# RadBioNET User Guide

**Version 1.0**

**File summary:** This document provides a guide for RadBioNET, including system access, database browsing, multidimensional filtering, factor-level evidence review, interactive analysis, knowledge-graph exploration, optional AI-assisted querying, data export, field definitions, worked examples, and troubleshooting guidance.

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# 1 Scope and intended use

RadBioNET is a web-based radiobiology knowledge base that structures evidence from the scientific literature into searchable records. It supports multidimensional filtering, factor-level evidence review, descriptive analysis, knowledge-graph exploration, data export, and optional domain-focused AI assistance.

Each database row represents a literature-derived relationship between a biological or therapeutic factor and a radiation-response context. Records retain contextual information such as cancer type, radiation particle or modality, direction of effect, evidence type, supporting text, publication metadata, and DOI.

## 1.1 Intended users

- Radiation oncology and radiobiology researchers.
- Clinical investigators conducting literature-based or translational studies.
- Bioinformatics researchers analysing radiation-response evidence.
- Students and trainees who require structured access to radiobiology concepts and publications.

## 1.2 Appropriate use

- Evidence discovery and hypothesis generation.
- Identification of candidate radiosensitising or radioresistance-associated factors.
- Comparison of radiation modalities, particle types, cancer contexts, and evidence classes.
- Preparation of reproducible literature-derived datasets for downstream analysis.

RadBioNET is a research resource. It does not provide diagnosis, treatment recommendations, dose prescriptions, or clinical decision support. All important interpretations should be verified against the original publications.

## 1.3 Version scope

This guide describes the public interface and functions available in RadBioNET Version 1.0. Database counts and individual records may change as curation and maintenance continue. Users should therefore record the access date and applied filters whenever results are exported or reported.

# 2 System access and interface structure

## 2.1 Access

Public URL: https://radbionet.com

Core browsing, filtering, visualisation, and export functions are available through a standard web browser and do not require a user account.

## 2.2 Client requirements

- A current version of Chrome, Microsoft Edge, Safari, or another modern standards-compliant browser.
- A display resolution of at least 1366 × 768 pixels; browser zoom at 100% is recommended.
- JavaScript enabled for interactive tables, visualisations, and network functions.
- A stable network connection, particularly when loading large tables or external DOI links.

## 2.3 Page layout

The interface uses a persistent top navigation bar and a page-specific content workspace. The Data page additionally contains a left-side filter panel. Analysis pages organise results into cards, plots, and interactive network elements.

| Module | Primary function |
|---|---|
| Home | Overview of database scope, record coverage, and research trends. |
| Data | Browse, filter, search, sort, inspect, and export structured evidence records. |
| Factor Detail | Aggregate evidence associated with a selected factor. |
| Analysis | Explore timelines, modalities, equipment, dose information, toxicity endpoints, and networks. |
| Chat-Radbio | Optional AI-assisted explanation and query formulation. |
| Resource Hub | Open curated links to external scientific resources. |
| About us | Review project information, version history, and contact details. |

## 2.4 Recommended research workflow

1. Define a focused research question, including the cancer context, radiation setting, factor class, and direction of effect.
2. Use the Data page to apply structured filters and table-level keyword search.
3. Open factor pages and inspect the supporting sentence, evidence type, quality flag, and DOI.
4. Use Analysis and Knowledge Graph views to identify broader patterns or candidate associations.
5. Return to the underlying Data records and original publications before drawing conclusions.

6. Export the final filtered result set and document the version, access date, and filters.

# 3 Home page and navigation

The Home page summarises the scope of RadBioNET and provides rapid access to the main modules. Overview cards and plots may show record counts, factor categories, cancer distributions, radiation types, and publication trends. These displays provide context rather than inferential statistics.

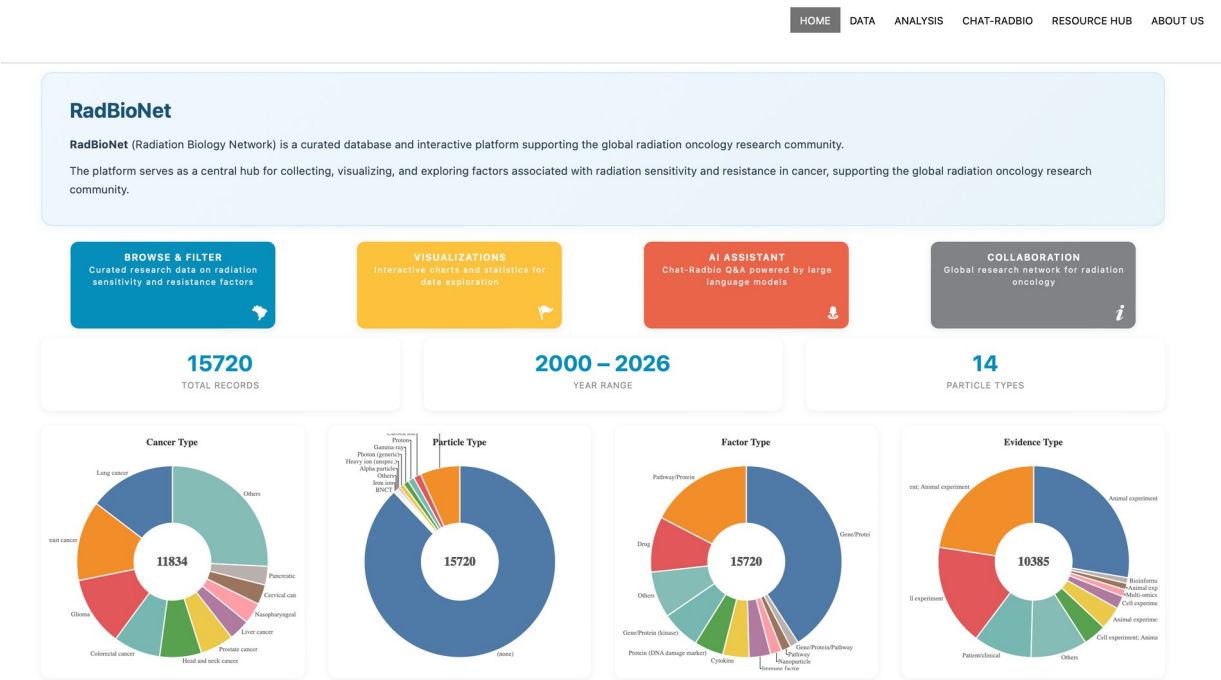



**Figure S1. RadBioNET Home page. The landing page provides a database overview, summary cards, descriptive visualisations, and persistent navigation to the Data, Analysis, Chat-Radbio, Resource Hub, and About us modules.**

## 3.1 Using the navigation bar

1. Select Home to return to the database overview.
2. Select Data to open the primary evidence browser.
3. Select Analysis to access descriptive plots and the Knowledge Graph.
4. Select Chat-Radbio to open the optional domain-focused assistant.
5. Select Resource Hub to browse external scientific resources.
6. Select About us to view the project description and version history.

Summary counts reflect the current database composition and literature coverage. They should not be interpreted as measures of biological effect size, clinical importance, or comparative treatment efficacy.

# 4 Data browsing, filtering, and export

## 4.1 Data page

The Data page is the principal entry point for evidence retrieval. A multidimensional filter panel is displayed on the left. Dynamic summary cards and a searchable, sortable results table are displayed in the main workspace.

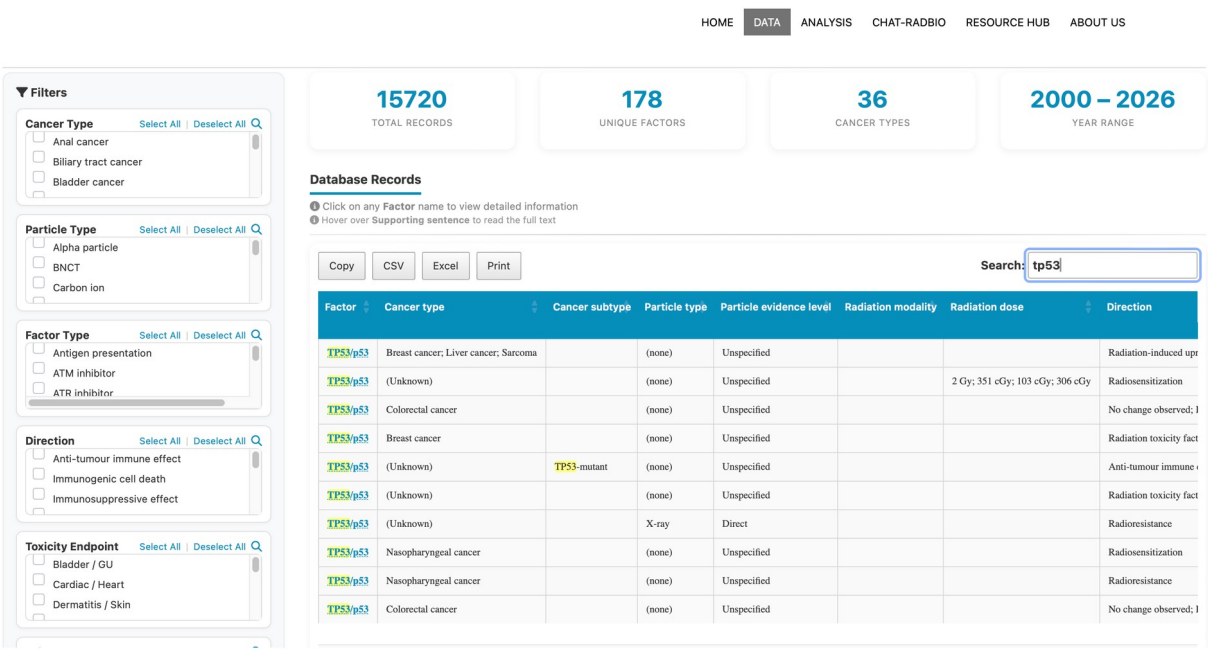



**Figure S2. Data browser. The Data page combines a left-side filter panel with dynamic result summaries and a structured evidence table. Available controls may be combined to narrow records by disease, radiation context, factor class, response direction, toxicity endpoint, evidence type, and quality flag.**

## 4.2 Filter groups

| Filter | Purpose |
|---|---|
| Cancer Type | Restricts records to selected cancer categories, such as lung, breast, prostate, or brain tumours. |
| Particle Type | Restricts records by reported radiation source, including X-rays, gamma rays, protons, carbon ions, neutrons, or electrons. |
| Factor Type | Selects genes/proteins, drugs, pathways, inhibitors, immune factors, nanoparticles, or other entity classes. |
| Direction | Selects radiosensitisation, radioresistance, immune effects, radiation toxicity, toxicity-sparing effects, or radiation-induced expression changes. |
| Toxicity Endpoint | Restricts toxicity-related records to organ or phenotype categories. |
| Evidence Type | Selects cellular, animal, organoid, clinical, bioinformatic, multi-omics, or computational evidence. |
| Quality Flag | Selects records labelled Strong or Weak according to the directness of textual support. |

## 4.3 Applying combined filters

1. Open the required filter group in the left panel.
2. Select one or more values. Use Select All or Deselect All when available.
3. Add filters from other groups to construct the desired combination.
4. Confirm that both the result count and the table update after each selection.
5. Select Reset All to clear filters and restore the default result set.

Selections within a filter group broaden that group, whereas filters from different groups narrow the overall result set. If no records remain, remove constraints one at a time to identify the restrictive condition.

### 4.4 Keyword search and sorting

1. Enter a factor, drug, cancer, journal, title term, or other keyword in the Search field above the table.
2. Remember that keyword search operates on the records remaining after structured filters have been applied.
3. Select a column heading to sort the visible records in ascending or descending order.
4. Use pagination controls to browse additional rows and the horizontal scrollbar to inspect later columns.

### 4.5 Inspecting evidence

- Select a linked factor name to open the factor-level evidence page.
- Inspect the Supporting sentence to understand the textual basis for the curated relation.
- Review the Evidence type and Quality flag before interpreting a record.
- Open the DOI link to verify experimental design, population, radiation conditions, and conclusions in the original publication.

### 4.6 Export controls

| Control | Recommended use | Caution |
|---|---|---|
| CSV | Scripted analysis and cross-platform exchange. | Check encoding, delimiters, and multi-valued fields. |
| Excel | Manual review, annotation, and sharing. | Prevent automatic conversion of gene symbols or date-like values. |
| Copy | Temporary transfer of a small number of rows. | Not suitable for long-term preservation of full metadata. |
| Print | A printable representation of the current table view. | Output may depend on browser page settings and column widths. |

## 5 Factor-level evidence pages

Selecting a factor name from the Data table opens a consolidated factor page. This view groups the factor's records across cancer types, radiation conditions, effect directions, and publications, supporting rapid review without removing the original record-level context.

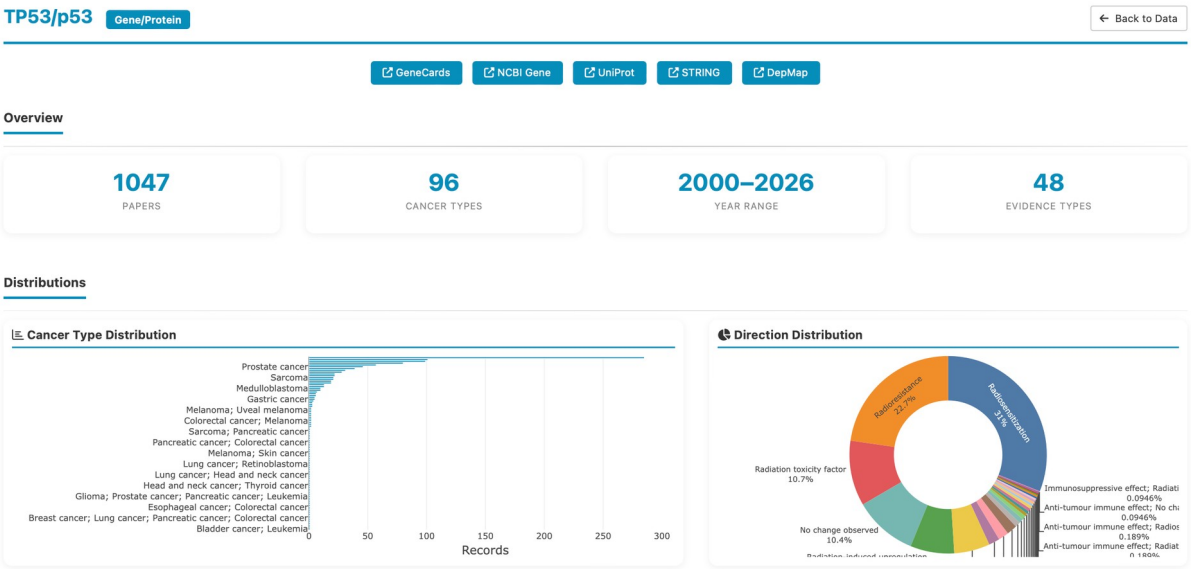



**Figure S3. Factor detail page. Example factor-level view for TP53/p53. The page consolidates factor identity, response direction, cancer and radiation contexts, mechanistic summaries, evidence attributes, supporting text, publication metadata, DOI links, and relevant external resources.**

## 5.1 Information shown

- Factor name and entity class.
- Reported directions of radiation response.
- Associated cancer types and subtypes.
- Particle type, radiation modality, equipment, and dose where available.
- Mechanistic descriptions and evidence classes.
- Quality flags and supporting text.
- Publication title, journal, year, DOI, and selected external database links.

## 5.2 Recommended review sequence

1. Confirm that the selected factor corresponds to the intended gene, protein, drug, pathway, or other entity.
2. Review whether the direction is consistent across cancer and radiation contexts.
3. Compare evidence types and experimental models before combining records.
4. Read the supporting text and use the DOI to inspect the source article.
5. Treat contradictory directions as context-dependent evidence rather than automatically removing one result.

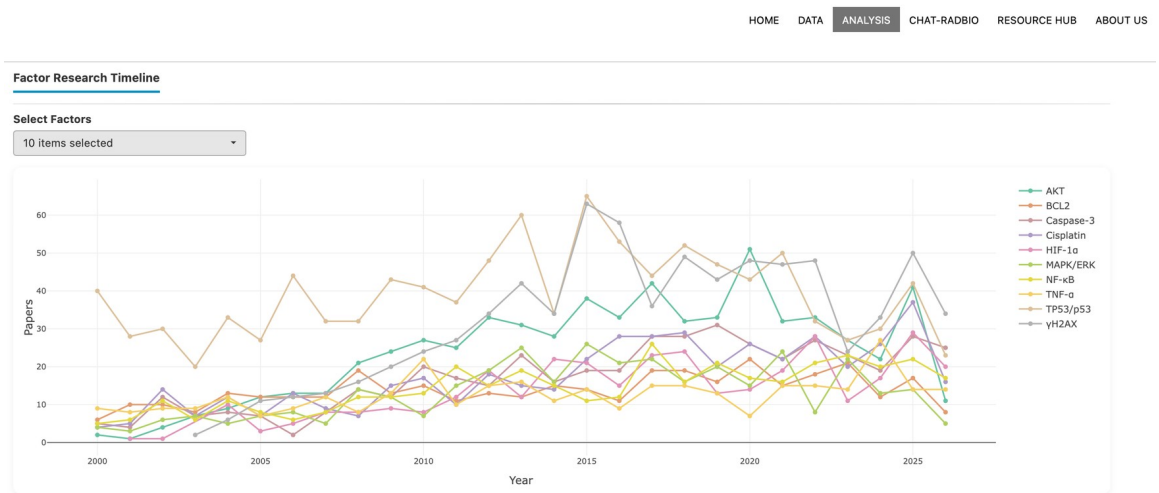
**Caution:** A Strong flag indicates comparatively direct textual support for the curated relation. It is not a formal grade of experimental design, risk of bias, clinical validity, or guideline-level evidence.

# 6 Interactive analysis and Knowledge Graph

## 6.1 Analysis page

The Analysis page converts the current database content into interactive descriptive displays. Depending on the selected view, users can examine publication timelines, radiation modalities and equipment, reported dose information, toxicity endpoints, and entity relationships.

(a)



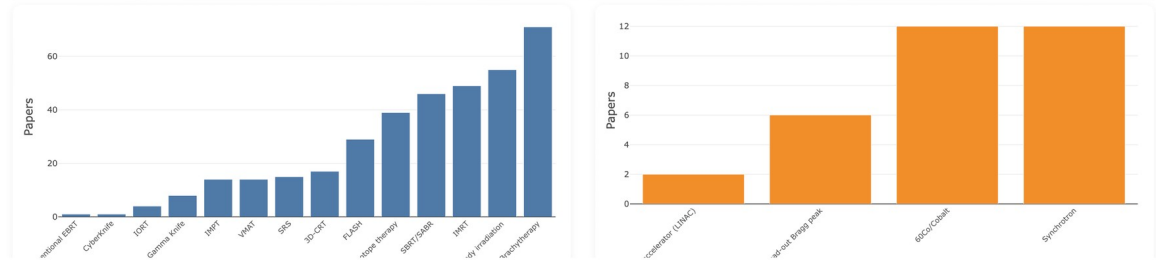

(b)

| Factor | Papers | Strong Ev. | Trend | Slope | P-value | Peak Year | Peak Count |
|---|---|---|---|---|---|---|---|
| TP53/p53 | 1057 | 513 | declining | -1.11 | 0.0475 | 2015 | 65 |
| γH2AX | 774 | 187 | stable | 0.34 | 0.5591 | 2015 | 63 |
| AKT | 645 | 304 | stable | -0.18 | 0.6948 | 2020 | 51 |
| Cisplatin | 469 | 196 | rising | 0.73 | 0.0263 | 2025 | 37 |
| Caspase-3 | 465 | 104 | rising | 0.52 | 0.0251 | 2019 | 31 |
| NF-κB | 389 | 199 | rising | 0.34 | 0.0916 | 2017 | 26 |
| BCL2 | 373 | 121 | stable | 0.14 | 0.4633 | 2020 | 22 |
| MAPK/ERK | 359 | 153 | stable | -0.31 | 0.3373 | 2015 | 26 |
| HIF-1α | 352 | 180 | rising | 0.5 | 0.0954 | 2025 | 29 |
| PD-L1/CD274 | 342 | 191 | rising fast | 5.9 | 0.0001 | 2025 | 75 |

Show 10 entries

Showing 1 to 10 of 178 entries

Previous 1 2 3 4 5 ... 18 Next




(c)

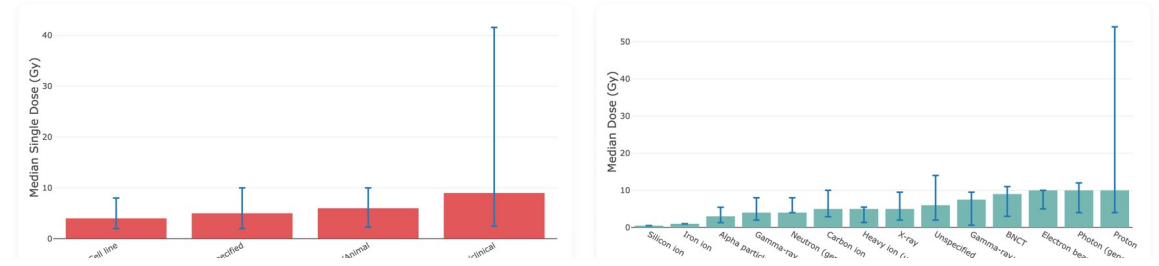


**Figure S4. Interactive Analysis page. Representative analysis views for TP53. Panels show complementary descriptive summaries and interactive plots. These displays describe the composition of curated records and should not be interpreted as causal estimates or comparative clinical effectiveness.**

## 6.2 Available analysis components

| Component | Purpose |
|---|---|
| Research Timeline | Displays how records for a selected factor, direction, or category vary by publication year. |
| Modality & Equipment | Summarises reported radiotherapy modalities, irradiation sources, and equipment categories. |
| Dose Distribution | Explores reported total dose, per-fraction dose, or dose schemes when extractable. |
| Toxicity Endpoint | Displays organ- or phenotype-based categories among toxicity-related records. |
| Knowledge Graph | Represents factors, cancers, directions, and other entities as connected nodes and edges. |

## 6.3 Interpretation safeguards

- Counts are influenced by curation scope, publication volume, and data availability.
- Differences between particle types or cancer categories may reflect research activity rather than biological superiority.
- Dose values originate from heterogeneous experimental and clinical contexts; fractionation and model differences must be considered.
- Visualisations are intended for exploration and hypothesis generation, not causal inference.

## 6.4 Knowledge Graph

The Knowledge Graph represents curated relations as a network of nodes and edges. It can be used to identify densely connected entities, cross-cancer associations, candidate mechanisms, and topics for targeted evidence review.

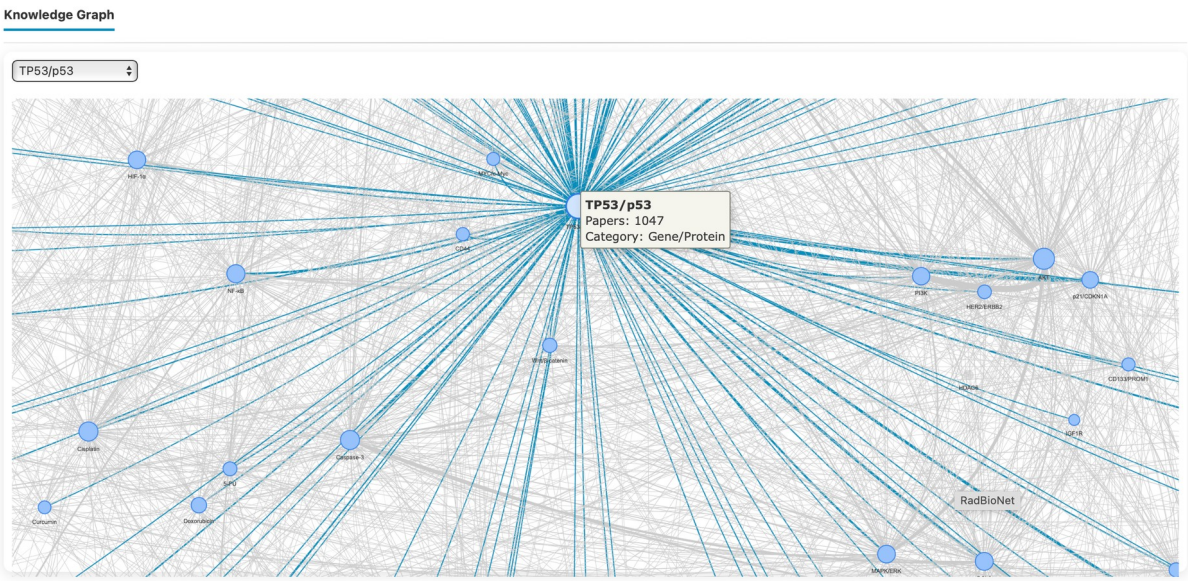



**Figure S5. Knowledge Graph. Interactive network view centred on TP53/p53. Nodes represent curated entities and edges represent structured relations. Network patterns are exploratory and should be traced back to individual Data records and source publications.**

## 6.5 Network interaction

1. Open Analysis and locate the Knowledge Graph section.
2. Select the target factor, cancer type, or relation category.
3. Drag nodes to adjust the layout and use the scroll wheel or trackpad gesture to zoom.
4. Select or hover over a node to inspect its name and available relationship information.
5. Record associations of interest, then return to Data to locate the supporting records and DOI links.

# 7 Chat-Radbio, Resource Hub, and About

## 7.1 Chat-Radbio

Chat-Radbio is an optional assistant for radiobiology-oriented explanation, concept clarification, and query formulation. It can connect to a local Ollama model or an OpenAI-compatible application programming interface (API). Its output is generated text and is not a curated database record.

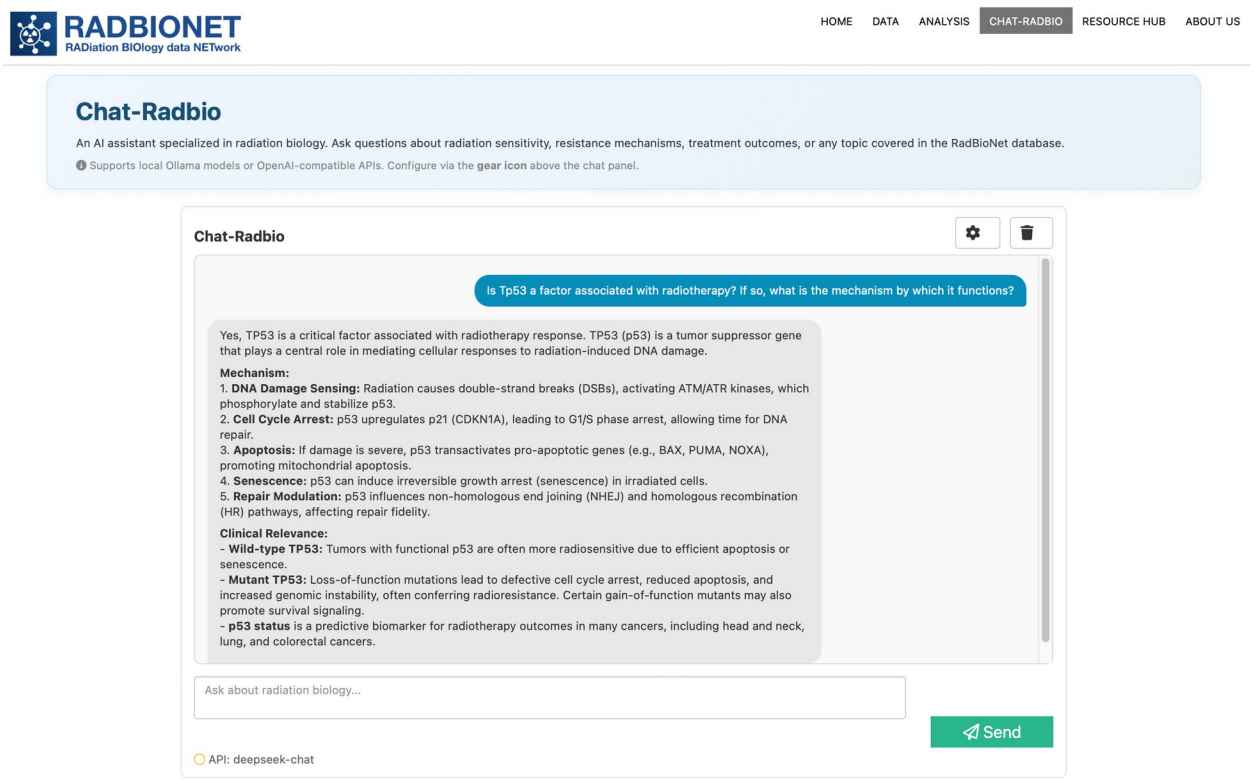



**Figure S6. Chat-Radbio. The optional assistant provides a conversational interface and settings for supported local or cloud-compatible model backends. Generated responses should be used to formulate searches and must not replace record-level verification or reading of original publications.**

## 7.2 Configuring a model backend

1. Open Chat-Radbio and display the settings panel.
2. Choose a local Ollama backend or a compatible cloud API.
3. Provide the API address and model name; provide an API key only when required by the selected cloud service.
4. Save the settings and return to the conversation panel.
5. Enter a radiobiology question, then use extracted factor, cancer, or mechanism terms to perform a structured Data search.

**Security and verification:** Never include patient identifiers, confidential research data, unpublished sensitive information, or visible API keys. Cloud data handling is governed by the selected service provider. Generated answers may be incomplete or incorrect and must be independently verified.

## 7.3 Resource Hub

The Resource Hub organises links to external databases and scientific tools, including resources for genes and proteins, drugs, molecular interactions, cancer omics, clinical trials, and particle therapy. Selecting a resource opens the third-party website in the browser.

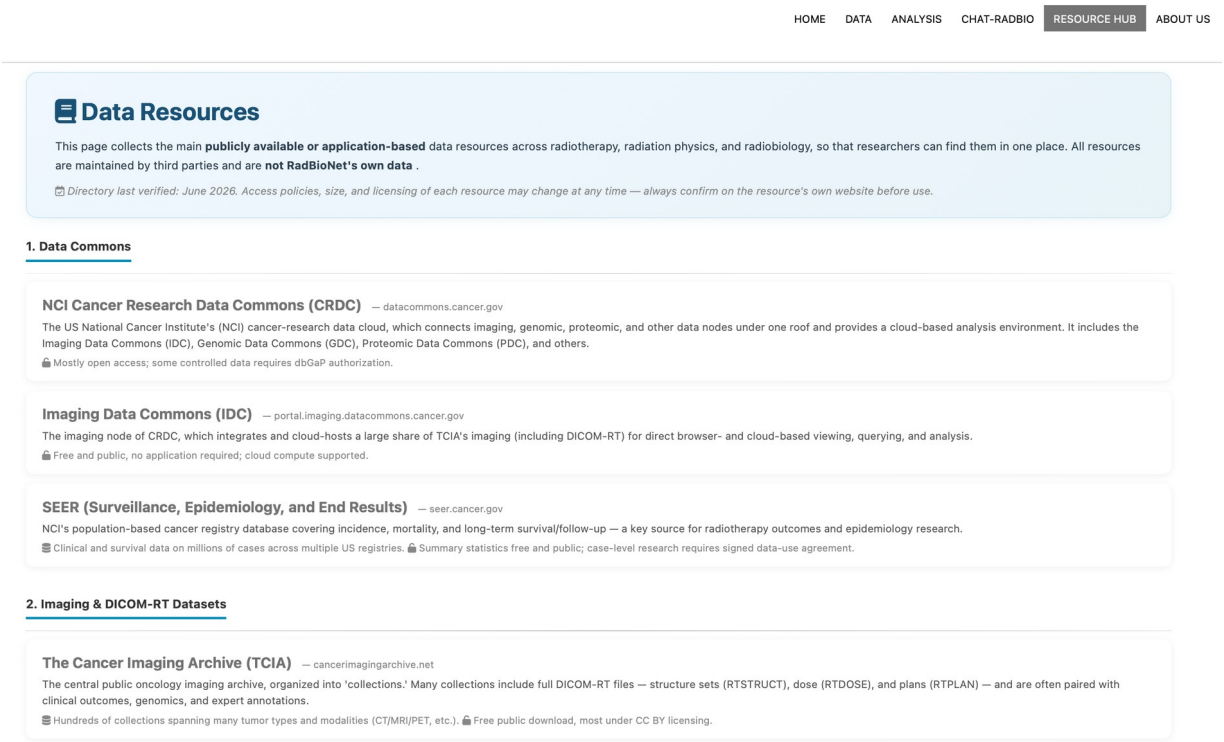



**Figure S7. Resource Hub. External resources are grouped by research purpose. RadBioNET provides navigation links only; availability, content, licences, and access policies are controlled by the respective third-party providers.**

## 7.4 About page

The About us page describes the purpose of RadBioNET, provides version information, and records platform updates. Version 1.0 is identified with a release date of 18 June 2026.

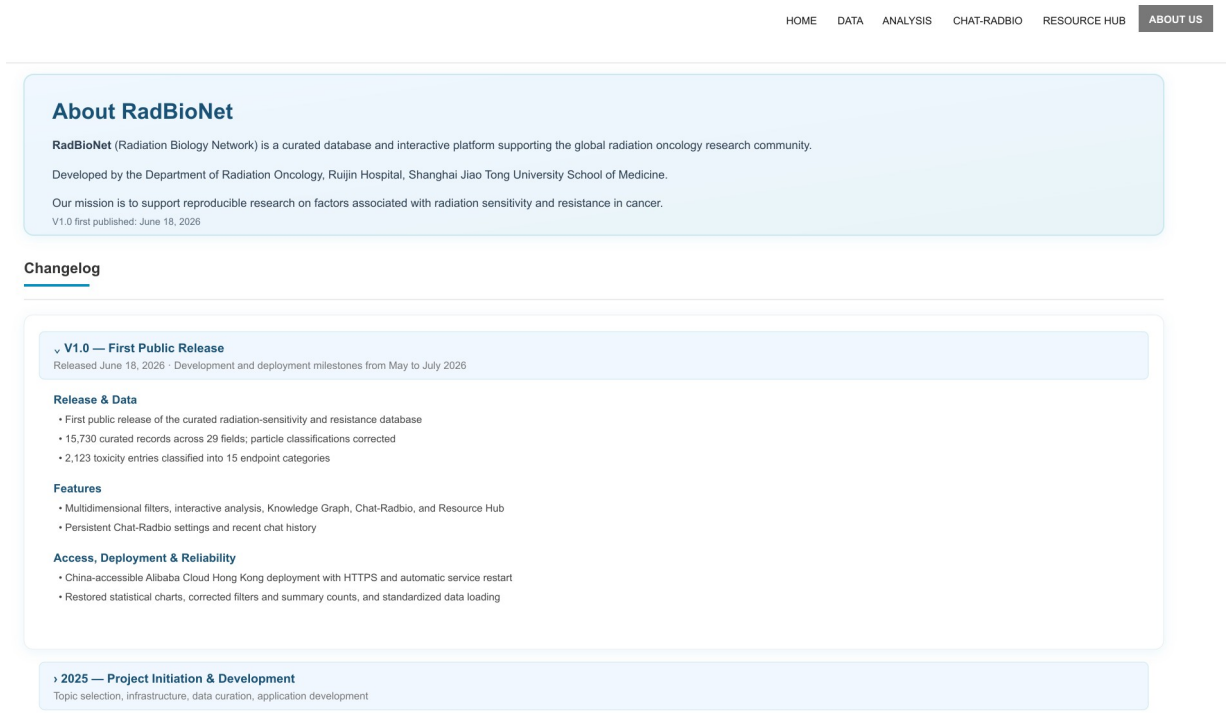



**Figure S8. About page and version information. The About us page provides the project description, version history, contact information, and technical update notes associated with RadBioNET Version 1.0.**

# 8 Data dictionary

Each row in the Data table represents a curated factor–radiation-response relation in a defined literature context. Field values should be interpreted jointly; a single column rarely captures the complete experimental or clinical setting.

## 8.1 Biological and disease fields

| Field | Definition and interpretation |
|---|---|
| Factor | The gene, protein, drug, pathway, immune factor, nanoparticle, or other regulator described in the record. |
| Factor type | The entity class used to organise and filter factors. |
| Cancer type | The broad tumour category reported in the source; may be Unknown or Unspecified when not clearly stated. |
| Cancer subtype | A histological, molecular, or clinical subtype when explicitly reported. |
| Biological mechanism | A concise description of the reported mechanism, such as DNA repair, cell death, immune regulation, or metabolism. |
| Clinical outcome association | A reported association with response, survival, recurrence, toxicity, or another clinical outcome. |
| Toxicity endpoint | An organ- or phenotype-based category for radiation-associated toxicity. |

## 8.2 Radiation fields

| Field | Definition and interpretation |
|---|---|
| Particle type | The reported radiation source, such as X-ray, gamma ray, proton, carbon ion, neutron, or electron. |
| Particle evidence level | The evidence basis for assigning particle identity, such as direct wording, title-level evidence, article-level evidence, or contextual inference. |
| Radiation modality | The reported experimental or clinical technique, such as IMRT, SBRT, or brachytherapy. |
| Radiation dose | The total dose, per-fraction dose, or fractionation scheme as reported. Cross-study comparisons require caution. |

## 8.3 Direction and evidence fields

| Field | Definition and interpretation |
|---|---|
| Direction | The curated response category, including radiosensitisation, radioresistance, antitumour immunity, immunosuppression, toxicity, toxicity sparing, or expression change. |
| Evidence type | The study context, such as cell, animal, organoid, patient/clinical, bioinformatic, multi-omics, or computational evidence. |
| Quality flag | Strong indicates comparatively direct textual support; Weak indicates that the relation requires closer source verification. |
| Supporting sentence | The source-context summary supporting the factor–radiation relation. |

## 8.4 Publication fields

| Field | Definition and interpretation |
|---|---|
| Journal | The journal in which the source study or review was published. |
| Publication year | The publication year used for timeline analysis and date filtering. |
| Title | The publication title, which provides additional context for study scope. |
| DOI | The persistent digital identifier used to trace the record to the original publication. |

## 8.5 Missing and unspecified information

When the available source text does not clearly report a cancer type, dose, particle, model, or other attribute, RadBioNET retains a blank value or a label such as Unknown, Unspecified, or none. Missing values are not automatically invalid and should not be imputed from general knowledge without checking the original publication.

# 9 Worked examples

## 9.1 Identifying radiosensitisation factors in lung cancer

1. Open Data and wait for the table to finish loading.

2. Under Cancer Type, select Lung cancer.
3. Under Direction, select Radiosensitization.
4. Optionally select Strong under Quality Flag to focus on more directly supported text relations.
5. Confirm that the result count and table update.
6. Review candidate factors, open relevant factor pages, and inspect supporting text.
7. Follow DOI links to verify the source studies.

## 9.2 Reviewing proton or carbon-ion evidence

1. Under Particle Type, select Proton or Carbon ion.
2. Add Cancer Type, Factor Type, or Direction filters according to the research question.
3. Review Particle evidence level and prioritise records with direct support for particle identity.
4. Inspect Radiation dose and Radiation modality to assess contextual compatibility.
5. Export the result set while retaining particle evidence, supporting text, and DOI fields.

## 9.3 Reviewing radiation-toxicity factors

1. Under Direction, select Radiation toxicity factor or Toxicity-sparing benefit.
2. Select the target Toxicity Endpoint, such as Pneumonitis / Pulmonary.
3. Add cancer, evidence-type, or quality filters if needed.
4. Review Clinical outcome association and Supporting sentence to distinguish clinical toxicity from experimental injury phenotypes.

## 9.4 Keyword-first retrieval

1. Clear unnecessary structured filters to avoid unintended restriction.
2. Enter a factor, drug, pathway, journal, or title keyword in Search.
3. If no result appears, check spelling and try a shorter or more general term.
4. Sort a relevant column or open a factor page for detailed review.

## 9.5 Moving from a network association to source evidence

1. Select a factor or cancer in the Knowledge Graph.
2. Record a connected entity or relation of interest.
3. Return to Data and use the entity as a Factor, Cancer Type, or keyword condition.

4. Inspect the supporting text and DOI to verify the literature basis of the network edge.

### 9.6 Troubleshooting a zero-result query

- Select Reset All and confirm that the full table is restored.
- Reapply one filter at a time to identify the condition that removes all records.
- Broaden an overly specific particle category or include unspecified records where appropriate.
- Check spelling, hyphenation, abbreviations, Greek letters, and gene/protein naming variants.
- Use a broader factor type or cancer category before applying more specific filters.

## 10 Export, citation, limitations, and troubleshooting

### 10.1 Reproducible export

- Record the complete database name, version (V1.0), URL, and access date.
- Record all selected filter values and the table-level search term.
- Retain Factor, Direction, Cancer type, Particle type, Evidence type, Quality flag, Supporting sentence, and DOI where possible.
- Define the analytical unit before counting records: a literature relation, publication, factor, and unique entity are not interchangeable.
- Preserve contextual fields when the same factor exhibits different directions across cancer types, doses, models, or interventions.

### 10.2 Recommended citation information

When reporting use of RadBioNET, cite the associated article after publication and include the resource name, database version, URL, access date, and principal filter conditions in the Methods, Data Availability, or Usage Notes section as appropriate.

**Suggested wording:** RadBioNET Version 1.0 (https://radbionet.com; accessed [date]) was queried using [filters and search terms].

### 10.3 Limitations

- Coverage depends on the literature search, curation rules, publication accessibility, and update schedule.

- A record count is not an effect-size estimate and does not measure the strength of a biological mechanism.
- Evidence derived from abstracts or concise source text may omit methodological details available only in the full article.
- The same factor can have context-dependent or apparently conflicting effects.
- Quality flags describe textual support and do not replace formal risk-of-bias or clinical-evidence grading.
- Knowledge-graph edges and AI-generated responses require verification against structured records and original publications.

## 10.4 Common problems

| Problem | Recommended action |
|---|---|
| Slow page loading | Check the network, wait for tables and plots to initialise, and refresh if needed. |
| No records after filtering | Select Reset All and rebuild the query one condition at a time. |
| Some table fields are hidden | Use the horizontal scrollbar or export to Excel/CSV. |
| A plot does not finish loading | Use a current browser, refresh, and check whether scripts are blocked. |
| Chat-Radbio cannot connect | Check the backend, API address, model, local service, and credentials. |
| Generated answer conflicts with evidence | Prioritise the structured Data record and DOI-linked publication. |
| External link is unavailable | Search the DOI or resource name independently. |

## 10.5 Final interpretation checklist

- Have the relevant supporting sentences and DOI-linked publications been checked?
- Are cancer type, experimental model, radiation modality, particle, and dose compatible with the research question?
- Have Strong and Weak flags been interpreted as textual-support labels rather than clinical grades?
- Have apparently conflicting records been retained with their context?