

# Report

	TARA_ASE_RAW
# contigs (>= 1000 bp)	39
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	84687
Total length (>= 5000 bp)	23930
Total length (>= 10000 bp)	12662
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	39
Largest contig	12662
Total length	84687
Reference length	4234461
GC (%)	46.18
Reference GC (%)	41.03
N50	1888
N75	1477
L50	10
L75	22
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	3 + 36 part
Unaligned length	81373
Genome fraction (%)	0.020
Duplication ratio	3.922
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10769.23
# indels per 100 kbp	118.34
Largest alignment	180
Total aligned length	3314
NGA50	-

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

## Misassemblies report

	TARA_ASE_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	35
# possible misassemblies	38
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	91
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	2

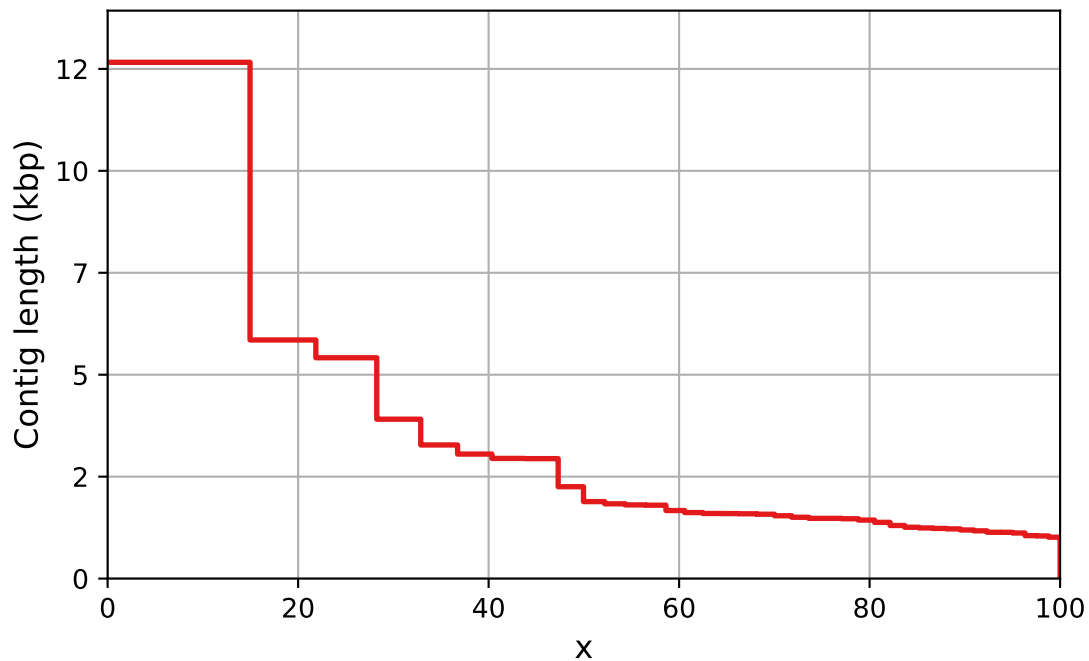
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	TARA_ASE_RAW
# fully unaligned contigs	3
Fully unaligned length	4022
# partially unaligned contigs	36
Partially unaligned length	77351
# N's	0

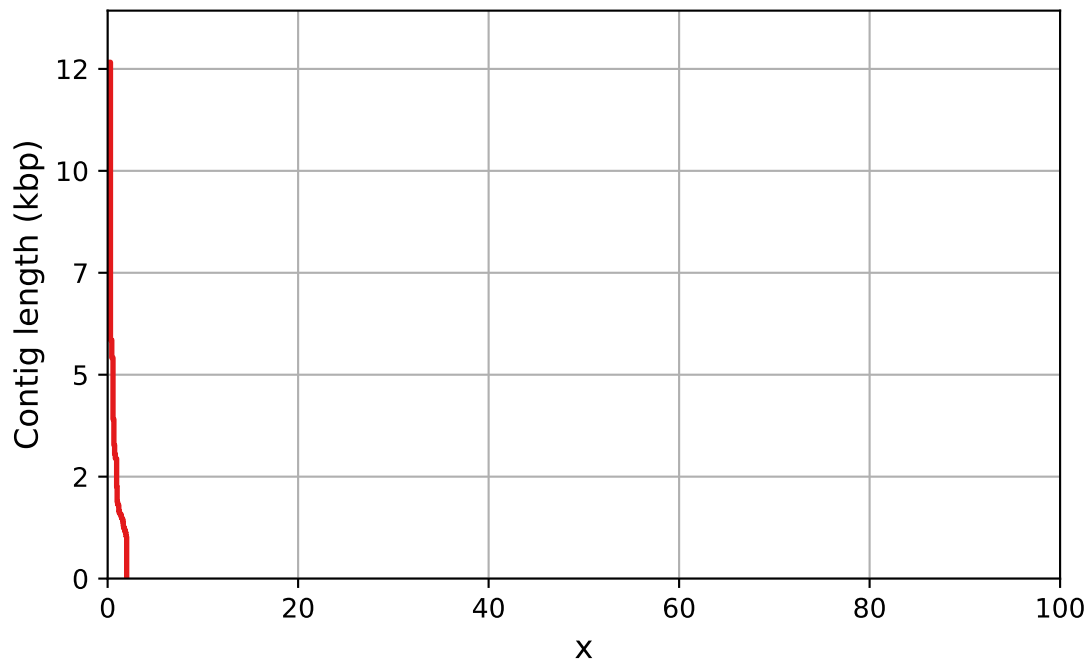
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

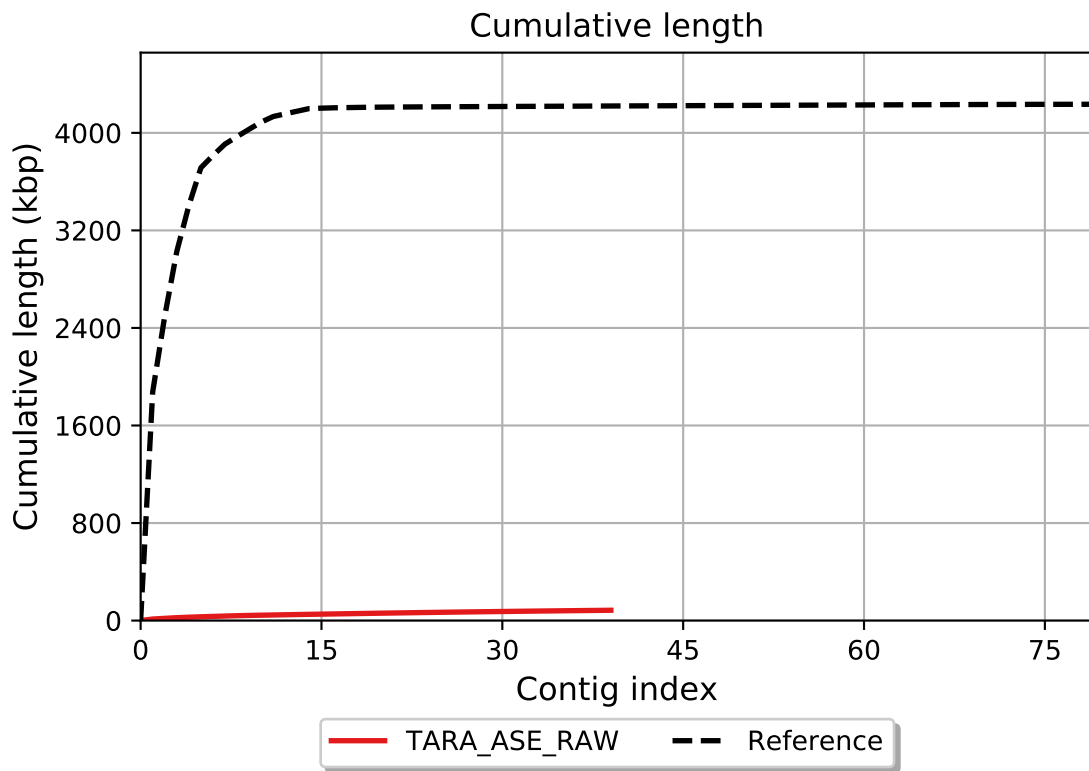


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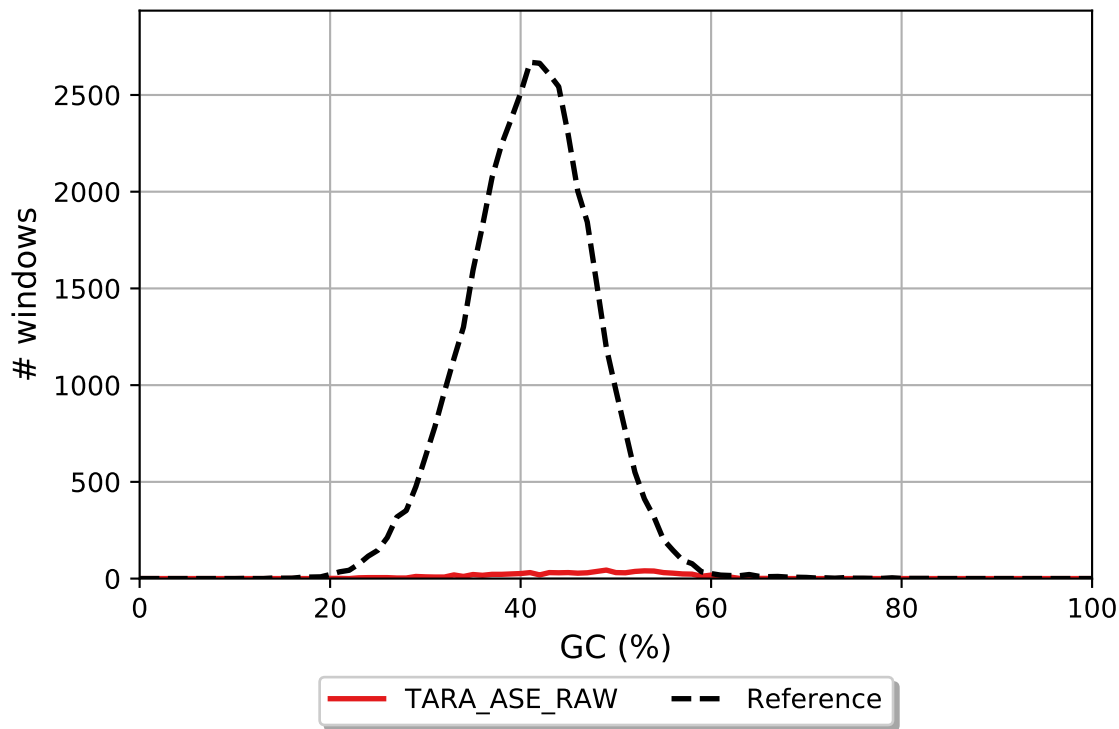
NGx



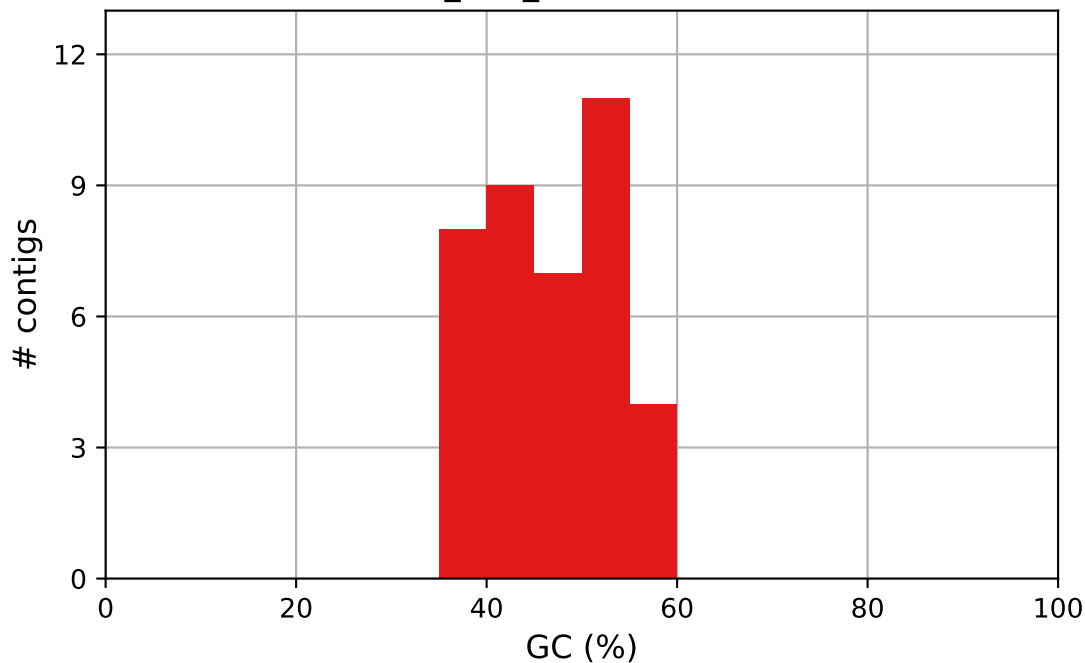
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## GC content



TARA\_ASE\_RAW GC content



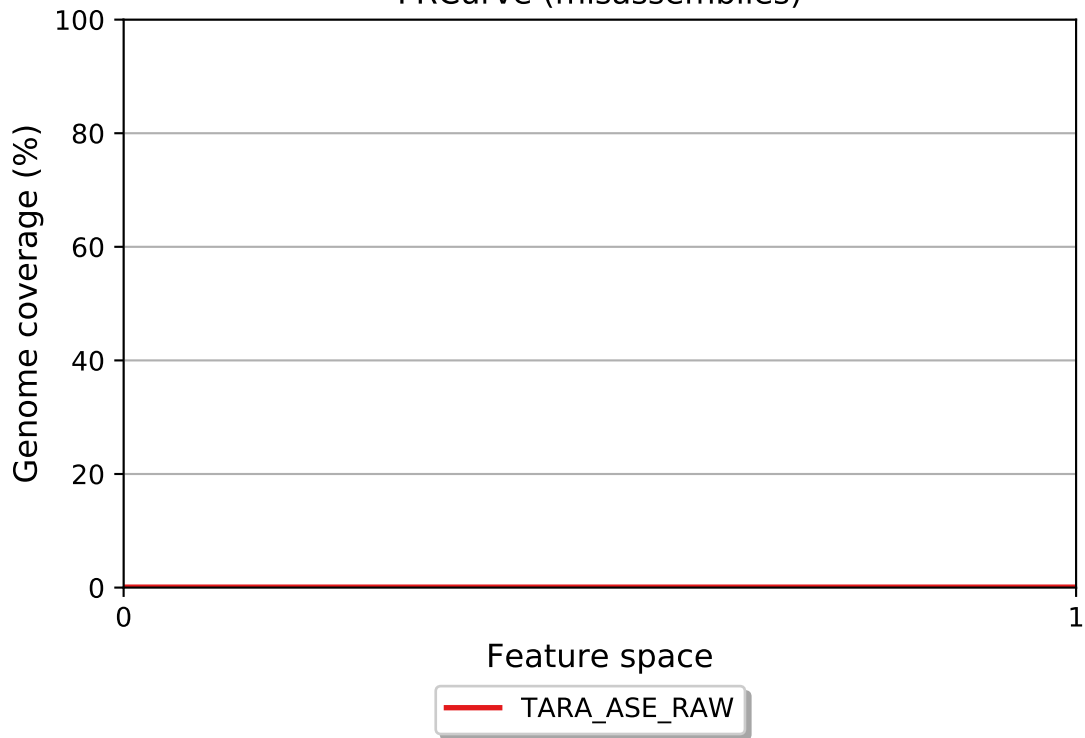
TARA\_ASE\_RAW



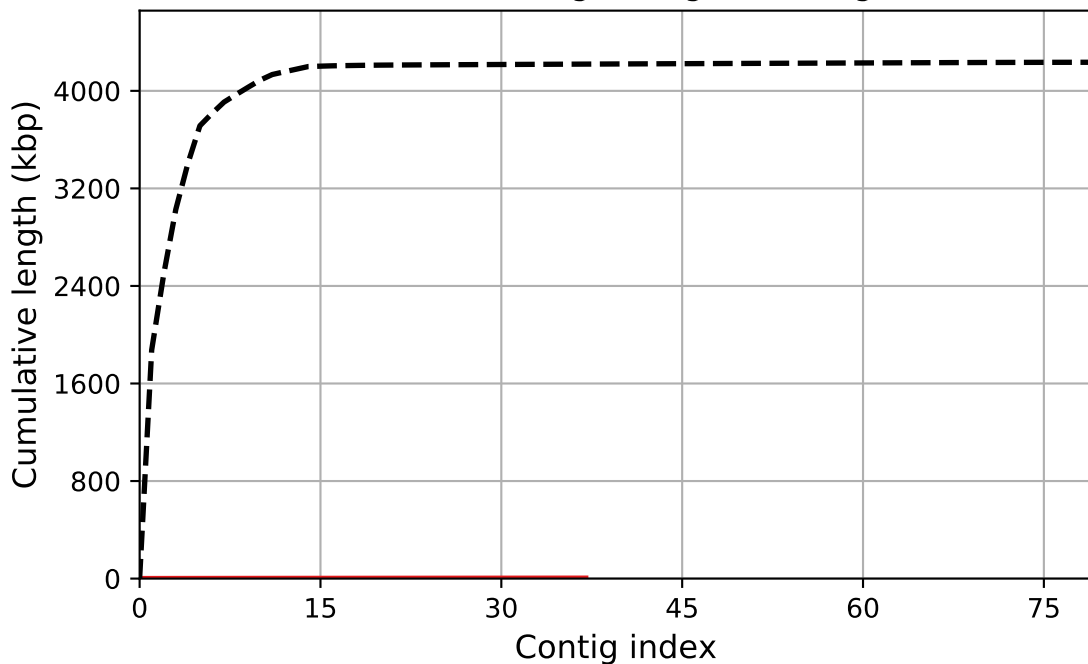
## Misassemblies



FRCurve (misassemblies)

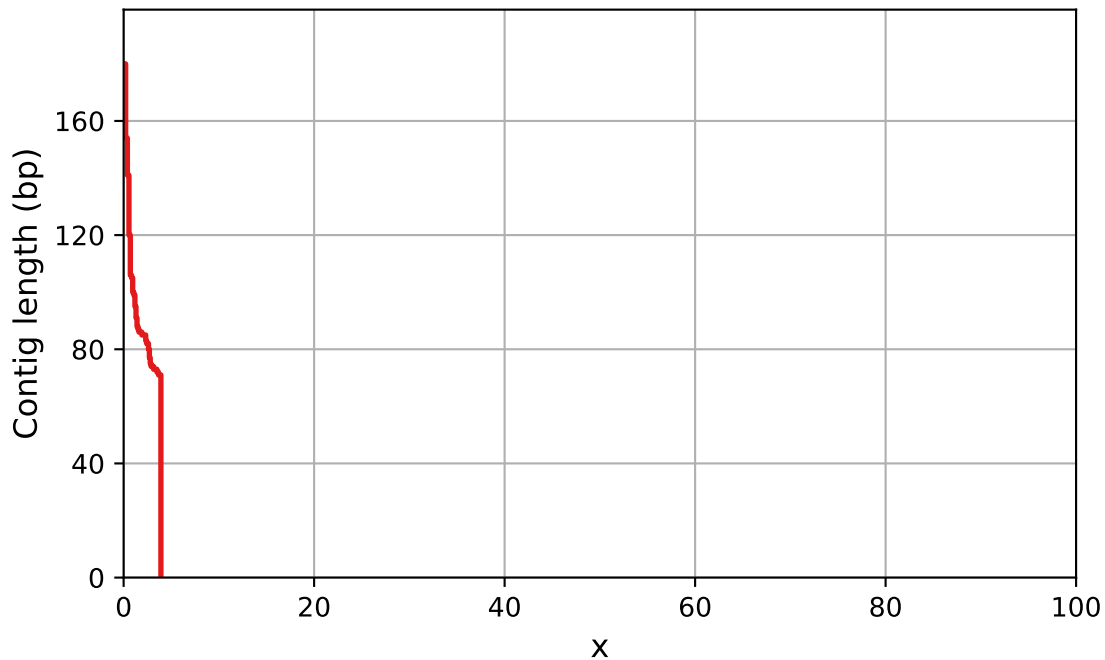


Cumulative length (aligned contigs)



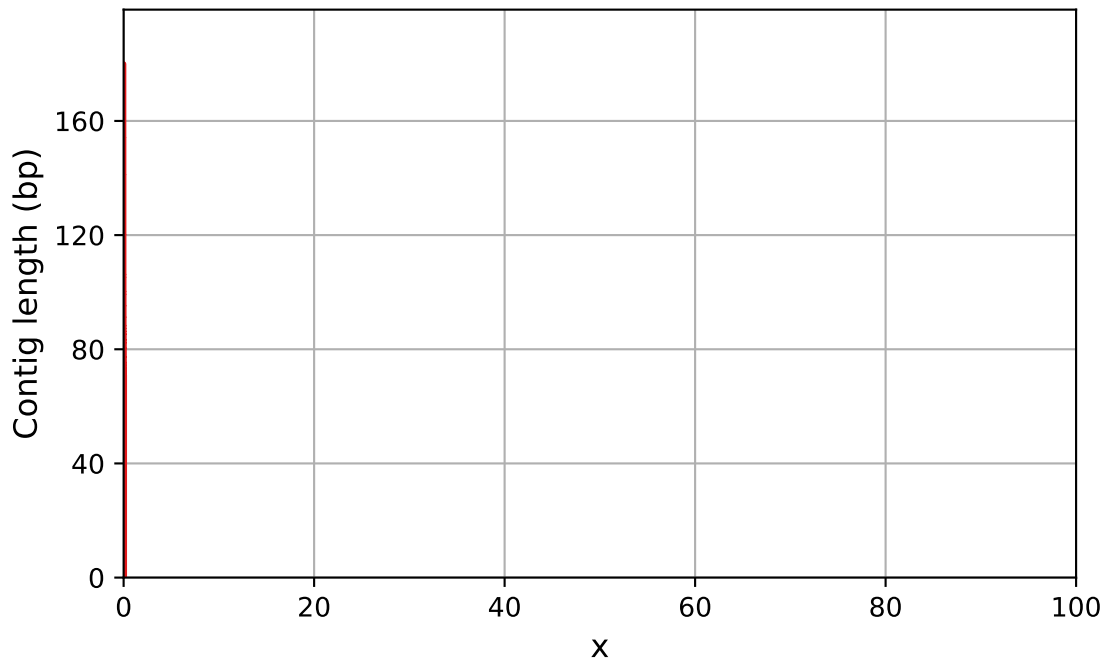
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NAx



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# NGAx



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