

## **Analisi dei requisiti per la definizione di web API del Catalogo Servizi di LifeWatch ITA per consentire l'interoperabilità con il software Taverna**

**Versione 1.0**

Prodotto da LifeWatch Italy: nodo nazionale dell'Infrastruttura di Ricerca Europea su Biodiversità ed Ecosistemi LifeWatch-ERIC

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**Ottobre 2017**

## **Citare come segue:**

P. Tagliolato, A. Oggioni (2017). *Analisi dei requisiti per la definizione di web API del Catalogo Servizi di LifeWatch ITA per consentire l'interoperabilità con il software Taverna. Versione 1.0.* Roma, CNR Pubblicazioni 2017. pp. 22, ISBN 978-88-8080-264-8 (online)

Piano attività LifeWatch-ITA 2016

Area di Intervento: evolutive piattaforma

Attività 5.1

## Report sull'Attività 5.1: Esposizione Servizi REST Catalogo Servizi compatibile con Taverna

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Con il contributo di: Ilaria Rosati

### Storia delle revisioni

Data	Versione	Editor	Descrizione
31/12/2016	0.1	Paolo Tagliolato	Aggiunti contenuti
6/10/2017	0.2	Paolo Tagliolato, Alessandro Oggioni	Revisione dei capitoli; aggiunto glossario
9/10/2017	0.3	Ilaria Rosati	Revisione del documento
10/10/2017	1.0	Paolo Tagliolato	Integrazione revisioni e preparazione per la pubblicazione

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### Introduzione.

Il Catalogo Servizi è un particolare registro informatico in cui sono catalogati e documentati i servizi web presenti nell’infrastruttura distribuita LifeWatch-ITA e che sono messi a disposizione dei laboratori virtuali, ambienti ospitati dalla stessa infrastruttura per la conduzione di flussi di lavoro scientifico mediante strumenti informatici di calcolo.

Il primo laboratorio virtuale di LifeWatch ITA è quello del “Caso studio Specie Aliene”, attualmente implementato come desktop remoto, accessibile tramite l’applicazione client “Microsoft remote desktop”. Nel Laboratorio Virtuale gli utenti dispongono di risorse informatiche (software, servizi di accesso ai dati, dati, servizi di calcolo) che sono state individuate, sviluppate e impiegate dai ricercatori impegnati nel caso studio.

L’idea di fondo nella costruzione dei laboratori virtuali è di fornire agli utenti un punto d’accesso a risorse che sono distribuite in rete, nonché proporre delle modalità appropriate per poter “assemblare” tali risorse in flussi di lavoro scientifici. In questo senso nel laboratorio suddetto viene messo a disposizione il software “Taverna” (cf. <http://www.taverna.org.uk>) che permette di “orchestrare” servizi web tramite la formalizzazione e la programmazione (informatica) di flussi di scientifici, secondo un relativamente semplice linguaggio di programmazione visuale.

### Obiettivo

Di grande interesse è la possibilità di integrare il catalogo servizi nel programma di orchestrazione, in modo che da semplificare il lavoro dei ricercatori rendendo visibili e selezionabili i servizi annoverati nel catalogo direttamente dall’interfaccia del programma.

L’attività mira a fornire delle indicazioni che possano guidare l’evoluzione del *Catalogo Servizi* della piattaforma del *Centro Servizi LifeWatch-ITA* in modo che questo possa essere utilizzato dal software Taverna ospitato nei Laboratori Virtuali.

### Analisi.

Il programma Taverna, nella versione fornita nei laboratori virtuali (Taverna Workbench Biodiversity, v.2.5.0), è dotato di una funzionalità che permette di collegarsi a un catalogo di servizi web e di cercare risorse ivi annoverate e utilizzarle all’interno dei flussi di lavoro. La

funzionalità è stata sviluppata per collegare Taverna specificamente<sup>1</sup> al software di catalogo BioCatalogue<sup>2</sup> (cf. la pagina introduttiva del progetto originale <https://www.biocatalogue.org/wiki/home> e il repository github con il codice sorgente del software <https://github.com/myGrid/biocatalogue>) ed in particolare:

1. alle interfacce di programmazione (API) di quest'ultimo, la cui definizione è documentata pubblicamente (cf. [https://www.biocatalogue.org/wiki/public:api#table\\_of\\_endpoints](https://www.biocatalogue.org/wiki/public:api#table_of_endpoints)) e formalizzata nello schema XML reperibile all'URL <https://www.biocatalogue.org/2009/xml/rest/schema-v1.xsd>.
2. al modello dati con cui BioCatalogue rappresenta i servizi web (cf. [https://www.biocatalogue.org/wiki/public:api#data\\_model](https://www.biocatalogue.org/wiki/public:api#data_model))

In seguito alla ricerca operata tramite il modulo di Taverna, l'utente può scegliere uno dei servizi REST o SOAP trovati e aggiungerlo al proprio spazio di lavoro (come componente da utilizzare in seguito) o nel flusso di lavoro correntemente aperto nel programma. Il software, leggendo le informazioni esposte dal catalogo, è in grado di configurare un elemento "REST service" (risp. "SOAP service") conformemente alle specifiche necessarie ad effettuare chiamate corrette al servizio (per esempio se un servizio REST viene specificato come URI template<sup>3</sup>, Taverna proporrà all'utente un componente REST che avrà tra gli input le variabili specificate nel template).

Il Centro Servizi LifeWatch espone sulla sua piattaforma un catalogo di servizi (<http://www.servicecentrelifewatch.eu/catalogue-of-services>) sviluppato ad hoc, che allo stato attuale segue parzialmente il modello dati definito da BioCatalogue ma non consente l'interrogazione tramite API equivalenti a quelle esposte da BioCatalogue, e non è dunque direttamente utilizzabile da Taverna.

Si è condotta un'analisi sulla versione disponibile in rete del codice sorgente del modulo di Taverna che esegue il collegamento alle API del software BioCatalogue<sup>4</sup> e un'analisi del log (*service\_catalogue\_api.log*) prodotto da tale modulo durante il suo funzionamento<sup>5</sup>. Risultano in Tabella 1 le API invocate (cfr. estratto dal log in Appendice I) dal modulo analizzato.

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<sup>1</sup> come già evidenziato in passato (cfr. relazione assegno LifeWatch Italia P. Tagliolato anno 2014-15).

<sup>2</sup> Bhagat, J., Tanoh, F., Nzuobontane, E., Laurent, T., Orłowski, J., Roos, M., Wolstencroft, K., Aleksejevs, S., Stevens, R., Pettifer, S., Lopez, R., Goble, C.A.: **BioCatalogue: a universal catalogue of web services for the life sciences**, Nucl. Acids Res., 2010. [doi:10.1093/nar/gkq394](https://doi.org/10.1093/nar/gkq394)

<sup>3</sup> cf. RFC 6570 URI Template specification <https://tools.ietf.org/html/rfc6570>

<sup>4</sup> <https://github.com/taverna-extras/taverna-perspective-biocatalogue/blob/master/taverna-perspective-biocatalogue/src/main/java/io/github/tavernaextras/biocatalogue/model/connectivity/BioCatalogueClient.java>

<sup>5</sup> Su piattaforma OSX i log di Taverna si trovano alla posizione ~/Library/Application/Support/taverna-biodiversity-2.5.0/logs/

**Tabella 1 - API invocate dal modulo BioCatalogue client di Taverna**

API	Rappresentazione richiesta	parametri di richiesta (query string parameters)						
		q (search query)	per_page (pagina parameter)	include_archived	page (pagina parameter)	sort_by	sort_order	include
<b>/soap_operations</b>	bljson	q=taxon	per_page=20	include_archived=false		sort_by=name	sort_order=asc	include=ancestors,inputs,outputs
<b>/rest_methods/filters</b>	xml	q=taxon						
<b>/soap_operations/filters</b>	xml	q=taxon						
<b>/rest_methods</b>	bljson	q=taxon	per_page=20	include_archived=false		sort_by=name	sort_order=asc	include=ancestors,inputs,outputs
<b>/soap_operations</b>	xml	q=taxon	per_page=20	include_archived=false	page=1	sort_by=name	sort_order=asc	include=ancestors,inputs,outputs
<b>/rest_methods</b>	xml	q=taxon	per_page=20	include_archived=false	page=1	sort_by=name	sort_order=asc	include=ancestors,inputs,outputs
<b>/services/3324/monitoring</b>	xml							
<b>/rest_methods/filters/index</b>	Xml (via POST)	q=taxon	per_page=20	include_archived=false	page=1	sort_by=name	sort_order=asc	include=ancestors,inputs,outputs

## Conclusioni

In assenza del software BioCatalogue ad implementazione delle funzionalità di catalogo dei servizi, sembra si possa suggerire, per adattare l'attuale catalogo dei servizi ad un'integrazione con Taverna, l'implementazione di quelle API individuate in questo documento come quelle necessarie al funzionamento del modulo di Taverna BioCatalogue client.

Resta da valutare la fattibilità di mappare l'attuale modello dati del Catalogo Servizi LW sul modello dati di BioCatalogue (almeno per quella parte toccata dalle API individuate). Risulta quindi indispensabile, per concludere questa parte di analisi, disporre dello schema del modello dati la cui documentazione è prevista nell'attività 1.3 del piano attività di LifeWatch Italia.

Allo stato attuale la piattaforma del Centro Servizi è dotata di alcune API "sperimentali" (per esempio il "dataportal" espone alcune REST API alternative alle interfacce web, che possono essere utilizzate per effettuare ricerche a testo libero nel portale dati). In seguito alle informazioni che saranno redatte nel deliverable 1.3, sarà possibile valutare se le eventuali API sviluppate per il Catalogo Servizi, al momento non disponibili, possano essere sfruttate, per esempio tramite un *strato adapter*. Questo potrebbe anche essere implementato come sistema a sé stante rispetto all'attuale Catalogo Servizi, di cui potrebbe essere solo *client*, incaricandosi di tradurre nelle API del Catalogo Servizi le richieste fatte da Taverna secondo le specifiche dettate da BioCatalogue.

## Glossario

*Servizi web*. Sistema software progettato per supportare l'interoperabilità tra diversi elaboratori su di una medesima rete in un contesto distribuito.

*Catalogo Servizi*. Risorsa del portale LifeWatch servicecentre dove sono registrati i servizi web offerti dall'infrastruttura distribuita, con informazioni per utilizzarli tramite interfacce utente e interfacce macchina-macchina.

*Laboratori virtuali*. Ambienti virtuali per condurre esperimenti scientifici in silico con gli strumenti messi a disposizione dall'infrastruttura

*Desktop remoto*. Computer remoto con interfaccia grafica messo a disposizione tramite un apposito applicativo, in modo che l'utente finale possa da un altro computer agire all'interno del D.R. come se vi fosse direttamente connesso.

*Orchestrazione di servizi*. Coordinamento di più servizi web, tipicamente presente in un'architettura distribuita

*Servizio REST*. Servizio web ispirato ai principi dell'architettura REST: REpresentational State Transfer (REST) è un tipo di architettura software per i sistemi di ipertesto distribuiti come il World Wide Web. Il termine REST è spesso usato per descrivere ogni semplice interfaccia che trasmetta dati su HTTP senza un livello opzionale come SOAP o la gestione della sessione tramite i cookie. Questi due concetti possono andare in conflitto così come in sovrapposizione.

*Servizio SOAP*. Servizio web aderente al protocollo SOAP: Simple Object Access Protocol è un protocollo per lo scambio di messaggi tra componenti software, tipicamente nella forma di

componentistica software. La parola object manifesta che l'uso del protocollo dovrebbe effettuarsi secondo il paradigma della programmazione orientata agli oggetti.

*URI.* Uniform Resource Identifier è una sequenza di caratteri che identifica univocamente una risorsa generica. Sono esempi di URI: un indirizzo web (URL), un documento, un'immagine, un file, un servizio, un indirizzo di posta elettronica, ecc.

*URI template.* Un URI Template è una sequenza compatta di caratteri per descrivere un insieme di Uniform Resource Identifiers tramite espansione di variabili.



## Appendice I – Estratto dal log di Taverna “service\_catalogue\_api.log”

```
10-dic-2016 17.37.50, 327, GET,
https://www.biocatalogue.org/rest_methods.bljson?per_page=20&include_archived=false&sort_by=name&q=t
axa&sort_order=asc&include=ancestors,inputs,outputs
10-dic-2016 17.37.50, 395, GET,
https://www.biocatalogue.org/soap_operations.bljson?per_page=20&include_archived=false&sort_by=name&
q=taxa&sort_order=asc&include=ancestors,inputs,outputs
10-dic-2016 17.37.50, 432, GET, https://www.biocatalogue.org/rest_methods/filters.xml?q=taxa
10-dic-2016 17.37.50, 5, xml_parsing, https://www.biocatalogue.org/rest_methods/filters.xml?q=taxa
10-dic-2016 17.37.50, 444, GET, https://www.biocatalogue.org/rest_methods/filters.xml?q=taxa
10-dic-2016 17.37.50, 1, xml_parsing, https://www.biocatalogue.org/rest_methods/filters.xml?q=taxa
10-dic-2016 17.37.50, 1322, GET, https://www.biocatalogue.org/soap_operations/filters.xml?q=taxa
10-dic-2016 17.37.51, 2, xml_parsing,
https://www.biocatalogue.org/soap_operations/filters.xml?q=taxa
10-dic-2016 17.37.50, 1748, GET, https://www.biocatalogue.org/soap_operations/filters.xml?q=taxa
10-dic-2016 17.37.52, 1, xml_parsing,
https://www.biocatalogue.org/soap_operations/filters.xml?q=taxa
10-dic-2016 17.37.51, 869, GET,
https://www.biocatalogue.org/soap_operations.xml?per_page=20&include_archived=false&page=1&sort_by=n
ame&q=taxa&sort_order=asc&include=ancestors,inputs,outputs
10-dic-2016 17.37.52, 82, xml_parsing,
https://www.biocatalogue.org/soap_operations.xml?per_page=20&include_archived=false&page=1&sort_by=n
ame&q=taxa&sort_order=asc&include=ancestors,inputs,outputs
10-dic-2016 17.38.00, 546, GET,
https://www.biocatalogue.org/soap_operations.bljson?per_page=20&include_archived=false&sort_by=name&
q=taxon&sort_order=asc&include=ancestors,inputs,outputs
10-dic-2016 17.38.00, 583, GET, https://www.biocatalogue.org/rest_methods/filters.xml?q=taxon
10-dic-2016 17.38.01, 4, xml_parsing, https://www.biocatalogue.org/rest_methods/filters.xml?q=taxon
10-dic-2016 17.38.00, 892, GET, https://www.biocatalogue.org/rest_methods/filters.xml?q=taxon
10-dic-2016 17.38.01, 2, xml_parsing, https://www.biocatalogue.org/rest_methods/filters.xml?q=taxon
10-dic-2016 17.38.00, 990, GET, https://www.biocatalogue.org/soap_operations/filters.xml?q=taxon
10-dic-2016 17.38.01, 1, xml_parsing,
https://www.biocatalogue.org/soap_operations/filters.xml?q=taxon
10-dic-2016 17.38.00, 1333, GET, https://www.biocatalogue.org/soap_operations/filters.xml?q=taxon
10-dic-2016 17.38.01, 1, xml_parsing,
https://www.biocatalogue.org/soap_operations/filters.xml?q=taxon
10-dic-2016 17.38.00, 2010, GET,
https://www.biocatalogue.org/rest_methods.bljson?per_page=20&include_archived=false&sort_by=name&q=t
axon&sort_order=asc&include=ancestors,inputs,outputs
10-dic-2016 17.38.01, 1753, GET,
https://www.biocatalogue.org/soap_operations.xml?per_page=20&include_archived=false&page=1&sort_by=n
ame&q=taxon&sort_order=asc&include=ancestors,inputs,outputs
10-dic-2016 17.38.03, 108, xml_parsing,
https://www.biocatalogue.org/soap_operations.xml?per_page=20&include_archived=false&page=1&sort_by=n
ame&q=taxon&sort_order=asc&include=ancestors,inputs,outputs
10-dic-2016 17.38.04, 577, GET,
https://www.biocatalogue.org/rest_methods.xml?per_page=20&include_archived=false&page=1&sort_by=name
&q=taxon&sort_order=asc&include=ancestors,inputs,outputs
10-dic-2016 17.38.04, 56, xml_parsing,
https://www.biocatalogue.org/rest_methods.xml?per_page=20&include_archived=false&page=1&sort_by=name
&q=taxon&sort_order=asc&include=ancestors,inputs,outputs
10-dic-2016 17.38.34, 230, GET, https://www.biocatalogue.org/services/3324/monitoring.xml
10-dic-2016 17.38.34, 6, xml_parsing, https://www.biocatalogue.org/services/3324/monitoring.xml
10-dic-2016 17.38.52, 249, GET, https://www.biocatalogue.org/rest_methods/314.xml
10-dic-2016 17.38.53, 12, xml_parsing, https://www.biocatalogue.org/rest_methods/314.xml
10-dic-2016 17.39.13, 358, GET, https://www.biocatalogue.org/rest_methods/314.xml
10-dic-2016 17.39.13, 3, xml_parsing, https://www.biocatalogue.org/rest\_methods/314.xml

10-dic-2016 19.43.14, 705, POST,
https://www.biocatalogue.org/rest_methods/filtered_index.bljson?per_page=20&include_archived=false&s
ort_by=name&q=taxon&sort_order=asc&include=ancestors,inputs,outputs
10-dic-2016 19.43.15, 437, POST,
https://www.biocatalogue.org/rest_methods/filtered_index.xml?per_page=20&include_archived=false&page
=1&sort_by=name&q=taxon&sort_order=asc&include=ancestors,inputs,outputs
10-dic-2016 19.43.16, 56, xml_parsing,
https://www.biocatalogue.org/rest_methods/filtered_index.xml?per_page=20&include_archived=false&page
=1&sort_by=name&q=taxon&sort_order=asc&include=ancestors,inputs,outputs
10-dic-2016 19.43.19, 74, POST,
https://www.biocatalogue.org/rest_methods/filtered_index.bljson?per_page=20&include_archived=false&s
ort_by=name&q=taxon&sort_order=asc&include=ancestors,inputs,outputs
10-dic-2016 19.43.20, 642, POST,
https://www.biocatalogue.org/rest_methods/filtered_index.xml?per_page=20&include_archived=false&page
=1&sort_by=name&q=taxon&sort_order=asc&include=ancestors,inputs,outputs
```

10-dic-2016 19.43.21, 56, xml\_parsing,  
[https://www.biocatalogue.org/rest\\_methods/filtered\\_index.xml?per\\_page=20&include\\_archived=false&page=1&sort\\_by=name&q=taxon&sort\\_order=asc&include=ancestors,inputs,outputs](https://www.biocatalogue.org/rest_methods/filtered_index.xml?per_page=20&include_archived=false&page=1&sort_by=name&q=taxon&sort_order=asc&include=ancestors,inputs,outputs)  
10-dic-2016 19.43.22, 74, POST,  
[https://www.biocatalogue.org/rest\\_methods/filtered\\_index.bljson?per\\_page=20&include\\_archived=false&sort\\_by=name&q=taxon&sort\\_order=asc&include=ancestors,inputs,outputs](https://www.biocatalogue.org/rest_methods/filtered_index.bljson?per_page=20&include_archived=false&sort_by=name&q=taxon&sort_order=asc&include=ancestors,inputs,outputs)  
10-dic-2016 19.43.23, 474, POST,  
[https://www.biocatalogue.org/rest\\_methods/filtered\\_index.xml?per\\_page=20&include\\_archived=false&page=1&sort\\_by=name&q=taxon&sort\\_order=asc&include=ancestors,inputs,outputs](https://www.biocatalogue.org/rest_methods/filtered_index.xml?per_page=20&include_archived=false&page=1&sort_by=name&q=taxon&sort_order=asc&include=ancestors,inputs,outputs)  
10-dic-2016 19.43.23, 55, xml\_parsing,  
[https://www.biocatalogue.org/rest\\_methods/filtered\\_index.xml?per\\_page=20&include\\_archived=false&page=1&sort\\_by=name&q=taxon&sort\\_order=asc&include=ancestors,inputs,outputs](https://www.biocatalogue.org/rest_methods/filtered_index.xml?per_page=20&include_archived=false&page=1&sort_by=name&q=taxon&sort_order=asc&include=ancestors,inputs,outputs)  
10-dic-2016 19.43.26, 71, POST,  
[https://www.biocatalogue.org/rest\\_methods/filtered\\_index.bljson?per\\_page=20&include\\_archived=false&sort\\_by=name&q=taxon&sort\\_order=asc&include=ancestors,inputs,outputs](https://www.biocatalogue.org/rest_methods/filtered_index.bljson?per_page=20&include_archived=false&sort_by=name&q=taxon&sort_order=asc&include=ancestors,inputs,outputs)  
10-dic-2016 19.43.26, 420, POST,  
[https://www.biocatalogue.org/rest\\_methods/filtered\\_index.xml?per\\_page=20&include\\_archived=false&page=1&sort\\_by=name&q=taxon&sort\\_order=asc&include=ancestors,inputs,outputs](https://www.biocatalogue.org/rest_methods/filtered_index.xml?per_page=20&include_archived=false&page=1&sort_by=name&q=taxon&sort_order=asc&include=ancestors,inputs,outputs)  
10-dic-2016 19.43.27, 56, xml\_parsing,  
[https://www.biocatalogue.org/rest\\_methods/filtered\\_index.xml?per\\_page=20&include\\_archived=false&page=1&sort\\_by=name&q=taxon&sort\\_order=asc&include=ancestors,inputs,outputs](https://www.biocatalogue.org/rest_methods/filtered_index.xml?per_page=20&include_archived=false&page=1&sort_by=name&q=taxon&sort_order=asc&include=ancestors,inputs,outputs)

## Appendice II – estratti dalle risposte ottenute dalle diverse API elencate in tabella 1

Descrizione: chiamate rivolte a <https://www.biocatalogue.org> che espone la versione del software Biocatalogue 2.2.0 e la versione delle API 1.2.1

API soap\_operations (bljson)

`/soap_operations.bljson?per_page=20&include_archived=false&sort_by=name&q=taxon&sort_order=asc&include=ancestors,inputs,outputs`

```
"soap_operations": [
  {
    "resource": "https://www.biocatalogue.org/soap_operations/37893",
    "name": "footprint_discovery"
  },
  {
    "resource": "https://www.biocatalogue.org/soap_operations/39149",
    "name": "footprint_discovery"
  },
  ...
  {
    "resource": "https://www.biocatalogue.org/soap_operations/39153",
    "name": "supported_organisms"
  }
]
```

API soap\_operations (xml)

`/soap_operations.xml?per_page=20&include_archived=false&page=1&sort_by=name&q=taxon&sort_order=asc&include=ancestors,inputs,outputs`

```
<?xml version="1.0" encoding="UTF-8"?>
<soapOperations
  xlink:href="https://www.biocatalogue.org/soap_operations?include=ancestors%2Cinputs%2Coutputs&include_archived=false&page=1&per_page=20&q=taxon&sort_by=name&sort_order=asc"
  xmlns="http://www.biocatalogue.org/2009/xml/rest" xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance"
  xsi:schemaLocation="http://www.biocatalogue.org/2009/xml/rest https://www.biocatalogue.org/2009/xml/rest/schema-v1.xsd" xmlns:xlink="http://www.w3.org/1999/xlink" xmlns:dc="http://purl.org/dc/elements/1.1/"
  xmlns:dcterms="http://purl.org/dc/terms/" resourceType="SoapOperations">
  <parameters>
    <filters>
    </filters>
    <query urlKey="q">taxon</query>
    <sortBy urlKey="sort_by" urlValue="name"></sortBy>
    <sortOrder urlKey="sort_order" urlValue="asc">Ascending</sortOrder>
    <page urlKey="page">1</page>
    <pageSize urlKey="per_page">20</pageSize>
  </parameters>
  <statistics>
    <pages>1</pages>
    <results>11</results>
    <total>21084</total>
  </statistics>
```

```

<results>
  <soapOperation xlink:href="https://www.biocatalogue.org/soap_operations/37893" xlink:title="Soap Operation - footprint_discovery" resourceName="footprint_discovery" resourceType="SoapOperation">
    ...
  </soapOperation>
  ...
  <soapOperation xlink:href="https://www.biocatalogue.org/soap_operations/39153" xlink:title="Soap Operation - supported_organisms" resourceName="supported_organisms" resourceType="SoapOperation">
    <dc:title>Soap Operation - supported_organisms[]</dc:title>
    <name>supported_organisms</name>
    <dc:description>List RSAT supported organisms.[]</dc:description>
    <parameterOrder></parameterOrder>
    <dcterms:created>2014-08-06T18:16:27Z[]</dcterms:created>
    <inputs xlink:href="https://www.biocatalogue.org/soap_operations/39153/inputs" resourceType="SoapOperation">
      <soapInput xlink:href="https://www.biocatalogue.org/soap_inputs/48924" xlink:title="Soap Input - parameters" resourceName="parameters" resourceType="SoapInput">
        <dc:title>Soap Input - parameters[]</dc:title>
        <name>parameters</name>
        <dc:description>[]</dc:description>
        <computationalType></computationalType>
        <computationalTypeDetails>{"name"=&gt;"" , "type"=&gt;[{"name"=&gt;"request" , "type"=&gt;[{"name"=&gt;"SupportedOrganismsRequest" , "type"=&gt;[{"name"=&gt;"output" , "type"=&gt;"string"}] , {"name"=&gt;"return" , "type"=&gt;"string"}] , {"name"=&gt;"format" , "type"=&gt;"string"}] , {"name"=&gt;"taxon" , "type"=&gt;"string"}] , {"name"=&gt;"depth" , "type"=&gt;"int"}]}} , {}</computationalTypeDetails>
        <dcterms:created>2014-08-06T18:16:27Z[]</dcterms:created>
      </soapInput>
    </inputs>
    <outputs xlink:href="https://www.biocatalogue.org/soap_operations/39153/outputs" resourceType="SoapOperation">
      <soapOutput xlink:href="https://www.biocatalogue.org/soap_outputs/36726" xlink:title="Soap Output - output" resourceName="output" resourceType="SoapOutput">
        <dc:title>Soap Output - output[]</dc:title>
        <name>output</name>
        <dc:description>[]</dc:description>
        <computationalType></computationalType>
        <computationalTypeDetails>{"name"=&gt;"" , "type"=&gt;[{"name"=&gt;"response" , "type"=&gt;[{"name"=&gt;"SupportedOrganismsResponse" , "type"=&gt;[{"name"=&gt;"server" , "type"=&gt;"string"}] , {"name"=&gt;"command" , "type"=&gt;"string"}] , {"name"=&gt;"client" , "type"=&gt;"string"}]}} , {}</computationalTypeDetails>
        <dcterms:created>2014-08-06T18:16:27Z[]</dcterms:created>
      </soapOutput>
    </outputs>
    <ancestors>
      <service xlink:href="https://www.biocatalogue.org/services/2003" xlink:title="Service - retrieve_ensembl_seq" resourceName="retrieve_ensembl_seq" resourceType="Service">
        <dc:title>Service - retrieve_ensembl_seq[]</dc:title>
        <name>retrieve_ensembl_seq</name>
        <originalSubmitter xlink:href="https://www.biocatalogue.org/users/427" xlink:title="Member - olisand" resourceName="olisand" resourceType="User" resourceName="olisand"/>
        <dc:description>Web services for the Regulatory Sequence Analysis Tools (RSAT). Tools developed by Jacques van Helden (jvanheld@bigre.ulb.ac.be), SOAP/WSDL interface developed by Olivier Sand (oly@bigre.ulb.ac.be).[]</dc:description>
        <serviceTechnologyTypes>
          <type>SOAP</type>
        </serviceTechnologyTypes>
        <latestMonitoringStatus>
          <label>WARNING</label>
          <message>Some or all of the tests for this service did not succeed&lt;p&gt;&lt;ul&gt;&lt;li&gt; Could not

```

```

access <lt;b>wsdl_location </b>.</li>
</ul></p></message>
  <symbol xlink:href="https://www.biocatalogue.org/assets/pling-sphere-50-
d62347d509c1e44124f531d17a552c0f.png" xlink:title="Large status symbol icon for this monitoring status"/>
  <smallSymbol xlink:href="https://www.biocatalogue.org/assets/small-pling-sphere-50-
34c8d0501dca95e9090fe68c3ceb8871.png" xlink:title="Small status symbol icon for this monitoring status"/>
  <lastChecked>2016-12-15T12:08:58Z</lastChecked>
</latestMonitoringStatus>
<dcterms:created>2009-06-26T11:34:23Z</dcterms:created>
<monitoring xlink:href="https://www.biocatalogue.org/services/2003/monitoring" resourceType="Service">
  <tests>
    <serviceTest xlink:href="https://www.biocatalogue.org/service_tests/2023" resourceType="ServiceTest">
      <testType>
        <urlMonitor>
          <url>http://rsat.ulb.ac.be/rsat/web_services/RSATWS.cgi</url>
          <resource resourceType="ServiceDeployment"
xlink:href="https://www.biocatalogue.org/service_deployments/2003" xlink:title="The resource from which the URL to
be monitored is obtained from"/>
        </urlMonitor>
      </testType>
      <dcterms:created>2010-03-09T15:46:22Z</dcterms:created>
      <activated>true</activated>
      <activatedAt>2009-06-26T13:10:29Z</activatedAt>
      <latestStatus>
        <label>PASSED</label>
        <message>The last check for this test was successful</message>
        <symbol xlink:href="https://www.biocatalogue.org/assets/tick-sphere-50-
6b7197514ef994d9cd0ee925b9f2332f.png" xlink:title="Large status symbol icon for this monitoring status"/>
        <smallSymbol xlink:href="https://www.biocatalogue.org/assets/small-tick-sphere-50-
8703d0772f35d31d0f41e1874f7a20e8.png" xlink:title="Small status symbol icon for this monitoring status"/>
        <lastChecked>2016-12-15T12:08:28Z</lastChecked>
      </latestStatus>
    </serviceTest>
    <serviceTest xlink:href="https://www.biocatalogue.org/service_tests/2024" resourceType="ServiceTest">
      <testType>
        <urlMonitor>
          <url>http://rsat.bigre.ulb.ac.be/rsat/web_services/RSATWS.wsdl</url>
          <resource resourceType="SoapService" xlink:href="https://www.biocatalogue.org/soap_services/1999"
xlink:title="The resource from which the URL to be monitored is obtained from"/>
        </urlMonitor>
      </testType>
      <dcterms:created>2010-03-09T15:46:33Z</dcterms:created>
      <activated>true</activated>
      <activatedAt>2009-06-26T13:10:29Z</activatedAt>
      <latestStatus>
        <label>FAILED</label>
        <message>The last check failed <p><b>Note :</b> Test is failing since Thursday
December 10 , 2015</p></message>
        <symbol xlink:href="https://www.biocatalogue.org/assets/cross-sphere-50-
1a56159eb22a78259bc76974dad29f55.png" xlink:title="Large status symbol icon for this monitoring status"/>
        <smallSymbol xlink:href="https://www.biocatalogue.org/assets/small-cross-sphere-50-
7ed858fb697e10f07bf920dec93806ff.png" xlink:title="Small status symbol icon for this monitoring status"/>
        <lastChecked>2016-12-15T12:08:58Z</lastChecked>
      </latestStatus>
    </serviceTest>
    <serviceTest xlink:href="https://www.biocatalogue.org/service_tests/2365" resourceType="ServiceTest">
      <testType>
        <testScript>
          <name>purge_seq_perl_test1</name>

```

```

    <dc:description>This test masks redundant stretches of sequence in a pair of DNA
sequences.[]</dc:description>
    <contentType>application/zip</contentType>
    <programmingLanguage>perl</programmingLanguage>
    <executableFilename>purge_seq_test1.pl</executableFilename>
    <download xlink:href="https://www.biocatalogue.org/test_scripts/2/download" xlink:title="The download
link to the test script file/package"/>
    <submitter xlink:href="https://www.biocatalogue.org/users/427" xlink:title="Member - olisand"
resourceType="User" resourceName="olisand"/>
    <dcterms:created>2010-03-10T12:38:54Z[]</dcterms:created>
    <activatedAt xsi:nil="true"/>
</testScript>
</testType>
<dcterms:created>2010-03-10T12:38:54Z[]</dcterms:created>
<activated>>false</activated>
<activatedAt xsi:nil="true"/>
<latestStatus>
<label>FAILED</label>
<message>The last check failed &lt;p>&lt;b>Note :&lt;/b> Test is failing since Thursday
March 11 , 2010&lt;p></message>
<symbol xlink:href="https://www.biocatalogue.org/assets/cross-sphere-50-
1a56159eb22a78259bc76974dad29f55.png" xlink:title="Large status symbol icon for this monitoring status"/>
<smallSymbol xlink:href="https://www.biocatalogue.org/assets/small-cross-sphere-50-
7ed858fb697e10f07bf920dcc93806ff.png" xlink:title="Small status symbol icon for this monitoring status"/>
<lastChecked>2013-01-10T06:35:28Z</lastChecked>
</latestStatus>
</serviceTest>
<serviceTest xlink:href="https://www.biocatalogue.org/service_tests/2372" resourceType="ServiceTest">
<testType>
<testScript>
<name>retrieve_ensembl_seq perl test 1</name>
<dc:description>This test retrieves 50 base pairs upstream the transcription start site of the human
ENSG00000139618 gene and compares it to the expected DNA sequence.[]</dc:description>
<contentType>application/zip</contentType>
<programmingLanguage>perl</programmingLanguage>
<executableFilename>retrieve-ensembl-seq_test1.pl</executableFilename>
<download xlink:href="https://www.biocatalogue.org/test_scripts/9/download" xlink:title="The download
link to the test script file/package"/>
<submitter xlink:href="https://www.biocatalogue.org/users/427" xlink:title="Member - olisand"
resourceType="User" resourceName="olisand"/>
<dcterms:created>2010-03-10T12:38:55Z[]</dcterms:created>
<activatedAt xsi:nil="true"/>
</testScript>
</testType>
<dcterms:created>2010-03-10T12:38:55Z[]</dcterms:created>
<activated>>false</activated>
<activatedAt xsi:nil="true"/>
<latestStatus>
<label>FAILED</label>
<message>The last check failed &lt;p>&lt;b>Note :&lt;/b> Test is failing since Thursday
March 11 , 2010&lt;p></message>
<symbol xlink:href="https://www.biocatalogue.org/assets/cross-sphere-50-
1a56159eb22a78259bc76974dad29f55.png" xlink:title="Large status symbol icon for this monitoring status"/>
<smallSymbol xlink:href="https://www.biocatalogue.org/assets/small-cross-sphere-50-
7ed858fb697e10f07bf920dcc93806ff.png" xlink:title="Small status symbol icon for this monitoring status"/>
<lastChecked>2013-01-10T06:31:57Z</lastChecked>
</latestStatus>
</serviceTest>
</tests>

```

```

</monitoring>
</service>
<soapService xlink:href="https://www.biocatalogue.org/soap_services/1999" xlink:title="Soap Service -
RSATWebServices" resourceName="RSATWebServices" resourceType="SoapService">
  <dc:title>Soap Service - RSATWebServices</dc:title>
  <name>RSATWebServices</name>
  <wsdlLocation>http://rsat.bigre.ulb.ac.be/rsat/web_services/RSATWS.wsdl</wsdlLocation>
  <submitter xlink:href="https://www.biocatalogue.org/users/427" xlink:title="Member - olisand"
resourceType="User" resourceName="olisand"/>
  <dc:description>Web services for the Regulatory Sequence Analysis Tools (RSAT). Tools developed by
Jacques van Helden (jvanheld@bigre.ulb.ac.be), SOAP/WSDL interface developed by Olivier Sand
(oly@bigre.ulb.ac.be).</dc:description>

<documentationUrl>http://rsat.bigre.ulb.ac.be/rsat/web_services/RSATWS_documentation.xml</documentation
Url>
  <dcterms:created>2009-06-26T11:34:12Z</dcterms:created>
</soapService>
</ancestors>
<related>
  <inputs xlink:href="https://www.biocatalogue.org/soap_operations/39153/inputs" xlink:title="All SOAP Inputs
for this SOAP Operation" resourceType="SoapOperation"/>
  <outputs xlink:href="https://www.biocatalogue.org/soap_operations/39153/outputs" xlink:title="All SOAP
outputs for this SOAP Operation" resourceType="SoapOperation"/>
  <annotations xlink:href="https://www.biocatalogue.org/soap_operations/39153/annotations" xlink:title="All
annotations on this SOAP Operation" resourceType="Annotations"/>
  <annotationsOnAll
xlink:href="https://www.biocatalogue.org/soap_operations/39153/annotations?also=inputs%2Coutputs" xlink:title="All
annotations on ALL parts of this SOAP Operation. I.e.: including all the inputs and outputs"
resourceType="Annotations"/>
  </related>
</soapOperation>
</results>
<related>
  <filters xlink:href="https://www.biocatalogue.org/soap_operations/filters" xlink:title="Filters for the SOAP
operations index" resourceType="Filters"/>
  <filtersOnCurrentResults
xlink:href="https://www.biocatalogue.org/soap_operations/filters?include=ancestors%2Cinputs%2Coutputs&inclu
de_archived=false&per_page=20&q=taxon&sort_by=name&sort_order=asc" xlink:title="Filters for
the SOAP operations index that will be applied on top of the current results set" resourceType="Filters"/>
  </related>
</soapOperations>

```

API rest\_methods (bljson)

/rest\_methods.bljson?per\_page=20&include\_archived=false&sort\_by=name&q=taxon&sort\_orde  
r=asc&include=ancestors,inputs,outputs

```

{
  "rest_methods": [
    {
      "resource": "https://www.biocatalogue.org/rest_methods/314",
      "name": "/help"
    },
    ...

```

```
{
  "resource": "https://www.biocatalogue.org/rest_methods/381",
  "name": "/data/view/Taxon:{id}"
}
]
```

API rest\_methods (xml)

/rest\_methods.xml?per\_page=20&include\_archived=false&page=1&sort\_by=name&q=taxon&sort\_order=asc&include=ancestors,inputs,outputs

```
<?xml version="1.0" encoding="UTF-8"?>
<restMethods
  xlink:href="https://www.biocatalogue.org/rest_methods?include=ancestors%2Cinputs%2Coutputs&include_archived=false&page=1&per_page=20&q=taxon&sort_by=name&sort_order=asc"
  xmlns="http://www.biocatalogue.org/2009/xml/rest" xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance"
  xsi:schemaLocation="http://www.biocatalogue.org/2009/xml/rest https://www.biocatalogue.org/2009/xml/rest/schema-v1.xsd" xmlns:xlink="http://www.w3.org/1999/xlink" xmlns:dc="http://purl.org/dc/elements/1.1/"
  xmlns:dcterms="http://purl.org/dc/terms/" resourceType="RestMethods">
  <parameters>
    <filters>
    </filters>
    <query urlKey="q">taxon</query>
    <sortBy urlKey="sort_by" urlValue="name"></sortBy>
    <sortOrder urlKey="sort_order" urlValue="asc">Ascending</sortOrder>
    <page urlKey="page">1</page>
    <pageSize urlKey="per_page">20</pageSize>
  </parameters>
  <statistics>
    <pages>1</pages>
    <results>3</results>
    <total>582</total>
  </statistics>
  <results>
    <restMethod xlink:href="https://www.biocatalogue.org/rest_methods/314" xlink:title="Rest Method - GET /help"
  resourceName="" resourceType="RestMethod">
    ...
  </restMethod>
    ...
    <restMethod xlink:href="https://www.biocatalogue.org/rest_methods/381" xlink:title="Rest Method - Taxonomy
  portal" resourceName="Taxonomy portal" resourceType="RestMethod">
      <dc:title>Rest Method - Taxonomy portal</dc:title>
      <name>Taxonomy portal</name>
      <endpointLabel>GET /data/view/Taxon:{id}</endpointLabel>
      <httpMethodType>GET</httpMethodType>
      <urlTemplate>http://www.ebi.ac.uk/ena/data/view/Taxon:{id}?portal={portal}</urlTemplate>
      <dc:description>This REST endpoint supports the retrieval of nucleotide sequence and associated data using
  a taxon identifier.</dc:description>
      <documentationUrl/>
      <submitter xlink:href="https://www.biocatalogue.org/users/671" xlink:title="Member - rasko.leinonen"
  resourceName="User" resourceType="User">
      <dcterms:created>2013-05-15T15:42:25Z</dcterms:created>
      <inputs xlink:href="https://www.biocatalogue.org/rest_methods/381/inputs" resourceType="RestMethod">
      <parameters>
        <restParameter xlink:href="https://www.biocatalogue.org/rest_parameters/471" xlink:title="Rest Parameter -
  id" resourceName="id" resourceType="RestParameter">
```



```

<dc:title>Rest Parameter - id</dc:title>
<name>id</name>
<dc:description>The taxon identifier.</dc:description>
<computationalType/>
<defaultValue/>
<paramStyle>template</paramStyle>
<isOptional>>false</isOptional>
<constrainedValues>
</constrainedValues>
<submitter xlink:href="https://www.biocatalogue.org/users/671" xlink:title="Member - rasko.leinonen"
resourceType="User" resourceName="rasko.leinonen"/>
<dcterms:created>2013-05-15T15:50:16Z</dcterms:created>
</restParameter>
<restParameter xlink:href="https://www.biocatalogue.org/rest_parameters/472" xlink:title="Rest Parameter -
portal" resourceName="portal" resourceType="RestParameter">
<dc:title>Rest Parameter - portal</dc:title>
<name>portal</name>
<dc:description>The result to fetch</dc:description>
<computationalType/>
<defaultValue/>
<paramStyle>query</paramStyle>
<isOptional>>true</isOptional>
<constrainedValues>
<value>analysis</value>
<value>analysis_study</value>
<value>assembly</value>
<value>read_experiment</value>
<value>read_run</value>
<value>read_study</value>
<value>read_trace</value>
<value>sample</value>
<value>sequence_coding</value>
<value>sequence_release</value>
<value>sequence_update</value>
<value>study</value>
</constrainedValues>
<submitter xlink:href="https://www.biocatalogue.org/users/671" xlink:title="Member - rasko.leinonen"
resourceType="User" resourceName="rasko.leinonen"/>
<dcterms:created>2013-05-15T15:52:50Z</dcterms:created>
</restParameter>
</parameters>
<representations>
</representations>
</inputs>
<outputs xlink:href="https://www.biocatalogue.org/rest_methods/381/outputs" resourceType="RestMethod">
<parameters>
</parameters>
<representations>
</representations>
</outputs>
<ancestors>
<service xlink:href="https://www.biocatalogue.org/services/2752" xlink:title="Service - European Nucleotide
Archive (ENA) Browser" resourceName="European Nucleotide Archive (ENA) Browser" resourceType="Service">
<dc:title>Service - European Nucleotide Archive (ENA) Browser</dc:title>
<name>European Nucleotide Archive (ENA) Browser</name>
<originalSubmitter xlink:href="https://www.biocatalogue.org/users/671" xlink:title="Member - rasko.leinonen"
resourceType="User" resourceName="rasko.leinonen"/>
<dc:description>The European Nucleotide Archive (ENA) Browser provides functionality to view and
retrieve nucleotide sequence data archived and exchanged by the International Sequence Database

```

## Collaboration (INSDC).

```

</dc:description>
  <serviceTechnologyTypes>
    <type>REST</type>
  </serviceTechnologyTypes>
  <latestMonitoringStatus>
    <label>PASSED</label>
    <message>All tests were successful for this service</message>
    <symbol xlink:href="https://www.biocatalogue.org/assets/tick-sphere-50-6b7197514ef994d9cd0ee925b9f2332f.png" xlink:title="Large status symbol icon for this monitoring status"/>
    <smallSymbol xlink:href="https://www.biocatalogue.org/assets/small-tick-sphere-50-8703d0772f35d31d0f41e1874f7a20e8.png" xlink:title="Small status symbol icon for this monitoring status"/>
    <lastChecked>2016-12-15T13:47:28Z</lastChecked>
  </latestMonitoringStatus>
  <dcterms:created>2010-12-07T14:11:27Z</dcterms:created>
  <monitoring xlink:href="https://www.biocatalogue.org/services/2752/monitoring" resourceType="Service">
    <tests>
      <serviceTest xlink:href="https://www.biocatalogue.org/service_tests/4203" resourceType="ServiceTest">
        <testType>
          <urlMonitor>
            <url>http://www.ebi.ac.uk/ena/data/search?query=histone</url>
            <resource resourceType="Annotation" xlink:href="https://www.biocatalogue.org/annotations/55081"
xlink:title="The resource from which the URL to be monitored is obtained from"/>
          </urlMonitor>
        </testType>
        <dcterms:created>2010-12-08T05:00:24Z</dcterms:created>
        <activated>true</activated>
        <activatedAt>2010-12-08T05:00:24Z</activatedAt>
        <latestStatus>
          <label>PASSED</label>
          <message>The last check for this test was successful</message>
          <symbol xlink:href="https://www.biocatalogue.org/assets/tick-sphere-50-6b7197514ef994d9cd0ee925b9f2332f.png" xlink:title="Large status symbol icon for this monitoring status"/>
          <smallSymbol xlink:href="https://www.biocatalogue.org/assets/small-tick-sphere-50-8703d0772f35d31d0f41e1874f7a20e8.png" xlink:title="Small status symbol icon for this monitoring status"/>
          <lastChecked>2016-12-15T13:47:27Z</lastChecked>
        </latestStatus>
      </serviceTest>
      <serviceTest xlink:href="https://www.biocatalogue.org/service_tests/4204" resourceType="ServiceTest">
        <testType>
          <urlMonitor>
            <url>http://www.ebi.ac.uk/ena</url>
            <resource resourceType="ServiceDeployment"
xlink:href="https://www.biocatalogue.org/service_deployments/2752" xlink:title="The resource from which the URL to
be monitored is obtained from"/>
          </urlMonitor>
        </testType>
        <dcterms:created>2010-12-08T05:39:09Z</dcterms:created>
        <activated>true</activated>
        <activatedAt>2010-12-08T05:39:09Z</activatedAt>
        <latestStatus>
          <label>PASSED</label>
          <message>The last check for this test was successful</message>
          <symbol xlink:href="https://www.biocatalogue.org/assets/tick-sphere-50-6b7197514ef994d9cd0ee925b9f2332f.png" xlink:title="Large status symbol icon for this monitoring status"/>
          <smallSymbol xlink:href="https://www.biocatalogue.org/assets/small-tick-sphere-50-8703d0772f35d31d0f41e1874f7a20e8.png" xlink:title="Small status symbol icon for this monitoring status"/>
          <lastChecked>2016-12-15T13:47:28Z</lastChecked>
        </latestStatus>
      </serviceTest>
    </tests>
  </monitoring>
</dc:description>

```

```

</serviceTest>
</tests>
</monitoring>
</service>
<restService xlink:href="https://www.biocatalogue.org/rest_services/89" xlink:title="Rest Service - European Nucleotide Archive (ENA) Browser" resourceName="European Nucleotide Archive (ENA) Browser" resourceType="RestService">
  <dc:title>Rest Service - European Nucleotide Archive (ENA) Browser[]</dc:title>
  <name>European Nucleotide Archive (ENA) Browser</name>
  <submitter xlink:href="https://www.biocatalogue.org/users/671" xlink:title="Member - rasko.leinonen" resourceType="User" resourceName="rasko.leinonen"/>
  <dc:description>The European Nucleotide Archive (ENA) Browser provides functionality to view and retrieve nucleotide sequence data archived and exchanged by the International Sequence Database Collaboration (INSDC).
[]</dc:description>
  <documentationUrl>http://www.ebi.ac.uk/ena/about/browser</documentationUrl>
  <dcterms:created>2010-12-07T14:11:26Z[]</dcterms:created>
</restService>
<restResource xlink:href="https://www.biocatalogue.org/rest_resources/454" xlink:title="Rest Resource - /data/view/Taxon:{id}" resourceName="/data/view/Taxon:{id}" resourceType="RestResource">
  <dc:title>Rest Resource - /data/view/Taxon:{id}[]</dc:title>
  <path>/data/view/Taxon:{id}</path>
  <submitter xlink:href="https://www.biocatalogue.org/users/671" xlink:title="Member - rasko.leinonen" resourceType="User" resourceName="rasko.leinonen"/>
  <dcterms:created>2013-05-15T15:50:14Z[]</dcterms:created>
</restResource>
</ancestors>
<related>
  <inputs xlink:href="https://www.biocatalogue.org/rest_methods/381/inputs" xlink:title="All REST Inputs on this REST endpoint" resourceType="RestMethod"/>
  <outputs xlink:href="https://www.biocatalogue.org/rest_methods/381/outputs" xlink:title="All REST Outputs on this REST endpoint" resourceType="RestMethod"/>
  <annotations xlink:href="https://www.biocatalogue.org/rest_methods/381/annotations" xlink:title="All annotations on this REST endpoint" resourceType="Annotations"/>
</related>
</restMethod>
</results>
<related>
  <filters xlink:href="https://www.biocatalogue.org/rest_methods/filters" xlink:title="Filters for the REST Methods index" resourceType="Filters"/>
  <filtersOnCurrentResults
xlink:href="https://www.biocatalogue.org/rest_methods/filters?include=ancestors%2Cinputs%2Coutputs&include_archived=false&per_page=20&q=taxon&sort_by=name&sort_order=asc" xlink:title="Filters for the REST Methods index that will be applied on top of the current results set" resourceType="Filters"/>
</related>
</restMethods>

```

API rest\_methods/{methodID} (xml)

/rest\_methods/314.xml

```

<?xml version="1.0" encoding="UTF-8"?>
<restMethod xlink:href="https://www.biocatalogue.org/rest_methods/314" xlink:title="Rest Method - GET /help"
xmlns="http://www.biocatalogue.org/2009/xml/rest" xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance"
xsi:schemaLocation="http://www.biocatalogue.org/2009/xml/rest https://www.biocatalogue.org/2009/xml/rest/schema-v1.xsd" xmlns:xlink="http://www.w3.org/1999/xlink" xmlns:dc="http://purl.org/dc/elements/1.1/"

```



```

<dcterms:created>2011-11-24T07:32:28Z[]</dcterms:created>
<activated>true</activated>
<activatedAt>2011-11-24T07:32:28Z</activatedAt>
<latestStatus>
<label>FAILED</label>
<message>The last check failed &lt;p&gt;&lt;b&gt;Note :&lt;/b&gt; Test is failing since Thursday March
31 , 2016&lt;p&gt;</message>
<symbol xlink:href="https://www.biocatalogue.org/assets/cross-sphere-50-
1a56159eb22a78259bc76974dad29f55.png" xlink:title="Large status symbol icon for this monitoring status"/>
<smallSymbol xlink:href="https://www.biocatalogue.org/assets/small-cross-sphere-50-
7ed858fb697e10f07bf920dcc93806ff.png" xlink:title="Small status symbol icon for this monitoring status"/>
<lastChecked>2016-12-15T13:59:02Z</lastChecked>
</latestStatus>
</serviceTest>
<serviceTest xlink:href="https://www.biocatalogue.org/service_tests/5331" resourceType="ServiceTest">
<testType>
<urlMonitor>
<url>http://data.gbif.org/ws/rest/taxon/help</url>
<resource resourceType="Annotation" xlink:href="https://www.biocatalogue.org/annotations/58426"
xlink:title="The resource from which the URL to be monitored is obtained from"/>
</urlMonitor>
</testType>
<dcterms:created>2011-11-26T04:30:30Z[]</dcterms:created>
<activated>true</activated>
<activatedAt>2011-11-26T04:30:30Z</activatedAt>
<latestStatus>
<label>FAILED</label>
<message>The last check failed &lt;p&gt;&lt;b&gt;Note :&lt;/b&gt; Test is failing since Thursday March
31 , 2016&lt;p&gt;</message>
<symbol xlink:href="https://www.biocatalogue.org/assets/cross-sphere-50-
1a56159eb22a78259bc76974dad29f55.png" xlink:title="Large status symbol icon for this monitoring status"/>
<smallSymbol xlink:href="https://www.biocatalogue.org/assets/small-cross-sphere-50-
7ed858fb697e10f07bf920dcc93806ff.png" xlink:title="Small status symbol icon for this monitoring status"/>
<lastChecked>2016-12-15T13:59:04Z</lastChecked>
</latestStatus>
</serviceTest>
</tests>
</monitoring>
</service>
<restService xlink:href="https://www.biocatalogue.org/rest_services/144" xlink:title="Rest Service - GBIF taxon
web service" resourceName="GBIF taxon web service" resourceType="RestService">
<dc:title>Rest Service - GBIF taxon web service[]</dc:title>
<name>GBIF taxon web service</name>
<submitter xlink:href="https://www.biocatalogue.org/users/871" xlink:title="Member - Hannu Saarenmaa"
resourceType="User" resourceName="Hannu Saarenmaa"/>
<dc:description>Global Biodiversity Information Facility taxonomic web service from the centralised GBIF
data portal[]</dc:description>
<documentationUrl>http://www.gbif.org/developer/summary</documentationUrl>
<dcterms:created>2011-11-23T14:04:57Z[]</dcterms:created>
</restService>
<restResource xlink:href="https://www.biocatalogue.org/rest_resources/382" xlink:title="Rest Resource - /help"
resourceName="/help" resourceType="RestResource">
<dc:title>Rest Resource - /help[]</dc:title>
<path>/help</path>
<submitter xlink:href="https://www.biocatalogue.org/users/829" xlink:title="Member - Robert Haines"
resourceType="User" resourceName="Robert Haines"/>
<dcterms:created>2011-11-25T15:48:15Z[]</dcterms:created>
</restResource>
</ancestors>

```

```
<related>
  <inputs xlink:href="https://www.biocatalogue.org/rest_methods/314/inputs" xlink:title="All REST Inputs on this REST endpoint" resourceType="RestMethod"/>
  <outputs xlink:href="https://www.biocatalogue.org/rest_methods/314/outputs" xlink:title="All REST Outputs on this REST endpoint" resourceType="RestMethod"/>
  <annotations xlink:href="https://www.biocatalogue.org/rest_methods/314/annotations" xlink:title="All annotations on this REST endpoint" resourceType="Annotations"/>
</related>
</restMethod>
```