

# MolecularMatch Conditions 2018 Update

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In 2013, MolecularMatch integrated SNOMED-CT as our technology's primary condition (disease) dataset. For months and years after, oncologists and scientists at MM added a layer of curation so that it fits with modern cancer diagnoses. This included editing and adding new conditions and synonyms, and creating genetic composite conditions. Since then, SNOMED has improved in relation to oncology. Also, several open-source disease datasets have been launched. Matching patients to trials, drugs and assertion evidence guidelines depends on an accurate diagnoses and consistent interpretation between healthcare systems. Therefore in 2018, we upgraded our condition system, accomplishing the goals of:

1. Allowing cohesive code-based searching to improve EHR/Payer/LIMS integrations.
  2. Updating to the most modern data ontologies.
  3. Expanding operations outside of cancer.
  4. Data validation (duplicates merging) with pathologist oversight.
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MolecularMatch NLP entity extraction and search engines run on ontologies. These include our conditions and findings, our in-house developed [molecular ontology](#) and our global clinical trial aggregation. As our experience with data aggregation has grown, we've developed a protocol that allows for easy integration of big data to enhance our search engines. This high-level protocol is:

1. Acquire datasets in their native form on update intervals.
  2. Identification strategy and merging to allow diverse inputs and avoid duplicates.
  3. Incorporate into MMPower for broad use.
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## Condition Data Incorporated into MM

Condition terms are now searchable by prefix\_code (e.g. `SNOMEDID_12345`).

Search Prefix	Dataset Name	Records Count
SNOMEDID	Systematized Nomenclature of Medicine -- Clinical Terms	313,940
ICD10	10th rev. of the International Statistical Classification of Diseases	94,127



## Custom Conditions and Genetic Composites

Only a handful of genetic composite conditions exist in the public datasets, like "EGFR positive NSCLC". At MM, we've created many more composites, which are necessary in our NLP engine for coalescing meaning from medical documents.

Screenshot of internal MM tools for creating composite conditions.

The screenshot shows the 'Data Management' interface with tabs for Conditions, Clinical Findings, Anatomies, Stages, OncoTree, SNOMED, ICD10, DiseaseOntology, and Processes. The 'Conditions' tab is active, showing a list of conditions with columns for Name, Composite, Custom, and Suppress. A search bar is at the top. On the right, a form for creating a composite condition is visible, with fields for Name, Alias, and a list of associated tags. The 'Associated Tags' section shows a list of terms with checkboxes for Custom and Suppress. The 'ER+ HER2- PIK3CA Breast cancer' condition is highlighted in the list.

Name	Composite	Custom	Suppress
BCH-ABL1			
B lymphoblastic leukaemia/lymphoma with TEL-AML1			
B lymphoblastic leukaemia/lymphoma with t(1;19)(q23;p13.3)			
B lymphoblastic leukaemia/lymphoma with t(5;14)(q31;q32)			
B lymphoblastic leukaemia/lymphoma with t(v;11q23); MLL rearranged			
BRAF mutated colorectal cancer			
BRAF mutated melanoma			
Carney's Triad			
Childhood myelodysplastic syndrome			
Classical Hodgkin lymphoma type PTL			
EGFR mutated GBM			
ER+ HER2- PIK3CA Breast cancer			
FLT3 AML			
GIST - NF1			
GIST KIT exon 11			
GIST KIT exon 13			

Associated Tags (these tags get created in addition to this domain tag when this rec...)

Term	Custom	Suppress
PIK3CA		
Neoplasm of breast		
ERBB2 Loss		
ESR1		

## Lets Use It! (warning: not available on production yet)

These codes can now be used in the whole MM ecosystem. From the application search, to API queries, to EHR integration.

### App Search

- [http://app.molecularmatch.com/search/ICD10\\_D45](http://app.molecularmatch.com/search/ICD10_D45)
- [http://app.molecularmatch.com/search/SNOMEDID\\_12345](http://app.molecularmatch.com/search/SNOMEDID_12345)
- [http://app.molecularmatch.com/search/DOID\\_0121](http://app.molecularmatch.com/search/DOID_0121)
- [http://app.molecularmatch.com/search/ONCOTREE\\_AML](http://app.molecularmatch.com/search/ONCOTREE_AML)

### API Queries

See specs on [api.molecularmatch.com](http://api.molecularmatch.com)

```
#####  
# Trials Search -- save this as a .sh file  
#####
```

```
# to run include apiKey as first argument
# $ chmod 777 file.sh
# $ ./file.sh apiKey

curl -X POST 'https://api.molecularmatch.com/v2/search/trials' \
--data "apiKey=$1" \
--data-urlencode 'filters=[ \
    {"facet":"ICD10","term":"ICD10_D45"}, \
    {"facet":"STATUS", "term":"Enrolling"}, \
    {"facet":"TRIALTYPE", "term":"Interventional"} \
  ]'

curl 'https://api.molecularmatch.com/v2/search/trials' \
--data "apiKey=$1" \
--data-urlencode 'filters=[ {"facet" : "SNOMEDID", "term" : "SNOMEDID_254626006"}]'
```

```
#####
# Condition Search -- used to normalize conditions
# If you have a condition name, or code, you can search our conditions table to find the be
# This can then be used as a term in subsequent trials and drugs searches.
#####

curl -X POST 'https://api.molecularmatch.com/v2/search/conditions' \
--data "apiKey=$1" \
--data-urlencode 'filters=[{"facet":"PHRASE","term":"Lung cancer"}]'
```

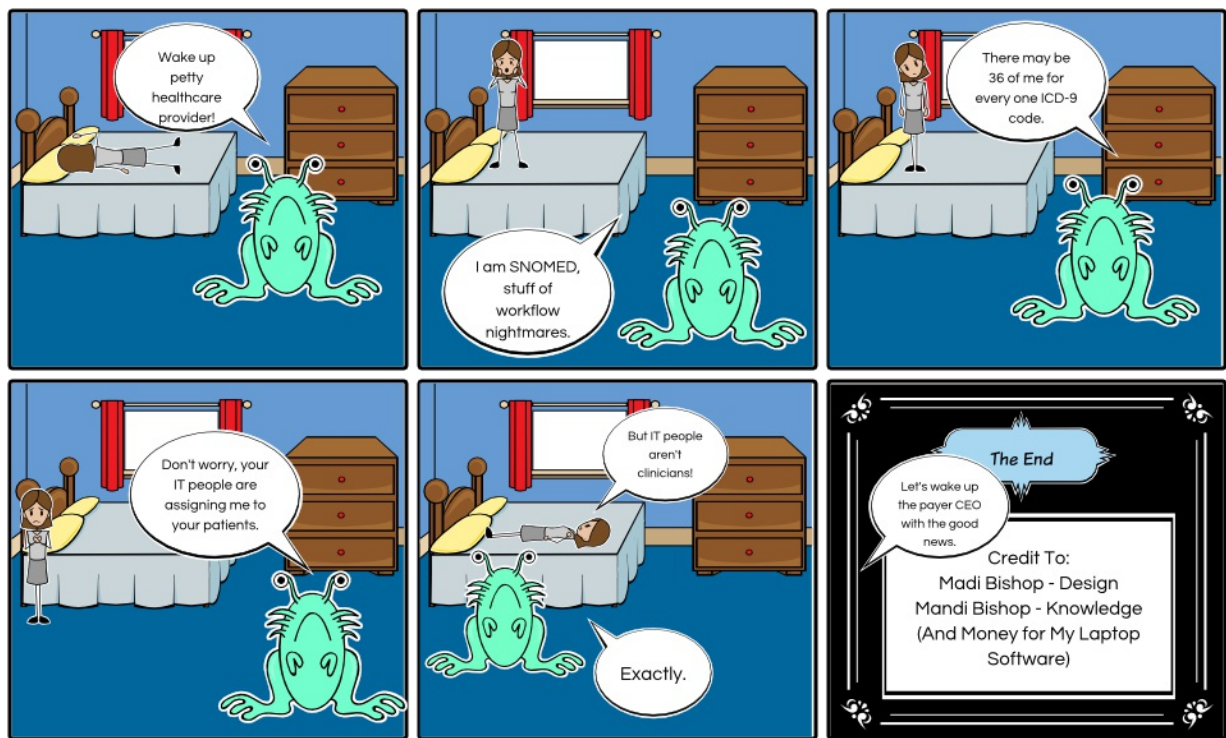
```
curl 'https://api.molecularmatch.com/v2/search/trials' \
--data "apiKey=$1" \
--data-urlencode 'filters=[ {"facet" : "SNOMEDID", "term" : "SNOMEDID_254626006"}]'
```

## EHR Integration

Contact Us at [info@molecularmatch.com](mailto:info@molecularmatch.com) for a demonstration of how to integrate with an EHR, payer system or LIMS.

## Mapping Trouble?

No mapping effort is perfect. Work with us to make sure you are getting the results you expect for your patients.



Create your own at [StoryboardThat.com](http://StoryboardThat.com)

From: <http://healthstandards.com/blog/2014/04/21/snomed-problems/>

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TODO: make a version of OHSU G2P disease\_normalizer using MM condition search:

<https://github.com/ohsu-comp-bio/g2p->

[agggregator/blob/cd2ffbecda4f3eeb946761d766929175018bd9fa/harvester/disease\\_normalizer](https://github.com/ohsu-comp-bio/g2p-agggregator/blob/cd2ffbecda4f3eeb946761d766929175018bd9fa/harvester/disease_normalizer)

.py