This documents how you call the API and a variety of options for customization of reports based on the data returned. The key customizations are:

- Ability to restrict the bacteria under consideration to specific ones
    - This is done by filtering to desired bacteria before making the API call
    - Example: you wish suggestions to based solely on species, genus and families. You just send those to the API
- Ability to set your own limits/ranges for each bacterium
    - Only bacterium outside of these ranges will be considered
- Ability to restrict suggestions / modifiers to only specific items
    - Example: Exclude antibiotics and other prescription drugs
- Ability to restrict suggestions to a specific number
    - The system often ranks/order over 1600 suggestions, this is excessive for presentation
- Ability to show suggestions with a positive impact, a negative impact or both
    - Typical presentation pattern is to give what to take and not what to avoid.
- Ability to customize names on your report using your own look up tables.
    - You may want to display **lactobacillus reuteri** instead of the current name of **Limosilactobacillus reuteri**
    - You may want to display **Hen of the Woods Mushroom** instead of the scientific name of **Grifola frondosa**
    - You may want to localize names in different languages based on the user's preferences

The intent of the API is to provide sufficient information for you to create a basic suggestions page customized to your preferences. Suggestions are based on the impact on all bacterium outside of your range (with some scaling depending on how far outside of your range). Suggestions are listed by those most probable to help after factoring in the number of studies. Often, a suggestion will increase a bacterium in 8 studies and decrease in 2 studies. The reason for this agreement is often the population used in the study, for example: athletes, people with diabetes and infants will display different shifts.

Filtered citations are provided that are safe to display without triggering support calls if someone reads the study. This is done by:

- Requiring the study to directly cite the bacterium and the suggestion
- The study does not report adverse effects on other bacterium being focused on.
- Study must have a **digital object identifier** (**DOI**) allowing it to be easily located

API formats

The basic pattern expected in the JSON call is shown on the next page. All properties must be in lower case.

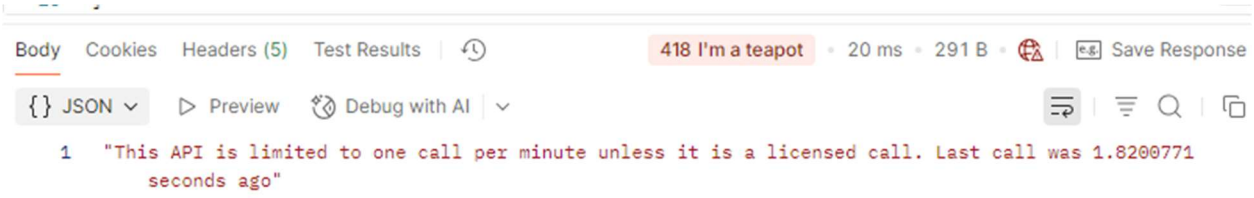
- **Labkey**: this is for billing purposes and to identify customizations to be used
- **Id**: your internal sample identifier
- **SuggestionCount**: the number of the most significant to take and to avoid to be return
- **Modifierclasses**: this is a coarse customization of suggestions until a customized suggestion list for your account is defined. See below.
- **Taxons**: information about the sample.
    - Percentile and/**or** Percentage ranges must be given
    - A matching Percentage or Percentile must be given (to determine if too high or too low)
    - Best results occur when both are provided
- **Conditions**: Used to request a cross-validated report. One or more supported medical conditions must be specified. This is covered in a separate document.

```
Key    Modifier Class
A      Antibiotics, Antivirals etc
B      Probiotics
C      Amino Acid and similar
D      Drug or "Non-drug"
E      Flavonoids, Polyphenols etc
F      Food (excluding seasonings)
G      Common and OTC Supplements
H      Herb or Spice
I      Prebiotics and similar
P      Prescription - Other
T      Diet Style
U      Sugar and similar
V      Vitamins, Minerals and similar
X      Food Preservatives
```

Example JSON Load


```
{
  "id": "a4bc0924-e16d-4d39-8526-57b5cbcf96e4",
  "labkey": "e49eedde-26fa-4879-a5ec-5761825d0a2a",
  "modifierclasses": "b,c,e,f,g,h,O,t,u,v",
  "suggestioncount": 20,
  "taxons": [
    {
      "percentage": 6.975,
      "percentagehigh": 88.161,
      "percentagelow": 8.9019,
      "percentile": 13,
      "percentilehigh": 99.95163240628779,
      "percentilelow": 14.897218863361548,
      "taxon": 816
    },
    {
      "percentage": 0.326,
      "percentagehigh": 8.359,
      "percentagelow": 0.001,
      "percentile": 100,
      "percentilehigh": 99.94997498749375,
      "percentilelow": 0.02501250625312656,
      "taxon": 200940
    },
    {
      "percentage": 0.307,
      "percentagehigh": 14.094,
      "percentagelow": 0.478,
      "percentile": 14,
      "percentilehigh": 98.5613265057303,
      "percentilelow": 17.62984637893197,
      "taxon": 375288
    }
  ]
}
```


Calls are limited to 1 call per minute in trial mode. A 400 status will be returned with information about the time since the last call.



Visual inspection of correct interpretation is recommended as shown below.

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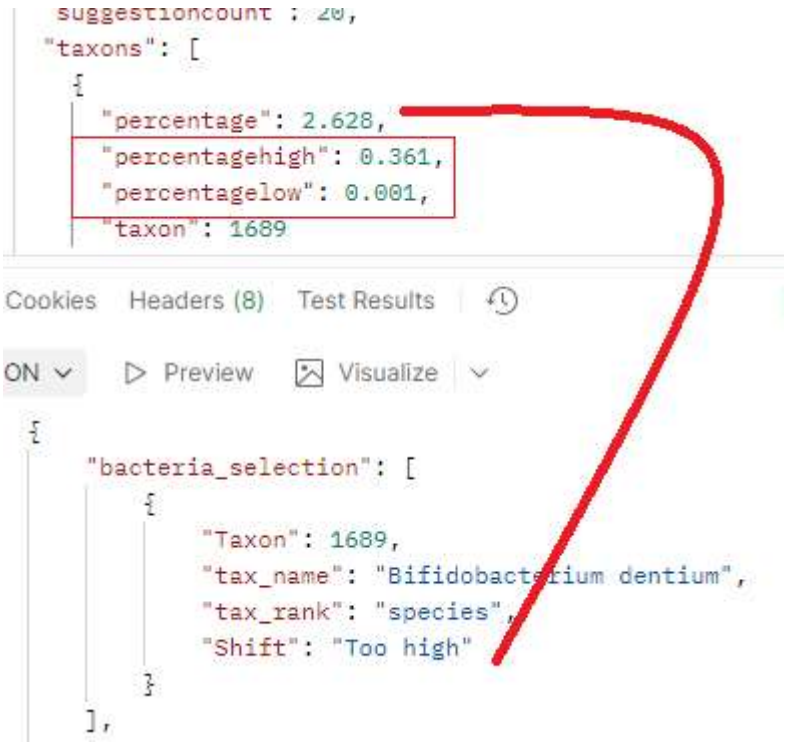


Testing API

Calling (get) https://microbiomeprescription.com/api/SampleExternalLab will return an example from our public database that is correctly formatted. This response is JSON and your browser will ask to save it to disk.

This example can often be of assistance to developers to see what is expected to be sent.

It is recommended that you use **PostMan** to test (and later triage) your API calls. This is free and may be downloaded from https://www.postman.com/. Images below are from PostMan.

- Open Postman
- Create a POST
- Enter the address: https://microbiomeprescription.com/api/SampleExternalLab
- Enter the sample download above OR your own data
- Click Post.

The result will be a collection of JSON starting with what was identified to be out of range by the data sent as shown below with the first set of data “bacteria_selection”

- It is recommended practice to compare this to the data sent.
- Manual review of some ranges is recommended for “bad bacteria”.
    - Our system accepts some amounts of “bad bacteria” to be normal. This may differ from your ideological assumptions.

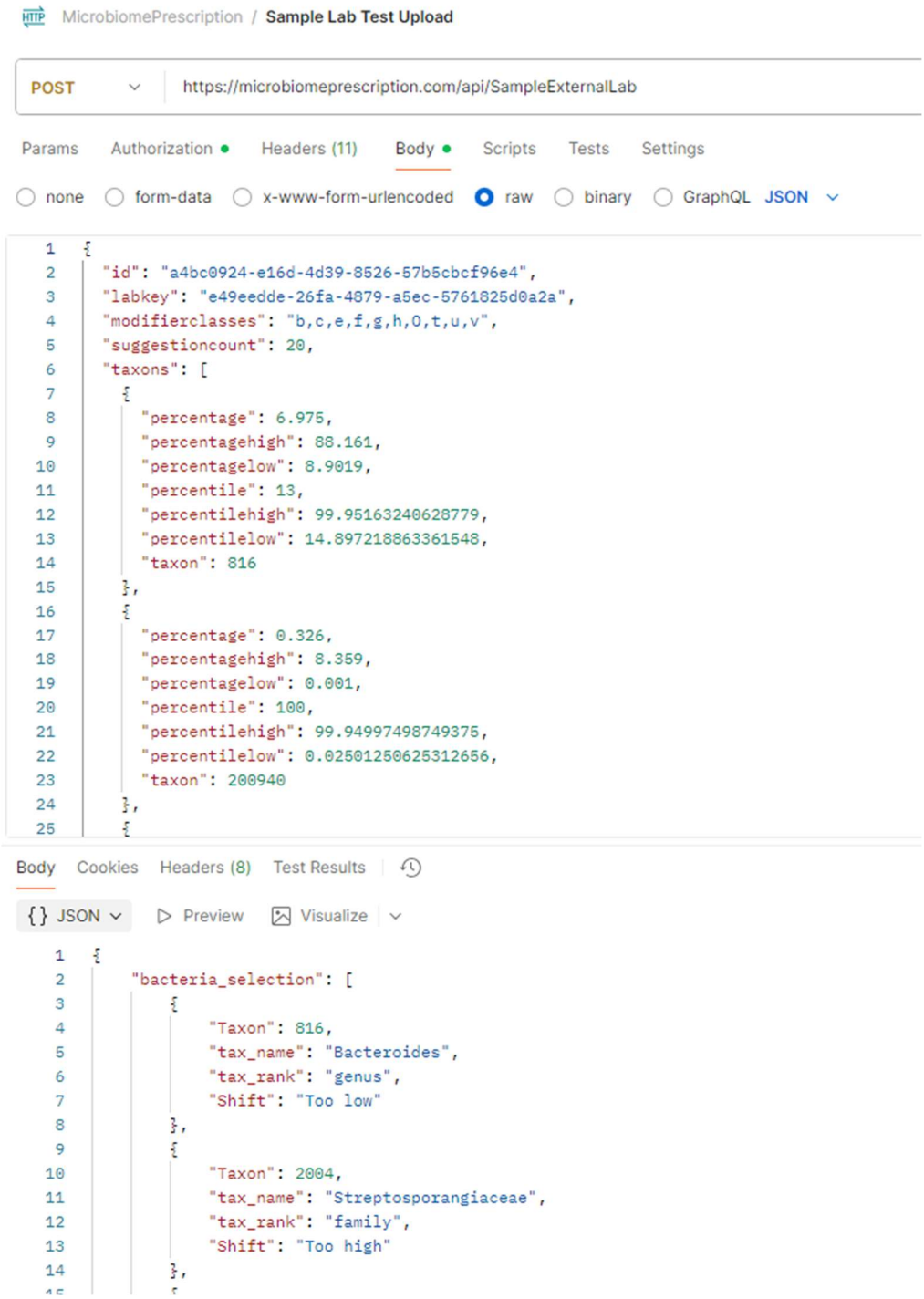
Other sets of data include

- “take_suggestions”
- “avoid_suggestions”
- “citations:
- “cross_reference”

Suggestions are in order of priority (maximum impact first) and provide alternative names.


```
{
    "mid": 86,
    "modifier2": "Inonotus obliquus {Chaga Mushroom}",
    "drugnames": "Chaga,Cinder conk, Birch canker polypore, Clinker polypore, Black mass,
        Sterile conk trunk rot of birch"
},
```

- To localize the name used in your report, use the mid value as a key into your replacement table.



Citations

The citations are “pure” and do not include *inferences*. They meet the following criteria to avoid support calls:

- The substance and the bacteria are *explicitly* referenced in the study
- There are no contra-indicated effects on other bacteria cited
- Only studies with a doi are listed

The suggestions are computed on a richer data set that addresses contra-indicated effects, includes inferences, etc.


```
"citations": [
    {
        "doi": "10.1007/s00394-013-0607-6",
        "Abstract": "Association of dietary type with fecal microbiota in vegetarians and
            omnivores in Slovenia."
    },
    {
        "doi": "10.3382/ps/pew389",
        "Abstract": "Effects of long-term Bacillus subtilis CGMCC 1.921 supplementation on
            performance, egg quality, and fecal and cecal microbiota of laying hens."
    },
```


After the references is a cross-reference section indicating how studies are connected to modifiers and bacteria.


```
],
"cross_reference": [
    {
        "doi": "10.3390/microorganisms9020238",
        "mid2": 67,
        "taxon": 818
    },
    {
        "doi": "10.1007/s00394-023-03308-4",
        "mid2": 120,
        "taxon": 818
    },
```

Note: that every bacterium may not be listed. In some cases, there are no existing studies on this bacterium for our modifiers. Our system uses inference: for example, if something impacts a genus, we infer that it was a *reduced* impact on species in that genus. This allows us to make reasonable suggestions when there are no explicit studies.

Example:

- Bifidobacterium dentium may return no citations
- Bifidobacterium will return dozens of citations

It is recommended that you just give citations without the cross references. The typical reader will read just a few citations.

Controlling Modifiers/Suggestions

Calling https://microbiomeprescription.com/api/modifiers [get] will list all available modifiers and return as JSON in alphabetical order. There are almost 1800 different ones in our database with new ones added periodically. You may exclude or include these as described below.


```
[
  {
    "mid": 212,
    "suggestion": " 3-Methylbutanoic acid {isovaleric acid}",
    "drugnames": "found as a result of fermentation, found in:
Cheese,Beer,sauerkraut,kimchi,wine "
  },
  {
    "mid": 40,
    "suggestion": " 5,6-dihydro-9,10-dimethoxybenzo[g]-1,3-benzodioxolo[5,6-
a]quinolizinium {Berberine}",
    "drugnames": "Found in goldenseal, Chinese goldthread, barberry, tree turmeric,
Oregon grape"
  },
  {
    "mid": 91,
    "suggestion": " chitosan oligomers {chitooligosaccharides}",
    "drugnames": "Chitooligosaccharides (COS) are produced from chitosan "
  }]
```


Current Approved Modifiers

To see your current set of approved modifiers, just change “test” to your lab code. If you are in trial mode, just enter and string and then use the same when asking for suggestions.

https://microbiomeprescription.com/api/modifiers?labcode=test

and you will get a full listing indicating which ones are used or not.

```
[
  {
    "used": false,
    "mid": 212,
    "suggestion": " 3-Methylbutanoic acid {isovaleric acid}",
    "drugnames": "found as a result of fermentation, found in:
Cheese,Beer,sauerkraut,kimchi,wine "
  },
  {
    "used": false,
    "mid": 40,
    "suggestion": " 5,6-dihydro-9,10-dimethoxybenzo[g]-1,3-benzodioxolo[5,6-
a]quinolizinium {Berberine}",
    "drugnames": "Found in goldenseal, Chinese goldthread, barberry, tree turmeric,
Oregon grape"
  },
  {
    "used": false,
    "mid": 91,
    "suggestion": " chitosan oligomers {chitooligosaccharides}",
    "drugnames": "Chitooligosaccharides (COS) are produced from chitosan "
  }]
```


Changing approved modifiers

The method is a simple post with the suggestion identifier (mid) that you wish to enabled. Any one not listed will be disabled.


```
{
  "labcode": "test",
  "mid": "40,91"
}
```


The items selected are echoed back. This allows typos to be caught early.

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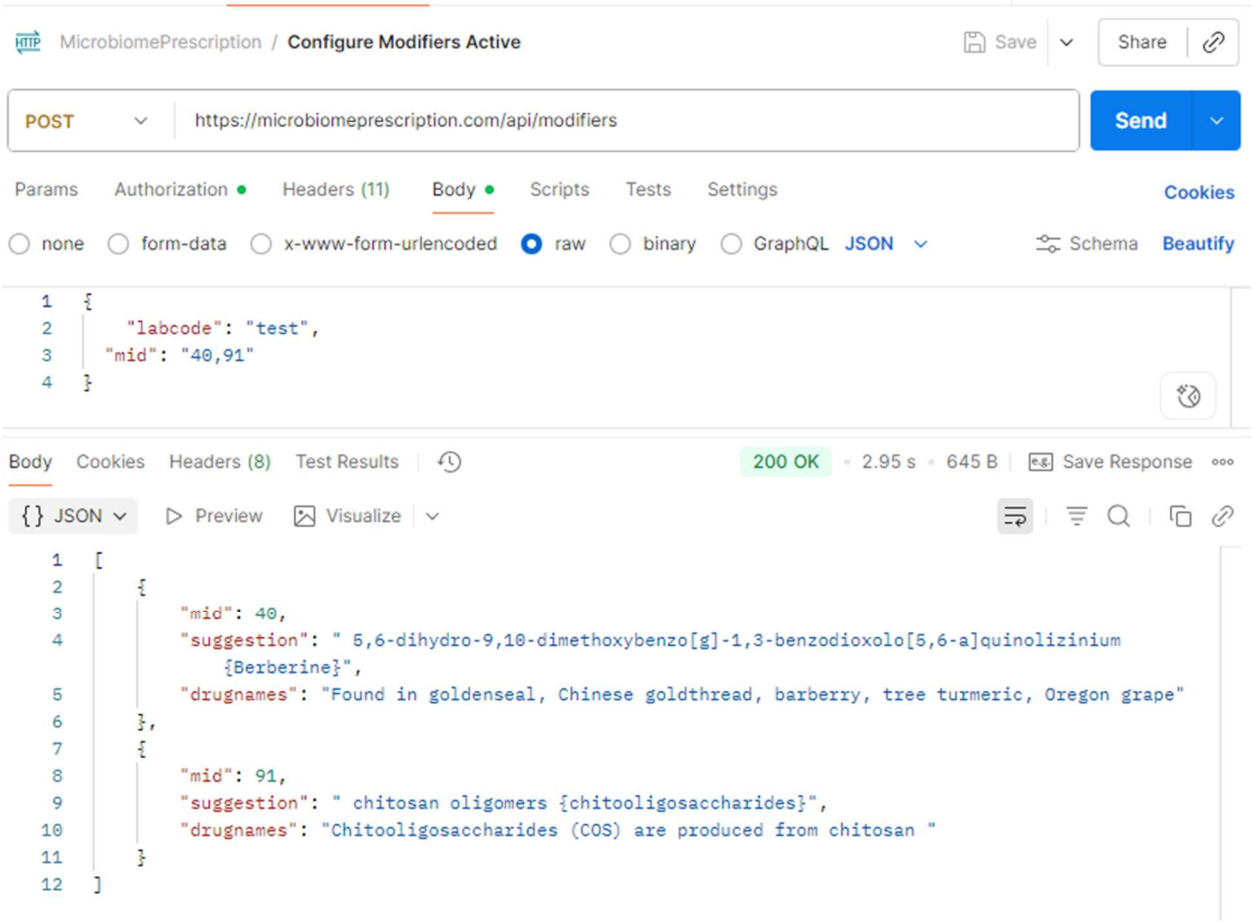

You can see the current list on the get page cited above.

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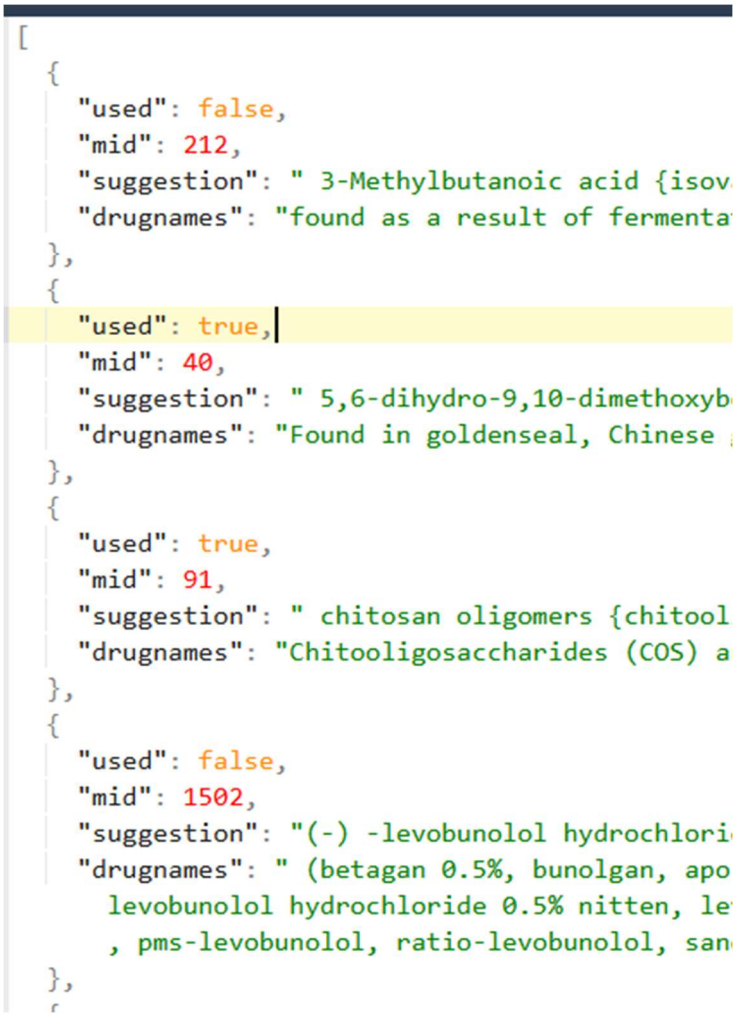

These choices will be applied automatically to any processing using the same lab code. You may experiment with as many different codes as you wish (one's not associated to a licensed account will be throttled at one call per minute across all of these ad hoc lab code

Example of Suggestions with Suggestion Restriction

Above we limited to just 2 suggestions. Only one was selected.


```
{
    "bacteria_selection": [
        {
            "Taxon": 1678,
            "tax_name": "Bifidobacterium",
            "tax_rank": "genus",
            "Shift": "Too low"
        }
    ],
    "take_suggestions": [
        {
            "mid": 40,
            "modifier2": " 5,6-dihydro-9,10
            "drugnames": "Found in goldense
        }
    ],
    "avoid_suggestions": [],
```


Summary

The intent of the API is simplicity with data sufficiency. Customizations should be keyed off the taxon identifier(taxon) and the suggestion identifier (mid) using your own lookup tables.

If there is a problem, just send the JSON payload to Research@MicrobiomePrescription.com . Typically issues are resolved within 24 hours.