

List of all available methods for BioModels Database Web Services.

Please note that by using the Java client library, users have access to more features: such as proxy settings, etc.

Method	Description
String[] getAllCuratedModelsId()	Return the identifier of all models in curated branch, and return them in a string array.
String[] getAllModelsId()	Return the identifier of all models in both curated and non-curated branch, and return them in a string array.
String[] getAllNonCuratedModelsId()	Return the identifier of all models in non-curated branch, and return them in a string array.
String getModelById(String id)	Deprecated: replaced by getModelSBMLById(String id)
String getModelNameById(String id)	Return the name of the model with the given identifier.
String getModelSBMLById(String id)	Return the model in SBML format by giving the identifier.
String[] getModelsIdByChEBI(String text)	Return the identifier of all models which annotations include the given text. The given text could be either a ChEBI identifier or ChEBI entry name.
String[] getModelsIdByChEBIId(String ChEBIid)	Return the identifier of all models which annotations include the given ChEBI identifier.
String[] getModelsIdByGO(String text)	Return the identifier of all models which annotations include the given text. The given text could be either a Gene Ontology identifier or Gene Ontology entry name.
String[] getModelsIdByName(String modelName)	Return the identifier of all models which names include the given modelName.
String[] getModelsIdByPerson(String personName)	Return the identifier of all models which authors and encoders' names include the given personName.
String[] getModelsIdByPublication(String publicationIdOrText)	Return the identifier of all models which corresponding publication has the given publication identifier or includes the given text. The publication identifier could be PubMed identifier, DOI or the URL of the published model.

<code>String[] getModelsIdByTaxonomy(String text)</code>	Return the identifier of all models which annotations include the given text. The given text could be either a Taxonomy identifier or Taxonomy entry name.
<code>String[] getModelsIdByTaxonomyId(String taxonomyId)</code>	Return the identifier of all models which annotations include the given Taxonomy identifier.
<code>String[] getModelsIdByUniprot(String text)</code>	Return the identifier of all models which annotations include the given text. The given text could be either a UniProt identifier or UniProt entry name.
<code>String[] getModelsIdByUniprotId(String UniProtId)</code>	Return the identifier of all models which annotations include the given UniProt identifier.
<code>String[] getModelsIdByUniprotIds(String[] UniProtIds)</code>	Return the identifier of all models which annotations include the given set of UniProt identifiers.
<code>String getSimpleModelById(String id)</code>	Return the model's meta data (identifier, name, publication, last modification date) in an XML. By using the provided Java client library, a <code>uk.ac.ebi.biomodels.SimpleModel</code> object which carries this meta data will be returned.
<code>String getSimpleModelsByChEBIIds(String[] ChEBIIds)</code>	Return the meta data (identifier, name, publication, last modification date) of the models which annotations include the given set of ChEBI identifiers. By using the provided Java client library, a set of <code>uk.ac.ebi.biomodels.SimpleModel</code> objects which carry this meta data will be returned.
<code>String getSimpleModelsByReactomeIds(String[] ReactomeIds)</code>	Return the meta data (identifier, name, publication, last modification date) of the models which annotations include the given set of Reactome identifiers. By using the provided Java client library, a set of <code>uk.ac.ebi.biomodels.SimpleModel</code> objects which carry this meta data will be returned.
<code>String getSimpleModelsByUniprotIds(String[] UniProtIds)</code>	Return the meta data (identifier, name, publication, last modification date) of the models which annotations include the given set of UniProt identifiers. By using the provided Java client library, a set of <code>uk.ac.ebi.biomodels.SimpleModel</code> objects which carry this meta data will be returned.
<code>String getSimpleModelsRelatedWithChEBI()</code>	Return the meta data (identifier, name, publication, last modification date) of all the models which has

	ChEBI annotations. By using the provided Java client library, a set of uk.ac.ebi.biomodels.SimpleModel objects which carry this meta data will be returned.
String getSubModelSBML(String modelId, String[] elementsIds)	Return the sub-model in SBML format. This method extracts all the related elements with the given elements identifiers and constructs them into a new model.
String helloBioModels()	Return “Hello BioModels”.