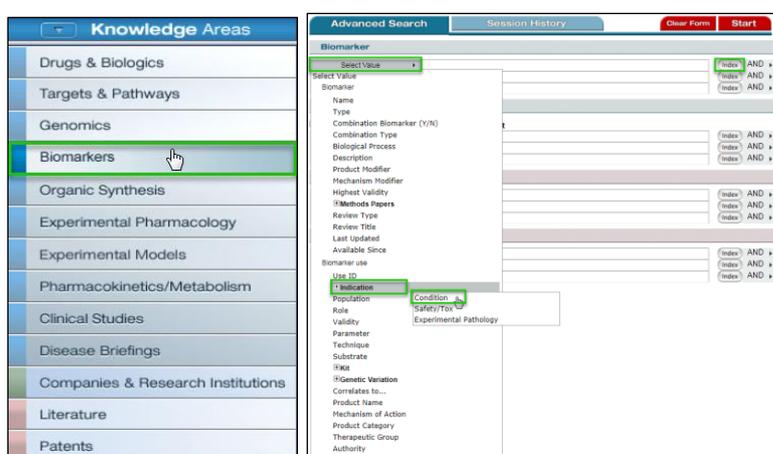


Find latest biomarkers for a specific disease

Are you interested in recent advances in discovery (identification and development) of biomarkers? Do you want to be able to find biomarkers early in their development that have been patented as having application to a disease of interest?

Biomarker Module of Clarivate Analytics Integrity enables you to find newly discovered and claimed biomarkers in connection to a disease of interest and keep up to date with advancements in development. Benefit from comprehensive manually curated intelligence on biomarkers captured from patents, literature and conferences. **Example Scenario:** you want to find the most recently patented biomarkers for multiple myeloma with any applications (you are interested in “white space” investigation or searching for new potential treatment targets).

Find recently reported multiple myeloma biomarkers:

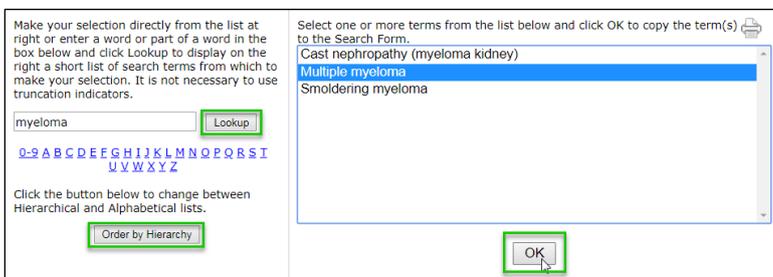


To find all biomarkers reported in source references related to a disease, go to the **Biomarkers** knowledge area.

Click **Select Value** in the Biomarker section and choose **Indication** -> **Condition** from the dropdown menu.

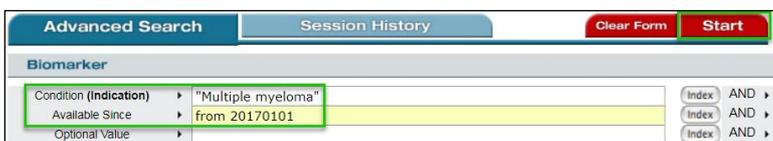
Click **Index** to the right of this field.

In the pop up window that appears, type “myeloma” into the text box on the left side of the window and click **Lookup**. Select **Order Alphabetically**, click on the specific term “multiple myeloma” from the list of options present on the right and click OK to copy the term into the search form.



Next, click **Optional Value** in the **Biomarker** section and choose **Available Since** from the dropdown menu.

Click **Index** to the right of this field to see the date format used in *Integrity*. In the search form, type “from 20170101” to retrieve biomarker records added to the database since January 1st, 2017.



Now with both fields entered, click the **Start** button at the top of the page to begin the search.

The search will retrieve all biomarkers reported in connection with multiple myeloma that are newly entered into the database since the given date regardless of validity levels.

Tip: Integrity includes multi-markers, such as gene signatures or protein panels, where a combination of components is used as biomarker. You can exclude multi-markers from your search results by selecting **Combination Biomarker (Y/N)** from the menu of optional values and typing “n” (for “No”) into the search form.

Tip:

- You can also define the validity level in the initial search as “emerging” using the **Highest Validity** field and selecting **Emerging** from the **Index**. This will restrict the search to biomarkers that have been reported to serve as a marker for multiple myeloma but are in early stages of development in addition to only having been added to the database since the given date.

Setting up alerts from newly added biomarkers:

In the results view use the **Options** drop-down menu to set up a **Save Query** alert to be notified when new biomarkers are added to the database that are connected to multiple myeloma. A pop-up menu will appear with various options for your alert.

Type your email address in the relevant box and select preferred alert frequency then save the alert by clicking **Save Query**. You will now be notified when new records that meet your search criteria enter the *Integrity* database.

Tip:

- You can find full definitions for **validity** phases, **source evidence** and other fields in the **Biomarker Frequently Asked Questions (FAQs)** document. There is a link to the FAQs from the **Learning Center** panel, located on the bottom left corner of the *Integrity* homepage or from the Biomarkers Advanced Search page by clicking the link in the left-hand column.

Changing the view:

Biomarker Name	Type	Use Indication Type and Validity	Options	Source	MetaCore
Caspase-9 subunit p33	Proteomic	Major Condition Cancer All	Integrity Reports Biomarker List Biomarker Full Record Biomarker Use Record Biomarker List with Kits	P ESH LSH R/A All Ref Pat Kits	
Choline kinases	Proteomic	Major Condition Cancer All	Integrity Reports Biomarker List Biomarker Full Record Biomarker Use Record Biomarker List with Kits	P ESH LSH R/A All Ref Pat Kits	
Chromosome locus 2q16.1 2q16.1	Genomic	Major Condition Cancer All	Integrity Reports Biomarker List Biomarker Full Record Biomarker Use Record Biomarker List with Kits	P ESH LSH R/A All Ref Pat Kits	
FGFR1-IGH fusion gene FGFR1-IGH; FGFR1-IGH DNA; FGFR1/IGH	Proteomic; Genomic	Major Condition Cancer	Integrity Reports Biomarker List Biomarker Full Record Biomarker Use Record Biomarker List with Kits Kit Development Status List All Related Information via Quick Search Printer Friendly Format	P ESH LSH R/A All Ref Pat Kits	FGFR1 IGH

With *Integrity Biomarkers*, the options to change the way the content is viewed can be a powerful way to explore the data. The initial search results are formatted in a table where the content pertaining to the biomarker record is displayed.

Using the **Options** drop-down menu, you can change this display using one of 5 different display formats. By selecting the **Biomarker List** option you can view the biomarkers from a new perspective with each biomarker use broken down.

If you have any questions please contact us at: DTStraining@clarivate.com

Multiple myeloma	Population Role	Technique (Substrate)	Parameter	Validity (Authority)	Sources
Caspase-9, submitil_p33	All	Monitoring Treatment Efficacy	Western blotting (Tissue)	NA	Early Studies in Humans
Choline Kinases	Adults to elderly	Predicting Treatment Efficacy	PET / CT (Whole body)	SUVmax	Early Studies in Humans
Chromosome locus 2q16.1	All	Prognosis	Oligonucleotide array analysis (DNA)	NA	Early Studies in Humans
EGFR_L1_TGFI fusion gene	p53 Mutation Carriers	Risk Factor	FISH (DNA)	NA	Early Studies in Humans

You may find the **Validity** and **Source Evidence** fields informative in understanding both how mature a biomarker is and whether the literature supports or refutes that biomarker use in a given context. This information can be found on the right-hand side of the display.

The results from a search can be refined using the fields within the records. The fields you can use to filter the results are set out in the **Filter By Statistics** box. Using these options, you can quantify the number of records that contain a given value and take a subset by either clicking on the bar or selecting a number of fields using the tick boxes to view these subsets together.

For example, the biomarkers in the results can be filtered by their **Validity**. By selecting the **Emerging** bar, you can view that only 1 biomarker falls within this category.

A subset can be further refined by filtering on another field such as **Source Evidence**. In this example, you can take **"at least 1 + source"** subset to include only those results where a significant association ($p < 0.05$) has been found between biomarker and condition in at least one published reference.

Filter by Statistics

- Biomarker Type
 - Highest Validity
 - Combination Type
 - Component Biomarker
 - Component Of
 - Biological Process
 - Product Modifier
 - Mechanism Modifier
 - Method Papers (Y/N)
- Biomarker Use
 - Indication Type
 - Major Condition
 - Condition
 - Safety/Tox
 - Experimental Pathology
 - Population
 - Role
 - Technique
 - Substrate
 - Genetic Variation Type
 - Parameter
 - Validity
 - Scientific Authority
 - Source Evidence
- Biomarker Kit
 - Kit Name
 - Organization
 - Status
 - Country / Area
 - Regulatory Authority

Validity

Condition (Indication) = "Multiple myeloma" AND Available Since = from 20170101

Early Studies in Humans

Late Studies in Humans

Experimental

Emerging

Check All 0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

Source Evidence

Condition (Indication) = "Multiple myeloma" AND Available Since = from 20170101

at least 1 + source

+ sources only

- sources only

at least 1 - source

Check All 0 3 6 9 12 15 18 21 24 27 30

Exporting your results:

Options

- Save Query
- Keep Me Posted
- Export Center
- Integrity Reports
- Biomarker Table
- Biomarker Full Record
- Biomarker Use Record
- Biomarker List with Kits
- Kit Development Status List
- All Related Information via Quick Search
- Printer Friendly Format

Export Center - Biomarkers

This feature allows users to export selected data from Integrity for use in other applications. Up to 2000 records (Format as Table Data, 2000 user-defined sources (not Format as Table Data) or exports can be exported at a time from this knowledge base including a maximum number of 200 fields per record, either as flat files of records or as selected records by clicking the record selection feature.

1) Use the pull-down menu to choose an export format:

Export type: Excel

2) Check the fields you wish to export for each record:

Format as table data

3) Select the records to export:

1. Biomarker

- Biomarker Name
- Last Updated Date
- Synonyms
- Biomarker Type
- Highest Validity
- Combination Type
- Component Biomarker
- Combination Biomarker (Y/N)

2. Biomarker Use

- Component Of
- Biological Process
- Description
- Product Modifier
- Mechanism Modifier
- Method Papers
- Link to Integrity
- MetaCare

3. Biomarker Kit

- Parameter
- Use ID
- Major Condition
- Condition
- Safety/Tox
- Experimental Pathology
- Population
- Role
- Technique
- Substrate
- Scientific Authority
- Sources (Type, Evidence, Citation)
- Link to Integrity
- Related Products
- Genetic Variations
- Connotations
- Kit

4) Click Export.

Export Close

Once filtered, the results will contain only those biomarkers that are most interesting. It may, therefore, be useful to export the relevant data to external files for further analysis and distribution to colleagues and project partners.

Using the **Options** drop-down menu select the **Export Center** where there is a variety of options for the format and fields that the data can be exported into.

There is the option to export into MS **Word** or **Excel** file formats. To customize the export so that you have the data that is needed, you can select from the fields contained within the records. You can select fields from both the **Biomarker** and **Biomarker Use** records.