Ensembl API Course: REST API

Magali Ruffier

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EMBL – European Bioinformatics Institute
Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SD, UK

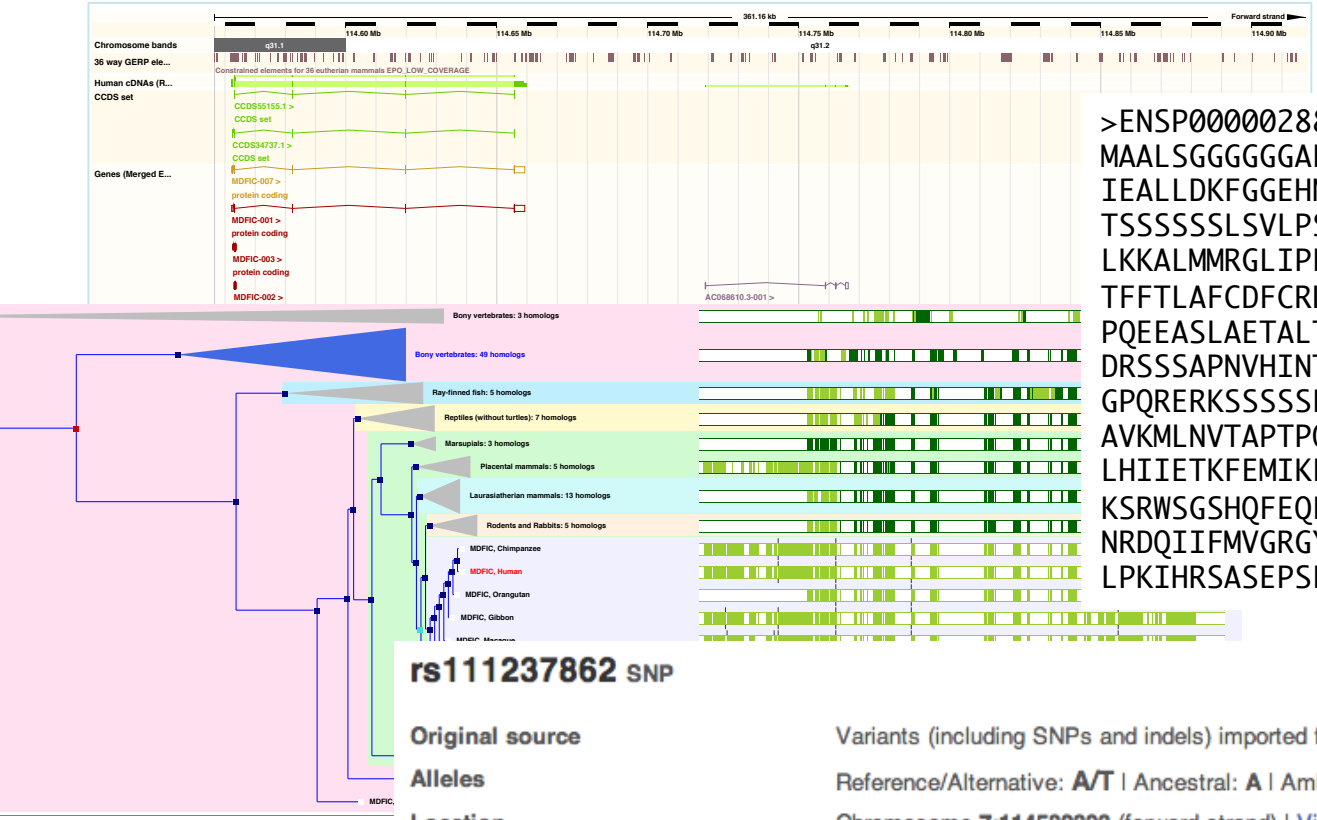
Outline

1. Ensembl
    1. Data available
    2. Data access
2. The REST API
    1. What is it
    2. How to query it
    3. Examples
        1. Retrieve sequence
        2. From region to variation
        3. Write a script

Outline

1. Introduction to the Ensembl REST APIs on rest.ensembl.org and grch37.rest.ensembl.org
2. How to make REST requests
3. How to fetch data with Python, Ruby, Perl or from the UNIX command line
4. Data available:
    1. sequences and genomic features
    2. genomic alignments or gene trees
    3. convert coordinates between two different assemblies
    4. Fetch variant consequences based on a SNP or a CNV

Data in Ensembl




```
>ENSP00000288602
MAALSGGGGGGAEPGQALFNGDMEPEAGAGAGAAASSAADPAIPEEV
IEALLDKFGGEHNPPSIYLEAYEEYTSKLDALQQREQQLLESLGNGT
TSSSSSSLSVLPSSLSVFQNPTDVARSNPKSPQKPIVRVFLPNKQRT
LKKALMMRGLIPECCAVYRIQDGEKKPIGWDTDISWLTGEELHVEVL
TFFTLAFCDFCRKLLFQGFRCQTCGYKFHQRCSTEVPLMCVNYDQLD
PQEEASLAETALTSGSSPSAPASDSIGPQILTSPSPSKSIPIPQPFF
DRSSSAPNVHINTIEPVNIDDLIRDQGFRGDGGSTTGLSATPPASLF
GPQRERKSSSSSEDRNRMKTLGRRDSSDDWEIPDGQITVGQRIGSGS
AVKMLNVTAPTPQQLQAFKNEVGVLRKTRHVNILLFMGYSTKPQLAI
LHIIETKFEMIKLIDIARQTAQGMDYLHAKSIIHRDLKSNNIFLHED
KSRWSGSHQFEQLSGSILWMAPEVIRMQDKNPYSFQSDVYAFGIVLY
NRDQIIFMVGRGYLSPDLSKVRSNCPKAMKRLMAECLKKKRDERPLF
LPKIHRSASEPSLNRAGFQTEDFSLYACASPKTPIQAGGYGAFPVH
```

rs111237862 SNP

Original source	Variants (including SNPs and indels) imported from dbSNP (release 137) | View in dbSNP
Alleles	Reference/Alternative: **A/T** | Ancestral: **A** | Ambiguity code: **W**
Location	Chromosome **7:114582393** (forward strand) | View in location tab
Evidence status	
Synonyms	None currently in the database
HGVS names ⊞	This variation has **10** HGVS names - click the plus to show

Access to data

- Ensembl web site http://www.ensembl.org
- *Pre!* web site http://pre.ensembl.org
- *Archive!* web site http://archive.ensembl.org
- GRCh37 web site http://grch37.ensembl.org

- BioMart http://www.ensembl.org/biomart/martview

- FTP site ftp://ftp.ensembl.org
- MySQL http://www.ensembl.org/info/data/mysql.html
- Perl API http://www.ensembl.org/info/data/api.html
- REST API http://rest.ensembl.org
- GRCh37 REST API http://grch37.rest.ensembl.org

What Is A REST API

- **RE**presentational **S**tate **T**ransfer
- Simple APIs with very few external dependencies
- Can use the web (HTTP) to communicate
- Can be queried by
  - Web browsers
  - Command line tools
  - Programming languages

How Do You Query A REST API?

- With URLs; the same way you go to any webpage

How A URL Is Formed

Server | **Endpoint and parameters** | **Optional parameters**

http://rest.ensembl.org/info/ping?content-type=application/json

How Do You Query?

- The web browser can be used as a test client
- Plugins are available for most browsers
  - Firefox – RESTClient
  - Chrome – REST Console or Postman
- All major programming languages can perform HTTP requests

Constructing a URL

1. Find the endpoint you need
   - Use find on the main page for more information

2. Copy an example URL into a text editor

3. Edit with your variables
   - Check the options available

4. Paste back into the address bar and press return

http://rest.ensembl.org/sequence/region/*:species*/*:region*.fasta

human

6:2198711..2198900

Example

Using the stable ID ENSG00000157764 (human BRAF)

a) Retrieve its genomic sequence in plain text
b) Soft mask this in FASTA format
c) Retrieve all linked protein sequences in JSON

Example

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a) **Retrieve its genomic sequence in plain text**
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Start from the main page

http://rest.ensembl.org

e!Ensembl | Endpoints | User Guide | Change Log | About the Ensembl Project | Contact Ensembl

Ensembl REST API Endpoints

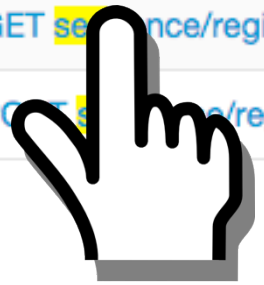
Archive

Resource	Description
GET archive/id/:id	Uses the given identifier to return the archived sequence
POST archive/id/	Retrieve the archived sequence for a set of identifiers

Find the correct endpoint

Sequence

Resource	Description
GET sequence/id/:id	Request multiple types of sequence by stable identifier.
POST sequence/id	Request multiple types of sequence by a stable identifier list.
GET sequence/region/:species/:region	Returns the genomic sequence of the specified region of the given species.
POST sequence/region/:species	Request multiple types of sequence by a list of regions.



Find and click sequence/id/:id

⌘ / Ctrl + f = find within page

Check the options available

The URL and required parameters

GET sequence/id/:id

Request multiple types of sequence by stable identifier.

Supported HTTP methods and output formats

Required parameters and examples

Parameters

Required

Name	Type	Description	Default	Example Values
id	*String*	An Ensembl stable ID	-	*ENSG00000157764* *ENSG00000157764.fasta (supported on some deployments)*

Optional

Name	Type	Description	Default	Example Values
callback	*String*	Name of the callback subroutine to be returned by the requested JSONP response. Required ONLY when using JSONP as the serialisation method. Please see the user guide.	-	*randomlygeneratedname*
db_type	*String*	Restrict the search to a database other than the default. Useful if you need to use a DB other than core	-	*core*
expand_3prime	*Int*	Expand the sequence downstream of the sequence by this many basepairs. Only available when using genomic sequence type.	-	*1000*

Resource Information

Methods	GET
Response formats	fasta json text yaml jsonp
Slice length	1e7

The optional parameter set

Select an example

/sequence/id/ENSG00000157764?content-type=text/plain

Example output | Perl | Python2 | Python3 | Ruby | Java | Curl | Wget

```
CGCCTCCCTTCCCCCTCCCCGCCCGACAGCGGCCGCTCGGGCCCCGGCTCTCGGTTATAAGATGGCGGCGCTGAGCGGTGGCGGTGGTGGCGGCGCGGAGCCGGGCCAGGCTCTGTTCAACGGGGACA
TGGAGCCCGAGGCCGGCGCCGGCGCCGGCGCCGCGGCCTCTTCGGCTGCGGACCCTGCCATTCCGGAGGAGGTGAGTGCTGGCGCCACCCTGCCGCCCTCCCGACTCCGGGCTCGGCGGCTGGCTGGTG
TTTATTTTGGAAAGAGGCGGCGGTGGGGGCTTGATGCCCTCAGCCACCTTCTCGGGCCAGCTCCGCGGGCTGGGAGGTGGGCATCGCCCCCGTGTCCCTCTCCGTCATGCAGCGCCTTCCTACGTAAAC
ACACACAATGGCCCGGGGGGTTTCCCTGGCCCCCACCCCAGATGTGGGGATTGGGGCAGCGGTGGTTGAGCGGGAGGCTATCAATAGGGGGCGAAACTCAGGGTTGGTCCGAGAAGGTCACGATTGGCT
GAAGTATCCAGCTCTGCATCTCTGTGGGGTGGGGGCGGCGGCGGCCTCGACGTGGAGGATATAGGTTAGTTGCTGGGGCTGAGACAACAGCCCGAGTTACTGTCGCGTGTAATTCTTACATGGTCGTGG
GGATGATGGGGCTCATCATTTCCTCTCTCCTCTCCCGGACTGCCCCCCTTCTCAGTCCGCTGCCCTTTTTCACTTTTCTATTTGGGGATTTCTCTTCACCTGTTTTACCCAGCAAATTATTTTGATTTA
GTCTTTACTTTTTCAATCCTAAATCGCAGTTTCCGATGCCTTTTCTGGTCTCTGGTCCTCTGTTCCTAATGTTTGTCAGCGCTCTGTCGCTGATTGGTAACCCCCATTCTATTCCCATCTACCGCCCGC
TCATTTTCCAGTTGTCGGACCTGCCTGCCTTCTAACCCCAGCTCCCACTTAAGAGCATTTTTGCACTTCTCTTACCCTGGTCCTCTTGAGGCTCTGTACTTGATCTCACCACTCCCTAACATTGTTGTC
TGTTGTTATCTTCACAAATCCTCCTGGACACTTTGGAGCTACTTGTTTTCTGAGCCCAGAAGCTGTCAAGATTCCATCAGGTTTCACTTGGCTCTTTTCGCGCTTGCACTACTGGCACTTTTTGGCTAG
TCGTCCATTGTGCATTCACACCTCTTTATTCCTACCCATTTTTATAGGTCTGATTGATTTCTTAGTGTTGTCCTCCTTTTTGTCCTATTTTTTTCCTTTTCCTTTTTCCTCTCCAGTCCTTGCTTCTCT
CAGCCTGTTTTTGCATTAGTCAGCCTCTTAGCACTGTGTCAAATTATTTACGTTTTTTTATTACATAAAATTTATTACAAATATTTGGTATTTTATTACAGAAAATAATACTTTATTATGCTTTACAAA
TAAGATATGGTATAATAATTGTGGTTTACAGTTATTGATTAGGTAATGTGACTTACTCTGTTGACTTTGCTCGAAGTTCTCTTTGCTACTTACTATTAACATCTAATTTCTCAATTCTCATAACATCTC
ATTCTCTCTGCAATTTTTTTTTTGCATCATCATCTTTGGAAATTCATCCAATATGCTTGCTTTATTCAGCATCAGCTTGTTTATGATAATGTTTGTTTTCTACTCTTTATATCATCTTTGTTACATGCC
CAAAATGTGTTCTGTACCATCATTTGATCTGTTCTAAAATTTCTCATTTTTAAGTTTCTTAAAATCATTCCACTTTTCAGTATGCATTTTTGCTTAGATCAGTTTCCTCTCATATCTGTTCCTTTCCCC
CAGCTTCTTGATTTCTAAGGAGAAAGCTCTTCTCTACTTCAATTTCCTAGTTTATTCTGTTTCCCTTGTTTCCAGTTACCATTCATTTTGCCTTGTTTCCTGGCTTTTGGTACTTAACTTTCTGAAGCT
TCCTCTTTTCTTCTCCACACCTCCACGTTCCTTCTTATTTATAAACATCTTTGTTTCCTTTGACATGGAAATTTATTTTTAGGATACATTGTTTTTAATGGATAAATACTAGGGGTCACATCTGCTGTC
TGTTTTCTCCAGGAATCGGATATGCCTTTGTCTTAACCAGGCACAGGTGCCTCTGGATTTTATTTTACTCTGTAATAGATGTGTAGTTTTGTTGAATTGTATCTTGTTTGAAGACTACTACAGAGTGGA
```

Copy and paste in the navigation bar

rest.ensembl.org/sequence/id/ENSG00000157764?content-type=text/plain

```
CGCCTCCCTTCCCCCTCCCCGCCCGACAGCGGCCGCTCGGGCCCCGGCTCTCGGTTATAAGATGGCGGCGCTGAGCGGTGGCGC
AAGAGGCGGCGGTGGGGGCTTGATGCCCTCAGCCACCTTCTCGGGCCAGCTCCGCGGGCTGGGAGGTGGGCATCGCCCCCGTGT
CTGTGGGGTGGGGGCGGCGGCGGCCTCGACGTGGAGGATATAGGTTAGTTGCTGGGGCTGAGACAACAGCCCGAGTTACTGTCC
TCCGATGCCTTTTCTGGTCTCTGGTCCTCTGTTCCTAATGTTTGTCAGCGCTCTGTCGCTGATTGGTAACCCCCATTCTATTCC
CTTGTTTTCTGAGCCCAGAAGCTGTCAAGATTCCATCAGGTTTCACTTGGCTCTTTTCGCGCTTGCACTACTGGCACTTTTTGC
GTTTTTTTATTACATAAAATTTATTACAAATATTTGGTATTTTATTACAGAAAATAATACTTTATTATGCTTTACAAATAAGAT
TTATTCAGCATCAGCTTGTTTATGATAATGTTTGTTTTCTACTCTTTATATCATCTTTGTTACATGCCCAAAATGTGTTCTGTA
CCAGTTACCATTCATTTTGCCTTGTTTCCTGGCTTTTGGTACTTAACTTTCTGAAGCTTCCTCTTTTCTTCTCCACACCTCCAC
TGTAGTTTTGTTGAATTGTATCTTGTTTGAAGACTACTACAGAGTGGAACAATGAGTGAAGTAATAAGTAGGGGTTATGAAATT
GCCATGGATTTCTGTATTTGGCACATGTCTTGAGCAGTTCCCATGTACCAATCCTTGAGAACCTCTAGGCTAGCTGAATTTAAC
GGAGGGTGACATTGATTAAAAAATGTATCTCTTGAATGTAAATATCAGTATTACAGATGATAAAATAAATTCCTCCAAGAAATA
AGGTTTTTTTTTTTTAAATAAAAGTTTCCCAGAGGGAAATTTCATCTAAAAAAAAAGTCTGATTTCAAAGGGAAAGCAAGTCAT
```

Example

Using the stable ID ENSG00000157764 (human BRAF)

a) Retrieve its genomic sequence in plain text
b) **Soft mask this in FASTA format**
c) Retrieve all linked protein sequences in JSON

Check the parameters

mask	*Enum(hard,soft)*	Request the sequence masked for repeat sequences. Hard will mask all repeats as N's and soft will mask repeats as lowercased characters. Only available when using genomic sequence type.	-	*hard*

Check the formats available

Resource Information

Methods	GET
Response formats	fasta json text yaml jsonp
Slice length	1e7

Output formats

- https://github.com/Ensembl/ensembl-rest/wiki/Output-formats

Format	Content-type	Extension	Notes
FASTA	`text/x-fasta`	`.fasta`	Sequence serialisation format. Only supported on the /sequence endpoint.
GFF3	`text/x-gff3`	`.gff3`	Genomic feature serialisation format. Only supported on the /overlap endpoint.
BED	`text/x-bed`	`.bed`	Browser Extensible Data format as defined by UCSC. Only supported on the /overlap endpoint.

Modify the required parameters

rest.ensembl.org/sequence/id/ENSG00000157764.fasta?mask=soft

```
>ENSG00000157764 chromosome:GRCh38:7:140719327:140924764:-1
cgcctcccttcccccctccccgcccgaCAGCGGCCGCTCGGGCCCCGGCTCTCGGTTATAA
GATGGCGGCGCTGAGCGGTGGCGGTGGTGGCGGCGCGGAGCCGGGCCAGGCTCTGTTCAA
CGGGGACATGGAGCCCGAggccggcgccggcgccggcgccgcggccTCTTCGGCTGCGGA
CCCTGCCATTCCGGAGGAGGTGAGTGCTGGCGCCACCCTGCCGCCCTCCCGACTCCGGGC
TCGGCGGCTGGCTGGTGTTTATTTTGGAAAGAGGCGGCGGTGGGGGCTTGATGCCCTCAG
CCACCTTCTCGGGCCAGCTCCGCGGGCTGGGAGGTGGGCATCGCCCCCGTGTCCCTCTCC
GTCATGCAGCGCCTTCCTACGTAAACACACACAATGGCCCGGGGGGTTTCCCTGGCCCCC
ACCCCAGATGTGGGGATTGGGGCAGCGGTGGTTGAGCGGGAGGCTATCAATAGGGGGCGA
AACTCAGGGTTGGTCCGAGAAGGTCACGATTGGCTGAAGTATCCAGCTCTGCATCTCTGT
GGGGTGGGGGCGGCGGCGGCCTCGACGTGGAGGATATAGGTTAGTTGCTGGGGCTGAGAC
AACAGCCCGAGTTACTGTCGCGTGTAATTCTTACATGGTCGTGGGGATGATGGGGCTCAT
CATTTCCTCTCTCCTCTCCCGGACTGCCCCCCTTCTCAGTCCGCTGCCCTTTTTCACTTT
TCTATTTGGGGATTTCTCTTCACCTGTTTTACCCAGCAAATTATTTTGATTTAGTCTTTA
CTTTTTCAATCCTAAATCGCAGTTTCCGATGCCTTTTCTGGTCTCTGGTCCTCTGTTCCT
AATGTTTGTCAGCGCTCTGTCGCTGATTGGTAACCCCCATTCTATTCCCATCTACCGCCC
GCTCATTTTCCAGTTGTCGGACCTGCCTGCCTTCTAACCCCAGCTCCCACTTAAGAGCAT
TTTTGCACTTCTCTTACCCTGGTCCTCTTGAGGCTCTGTACTTGATCTCACCACTCCCTA
```

Example

Using the stable ID ENSG00000157764 (human BRAF)

a) Retrieve its genomic sequence in plain text
b) Soft mask this in FASTA format
c) **Retrieve all linked protein sequences in JSON**

Check the parameters

type	*Enum(genomic,cds,cdna,protein)*	Type of sequence. Defaults to genomic where applicable, i.e. not translations. cdna refers to the spliced transcript sequence with UTR; cds refers to the spliced transcript sequence without UTR.	*genomic*	*cds*

Modify the required parameters

rest.ensembl.org/sequence/id/ENSG00000157764?content-type=text/plain;type=protein

{"error":"Requesting a gene and type not equal to \"genomic\" can result in multiple sequences. 4 sequences detected. Please rerun your request and specify the multiple_sequences parameter"}

Check the parameters (again)

multiple_sequences	*Boolean*	Allow the service to return more than 1 sequence per identifier. This is useful when querying for a gene but using a type such as protein.	*0*	-

Modify the required parameters

rest.ensembl.org/sequence/id/ENSG00000157764?type=protein;multiple_sequences=1

```
>ENSP00000419060
XSTTGLSATPPASLPGSLTNVKALQKSPGPQRERKSSSSSEDRNRMKTLGRRDSSDDWEI
PDGQITVGQRIGSGSFGTVYKGKWHGDVAVKMLNVTAPTPQQLQAFKNEVGVLRKTRHVN
ILLFMGYSTKPQLAIVTQWCEGSSLYHHLHIIETKFEMIKLIDIARQTAQGMDYLHAKSI
IHRDLKSNNIFLHEDLTVKIGDFGLATVKSRWSGSHQFEQLSGSILWMAPEVIRMQDKNP
YSFQSDVYAFGIVLYELMTGQLPYSNINNRDQIIFMVGRGYLSPDLSKVRSNCPKAMKRL
MAECLKKKRDERPLFPQILASIELLARSLPKIHRSASEPSLNRAGFQTEDFSLYACASPK
TPIQAGGYGEFAAFK
>ENSP00000288602
MAALSGGGGGGAEPGQALFNGDMEPEAGAGAGAAASSAADPAIPEEVWNIKQMIKLTQEH
IEALLDKFGGEHNPPSIYLEAYEEYTSKLDALQQREQQLLESLGNGTDFSVSSSASMDTV
TSSSSSSLSVLPSSLSVFQNPTDVARSNPKSPQKPIVRVFLPNKQRTVVPARCGVTVRDS
LKKALMMRGLIPECCAVYRIQDGEKKPIGWDTDISWLTGEELHVEVLENVPLTTHNFVRK
TFFTLAFCDFCRKLLFQGFRCQTCGYKFHQRCSTEVPLMCVNYDQLDLLFVSKFFEHHPI
PQEEASLAETALTSGSSPSAPASDSIGPQILTSPSPSKSIPIPQPFRPADEDHRNQFGQR
DRSSSAPNVHINTIEPVNIDDLIRDQGFRGDGGSTTGLSATPPASLPGSLTNVKALQKSP
GPQRERKSSSSSEDRNRMKTLGRRDSSDDWEIPDGQITVGQRIGSGSFGTVYKGKWHGDV
AVKMLNVTAPTPQQLQAFKNEVGVLRKTRHVNILLFMGYSTKPQLAIVTQWCEGSSLYHH
LHIIETKFEMIKLIDIARQTAQGMDYLHAKSIIHRDLKSNNIFLHEDLTVKIGDFGLATV
KSRWSGSHQFEQLSGSILWMAPEVIRMQDKNPYSFQSDVYAFGIVLYELMTGQLPYSNIN
NRDQIIFMVGRGYLSPDLSKVRSNCPKAMKRLMAECLKKKRDERPLFPQILASIELLARS
LPKIHRSASEPSLNRAGFQTEDFSLYACASPKTPIQAGGYGAFPVH
>ENSP00000418033
IHRDLKSNNIFLHEDLTVKIGDFGLATVKSRWSGSHQFEQLSGSILWMAPEVIRMQDKNP
YSFQSDVYAFGIVLYELMTGQLPYSNINNRDQVLCPPWEYNK
>ENSP00000420119
QALFNGDMEPEAGAGAGAAASSAADPAIPEEVWNIKQMIKLTQEHIEALLDKFGGEHNPP
SIYLEAYEEYTSKLDALQQREQQLLESLGNGTDFSVSSSASMDTVTSSSSSSLSVLPSSL
SVFQNPTDVARSNPKSPQKPIVRVFLPNKQRTVVPARCGVTVRDSLKKALMMRGLIPECC
AVYRIQDGSFLELT
```

Existing endpoints

Endpoint	Entry point	Output data
/alignment	A region	Whole genome alignments from Compara
/genetree	A gene or tree identifier	The corresponding gene tree
/homology	A gene	Corresponding orthologs and paralogs
/xrefs	An external symbol	Corresponding Ensembl object
/info	Species or nothing	Information about data available
/lookup	A stable identifier	Information related to that feature
/map	A region to convert	Equivalent coordinates in another context
/overlap	A region or feature	All features overlapping that region
/regulatory	A stable identifier	Corresponding regulatory features
/sequence	A stable identifier	The corresponding sequence
/variation	A variation id	Corresponding variation features
/vep	A region or a variation id	Corresponding variant consequences

Example

Starting with a region in GRCh37,

a) Find the corresponding region in assembly GRCh38
b) Find genes overlapping this region
c) Explore the corresponding gene tree
d) Look for variations

Example

Starting with a region in GRCh37, 17:64216194-64218564:1

a) **Find the corresponding region in assembly GRCh38**
b) Find genes overlapping this region
c) Explore the corresponding gene tree
d) Look for variant consequences

Find the correct endpoint

Resource	Description
GET map/cdna/:id/:region	Convert from cDNA coordinates to genomic coordinate API.
GET map/cds/:id/:region	Convert from CDS coordinates to genomic coordinates
GET map/:species/:asm_one/:region/:asm_two	Convert the co-ordinates of one assembly to another
GET map/translation/:id/:region	Convert from protein (translation) coordinates to genom the Ensembl API.

Select an example

Example Requests

/map/human/GRCh37/X:1000000..1000100:1/GRCh38?content-type=application/json

Example output | Perl | Python2 | Python3 | Ruby | Java | Curl | Wget


```
{
 "mappings": [
   {
     "original": {
       "seq_region_name": "X",
       "strand": 1,
       "coord_system": "chromosome",
       "end": 1000100,
       "start": 1000000,
       "assembly": "GRCh37"
     },
     "mapped": {
       "seq_region_name": "X",
       "strand": 1,
       "coord_system": "chromosome",
       "end": 1039365,
       "start": 1039265
```

Copy and paste in the navigation bar

rest.ensembl.org/map/human/GRCh37/17:64216194-64218564:1/GRCh38


```
---
mappings:
  -
    mapped:
      assembly: GRCh38
      coord_system: chromosome
      end: 66222446
      seq_region_name: 17
      start: 66220076
      strand: 1
    original:
      assembly: GRCh37
      coord_system: chromosome
      end: 64218564
      seq_region_name: 17
      start: 64216194
      strand: 1
```


GRCh7:17:64216194-64218564:1 maps to GRCh38:17:66220076-66222446:1

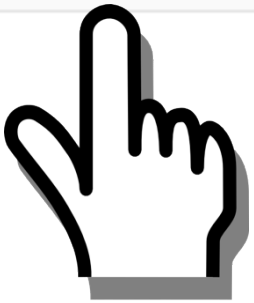
Example

Starting with a region in GRCh37, 17:64216194-64218564:1

a) Find the corresponding region in assembly GRCh38
b) **Find genes overlapping this region**
c) Explore the corresponding gene tree
d) Look for variant consequences

Find the correct endpoint

Resource	Description
GET overlap/id/:id	Retrieves features (e.g. genes, transcripts, variations et
GET overlap/region/:species/:region	Retrieves multiple types of features for a given region.
GET overlap/translation/:id	Retrieve features related to a specific Translation as de



Select an example

Example Requests

/overlap/region/human/7:140424943-140624564?feature=gene;feature=transcript;feature=cds;feature=exon;content-type=application/json

Example output | Perl | Python2 | Python3 | Ruby | Java | Curl | Wget


```
[
 {
   "source": "ensembl_havana",
   "logic_name": "ensembl_havana_gene",
   "feature_type": "gene",
   "external_name": "RAB19",
   "havana_version": "1",
   "seq_region_name": "7",
   "havana_gene": "OTTHUMG00000157410",
   "strand": 1,
   "id": "ENSG00000146955",
```

Copy and paste in the navigation bar

rest.ensembl.org/overlap/region/human/17:66220076-66222446:1?feature=gene;content-type=text/x-gff3

```
##gff-version 3
##sequence-region   17 66220076 66222446
17      ensembl_havana  gene    66220076        66222446        .       -       .       ID=gene:ENSG00000091583
Symbol%3BAcc:HGNC:616];gene_id=ENSG00000091583;havana_gene=OTTHUMG00000179530;havana_version=3;logic_name=ensemb
```

Found one gene: ENSG00000091583

Example

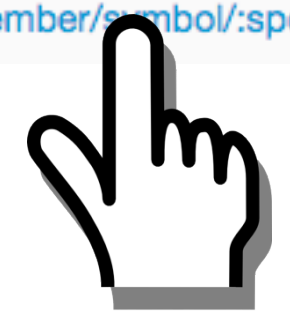
Starting with a region in GRCh37, 17:64216194-64218564:1

a) Find the corresponding region in assembly GRCh38
b) Find genes overlapping this region
c) **Explore the corresponding gene tree**
d) Look for variant consequences

Find the correct endpoint

Comparative Genomics

Resource	Description
GET genetree/id/:id	Retrieves a gene tree dump for a gene tree stable identifier
GET genetree/member/id/:id	Retrieves a gene tree that contains the stable identifier
GET genetree/member/symbol/:species/:symbol	Retrieves a gene tree containing the gene identified by a symbol



Select an example

Example Requests

/genetree/member/id/ENSG00000157764?content-type=text/x-phyloxml%2Bxml

Example output | Perl | Python2 | Python3 | Ruby | Java | Curl | Wget


```
<?xml version="1.0" encoding="UTF-8"?><phyloxml xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance" xmlns="http://www.phyloxml.org" xsi:schemaLocation="http://www.phyloxml.org http://www.phyloxml.org/1.10/phyloxml.xsd">
  <phylogeny rooted="true" type="gene tree">
    <clade branch_length="0">
      <confidence type="duplication_confidence_score">1.0000</confidence>
      <taxonomy>
        <id>33213</id>
        <scientific_name>Bilateria</scientific_name>
      </taxonomy>
      <events>
```

Copy and paste in the navigation bar

rest.ensembl.org/genetree/member/id/ENSG00000091583


```
<?xml version="1.0" encoding="UTF-8"?>

<phyloxml xsi:schemaLocation="http://www.phyloxml.org http://www.phy
  <phylogeny rooted="true" type="gene tree">
    <clade branch_length="0">
      <confidence type="duplication_confidence_score">0.9853</confic
      <taxonomy>
        <id>33213</id>
        <scientific_name>Bilateria</scientific_name>
      </taxonomy>
      <events>
        <type>speciation_or_duplication</type>
        <duplications>1</duplications>
      </events>
      <clade branch_length="0">
        <taxonomy>
          <id>33213</id>
          <scientific_name>Bilateria</scientific_name>
        </taxonomy>
        <clade branch_length="0.014137">
          <confidence type="duplication_confidence_score">0.1970</cc
          <taxonomy>
            <id>7711</id>
```

Example

Starting with a region in GRCh37, 17:64216194-64218564:1

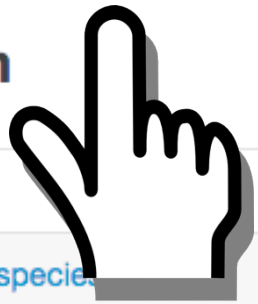
a) Find the corresponding region in assembly GRCh38
b) Find genes overlapping this region
c) Explore the corresponding gene tree
d) Look for variant consequences

Find the correct endpoint

VEP

Resource	Description
GET vep/:species/hgvs/:hgvs_notation	Fetch variant consequences based on a HGVS notation
GET vep/:species/id/:id	Fetch variant consequences based on a variation identifier
POST vep/:species/id	Fetch variant consequences for multiple ids
GET vep/:species/region/:region/:allele/	Fetch variant consequences
POST vep/:species/region	Fetch variant consequences for multiple regions

Variation



Resource	Description
GET variation/:species/	Uses a variation identifier (e.g. rsID) to return the variation features
POST variation/:species/	Uses a list of variation identifiers (e.g. rsID) to return the variation features

Select an example

Example Requests

/vep/human/region/9:22125503-22125502:1/C?content-type=application/json

Example output | Perl | Python2 | Python3 | Ruby | Java | Curl | Wget


```
[
 {
   "assembly_name": "GRCh38",
   "end": 22125502,
   "seq_region_name": "9",
   "transcript_consequences": [
     {
       "gene_id": "ENSG00000240498",
       "distance": 4930,
       "variant_allele": "C",
       "biotype": "antisense",
       "gene_symbol_source": "HGNC",
       "consequence_terms": [
         "downstream_gene_variant"
       ],
```

Copy and paste in the navigation bar

rest.ensembl.org/vep/human/region/17:66220076-66222446:1/C?content-type=text/xml

This XML file does not appear to have any style information associated with it. The document tree is shown below.


```
▼<opt>
  ▼<data id="temp"
   allele_string="AAAGATTTTTAAAATGTGTAACAATCAGACAGCAACCCAGTCTTAACCTTCATCTCCTAGGACTCTCCAATTTAACCCAGG
   assembly_name="GRCh38" end="66222446" most_severe_consequence="splice_acceptor_variant" seq_regi
   ▼<transcript_consequences biotype="protein_coding" gene_id="ENSG00000091583" gene_symbol="APOH"
      <consequence_terms>splice_acceptor_variant</consequence_terms>
      <consequence_terms>splice_donor_variant</consequence_terms>
      <consequence_terms>coding_sequence_variant</consequence_terms>
      <consequence_terms>intron_variant</consequence_terms>
    </transcript_consequences>
   ▼<transcript_consequences biotype="protein_coding" gene_id="ENSG00000091583" gene_symbol="APOH"
      <consequence_terms>splice_acceptor_variant</consequence_terms>
      <consequence_terms>splice_donor_variant</consequence_terms>
      <consequence_terms>coding_sequence_variant</consequence_terms>
      <consequence_terms>intron_variant</consequence_terms>
    </transcript_consequences>
   ▼<transcript_consequences biotype="protein_coding" gene_id="ENSG00000091583" gene_symbol="APOH"
      <consequence_terms>splice_donor_variant</consequence_terms>
      <consequence_terms>coding_sequence_variant</consequence_terms>
```

Write a script: documentation

Example output | **Perl** | Python2 | Python3 | Ruby | Java | Curl | Wget

Multiple stub clients designed to get you working with REST fast

```
8.  my $server = 'http://rest.ensembl.org';
9.  my $ext = '/overlap/region/human/7:140424943-140624564?feature=gene;feature=transcript;feature=cds;feature=exon';
10. my $response = $http->get($server.$ext, {
11.   headers => { 'Content-type' => 'application/json' }
12. });
13.
14. die "Failed!\n" unless $response->{success};
15.
16.
17. use JSON;
18. use Data::Dumper;
19. if(length $response->{content}) {
20.   my $hash = decode_json($response->{content});
21.   local $Data::Dumper::Terse = 1;
22.   local $Data::Dumper::Indent = 1;
23.   print Dumper $hash;
24.   print "\n";
25. }
26.
```

Show more advanced techniques e.g. providing headers and looking at server response codes for errors

Modify the example script

```
my $server = 'http://rest.ensembl.org';
my $ext = '/overlap/region/human/7:140424943-140624564?feature=gene';
my $response = $http->get($server.$ext, {
  headers => { 'Content-type' => 'application/json' }
});
```

Modify the example script

```
my $server = 'http://rest.ensembl.org';
my $ext = '/overlap/region/human/7:140424943-140624564?feature=gene';
my $response = $http->get($server.$ext, {
  headers => { 'Content-type' => 'application/json' }
});
```

```
my $server = 'http://rest.ensembl.org';
my $region = '7:140424943-140624564';
my $overlap_endpoint = '/overlap/region/human/';
my $overlap_options = '?feature=gene';
my $ext = $overlap_endpoint . $region . $overlap_options;
my $response = $http->get($server.$ext, {
  headers => { 'Content-type' => 'application/json' }
});
```

Create re-usable methods

```
sub perform_rest_action {
  my ($endpoint, $headers) = @_;
  $parameters ||= {};
  $headers ||= {};
  $headers->{'Content-Type'} = 'application/json' unless exists $headers->{'Content-Type'};

  my $url = $server.$endpoint;

  my $response = $http->get($url, {headers => $headers});
  my $status = $response->{status};
  if(!$response->{success}) {
     my ($status, $reason) = ($response->{status}, $response->{reason});
     die "Failed for $endpoint! Status code: ${status}. Reason: ${reason}\n";
    }
  }
  $request_count++;
  if(length $response->{content}) {
    return $response->{content};
  }
  return;
}
```

Multiple queries

/sequence/id

Example output | Example input | **Perl** | Python2 | Python3 | Ruby | Java | Curl | Wget

```perl
use strict;
use warnings;

use HTTP::Tiny;

my $http = HTTP::Tiny->new();

my $server = 'http://rest.ensembl.org';
my $ext = '/sequence/id';
my $response = $http->request('POST', $server.$ext, {
  headers => {
        'Content-type' => 'application/json',
        'Accept' => 'application/json'
  },
  content => '{ "ids" : ["ENSG00000157764", "ENSG00000248378" ] }'
});

die "Failed!\n" unless $response->{success};
```

https://github.com/Ensembl/ensembl-rest/wiki

Ensembl REST 4.3 User Guide

The following guide refers to the 4.3 release of the Ensembl REST API. For support please contact helpdesk or our dev mailing list.

Contents

Acknowledgements

Ensembl 2014

Paul Flicek[1,2,*], M. Ridwan Amode[2], Daniel Barrell[2], Kathryn Beal[1], Konstantinos Billis[2], Simon Brent[2], Denise Carvalho-Silva[1], Peter Clapham[2], Guy Coates[2], Stephen Fitzgerald[1], Laurent Gil[1], Carlos García Girón[2], Leo Gordon[1], Thibaut Hourlier[2], Sarah Hunt[1], Nathan Johnson[1], Thomas Juettemann[1], Andreas K. Kähäri[2], Stephen Keenan[1], Eugene Kulesha[1], Fergal J. Martin[2], Thomas Maurel[1], William M. McLaren[1], Daniel N. Murphy[2], Rishi Nag[2], Bert Overduin[1], Miguel Pignatelli[1], Bethan Pritchard[2], Emily Pritchard[1], Harpreet S. Riat[2], Magali Ruffier[1], Daniel Sheppard[2], Kieron Taylor[1], Anja Thormann[1], Stephen J. Trevanion[2], Alessandro Vullo[1], Steven P. Wilder[1], Mark Wilson[2], Amonida Zadissa[1], Bronwen L. Aken[2], Ewan Birney[1], Fiona Cunningham[1], Jennifer Harrow[2], Javier Herrero[1], Tim J.P. Hubbard[2], Rhoda Kinsella[1], Matthieu Muffato[1], Anne Parker[2], Giulietta Spudich[1], Andy Yates[1], Daniel R. Zerbino[1] and Stephen M.J. Searle[2]

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Standard Ensembl REST Parameters

:id – The global ID for that object. Normally a stable ID

ENSG00000157764

ENSGT00390000003602

:species – Species name (any Ensembl alias will do)

human

homo_sapiens

:region – 1 base locations CHR:START-END:STRAND

1:1000-2000

chr1:1000-2000:-1

:symbol – Reserved for Genes. Indicates a name to use

BRAF

BRCA2

Species Required

Specifying Output Formats

- File extension
  - http://rest.ensembl.org/sequence/id/ENST00000288602**.json**?type=cds
- HTTP Parameter
  - http://rest.ensembl.org/sequence/id/ENST00000288602?content-type=application/json;type=cds
- HTTP Header
  - http://rest.ensembl.org/sequence/id/ENST00000288602?type=cds
  - `Content-Type: application/json`

Programming Against REST

Build a URL

↓

Specify the response format

↓

Send HTTP query

↓

Read the response

- Parse the result if successful
- If not report the error

↓

Respect the rate limit

Rules When Writing a Client

- Choose your most convenient language
  - If you are a Python programmer, use Python
- Find a good HTTP and JSON library for your language
- Try to limit your requests to 15 per second
  - We will limit you to ~54,000 per hour
  - Basic way is to count & sleep for fractions of seconds
- Create reusable methods for querying
  - It will make things easier

Pre-Written REST Clients

All of these are 3rd party contributed

- R - https://github.com/acbb/EnsemblRest
- Node.js - https://github.com/jermth/EnsemblFetches
- Ruby - https://github.com/ALTree/bio-ensembl-rest
- Java - https://github.com/heuermh/ensembl-rest-client
- Python - https://github.com/pyOpenSci/pyEnsemblRest

REST Terminology

Term	Definition	Example
Endpoint	A URL which will respond to a HTTP request and return data	`/sequence/id/ENST00000288602.fasta`
HTTP Header	Sent to the server along side the requested URL.	`Accepts: application/json` `Content-type: application/json`
HTTP Parameter	Key value pairs separated by an = sign given to an endpoint after all required parameters.	`?type=cds`
HTTP Method	Tells the server the kind of operation you want to perform. Are you retrieving data or sending data to the server	`GET` `POST`

HTTP Status Code	Indicates to the client what the server did with a request ranging from “OK”, to “Server Error” and “Your Input Was Wrong”	`200`
		`400`
		`404`
		`500`

JSON	Common cross-language data structure interchange format	`{ “key”: [1, “two”]}`

Output Formats

Format	Content-Type	Extension	Notes
FASTA	`text/x-fasta`	`.fasta`	
GFF3	`text/x-gff3`	`.gff3`	
JSON	`application/json`	`.json`	Standard serialisation format
JSONP	`text/javascript`	`.jsonp`	Used to avoid browser sandbox issues. Use CORS instead
Newick	`text/x-nh`	`.nh`	Old tree format. Use PhyloXML instead
SeqXML	`text/x-seqxml+xml`	`.seqxml`	FASTA replacement
PhyloXML	`text/x-phyloxml+xml`	`.phyloxml`	Phylogenetic format
Text	`text/plain`	`.txt`	
XML	`text/xml`	`.xml`	
YAML	`text/x-yaml`	`.yaml`	

Response Codes - Server Meta Data

Code	Class	Meaning
200	Success	Everything is groovy!
4xx	Client error	Range specifying some kind of error in the user request.
400	Client error	User has made a bad request e.g. bad parameters
404	Client error	Location cannot be found
415	Client error	Unsupported media type; bad format request made
429	Client error	Too many requests made. Observe the Retry-After header
5xx	Server error	Anything in the 500 range is a server issue. You cannot fix this
503	Server error	Server unavailable. Probably down for maintenance.

HTTP Response Headers

Name	Data type	Meaning
Content-type	MIME type	Describes what format the response is. The formats are the same as those used in the content-type request header
Retry-After	Floating point seconds	If found you **must** wait for this long before retrying the server
X-RateLimit-Limit	Integer	What the total limit of requests is
X-RateLimit-Remaining	Integer	How many requests you have left
X-RateLimit-Reset	Floating point seconds	How long before your tokens reset to the amount given in X-RateLimit-Limit
X-Runtime	Floating point seconds	The amount of time this request took

Documentation and Help

- https://github.com/Ensembl/ensembl-rest/wiki
  - How to write your first client
  - How to write POST requests
- dev@ensembl.org mailing list:

  http://www.ensembl.org/info/about/contact/mailing.html

  searchable mailing list archive:

  http://blog.gmane.org/gmane.science.biology.ensembl.devel
- Ensembl helpdesk:

  helpdesk@ensembl.org