without changing their denominator. Compare glyhub_GPST000643_O_S10B for the complementary feature space.

Replicated GH20 measurements of PSGL-1 N-glycan features: The conditions are control, BT3178, BT3598, BT3868 and BT4681, each with Sample 1, Sample 2 and Sample 3. PSGL-1 expressing core 4 was pretreated with an enzyme mix. The expression-system species and biological versus technical replicate type are not established by these table columns. Percentages retain the source total-AUC denominator without renormalization after separation by glycan class.

Mass-labelled features 1317-1 and 1520 are source rows 11 and 12. Their compositions and complete putative-structure text are identical to S10B rows 25 and 26, located under its explicit N-glycans heading. This source correspondence supports the N classification independently of mass alone. The companion glyhub_GPST000643_O_S10C object contains the other three rows; the matrices share their observation identities and must not be counted as separate samples.

The three composition labels and putative structures are encoded, including the source reduced reducing ends.

Access

Use `glyhub_load("glyhub_GPST000643_N")` to load this dataset.

Source

GlycoPOST GPST000643. Supplementary Table S10B, N-glycan rows 25-27 (media-11.xlsx). Study: <https://doi.org/10.64898/2026.03.26.714468>. Repository: <https://glycopost.glycosmos.org/entry/GPST000643>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000643_O	<i>Fucosidase treatment of porcine colonic mucin O-glycans and related study experiments</i>
---------------------	--

Description

LC-MS profiles of porcine colonic mucin oligosaccharides exposed to individual *Bacteroides thetaio-*taomicron fucosidases. This experiment compares the effects of GH95 and GH29 enzymes on a complex O-glycan substrate containing different fucosylated epitopes. Supplementary Table S5 provides 108 features and 22 observations. Combined O-glycan quantitative profiles from GPST000643. 365 union features and 71 source observations are represented.

Usage

```
glyhub_GPST000643_O(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 365 features and 71 observations. The abundance assay is in percentage of source total glycan AUC. `rowData` includes a typed `glycan_structure` column; features without a supported structure are NA.

Details

Source experiments are identified in `colData` and original panel-specific metadata, annotations and measurements are retained in `metadata`. Feature identities are aligned only when supported by author identifiers or explicit molecular structures; other features retain source-specific identities. The `source_coverage` matrix distinguishes unmeasured combinations from measured missing values. Units: source-reported percentage of total glycan AUC.

Fucosidase treatment of porcine colonic mucin O-glycans: The conditions are a no-enzyme control and BT1777, BT3155, BT3173, BT1842, BT3665, BT1625, BT4136, BT3798, BT3956 and BT4713. Each condition has columns labelled Replicate 1 and Replicate 2; these labels alone do not identify biological versus technical replicates.

The source supplies glycan AUCs, retention times and percentages normalized to total glycan AUC per observation. The abundance assay uses the percentages. Fucose, sulfation and blood-group annotations are retained as source annotations, including their zero-valued categorical flags. Features include substrate glycans and enzymatic products; O-derived denotes their experimental origin.

GH89 treatment of porcine gastric mucin O-glycans: The no-enzyme control, BT0438 treatment and BT4359 treatment each have two source-labelled replicates. The assay contains total-AUC-normalized percentages; original AUC and retention-time entries are retained separately in `metadata`.

Source row 46 has a disagreement between its reported composition and putative structure residue counts. Rows 69 and 70 contain the unresolved composition token `HexHAc`, so their typed compositions are NA. Original labels and the `annotation_consistency` field identify these cases. Their quantitative measurements are retained; uncertain molecular assignments should be considered before feature-level interpretation.

GH2 treatment of bovine submaxillary mucin O-glycans: The seven source columns represent a control and separate treatments with BT1626, BT3179, BT3340, BT4050, BT4241 and BT4684. No replicate labels are supplied for these columns. This table concerns bovine submaxillary mucin without the sialidase/fucosidase pretreatment used in the separate S9C experiment.

Abundances are percentages of total source glycan AUC. Source galactose, sialylation, sulfate and fucose annotations accompany the molecular labels. A single column per condition should not be interpreted as replicated evidence for treatment effects.

GH20 activity on O-glycans from pretreated PSGL-1: The protein substrate was pretreated with BT0455 sialidase and the galactosidases BT1626 and BT4241 to expose terminal N-acetylglucosamine. The eight conditions are control, BT1621, BT1627, BT3178, BT3598, BT3868, BT4394 and BT4681. There is one source column per condition; biological replicate type and expression-system species are not established by these table columns.

Only the source O-glycan section is included here. Its N-glycan section is available as glyhub_GPST000643_N_S10B. Percentages retain the denominator supplied in the workbook; separating the sections does not renormalize either matrix. Source mass/isomer labels are local to the table and are not universal glycan identifiers.

Replicated GH20 measurements of PSGL-1 O-glycan core features: The conditions are control, BT3178, BT3598, BT3868 and BT4681, each with Sample 1, Sample 2 and Sample 3. PSGL-1 expressing core 4 was pretreated with an enzyme mix. The expression-system species and biological versus technical replicate type are not established by these table columns. Percentages retain the source total-AUC denominator without renormalization after separation by glycan class.

The retained mass-labelled features are 425-2, 628 and 716 (source rows 8-10). Their composition and full putative-structure labels match the explicitly labelled O-glycan section of S10B. The two N-glycan features from S10C are available in glyhub_GPST000643_N_S10C. Both objects describe the same observation columns; they are complementary feature partitions, not separate biological samples.

Colonic mucin O-glycan degradation by enzyme mixtures: Three source-labelled samples are reported for each of a no-enzyme control, an eleven-enzyme mixture and the same mixture supplemented with BT3868. The base mixture contains BT0455, BT4243, BT1625, BT3173, BT1636, BT1624, BT1626, BT4241, BT1628, BT4681 and BT0438. This is the S11B mixture; it does not include the additional BT4394 used in the distinct S11C experiment.

Measurements are percentages of source total glycan AUC. O-derived features include remaining substrate glycans and released enzymatic products. Sample 1-3 labels are retained without assigning a biological replicate type or pairing the conditions.

Gastric mucin oligosaccharides remaining after bacterial growth: The source conditions are Control (gMO), the double alpha-1,2-fucosidase deletion strain lacking bt3173 and bt4682, that double deletion with an additional bt1842 deletion, and wild-type B. thetaiotaomicron. These are culture-supernatant glycan profiles, not bacterial counts or gene-expression measurements. One percentage column is available for each condition; no biological replicate type is assigned.

Percentages are normalized to source total glycan AUC. Feature row 48 has conflicting composition and putative-structure residue counts; both source assignments are retained and flagged in annotation_consistency. Digestion products and residual substrate glycans should be interpreted together in this extracellular measurement space.

All 108 source composition labels are retained as typed compositions. Forty-seven source putative structures have explicit encodings; remaining structural descriptions are preserved as text without completing unspecified linkages.

Access

Use `glyhub_load("glyhub_GPST000643_0")` to load this dataset.

Source

GlycoPOST GPST000643. Supplementary Table S5 (media-6.xlsx). Study: <https://doi.org/10.64898/2026.03.26.714468>. Repository: <https://glycopost.glycosmos.org/entry/GPST000643>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000647_N	<i>Whole-brain N-glycans in Slc35a3-deficient mice</i>
---------------------	--

Description

N-glycan amounts in whole-brain tissue from wild-type, heterozygous and Slc 35 a 3-knockout mice, with three source observations per genotype.

Usage

```
glyhub_GPST000647_N(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A `glyexp::GlycomicSE` with 179 features and 9 observations. The abundance assay is in pmol per 100 micrograms protein. `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

The 179 rows include paucimannose, high-mannose, hybrid, neutral-complex and acidic-complex features. Paucimannose counts are literal; other source counts describe residues beyond the Hex 3 HexNAc 2 N-glycan core. Full compositions include this core, consistent with the reported mass series and the paper core-plus-HexNAc convention. Source alpha 2,3/alpha 2,6 sialic-acid counts are retained as partial linkage annotations; predicted SNFG cartoons are not promoted to experimentally resolved isomer structures.

Source-derived composition annotations; linkage information is retained as source annotation without inferring a full topology. No complete unambiguous structures are asserted.

Access

Use `glyhub_load("glyhub_GPST000647_N")` to load this dataset.

Source

GlycoPOST GPST000647. Supplementary Table 1. Study: <https://doi.org/10.3390/ijms27041643>. Repository: <https://glycopost.glycosmos.org/entry/GPST000647>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000650_O	<i>Whole-brain O-glycans in Slc35a3-deficient mice</i>
---------------------	--

Description

O-glycan amounts in whole-brain tissue from wild-type, heterozygous and Slc 35 a 3-knockout mice, with three source observations per genotype.

Usage

```
glyhub_GPST000650_O(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A `glyexp::GlycomicSE` with 25 features and 9 observations. The abundance assay is in pmol per 100 micrograms protein. `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

The source study profiles nucleotide-sugar transporter deficiency using MALDI-TOF MS. Twenty-five annotated features are retained, including source-undetected rows. Sialic-acid linkage labels remain in row annotations; the paper describes composition-based assignments and does not resolve all isomeric structures. Quantitative zeros are represented as missing values, with original measurements and masks retained.

Source-derived composition annotations; linkage information is retained as source annotation without inferring a full topology. No complete unambiguous structures are asserted.

Access

Use `glyhub_load("glyhub_GPST000650_0")` to load this dataset.

Source

GlycoPOST GPST000650. Supplementary Table 2. Study: <https://doi.org/10.3390/ijms27041643>. Repository: <https://glycopost.glycosmos.org/entry/GPST000650>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000667_N	<i>N-glycan profiles of A549 and BEAS-2B small extracellular vesicles and culture media</i>
---------------------	---

Description

GlycoGenius-derived N-glycan abundance profiles from tumorigenic A549 and non-tumorigenic BEAS-2B small extracellular vesicles, with BEGM and F12 culture-medium profiles from the same study.

Usage

```
glyhub_GPST000667_N(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 271 features and 4 observations. The abundance assay is in Glyco-Genius abundance. rowData has no glycan_structure column because no feature has a supported structural annotation.

Details

All four source profile columns are retained. These are single profiles rather than six-replicate glycoproteomic measurements reported elsewhere in the paper. Migration-time-filtered assignments can contain alternative compositions separated by slashes; those alternatives remain explicit and are not arbitrarily resolved. Missing medium signals remain NA. This accession shares its publication with GPST000562, whose CS/DS disaccharides are represented separately because the glycan type and quantification differ.

H, N and F encode Hex, HexNAc and Fuc. Am and E encode derivatized alpha2,3 and alpha2,6 Neu5Ac; native NeuAc totals are represented as composition, and derivative/linkage counts are retained. Phosphorylation is retained where explicitly reported. Features with incompatible alternative compositions have missing typed composition and retain every author candidate.

Access

Use `glyhub_load("glyhub_GPST000667_N")` to load this dataset.

Source

GlycoPOST GPST000667. . Study: <https://doi.org/10.1016/j.mcpro.2026.101524>. Repository: <https://glycopost.glycosmos.org/entry/GPST000667>. Quantitative source: <https://glycopost.glycosmos.org/data/GPST000667.0/N-glycan-identifications.csv>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000671_N	<i>N-glycomes of influenza-infected A549 organelle and secreted fractions</i>
---------------------	---

Description

131 released N-glycan chromatographic features in organelle and secreted protein fractions of A549 cells 24 hours after PR8 (H1N1), x31 (H3N2) or mock infection.

Usage

```
glyhub_GPST000671_N(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A `glyexp::GlycomicSE` with 131 features and 24 observations. The abundance assay is in relative abundance fraction. `rowData` includes a typed `glycan_structure` column; features without a supported structure are NA.

Details

PGC-LC-MS/MS glycan abundances are author-normalized proportions of all glycans in each sample. Compatible organelle and secreted fractions are combined with explicit compartment and infection metadata. Four biological replicates per condition were planned. The O-glycan secreted x31 block contains only two observations in the deposited quantitative table; missing observations are not invented. Source isomer identifiers and diagnostic evidence are retained. The deposited N-glycan table contains 131 quantitative features, whereas the publication describes 142 identified N-glycan structures; this object reproduces the available quantitative matrix rather than claiming

to include undocumented features. The corresponding molecular feature blocks in official Supplementary Data 4 were checked cell-by-cell and match the deposited workbook.

Source monosaccharide counts and author GlyTouCan accessions are retained. Where an accession resolves to a parseable WURCS structure with composition consistent with the source row, its structure is included. Unresolvable accessions, incompatible compositions and rows without sequence-level structure remain unfilled. Sulfate/phosphate identity is resolved only when the row explicitly names it; ambiguous substitution remains source annotation without a falsely complete composition. Glycans were chemically reduced for measurement; structures represent the source-referenced glycan identity.

Access

Use `glyhub_load("glyhub_GPST000671_N")` to load this dataset.

Source

GlycoPOST GPST000671. . Study: <https://doi.org/10.1038/s42003-026-10759-y>. Repository: <https://glycopost.glycosmos.org/entry/GPST000671>. Quantitative source: https://glycopost.glycosmos.org/data/GPST000671.0/Supplementary%20File_4_Glycomics.xlsx.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000671_N_Glycoproteomics

Site-resolved N-glycoform proportions during influenza infection of A549 cells

Description

Complete source N-site glycoforms from Supplementary File 5: union of ten organelle/secreted fraction panels at 0,6,12,18,24 hours after mock, PR8(H1N1), or x31(H3N2) exposure. 3609 protein/site/glycan identities across 90 biological sample observations.

Usage

```
glyhub_GPST000671_N_Glycoproteomics(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A `glyexp::GlycoproteomicSE` with 3609 features and 90 observations. The abundance assay is in site-normalized glycoform proportion (fraction). `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

Assay values are author site-normalized proportions F:N, not raw signal or whole-sample glycan abundance. All source rows assigned to this glycan class are retained. Features are aligned only by the exact Protein/site/Glycans triplet; source Concat was checked to match this triplet in every row. No within-panel duplicate triplets occur. Union cells for a feature absent from a source panel remain NA with `source_coverage=false`; source blanks and actual zeros remain separately recoverable. Only quantitative zeros become NA. No curation-stage imputation, renormalization or replicate averaging occurs. O:W raw intensities are preserved in columns O:W of the pinned source extraction and original workbook. The three biological replicates per condition follow the paper; replicate numbers 1:3 encode within-condition source-column order, not demonstrated longitudinal pairing across time or compartment. TMT channels are preserved because assignments change with time. Human, bovine and influenza-virus protein assignments are all retained exactly; the culture host is human A549, but row-level protein organism must be used for protein provenance. Released glycomics is a separate assay/object class.

Counts are parsed only from explicit author Glycans tokens. HexNAc, Hex, Fuc and NeuAc are preserved; explicit Phospho and Sulfo are retained as P and S substituents. Protein accession and site positions are author assignments, not independently revalidated peptide localization. All observed source sites are single N/S/T positions; ambiguous or multiple source sites would remain untyped. Full glycan structures are not inferred from composition or site.

Access

Use `glyhub_load("glyhub_GPST000671_N_Glycoproteomics")` to load this dataset.

Source

GlycoPOST GPST000671. . Study: <https://doi.org/10.1038/s42003-026-10759-y>. Repository: <https://glycopost.glycosmos.org/entry/GPST000671>. Quantitative source: <https://www.nature.com/articles/s42003-026-10759-y>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000671_O	<i>O-glycomes of influenza-infected A549 organelle and secreted fractions</i>
---------------------	---

Description

49 released O-glycan chromatographic features in organelle and secreted protein fractions of A549 cells 24 hours after PR8 (H1N1), x31 (H3N2) or mock infection.

Usage

```
glyhub_GPST000671_O(  
  kind = c("curated", "raw"),  
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),  
  refresh = FALSE,  
  offline = FALSE  
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 49 features and 22 observations. The abundance assay is in relative abundance fraction. rowData includes a typed glycan_structure column; features without a supported structure are NA.

Details

PGC-LC-MS/MS glycan abundances are author-normalized proportions of all glycans in each sample. Compatible organelle and secreted fractions are combined with explicit compartment and infection metadata. Four biological replicates per condition were planned. The O-glycan secreted x31 block contains only two observations in the deposited quantitative table; missing observations are not invented. Source isomer identifiers and diagnostic evidence are retained. The deposited N-glycan table contains 131 quantitative features, whereas the publication describes 142 identified N-glycan structures; this object reproduces the available quantitative matrix rather than claiming

to include undocumented features. The corresponding molecular feature blocks in official Supplementary Data 4 were checked cell-by-cell and match the deposited workbook.

Source monosaccharide counts and author GlyTouCan accessions are retained. Where an accession resolves to a parseable WURCS structure with composition consistent with the source row, its structure is included. Unresolvable accessions, incompatible compositions and rows without sequence-level structure remain unfilled. Sulfate/phosphate identity is resolved only when the row explicitly names it; ambiguous substitution remains source annotation without a falsely complete composition. Glycans were chemically reduced for measurement; structures represent the source-referenced glycan identity.

Access

Use `glyhub_load("glyhub_GPST000671_O")` to load this dataset.

Source

GlycoPOST GPST000671. . Study: <https://doi.org/10.1038/s42003-026-10759-y>. Repository: <https://glycopost.glycosmos.org/entry/GPST000671>. Quantitative source: https://glycopost.glycosmos.org/data/GPST000671.0/Supplementary%20File_4_Glycomics.xlsx.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000671_O_Glycoproteomics

Site-resolved O-glycoform proportions during influenza infection of A549 cells

Description

Complete source O-site glycoforms from Supplementary File 5: union of ten organelle/secreted fraction panels at 0,6,12,18,24 hours after mock, PR8(H1N1), or x31(H3N2) exposure. 253 protein/site/glycan identities across 90 biological sample observations.

Usage

```
glyhub_GPST000671_O_Glycoproteomics(  
  kind = c("curated", "raw"),  
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),  
  refresh = FALSE,  
  offline = FALSE  
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A `glyexp::GlycoproteomicSE` with 253 features and 90 observations. The abundance assay is in site-normalized glycoform proportion (fraction). `rowData` has no `glycan_structure` column because no feature has a supported structural annotation.

Details

Assay values are author site-normalized proportions F:N, not raw signal or whole-sample glycan abundance. All source rows assigned to this glycan class are retained. Features are aligned only by the exact Protein/site/Glycans triplet; source Concat was checked to match this triplet in every row. No within-panel duplicate triplets occur. Union cells for a feature absent from a source panel remain NA with `source_coverage=false`; source blanks and actual zeros remain separately recoverable. Only quantitative zeros become NA. No curation-stage imputation, renormalization or replicate averaging occurs. O:W raw intensities are preserved in columns O:W of the pinned source extraction and original workbook. The three biological replicates per condition follow the paper; replicate numbers 1:3 encode within-condition source-column order, not demonstrated longitudinal pairing across time or compartment. TMT channels are preserved because assignments change with time. Human, bovine and influenza-virus protein assignments are all retained exactly; the culture host is human A549, but row-level protein organism must be used for protein provenance. Released glycomics is a separate assay/object class.

Counts are parsed only from explicit author Glycans tokens. HexNAc, Hex, Fuc and NeuAc are preserved; explicit Phospho and Sulfo are retained as P and S substituents. Protein accession and site positions are author assignments, not independently revalidated peptide localization. All observed source sites are single N/S/T positions; ambiguous or multiple source sites would remain untyped. Full glycan structures are not inferred from composition or site.

Access

Use `glyhub_load("glyhub_GPST000671_O_Glycoproteomics")` to load this dataset.

Source

GlycoPOST GPST000671. . Study: <https://doi.org/10.1038/s42003-026-10759-y>. Repository: <https://glycopost.glycosmos.org/entry/GPST000671>. Quantitative source: <https://www.nature.com/articles/s42003-026-10759-y>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000676_GAG *Sulfatase modifying factors control the timing of zebrafish convergence and extension morphogenesis. and related study experiments*

Description

Complete eight-component targeted heparan-sulfate disaccharide assay at 80% epiboly. Each sample is independent clutch of 100 embryos. Source Data genotype replicate counts exceed GlycoPOST metadata, so source column IDs are retained and no raw-file correspondence is asserted. Combined GAG-glycan quantitative profiles from GPST000676. 8 union features and 15 source observations are represented.

Usage

```
glyhub_GPST000676_GAG(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 8 features and 15 observations. The abundance assay is in percent total HS disaccharides. rowData has no glycan_structure column because no feature has a supported structural annotation.

Details

Source experiments are identified in colData and original panel-specific metadata, annotations and measurements are retained in metadata. Feature identities are aligned only when supported by author identifiers or explicit molecular structures; other features retain source-specific identities. The

source_coverage matrix distinguishes unmeasured combinations from measured missing values. Units: percent total HS disaccharides.

Sulfatase modifying factors control the timing of zebrafish convergence and extension morphogenesis.: Complete eight-component targeted heparan-sulfate disaccharide assay at 80% epiboly. Each sample is independent clutch of 100 embryos. Source Data genotype replicate counts exceed GlycoPOST metadata, so source column IDs are retained and no raw-file correspondence is asserted.

Sulfatase modifying factors control the timing of zebrafish convergence and extension morphogenesis.: Complete eight-component targeted heparan-sulfate disaccharide assay at 80% epiboly. Each sample is independent clutch of 100 embryos. Source Data genotype replicate counts exceed GlycoPOST metadata, so source column IDs are retained and no raw-file correspondence is asserted.

Molecular annotations retain source precision. Unresolved compositions or structures are NA; original annotations are retained in rowData. All quantitative source features are preserved.

Access

Use `glyhub_load("glyhub_GPST000676_GAG")` to load this dataset.

Source

GlycoPOST GPST000676. Figure 5 e,f. Study: <https://doi.org/10.1038/s41467-026-70804-6>. Repository: <https://glycopost.glycosmos.org/entry/GPST000676>. Quantitative source: https://media.springernature.com/full/springer-static/esm/art%3A10.1038%2Fs41467-026-70804-6/MediaObjects/41467_2026_70804_MOESM10_ESM.xlsx.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000738_N_B4GalT1

Galactosylation of bovine fetuin N-glycans in an enzyme reactor

Description

N-glycan profiles from bovine fetuin treated with an immobilised B4GalT1 reactor. The experiment examines galactose addition to desialylated, degalactosylated fetuin over repeated injections at two flow rates. It contains nine glycan and isomer features measured across 18 source observations.

Usage

```
glyhub_GPST000738_N_B4GalT1(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A `glyexp::GlycomicSE` with 9 features and 18 observations. The abundance assay is in percentage within the source glycan family. `rowData` includes a typed `glycan_structure` column; features without a supported structure are NA.

Details

The substrate is foetal bovine serum fetuin treated with sialidase and galactosidase. Four substrate-control columns are followed by two observations at each of 2, 4 and 8 hours at 25 microlitres/minute, and at 0, 2, 4 and 8 hours at 75 microlitres/minute. The first 25 microlitres/minute injection was excluded in the source study because of acquisition loss and poor signal.

Abundance is expressed as a percentage within the A2 or A3 glycan family, not of the total glycome. Flow and time are recorded in `colData`. The repeated control table is represented once; the columns do not establish biological replication or pairing.

Twelve A2/A2G1 treatment cells with duplicated, non-closing source values and twelve A3 control cells with unresolved cross-table correspondence are NA. Six additional zero measurements are NA. Original values and the separate masks remain in metadata. Summing the available values therefore need not give 100.

Nine typed compositions retain distinct source isomer labels. Four fully localized structures from Supplementary Figure S3 are encoded; ambiguous antennae and unresolved isomer mappings retain diagram evidence.

Access

Use `glyhub_load("glyhub_GPST000738_N_B4GalT1")` to load this dataset.

Source

GlycoPOST GPST000738. Supplementary Table 1, sheets 1 and 2; composition comparisons in sheets 5 and 6; Figure S3. Study: <https://doi.org/10.3389/fmolb.2026.1932584>. Repository: <https://glycopost.glycosmos.org/entry/GPST000738>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_GPST000738_N_ST6GAL1

Sialylation of bovine fetuin N-glycans in an enzyme reactor

Description

N-glycan profiles from desialylated bovine fetuin passed through an immobilised ST6GAL1 reactor. The experiment follows redistribution among sialylated forms of three precursor families during repeated injections at 25 and 75 microlitres/minute. Ten glycan features are represented across 28 source observations.

Usage

```
glyhub_GPST000738_N_ST6GAL1(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Format

A [glyexp::GlycomicSE](#) with 10 features and 28 observations. The abundance assay is in fraction within the source precursor glycan family. `rowData` includes a typed `glycan_structure` column; features without a supported structure are NA.

Details

Seven substrate-control columns accompany seven reactor observations at 25 microlitres/minute and fourteen at 75 microlitres/minute. Injection times are 0, 2, 4 and 8 hours. The 25 microlitres/minute series has one 0-hour column and two at each later time; the 75 microlitres/minute series has four at 0, 2 and 8 hours and two at 4 hours.

Values are fractions within the H6N5, H5N5 or H5N4 precursor family. They must not be interpreted as total-glycome fractions or mixed directly with the percentage scale of the B4GalT1 dataset.

Thirteen source n.d. values are NA. Ten 25 microlitres/minute 0-hour measurements are also NA because their omission from processed sheet 7 is unexplained. An extra processed-table control

lacks a raw-table identity and remains in metadata as unmatched observations. The repeated control table is represented once; biological replicate type is unresolved.

Ten typed compositions describe sialylated forms. Four fully localized Figure S3 structures are encoded; diagrams retain the evidence for unresolved positional forms.

Access

Use `glyhub_load("glyhub_GPST000738_N_ST6GAL1")` to load this dataset.

Source

GlycoPOST GPST000738. Supplementary Table 1, sheets 3 and 4; composition comparisons in sheets 7 and 8; Figure S3. Study: <https://doi.org/10.3389/fmolb.2026.1932584>. Repository: <https://glycopost.glycosmos.org/entry/GPST000738>.

See Also

[glyhub_data_conventions](#) for missing-value handling, annotations and access to original measurements and source coordinates.

glyhub_IPX0011099000_N_Brain

Mouse brain Glyco-Decipher chromatographic areas

Description

Mouse brain Glyco-Decipher chromatographic areas

Usage

```
glyhub_IPX0011099000_N_Brain(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

<code>kind</code>	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
<code>cache_dir</code>	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
<code>refresh</code>	Download the pinned resource again, even if cached.
<code>offline</code>	Prohibit downloads; require a verified local resource.

Details

20,191 source feature rows across 60 reported measurement columns.

Assay scale: Source untransformed chromatographic Area

Feature grain: Peptide / glycan / source sites / compensation voltage

Source selection: Raw Area exports preferred over Supplementary Data6 processed matrix

No normalization, log transform, imputation, filtering, aggregation or zero conversion

Exact source identity union; a row absent from a run becomes structural NA; reported zero remains zero

Separate FAIMS compensation voltages retained as separate features

Unambiguous single accession@position parsed; multiple site assignments retained verbatim with canonical NA

Run code and region code retained without guessing disease, age, or anatomical mapping

Source extraction and identification filtering precede these exports; unspecified extraction settings remain unknown

Measurement columns are not automatically independent biological samples. Source row identifiers, annotations and provenance are retained in metadata.

The assay preserves source numeric values. The metadata field raw_abundance means source numbers; it does not certify that the authors supplied unprocessed intensity.

Value

A [glyexp::GlycoproteomicSE](#).

Availability and source license

Downloaded from the existing data release through the verified cache. Source-license scope for the complete object remains unresolved; no new license is granted. See publication-decisions.tsv and object metadata for original sources and limitations.

Source

<https://doi.org/10.1038/s41467-025-60437-6>.

See Also

[glyhub_catalog\(\)](#), [glyhub_data_conventions](#)

glyhub_load	<i>Load any glyhub dataset</i>
-------------	--------------------------------

Description

Load any dataset from the shared external data release. Dataset identifiers also name convenience functions that call this loader with the same options.

Usage

```
glyhub_load(
  dataset,
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

dataset	Exact dataset identifier from glyhub_catalog() , for example "glyhub_GPST000738_N_B4GalT1" or "glyhub_CPTAC_CCRCC".
kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Details

Downloads and cached files are checked against the package's size and SHA-256 manifest before use. Files are cached by version and hash. Interrupted or invalid downloads never replace a verified cached file. `refresh = TRUE` cannot be combined with `offline = TRUE`. Delete downloaded files from `cache_dir` to clear the cache.

Dataset objects are no longer exposed through `LazyData` or `data()`. Use this loader or each dataset's same-named function. Both return identical objects and share the verified cache. Consult dataset help for scientific details.

Value

For `kind = "curated"`, a [glyexp::GlycomicSE](#) or [glyexp::GlycoproteomicSE](#). For `kind = "raw"`, an absolute file path.

See Also

[glyhub_catalog\(\)](#), [glyhub_data_conventions](#)

Examples

```
glyhub_catalog()[1:3, c("dataset", "bytes")]
```

```
glyhub_MSV000089484_N_HCC
```

```
pGlycoQuant HCC cell-line source intensities
```

Description

pGlycoQuant HCC cell-line source intensities

Usage

```
glyhub_MSV000089484_N_HCC(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Details

11,001 source feature rows across 12 reported measurement columns.

Assay scale: Source SILAC glycoform-site intensity; -1 mapped to NA by user-confirmed curation convention

Exactly 40338 source -1 entries mapped to assay NA by explicit user instruction; the author has not directly defined this code in inspected sources

Original -1 entries and every source value remain in metadata raw_abundance

All 2137 zeros and every positive intensity preserved exactly; no log transform, normalization, imputation or filtering

One record per source protein/site/glycan row; no invented peptide sequence or PSM

The 6435-row filtered sheet is not a separate dataset or cohort

Repeat labels do not establish independent biological replication

Measurement columns are not automatically independent biological samples. Source row identifiers, annotations and provenance are retained in metadata.

The assay maps source -1 to NA by user-confirmed convention, not an author-confirmed definition. All source values, including -1, remain in metadata raw_abundance; zeros and positive values are unchanged.

Value

A `glyexp::GlycoproteomicSE`.

Availability and source license

Downloaded from the existing data release through the verified cache. Source-license scope for the complete object remains unresolved; no new license is granted. See publication-decisions.tsv and object metadata for original sources and limitations.

Source

<https://doi.org/10.1038/s41467-022-35172-x>.

See Also

`glyhub_catalog()`, `glyhub_data_conventions`

glyhub_PXD011063_O_Dilution

Glyco-DIA precursor peak areas in a dilution experiment

Description

Glyco-DIA precursor peak areas in a dilution experiment

Usage

```
glyhub_PXD011063_O_Dilution(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Details

15,890 source feature rows across 10 reported measurement columns.

Assay scale: Source FG.MS2TotalPeakArea; untransformed summed MS2 fragment chromatographic peak area

Feature grain: Library-specific precursor and source decoy flag; source decoys retained and explicitly flagged

Source selection: MS2TotalPeakArea preferred over FG.Quantity, EG.TotalQuantity and supplementary glycopeptide quantities; MS1PeakArea retained in metadata

No normalization, log transform, imputation, zero conversion, confidence filtering or aggregation

Union of exact library/precursor/decoy keys; absent report rows become structural NA, not zero

Source decoy rows and unquantified or unidentified rows retained; use source flags before biological inference

Different libraries are alternative analyses, not independent biological samples

No glycan composition inferred solely from rounded modification mass; source modified sequence retained

Spectronaut extraction, interference handling and upstream settings are not fully recoverable from these exports

Measurement columns are not automatically independent biological samples. Source row identifiers, annotations and provenance are retained in metadata.

The assay preserves source numeric values. The metadata field raw_abundance means source numbers; it does not certify that the authors supplied unprocessed intensity.

Source decoys are retained and flagged; this is an unfiltered source-report representation, not a confidence-filtered biological feature set.

Value

A [glyexp::GlycoproteomicSE](#).

Availability and source license

Downloaded from the existing data release through the verified cache. Deposited PRIDE source data are CC0-1.0, explicitly declared in the project API. Cite the original authors and accession; see metadata redistribution and source provenance.

Source

<https://doi.org/10.1038/s41592-019-0504-x>.

See Also

[glyhub_catalog\(\)](#), [glyhub_data_conventions](#)

 glyhub_PXD011063_O_SerumSA

Glyco-DIA SA serum source precursor peak areas

Description

Glyco-DIA SA serum source precursor peak areas

Usage

```
glyhub_PXD011063_O_SerumSA(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Details

93,442 source feature rows across 6 reported measurement columns.

Assay scale: Source FG.MS2TotalPeakArea; untransformed MS2 chromatographic peak area

Feature grain: Library / precursor / decoy flag; all source row associations retained

Source selection: Original Spectronaut peak areas preferred over author-added Abundance and derived summary statistics

No normalization, logarithm, imputation, zero conversion, confidence filtering or numerical aggregation

Repeated DDA-association rows are represented by their shared quantitative cell only after exact MS1/MS2 equality is proven; no value averaging or conflict resolution

Every source association remains linked by file and row; a missing precursor/run pair becomes structural NA

Source decoy rows retained and flagged; biological independence of runs is not inferred from file-names

Source modified sequence and glycopeptide label retained; no glycan composition inferred solely from rounded mass

Upstream extraction and interference handling are not fully documented in these exports

Measurement columns are not automatically independent biological samples. Source row identifiers, annotations and provenance are retained in metadata.

The assay preserves source numeric values. The metadata field `raw_abundance` means source numbers; it does not certify that the authors supplied unprocessed intensity.

Only the SA source file is included, across six reported runs. The deSA source CSV contains independently confirmed embedded NUL bytes and an unparsable quantitative record; it is excluded, not repaired or filtered. All source decoys are retained and flagged. Biological independence and exact glycan compositions remain unassigned.

Value

A `glyexp::GlycoproteomicSE`.

Availability and source license

Downloaded from the existing data release through the verified cache. Deposited PRIDE source data are CC0-1.0, explicitly declared in the project API. Cite the original authors and accession; see metadata redistribution and source provenance.

Source

<https://doi.org/10.1038/s41592-019-0504-x>.

See Also

`glyhub_catalog()`, `glyhub_data_conventions`

glyhub_PXD046637_N_Lung

Paired lung nodule glycoproteomics

Description

Paired lung nodule glycoproteomics

Usage

```
glyhub_PXD046637_N_Lung(  
  kind = c("curated", "raw"),  
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),  
  refresh = FALSE,  
  offline = FALSE  
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Details

39,079 source feature rows across 165 reported measurement columns.

Assay scale: Deposited untransformed ion-level TMT reporter intensities; author software aggregated PSMs to ions

Feature grain: Peptide Sequence / Modified Sequence / Charge / Observed Modifications / Protein

Source selection: Raw deposited ion reporter table preferred. Processed clinical matrix retained as explicit alternative in metadata because original channel-to-patient mapping was not supplied in the inspected files.

No additional normalization, logarithm, imputation, zero conversion, confidence filtering or intensity aggregation

Exact molecular identity union across batches; an ion absent from a batch becomes structural NA

All source ion rows, including rows without glycan annotations, and all 11 channels per batch retained

165 reporter channels are not 165 patients: reference/unused roles and linkage to the 132 clinical specimens remain unresolved

Source annotation.txt only repeats channel labels; clinical specimen labels are not guessed

Source PSM-to-ion summarization precedes this deposit; upstream correction settings remain unverified

Unambiguous composition text parsed after removing its explicit terminal mass; ambiguous modifications retain full text and typed NA

Measurement columns are not automatically independent biological samples. Source row identifiers, annotations and provenance are retained in metadata.

The assay preserves source numeric values. The metadata field `raw_abundance` means source numbers; it does not certify that the authors supplied unprocessed intensity.

Value

A `glyexp::GlycoproteomicSE`.

Availability and source license

Downloaded from the existing data release through the verified cache. Source-license scope for the complete object remains unresolved; no new license is granted. See `publication-decisions.tsv` and object metadata for original sources and limitations.

Source

<https://doi.org/10.1038/s41467-025-57364-x>.

See Also

[glyhub_catalog\(\)](#), [glyhub_data_conventions](#)

glyhub_PXD052447_N_Microbiome

DQGlyco microbiome experiment reporter intensities

Description

DQGlyco microbiome experiment reporter intensities

Usage

```
glyhub_PXD052447_N_Microbiome(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Details

160,699 source feature rows across 18 reported measurement columns.

Assay scale: Deposited untransformed PSM-level TMT reporter intensities

Feature grain: PSM; all deposited rows retained, including rows without glycan annotation

Source selection: Deposited reporter intensities preferred over normalized supplementary glycopeptide matrices or ratios

No normalization, logarithm, imputation, filtering, aggregation or zero conversion

Source blanks are NA; numeric zero retained with no interpretation of its missingness semantics

All 18 deposited reporter channels retained; unmatched channel roles remain unknown

PSM counts are not counts of unique glycopeptides; no peptide-level aggregation performed

Protein sites are not inferred from peptide coordinates; original search annotations are retained

Source search/FDR and reporter extraction precede this deposit; any undocumented upstream correction remains unknown

Measurement columns are not automatically independent biological samples. Source row identifiers, annotations and provenance are retained in metadata.

The assay preserves source numeric values. The metadata field `raw_abundance` means source numbers; it does not certify that the authors supplied unprocessed intensity.

All deposited PSM rows are retained, including rows without a glycan annotation. All source reporter channels are retained; unmapped channels have unknown sample roles. Consult `sample_annotation_matched` before comparing biological groups.

Value

A `glyexp::GlycoproteomicSE`.

Availability and source license

Downloaded from the existing data release through the verified cache. Deposited PRIDE source data are CC0-1.0, explicitly declared in the project API. Cite the original authors and accession; see metadata redistribution and source provenance.

Source

<https://doi.org/10.1038/s41594-025-01485-w>.

See Also

`glyhub_catalog()`, `glyhub_data_conventions`

glyhub_PXD052447_N_PNGase

DQGlyco PNGase accessibility reporter intensities

Description

DQGlyco PNGase accessibility reporter intensities

Usage

```
glyhub_PXD052447_N_PNGase(  
  kind = c("curated", "raw"),  
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),  
  refresh = FALSE,  
  offline = FALSE  
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Details

118,216 source feature rows across 18 reported measurement columns.

Assay scale: Deposited untransformed PSM-level TMT reporter intensities

Feature grain: PSM; all deposited rows retained, including rows without glycan annotation

Source selection: Deposited reporter intensities preferred over normalized supplementary glycopeptide matrices or ratios

No normalization, logarithm, imputation, confidence filtering, aggregation or zero conversion; acquisition partitions use explicit source Spectrum prefixes

Source blanks are NA; numeric zero retained with no interpretation of its missingness semantics

All 18 deposited reporter channels retained; unmatched channel roles remain unknown

PSM counts are not counts of unique glycopeptides; no peptide-level aggregation performed

Protein sites are not inferred from peptide coordinates; original search annotations are retained

Source search/FDR and reporter extraction precede this deposit; any undocumented upstream correction remains unknown

Measurement columns are not automatically independent biological samples. Source row identifiers, annotations and provenance are retained in metadata.

The assay preserves source numeric values. The metadata field `raw_abundance` means source numbers; it does not certify that the authors supplied unprocessed intensity.

All deposited PSM rows are retained, including rows without a glycan annotation. All source reporter channels are retained; unmapped channels have unknown sample roles. Consult `sample_annotation_matched` before comparing biological groups.

Value

A `glyexp::GlycoproteomicSE`.

Availability and source license

Downloaded from the existing data release through the verified cache. Deposited PRIDE source data are CC0-1.0, explicitly declared in the project API. Cite the original authors and accession; see metadata redistribution and source provenance.

Source

<https://doi.org/10.1038/s41594-025-01485-w>.

See Also

[glyhub_catalog\(\)](#), [glyhub_data_conventions](#)

glyhub_PXD052447_N_ProteinaseK

DQGlyco proteinase K accessibility reporter intensities

Description

DQGlyco proteinase K accessibility reporter intensities

Usage

```
glyhub_PXD052447_N_ProteinaseK(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Details

125,755 source feature rows across 18 reported measurement columns.

Assay scale: Deposited untransformed PSM-level TMT reporter intensities

Feature grain: PSM; all deposited rows retained, including rows without glycan annotation

Source selection: Deposited reporter intensities preferred over normalized supplementary glycopeptide matrices or ratios

No normalization, logarithm, imputation, confidence filtering, aggregation or zero conversion; acquisition partitions use explicit source Spectrum prefixes

Source blanks are NA; numeric zero retained with no interpretation of its missingness semantics

All 18 deposited reporter channels retained; unmatched channel roles remain unknown

PSM counts are not counts of unique glycopeptides; no peptide-level aggregation performed

Protein sites are not inferred from peptide coordinates; original search annotations are retained

Source search/FDR and reporter extraction precede this deposit; any undocumented upstream correction remains unknown

Measurement columns are not automatically independent biological samples. Source row identifiers, annotations and provenance are retained in metadata.

The assay preserves source numeric values. The metadata field `raw_abundance` means source numbers; it does not certify that the authors supplied unprocessed intensity.

All deposited PSM rows are retained, including rows without a glycan annotation. All source reporter channels are retained; unmapped channels have unknown sample roles. Consult `sample_annotation_matched` before comparing biological groups.

Value

A `glyexp::GlycoproteomicSE`.

Availability and source license

Downloaded from the existing data release through the verified cache. Deposited PRIDE source data are CC0-1.0, explicitly declared in the project API. Cite the original authors and accession; see metadata redistribution and source provenance.

Source

<https://doi.org/10.1038/s41594-025-01485-w>.

See Also

`glyhub_catalog()`, `glyhub_data_conventions`

glyhub_PXD052447_N_Solubility

DQGlyco mouse brain solubility reporter intensities

Description

DQGlyco mouse brain solubility reporter intensities

Usage

```
glyhub_PXD052447_N_Solubility(  
  kind = c("curated", "raw"),  
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),  
  refresh = FALSE,  
  offline = FALSE  
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Details

89,115 source feature rows across 18 reported measurement columns.

Assay scale: Deposited untransformed PSM-level TMT reporter intensities

Feature grain: PSM; all deposited rows retained, including rows without glycan annotation

Source selection: Deposited reporter intensities preferred over normalized supplementary glycopeptide matrices or ratios

No normalization, logarithm, imputation, filtering, aggregation or zero conversion

Source blanks are NA; numeric zero retained with no interpretation of its missingness semantics

All 18 deposited reporter channels retained; unmatched channel roles remain unknown

PSM counts are not counts of unique glycopeptides; no peptide-level aggregation performed

Protein sites are not inferred from peptide coordinates; original search annotations are retained

Source search/FDR and reporter extraction precede this deposit; any undocumented upstream correction remains unknown

Measurement columns are not automatically independent biological samples. Source row identifiers, annotations and provenance are retained in metadata.

The assay preserves source numeric values. The metadata field `raw_abundance` means source numbers; it does not certify that the authors supplied unprocessed intensity.

All deposited PSM rows are retained, including rows without a glycan annotation. All source reporter channels are retained; unmapped channels have unknown sample roles. Consult `sample_annotation_matched` before comparing biological groups.

Value

A `glyexp::GlycoproteomicSE`.

Availability and source license

Downloaded from the existing data release through the verified cache. Deposited PRIDE source data are CC0-1.0, explicitly declared in the project API. Cite the original authors and accession; see metadata redistribution and source provenance.

Source

<https://doi.org/10.1038/s41594-025-01485-w>.

See Also

[glyhub_catalog\(\)](#), [glyhub_data_conventions](#)

glyhub_PXD052447_N_Tissues

DQGlyco mouse tissue reporter intensities

Description

DQGlyco mouse tissue reporter intensities

Usage

```
glyhub_PXD052447_N_Tissues(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Details

205,904 source feature rows across 18 reported measurement columns.

Assay scale: Deposited untransformed PSM-level TMT reporter intensities

Feature grain: PSM; all deposited rows retained, including rows without glycan annotation

Source selection: Deposited reporter intensities preferred over normalized supplementary glycopeptide matrices or ratios

No normalization, logarithm, imputation, filtering, aggregation or zero conversion

Source blanks are NA; numeric zero retained with no interpretation of its missingness semantics

All 18 deposited reporter channels retained; unmatched channel roles remain unknown

PSM counts are not counts of unique glycopeptides; no peptide-level aggregation performed

Protein sites are not inferred from peptide coordinates; original search annotations are retained

Source search/FDR and reporter extraction precede this deposit; any undocumented upstream correction remains unknown

Measurement columns are not automatically independent biological samples. Source row identifiers, annotations and provenance are retained in metadata.

The assay preserves source numeric values. The metadata field `raw_abundance` means source numbers; it does not certify that the authors supplied unprocessed intensity.

All deposited PSM rows are retained, including rows without a glycan annotation. All source reporter channels are retained; unmapped channels have unknown sample roles. Consult `sample_annotation_matched` before comparing biological groups.

Value

A `glyexp::GlycoproteomicSE`.

Availability and source license

Downloaded from the existing data release through the verified cache. Deposited PRIDE source data are CC0-1.0, explicitly declared in the project API. Cite the original authors and accession; see metadata redistribution and source provenance.

Source

<https://doi.org/10.1038/s41594-025-01485-w>.

See Also

`glyhub_catalog()`, `glyhub_data_conventions`

glyhub_PXD052447_N_TwoFF

DQGlyco 2-fluorofucose time course reporter intensities

Description

DQGlyco 2-fluorofucose time course reporter intensities

Usage

```
glyhub_PXD052447_N_TwoFF(  
  kind = c("curated", "raw"),  
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),  
  refresh = FALSE,  
  offline = FALSE  
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Details

91,409 source feature rows across 18 reported measurement columns.

Assay scale: Deposited untransformed PSM-level TMT reporter intensities

Feature grain: PSM; all deposited rows retained, including rows without glycan annotation

Source selection: Deposited reporter intensities preferred over normalized supplementary glycopeptide matrices or ratios

No normalization, logarithm, imputation, filtering, aggregation or zero conversion

Source blanks are NA; numeric zero retained with no interpretation of its missingness semantics

All 18 deposited reporter channels retained; unmatched channel roles remain unknown

PSM counts are not counts of unique glycopeptides; no peptide-level aggregation performed

Protein sites are not inferred from peptide coordinates; original search annotations are retained

Source search/FDR and reporter extraction precede this deposit; any undocumented upstream correction remains unknown

Measurement columns are not automatically independent biological samples. Source row identifiers, annotations and provenance are retained in metadata.

The assay preserves source numeric values. The metadata field `raw_abundance` means source numbers; it does not certify that the authors supplied unprocessed intensity.

All deposited PSM rows are retained, including rows without a glycan annotation. All source reporter channels are retained; unmapped channels have unknown sample roles. Consult `sample_annotation_matched` before comparing biological groups.

Value

A `glyexp::GlycoproteomicSE`.

Availability and source license

Downloaded from the existing data release through the verified cache. Deposited PRIDE source data are CC0-1.0, explicitly declared in the project API. Cite the original authors and accession; see metadata redistribution and source provenance.

Source

<https://doi.org/10.1038/s41594-025-01485-w>.

See Also

[glyhub_catalog\(\)](#), [glyhub_data_conventions](#)

glyhub_PXD065283_N_DiscoverySelected

HCC discovery cohort selected processed features

Description

HCC discovery cohort selected processed features

Usage

```
glyhub_PXD065283_N_DiscoverySelected(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Details

1,038 source feature rows across 140 reported measurement columns.

Assay scale: Source median-normalized, log2-transformed, normally imputed abundance; DE-selected features

Source selection: Only verified public individual clinical matrix; earliest unnormalized clinical table unavailable through inspected sources. QC linear table is a different experiment, not a substitute for clinical samples.

All source cells preserved; no new normalization, imputation, filtering, inverse transform or aggregation

Source workflow: MBR, source missingness filtering, median normalization, log2, normal-distribution interpolation, then differential-feature selection ($p \leq 0.01$ and absolute $\log_2 FC \geq 1$)

1038 selected features and 140 discovery samples; not the full 8902-feature matrix or 60-person validation cohort. Feature selection uses case labels; unsuitable for unbiased discovery or classifier performance estimates.

No exponentiation to claim recovered original intensity; unspecified upstream settings remain unknown

Measurement columns are not automatically independent biological samples. Source row identifiers, annotations and provenance are retained in metadata.

The assay preserves source numeric values. The metadata field `raw_abundance` means source numbers; it does not certify that the authors supplied unprocessed intensity.

Value

A `glyexp::GlycoproteomicSE`.

Availability and source license

Downloaded from the existing data release through the verified cache. Source-license scope for the complete object remains unresolved; no new license is granted. See `publication-decisions.tsv` and object metadata for original sources and limitations.

Source

<https://doi.org/10.1002/adv.s.202516299>.

See Also

`glyhub_catalog()`, `glyhub_data_conventions`

glyhub_PXD065283_N_QC	<i>HCC study quality-control injections</i>
-----------------------	---

Description

HCC study quality-control injections

Usage

```
glyhub_PXD065283_N_QC(  
  kind = c("curated", "raw"),  
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),  
  refresh = FALSE,  
  offline = FALSE  
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to <code>tools::R_user_dir("glyhub", "cache")</code> . Set option <code>glyhub.cache_dir</code> to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Details

8,030 source feature rows across 30 reported measurement columns.

Assay scale: Source linear MBR-derived glycosite/glycan quantities; upstream normalization not independently established

Source selection: Linear QC matrix chosen; clinical DE-selected log2 table is a separate cohort dataset.

All source cells preserved; no new normalization, imputation, filtering, inverse transform or aggregation

Source reports match-between-run quantification; source blank values retained as NA

30 QC injections (13 days, 3 repeated injections, 14 batch QC runs), not 30 independent people

No exponentiation to claim recovered original intensity; unspecified upstream settings remain unknown

Measurement columns are not automatically independent biological samples. Source row identifiers, annotations and provenance are retained in metadata.

The assay preserves source numeric values. The metadata field raw_abundance means source numbers; it does not certify that the authors supplied unprocessed intensity.

Value

A [glyexp::GlycoproteomicSE](#).

Availability and source license

Downloaded from the existing data release through the verified cache. Source-license scope for the complete object remains unresolved; no new license is granted. See publication-decisions.tsv and object metadata for original sources and limitations.

Source

<https://doi.org/10.1002/advs.202516299>.

See Also

[glyhub_catalog\(\)](#), [glyhub_data_conventions](#)

glyhub_PXD070547_N_HumanAtlas

Human organ atlas raw XIC matrix

Description

Human organ atlas raw XIC matrix

Usage

```
glyhub_PXD070547_N_HumanAtlas(
  kind = c("curated", "raw"),
  cache_dir = getOption("glyhub.cache_dir", tools::R_user_dir("glyhub", "cache")),
  refresh = FALSE,
  offline = FALSE
)
```

Arguments

kind	"curated" returns a data object; "raw" returns the path to a verified source archive. Raw archives are currently available for CPTAC.
cache_dir	Cache directory, defaulting to tools::R_user_dir("glyhub", "cache"). Set option glyhub.cache_dir to change the default.
refresh	Download the pinned resource again, even if cached.
offline	Prohibit downloads; require a verified local resource.

Details

57,884 source feature rows across 219 reported measurement columns.

Assay scale: Source Skyline extracted-ion chromatogram quantification; raw relative signal

Explicit source NA strings and blanks -> NA; no imputation, normalization, filtering, zero conversion or aggregation

Annotation joined only by exact ID: unmatched source rows retained with unknown molecular annotation

Source linkage notation retained, no unverified structure parser or inferred linkage

S monosaccharide is unspecified sialic acid; sialylated typed compositions remain NA

Source age/sex cells are cohort summaries, not person-level values; not propagated to samples

Use original measured columns, not the normalized or KNN/ComBat matrices

Measurement columns are not automatically independent biological samples. Source row identifiers, annotations and provenance are retained in metadata.

The assay preserves source numeric values. The metadata field raw_abundance means source numbers; it does not certify that the authors supplied unprocessed intensity.

Value

A [glyexp::GlycoproteomicSE](#).

Availability and source license

Downloaded from the existing data release through the verified cache. Source-license scope for the complete object remains unresolved; no new license is granted. See publication-decisions.tsv and object metadata for original sources and limitations.

Source

<https://doi.org/10.1038/s41467-026-74631-7>.

See Also

[glyhub_catalog\(\)](#), [glyhub_data_conventions](#)

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