

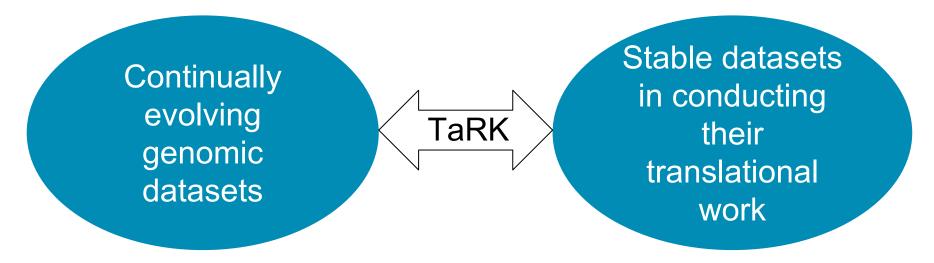




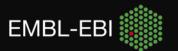
## Ensembl Updates - TaRK

Transforming Genomic Medicine Initiative

The challenge for researchers



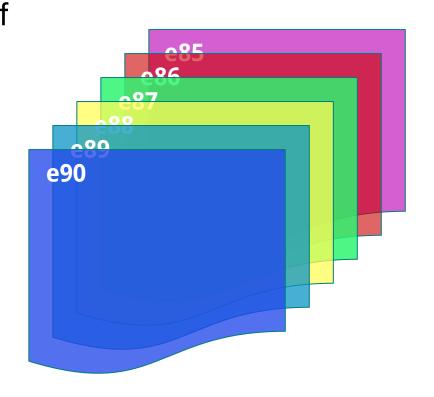
 The need to tag a stable transcript set that won't change on researchers between releases

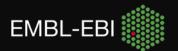




## Ensembl Updates - Sequence Store

- With the growing number of genomes, a way to reduce redundancy between releases was needed
- Annotations could go 10 or more releases without updates to sequence or structure in Ensembl

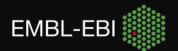






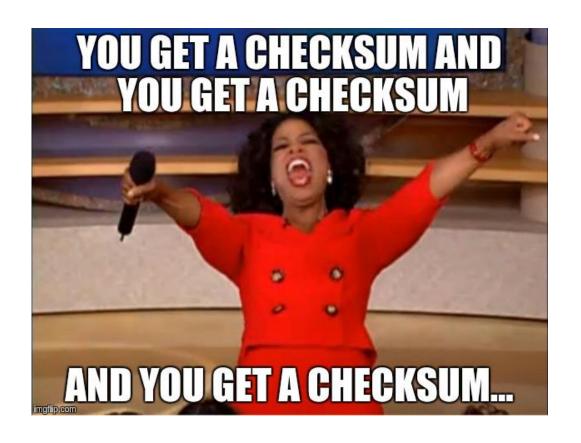
## TaRK & Sequence Store Goals

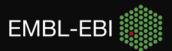
- Maintain persistent tagged transcript set across Ensembl releases
- Calculate differences between transcript set releases and Ensembl releases/data freezes
- Checksum datasets at multiple levels; from release level to individual feature
- RESTful interface, rich queries slicing over multiple tagsets, criteria in creating resultset





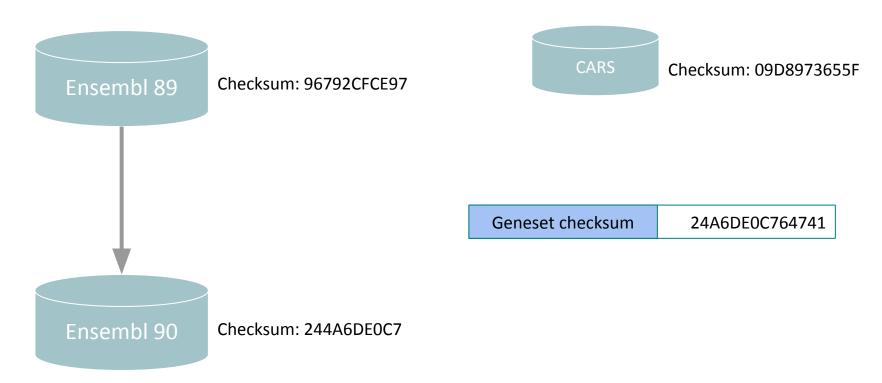
## TaRK - Checksums



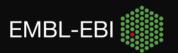




### Set checksums



 Checksums currently SHA1 based, but we will be regenerating the database using SHA-512 in the near future





### Set checksums

Dig down through sets finding difference between release or tag set at a fine grained level

Gene set checksum 24A6DE0C764741

ENSG00000633248.2				
FE96C119698C6CD				
Location Checksum	BEF9D96C149BB7			
Transcripts Checksum	BBE4996C1FB79D			
Sequence Checksum	6C1B499D9BEFB7			

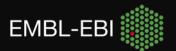
ENSG00000444909.4

ENSG00000364718.1







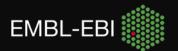


# Revision tracking

Dig down to find changes at sub-record level between two features
 eg. exon location shift

ENST00000444909.4				
7B6773A24743AA48				
Location Checksum	7BF3A24743AA48			
Exon set Checksum	43AA487BF3A247			
Sequence Checksum	E743AA4AF3AA48			

ENST00000444909.5				
FE96C119698C6CD				
Location Checksum	7BF3A24743AA48			
Exon set Checksum	6F0EB5E6A539			
Sequence Checksum	E743AA4AF3AA48			





## Reduced redundancy

- Redundant sequences are only stored once
- This includes across assemblies and species

ENST00000444909.4				
7B6773A24743AA48				
Assembly	GRCh37			
Location Checksum	7BF3A24743AA48			
Exon set Checksum	43AA487BF3A247			
Sequence Checksum	E743AA4AF3AA48			

ENST00000444909.4				
7B6773A24743AA48				
Assembly	GRCh38			
Location Checksum	7BF3A24743AA48			
Exon set Checksum	43AA487BF3A247			
Sequence Checksum	E743AA4AF3AA48			

CTGCAATCGACACCCTAGCGGACAATTTTAACCC
TGTGTCTGAGGAGCGTGGCAAAGTTGCCAAGATTGT
TTCTACCTCTTTGAGATGGATAGCAGCCTGGCCTGT
TCACCAGAGATCTCAGCCACCTCAGTGTGGGTTCCA
TCTTACTTGTCCTGGTAGCAGATGGCTGTGACTTTG
TCTGTACCGTTCTAAACCTCGAAATGTGCCTGCAGC
ATATCGTGGTGTGGGGGATGACCAGCTGGGAC

E743AA4AF3AA48

Sequence Checksum





# Rich queries

- Rich queries taking advantage of multiple tagsets available
  - "All human transcripts identical between E89 and E90 and in CARS"

Ensembl 89					Ensembl 90
ENST000005713 ENST000005888 ENST000005716 ENST000004492 ENST000004460 ENST000004487 ENST000004479 ENST000004479 ENST000004479 ENST000004492 ENST000004487 ENST000004487	340 585 252 074 297 766 562 503 045 591 252 766	ENST00000588756 ENST00000621238 ENST00000588756 ENST00000633248 ENST00000632612 ENST00000634057 ENST00000631475 ENST00000632514 ENST00000632736 ENST00000631707 ENST00000633036 ENST00000632953		ENS' ENS' ENS' ENS' ENS' ENS' ENS' ENS'	T00000431024 T00000449548 T00000416355 T00000440517 T00000429749 T00000418520 T00000415067 T00000449548 T00000440517 T00000416355 T00000363511 T00000363754
		CARS			



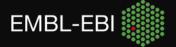


## **Ensembl Difference Set**

# Release comparison endpoint detailing changes between Ensembl releases

- Features added/removed
- Location and sequence changes
- Stable id remapping

```
stable_id: "ENSG00000122877",
    updated: 14,
    base: 13
* transcript_differences:
       exon_differences: [
              stable id: "ENSE00001760892",
              version: {
                  updated: 2,
                  base: 1
                  updated: "GRCh38:10:62816070:62816315:-1".
                  base: "GRCh38:10:62816070:62816366:-1"
              stable_id: "ENSE00000834013",
             missing: {
                  release: "84"
              stable id: "ENSE00003792399",
              added: {
                 release: "85"
        stable id: "ENST00000411732",
       version: {
           updated: 3,
           base: 2
      * location: {
           updated: "GRCh38:10:62812000:62816315:-1",
           base: "GRCh38:10:62812003:62816366:-1"
      * sequence: {
           updated:
        stable_id: "ENST00000637191",
       added: {
           release: "85"
```





### **Ensembl Difference Set**

Intersect the two datasets to get a sense of what changes might occur in the frozen transcript set between Ensembl releases.

```
        ENSG00000215474
        SKOR2
        protein_coding
        ENST00000620245

        ENSG00000173621
        LRFN4
        protein_coding
        ENST00000309602

        ENSG00000139624
        CERS5
        protein_coding
        ENST000000317551

        ENSG000000157326
        DHRS4
        protein_coding
        ENST000000313250

        ENSG00000087116
        ADAMTS2
        protein_coding
        ENST000000251582
```

```
stable id: "ENSG00000215474"
version: {
    updated: 7,
    base: 6
v location: {
    updated: "GRCh38:18:47206322:47251603:-1",
    base: "GRCh38:18:47212089:47249183:-1"
* transcript differences: [
     sequence: {
         updated:
         "CGTACCCACACTTTCTGCGGTGGAGGGGACGCCCCGCCGCAATTCAGGCCGTCATTCTCCCCAGGCCGGGGTTTGAGCGCCATTCGCTCGGGCC/
         * exon differences: [
            stable id: "ENSE00003792160",
          ▼ added: {
              release: "85"
         },
```

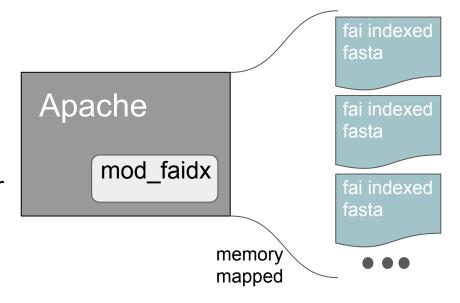




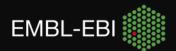
# Reference sequence (mod\_faidx)

Bulk sequence storage and serving is another growth pinch point.

- Apache module written in C
- Uses htslib to memory map compressed, indexed fasta files
- Can return individual sequences, or assemble a series of coordinates and translate to protein sequence
- Returns JSON, fasta or plain text sequence
- Working with ENA to create a proposal for a Reference Sequence API



/seq/region/GRCh38/?location=12:43768112-43768272,43771220-43771365,43772180-43772362,43773045-43773072&translate=1





### TaRK Beta



The goal of TarK is to create an archive of all iterations of gene sets, from Ensembl and other sources. To ensure robust tracking of exact changes between gene and transcript sets, checksums are included at a fine grained level and functionality provided to dig down and examine the exact changes from one release to the next. Ultimately, it is envisioned TArK could take the place as the primary sequence store for Ensembl releases.

This beta is provided to give the community an opportunity to explore TArK's functionality and provide feedback on possible improvements to help meet future needs. This is a beta and should not be counted upon to be stable, the API may change and this server may be unavailable at times.

Explore TArK

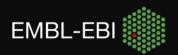
Funding:





TRANSFORMING GENETIC MEDICINE INITIATIVE

betatark.ensembl.org

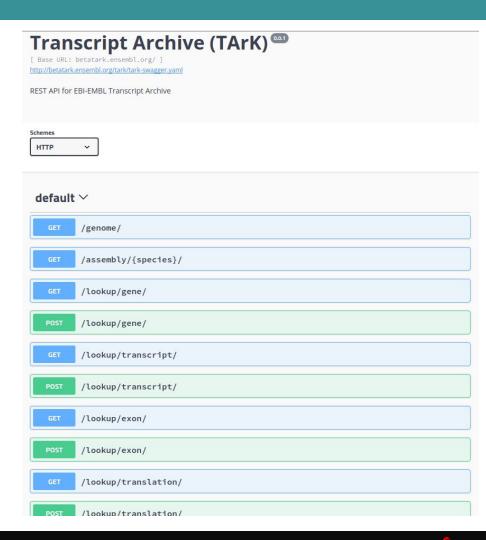


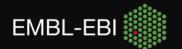


### TaRK Beta

- Swagger based site for exploring the API
- e86-90 loaded into the site
- Beta software, API may change at any time over the coming months
- Will become part of the Ensembl website backend

# betatark.ensembl.org







## Acknowledgements

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