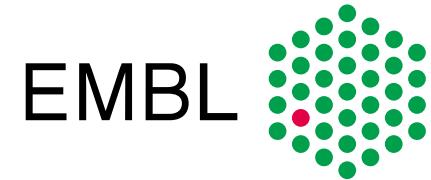


# Genome Annotation Report

Report generated: 2025-11-06



The {species\_name} genome assembly GCF\_902655055.1 was annotated by {facility/organisation/contact}. This annotation includes 4878 transcribed mRNAs from 4878 genes. The average transcript length is 1852.35649856499 bp, with an average of 1 coding transcripts per gene and 1.6 exons per transcript. The annotation file is available at {url}.

## Summary

<b>Number of genes:</b>	4878
<b>Number of transcripts:</b>	4878
<b>Mean transcript length:</b>	1852.36 bp
<b>Mean transcripts per gene:</b>	1
<b>Mean exons per transcript:</b>	1.6
<b>BUSCO summary:</b>	C:98.0%[S:97.6%,D:0.4%],F:0.6%,M:1.4%,n:1706
<b>BUSCO lineage dataset:</b>	ascomycota_odb10
<b>BUSCO mode:</b>	euk_genome_met

## Metadata

<b>Taxon ID</b>	{taxon_id}
<b>Species name</b>	{species_name}
<b>ToL prefix</b>	mLutLut
<b>Assembly accession</b>	GCF_902655055.1

## BUSCO Full Stats

<b>Version:</b>	5.4.3
<b>Lineage dataset:</b>	ascomycota_odb10
<b>Mode:</b>	euk_genome_met
<b>One line summary:</b>	C:98.0%[S:97.6%,D:0.4%],F:0.6%,M:1.4%,n:1706
<b>Complete BUSCOs:</b>	98%
<b>Single-copy:</b>	97.6%
<b>Duplicated:</b>	0.4%
<b>Fragmented:</b>	0.6%
<b>Missing:</b>	1.4%
<b>Total markers:</b>	1706

## AGAT Full Stats

### Counts

<b>Genes:</b>	4878
<b>Transcripts:</b>	4878
<b>Exons:</b>	7764
<b>CDS:</b>	4878
<b>Introns:</b>	2886
<b>Single exon genes:</b>	3006
<b>Single exon transcripts:</b>	3006

### Mean Ratios

<b>Transcripts per gene:</b>	1
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<b>Exons per transcript:</b>	1.6
<b>Exons per CDS:</b>	1.6
<b>CDS per transcript:</b>	1
<b>Introns per transcript:</b>	0.6

#### **Mean Lengths (bp)**

<b>Gene:</b>	1852.36
<b>Transcript:</b>	1852.36
<b>Exon:</b>	474.45
<b>CDS:</b>	755.14
<b>Intron:</b>	1854.54

#### **Median Lengths (bp)**

<b>Gene:</b>	747
<b>Transcript:</b>	747
<b>Exon:</b>	372
<b>CDS:</b>	372
<b>Intron:</b>	197.5

#### **Total Lengths (bp)**

<b>Genes:</b>	9035795
<b>Transcripts:</b>	9035795
<b>Exons:</b>	3683592
<b>CDS:</b>	3683592
<b>Introns:</b>	5352203

### **Longest Features (bp)**

**Gene:** 176339  
**Transcript:** 176339  
**Exon:** 3851  
**CDS:** 6429  
**Intron:** 59934

### **Shortest Features (bp)**

**Gene:** 201  
**Transcript:** 201

### **OMARK Full Stats**