



# **Biomeme Web API**







## **Biomeme for Developers**

The **Biomeme Web API** offers a simple, fast solution for requesting and consuming your PCR data. With 15+ endpoints, you have the freedom to build what you want and our team of developers are here to help you every step of the way. Whether you're looking to build a surveillance system like we did with the **Tick Pathogen Map** shown above, or simply connecting data between your disparate systems, leveraging the capabilities of the Biomeme API can and will play an integral part.

## **API Highlights**

In its most basic form, the Biomeme Web API is an interface that you can use to retrieve and manage your Biomeme data over the Internet. Our API uses the same HTTP protocol that's used by every Internet browser allowing you to easily integrate complex services and applications that go beyond the features the Biomeme Platform provides out of the box.



#### **Easy Integration**

Connect to the Biomeme API within minutes to extract and consolidate your data from multiple applications to present in a unified format for analysis and reporting.



#### **Detailed Documentation**

Access comprehensive documentation including resources, tutorials, sample code and best practices for getting the most out of our PCR technology.



#### Safe, Secure & Private

In an effort to safeguard your organization's data, we provide end-to-end encryption that keeps your PCR data safe from unauthorized access at all times.



#### **Dedicated Support**

Sometimes documentation just isn't enough and you need someone who understands the struggle to help you out. Our team of developers are here for you.

## Requests

The Biomeme Web API is based on REST principles. Data resources are accessed via standard HTTPS requests in UTF-8 format to an API endpoint. Where possible, the Biomeme API uses appropriate HTTP verbs for each action:

METHOD	ACTION
GET	Retrieves resources
POST	Creates resources
PUT	Changes and/or replaces resources
DELETE	Deletes resources

#### **Rate Limiting**

Rate limiting enables the Biomeme Web API to share access bandwidth to its resources equally across all users. Rate limiting is applied as per application, regardless of the number of users who use the application simultaneously, and is limited to 100 requests per second (RPS).



*Note:* If the Web API returns status code 429, it means that you have sent too many requests. Please wait a few seconds before you try your request again.

#### Responses

The Biomeme Web API returns all response data as a JSON object. See Addendum A and B for a description of **all** retrievable objects.

#### **Base Paths**

The base address of the Web API is https://api.biomeme.com/. In requests to the API and responses from it, you will frequently encounter the following paths:

PARAMETER	DESCRIPTION
Teams	Users are members of Teams
Folders	Groups of runs, folders and standards
Protocols	Thermocycling parameters
Runs	Information about experimental runs performed
Standards	Standard curve run, used in calculating quantitative runs

#### Timestamps

Timestamps are returned in ISO 8601 format as Coordinated Universal Time (UTC) with a zero offset: YYYY-MM-DDTHH:MM:SSZ.

### **Response Status Codes**

The Biomeme Web API uses the following response status codes:

STATUS CODE	DESCRIPTION
200	OK - the request has succeeded.
204	No Content - the request has succeeded but returns no message body.
400	Bad Request - the request could not be understood by the server due to malformed syntax.
404	Not Found - the requested resource could not be found.
405	Invalid date format for after query.
429	User has sent too many requests in a given amount of time (see "Rate Limiting").
500	Internal Server Error - you should never receive this error.

## Authentication

All requests to the Biomeme Web API require authentication. This is achieved by sending a valid access token in the request header. For more information about these authentication methods, please contact your Biomeme account representative.



#### **Contact Us**

Biomeme, Inc. 1015 Chestnut Street, Suite 1401 Philadelphia, PA, USA 19107 <u>support@biomeme.com</u>

## Addendum A

A full list of objects returned by the **Protocol** endpoint of the Biomeme API. All endpoints return data in JSON format.

KEY	VALUE TYPE	VALUE DESCRIPTION
id	String	UUID of the protocol
name	String	User input name of protocol
teamId	String	UUID of the team who created protocol
type	String	Protocol configuration
overshootTime	Number	Cycle overshoot duration in seconds
undershootTime	Number	Cycle undershoot duration in seconds
annealTime	Number	Cycle annealing duration in seconds
denatureTime	Number	Cycle denature duration in seconds
firstDenatureTime	Number	First denature duration in seconds
rtTime	Number	Reverse transcription duration in seconds
extensionTime?	Number	Cycle extension duration in seconds
denature	Number	Denature temperature in Celsius
overshoot	Number	Overshoot temperature in Celsius
undershoot	Number	Undershoot temperature in Celsius

#### Addendum A – Continued

KEY	VALUE TYPE	VALUE DESCRIPTION
anneal	Number	Annealing temperature in Celsius
extensionTemp?	Number	Extension temperature in Celsius
rtTemp	Number	Reverse Transcription temperature in Celsius
cycles	Number	Number of cycles
timestamp	Number	Protocol creation time
targets	Array	An array of ProtocolTarget
synced	Boolean	Are the device and smartphone synced?
fluorophore	String	Fluorophore name
emissionColor	String	Color that is emitted from the LED (blue, amber, red)
excitationColor	String	Color of the fluorophore (green, amber, red)
well	String	Well location within the strip (left, right middle)
strip	String	Location of the strip (A, B, C)
wellNumber	Integer	0 index well number, left most well being 0
abbreviation?	String	Abbreviated target name used in live view while test is running
name?	String	Target full name
sampleId?	String	User input sample name

#### Addendum A – Continued

KEY	VALUE TYPE	VALUE DESCRIPTION
notes?	String	User input notes about the protocol
startingQuanity?	Number	Starting quantity (used in standard curves)

## Addendum B

A full list of objects returned by the **Run** endpoint of the Biomeme API. All endpoints return data in JSON format.

KEY	VALUE TYPE	VALUE DESCRIPTION
id	String	UUID of the run
name	String	User input run name
protocolld	String	UUID of protocol
parentId	String	UUID of the parent folder
teamId	String	UUID of the team
isQuantitative	Boolean	Is the run quantitative?
targets	Array	An array of RunTarget
platform	String	Smartphone platform version number
appVersion	String	Smartphone application version number
baseboardHw?	String	Baseboard hardware version
baseboardFw?	String	Baseboard firmware version
heaterHw?	String	Heater hardware version
heaterFw?	String	Heater firmware version
detectorHw?	String	Detector hardware version

#### Addendum B - Continued

KEY	VALUE TYPE	VALUE DESCRIPTION
detectorFw?	String	Detector firmware version
serialNumber?	Number	Thermocycler serial number
bleName?	String	MAC address
notes	String	User input notes about the run
resultString	String	Description of the results as output from the algorithm
detailedResultString	String	More detailed result value
ipcResult	String	If an IPC was used, indicates if IPC amplified or not
timestamp	Number	Time of the run
duration	Number	Duration of thermocycling (MM:SS.ss)
lidFlag	Number	Is the lid open?
synced	Boolean	Are the device and smartphone synced?
complete	Boolean	Did the run finish or not?
locationString?	String	Name of the location as determined by the GPS coordinates
longitude?	Number	Longitude coordinates of location
latitude?	Number	Latitude coordinates of location
sku?	String	SKU number from scanned QR code (if one was used)

#### Addendum B - Continued

KEY	VALUE TYPE	VALUE DESCRIPTION
lotNumber?	String	Strips lot number from scanned QR code (if one was used)
expirationDate?	String	Expiration data from the scanned QR code (if one was used)
isHidden	Boolean	Has object been deleted or not?
fluorophore	String	Name of fluorophore
emissionColor	String	Color that is emitted from the LED (blue, amber, red)
excitationColor	String	Color of the fluorophore (green, amber, red)
well	String	Well location within the strip (left, right, middle)
strip	String	Location of the strip (A, B, C)
wellNumber	Number	0 index well number, left most well being 0
rawData	Number	Unmodified fluorescence data from thermocycler
baselineData	Number	Data that has been baselined and processed with algorithm
threshold	Number	Calculated threshold used in determining CQ value
cq	Number	Calculated CQ of well data
calculationMethod	String	How the data was processed (i.e. algorithm version)
abbreviation?	String	Abbreviated target name used in display while test is running
name?	String	Target full name

#### Addendum B - Continued

KEY	VALUE TYPE	VALUE DESCRIPTION
sampleId?	String	User input sample name
notes?	String	User input notes about the protocol
hidden	Boolean	Has this object been deleted or not?
calculatedCopy?	Number	Calculated copy number (only available in quantitative) curve runs
startingQuanity?	Number	Starting quantity (used in standard curves)