

Assertions API Detailed Docs

Based on documentation available at api.molecularmatch.com.

For background on assertions, see diagrams and publications [on this page](#).

Assertion Search

Image from the [web application](#). The app is good for discovery purposes or physician use.

The screenshot shows the MolecularMatch web application interface. At the top left is the MolecularMatch logo with the tagline "CLINICAL INTELLIGENCE ON-DEMAND". At the top right are a grid icon and a purple circle with the letter 'S'. The main search area has a text input field containing "Lung cancer BRAF V600E", a search button with a magnifying glass icon, and a "SEND TO" button with a dropdown arrow. Below the search bar are several filter dropdown menus: "Regulatory Body" (set to FDA), "Tiering Template" (set to AMPCAP), "Tier" (set to All), "Version" (set to 4), "Biomarker Class" (set to Predictive/Therapeutic), "Clinical Significance" (set to Sensitive), and "Direction" (set to Supports). At the bottom of the filter section are two buttons: "← Previous Page" and "Next Page →". Below the filters is a results box containing the text "1B - BRAF V600E confers sensitivity to Vemurafenib in patients with Non-small cell lung cancer".

Let's break down a typical search scenario

Looking for treatments with supporting evidence where the biomarker provided is predictive of drug sensitivity.

For Lung cancer patients with a BRAF mutation, where you only want to return exact mutation matches (strict), it would be queried like this:

```
filters = [
  {"facet": "CLINICAL_SIGNIFICANCE", "term": "sensitive"},
  {"facet": "BIOMARKER_CLASS", "term": "predictive"},
  {"facet": "ASSERTION-DIRECTION", "term": "supports"},
  {"facet": "MUTATION", "term": "BRAF V600E"},
  {"facet": "CONDITION", "term": "Lung cancer"}
]
payload = {
  'apiKey': '<my api key>',
  'filters': json.dumps(filters),
  'tieringTemplate': 'AMPCAP',
  'mode': 'strict'
}
```

```
url = 'https://api.molecularmatch.com/v2/assertion/search'
r = requests.post(url, json=payload)
print(json.dumps(r.json()))
```

For going through multiple pages of assertions, see the [paging example](#).

Valid Values:

- BIOMARKER_CLASS --- Predictive/Theranostic , Diagnostic , Prognostic , Unknown
- CLINICAL_SIGNIFICANCE --- Resistant , No Response , Sensitive , Favorable , Unfavorable , Unknown
- DIRECTION --- Supports , Does Not Support
- tieringTemplate --- AMPCAP , MVLD

Assertion Response

1B - KRAS G12C confers sensitivity to Selumetinib in patients with Non-small cell lung cancer

Selumetinib

Biomarker Class: predictive

Clinical Significance: sensitive

Direction: supports

Unmet Criteria

Non-small cell lung cancer +

SHOW LESS

Evidence	Classifications	Variant Info	Prevalence
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Regulatory Body	FDA	Guideline Body	Regulatory Body Approved	✖
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PUBMED - [23200175](#) - trial - prospective - [NCT00890825](#)
 PUBMED - [26125448](#) - trial - retrospective - [NCT00890825](#)
 PUBMED - [22425996](#) - preclinical - mouse_model

API Response

Here is the breakdown of the response, starting from the high-level, and digging into the fields of the assertion records.

High-level response.

```

JSON
├── rows
│   └── tieringTemplate : "AMPCAP"
├── tieringTemplateLegend
├── rationalized
├── inferred
├── unrecognized
├── totalPages : 1
├── total : 4
├── max_score : null
└── page : 1

```

An overview of the record's fields

```

JSON
├── id : "920e7cfe-3338-4cd0-b62b-3b93f5e0e899"
├── narrative : "BRAF V600E confers sensitivity to Trametinib + Dabrafenib in patients with Non-small cell lung cancer"
├── direction : "supports"
├── ampcap : "1A"
├── tierExplanation
│   ├── biomarkerClass : "predictive"
│   └── clinicalSignificance : "sensitive"
├── sources
│   ├── includeDrug1
│   ├── criteriaUnmet
│   ├── mutations
│   └── variantInfo
│       ├── mvld : "1"
│       ├── sixtier : "1"
│       ├── tier : "1A"
│       ├── civic : "A"
│       ├── guidelineBody : "NCCN"
│       ├── regulatoryBody : "FDA"
│       ├── regulatoryBodyApproved : true
│       └── expression : "'Non-small cell lung cancer' && 'BRAF V600E'"
├── includeCondition1

```

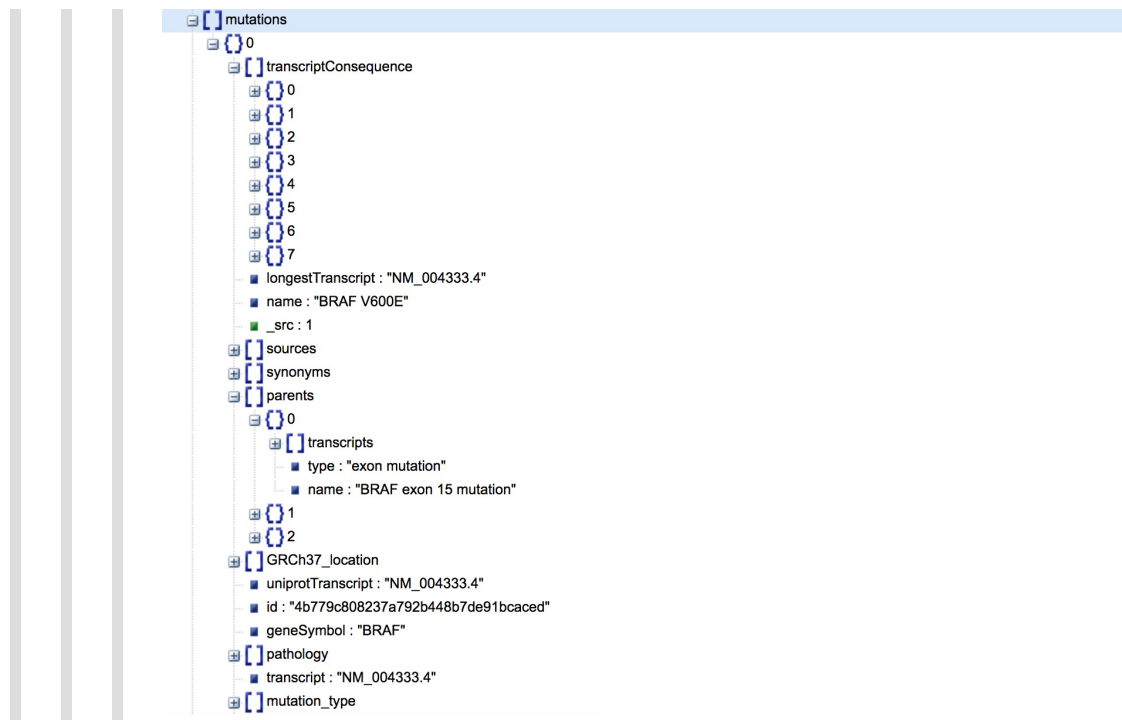
This is the data (trials, publications, abstracts) that support the conclusion of the assertion.

```

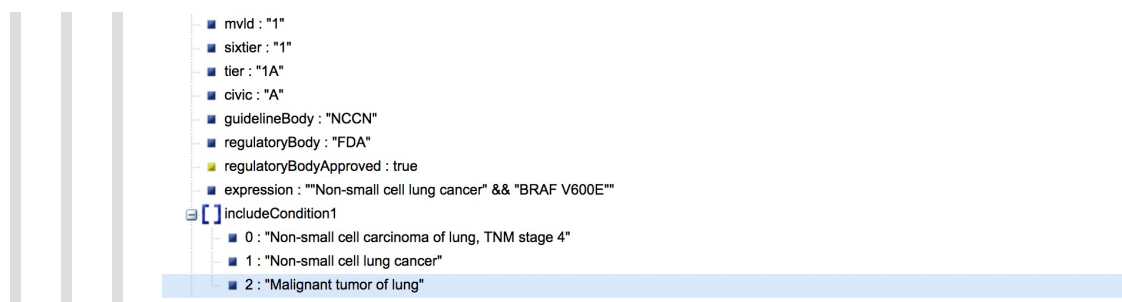
sources
├── 0
│   ├── type : "trial"
│   ├── name : "ASCO"
│   ├── suppress : false
│   ├── subType : "prospective"
│   ├── valid : true
│   ├── link : "http://ascopubs.org/doi/abs/10.1200/JCO.2017.35.15_suppl.9075"
│   ├── trialId : "NCT01336634"
│   └── id : "1519930784154"
├── 1
│   ├── type : "trial"
│   ├── name : "PUBMED"
│   ├── suppress : false
│   ├── pubId : "28919011"
│   ├── subType : "prospective"
│   ├── valid : true
│   ├── link : "https://www.ncbi.nlm.nih.gov/pubmed/28919011"
│   ├── trialId : "NCT01336634"
│   └── id : "1519930475732"
├── 2
├── 3
└── 4

```

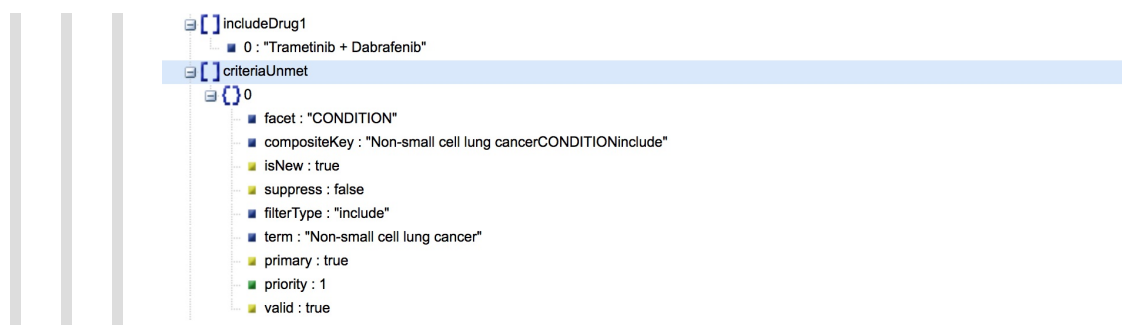
Detailed information on the mutations in this assertion.



Other tiering system's scores have also been calculated.



The criteria your search did not match. This assertion was for NSCLC, but you entered it's parent Lung cancer (root term = Malignant tumor of lung).



Back at the high-level response, you see explanations of the tiering and the root terms your query rationalized to.

[-]	tieringTemplateLegend	
[+]	3	
[+]	4	
[+]	2D	
[+]	N/A	
[-]	1A	<ul style="list-style-type: none"> ■ description : "FDA approved drugs OR professional guidelines" ■ label : "Tier 1A"
[-]	1B	<ul style="list-style-type: none"> ■ description : "Clinical trial that is Phase 2 or above" ■ label : "Tier 1B"
[+]	2C	
[-]	rationalized	
[+]	0	
[+]	1	
[+]	2	
[+]	3	
[+]	4	
[+]	5	
[+]	6	
[-]	7	<ul style="list-style-type: none"> ■ term : "Lung cancer" ■ rootTerm : "Malignant tumor of lung" [+]
[+]	inferred	
[+]	unrecognized	
	totalPages : 1	