

## WebTraceMiner Frequently Asked Questions (FAQs)

**[Question 01].** *Are the source codes available for local installation?*

At the current stage, we are not ready to release the source codes yet, since releasing source codes involves many issues such as detailed documentation, user support, license and so on. However, in the future, we will release the source codes if we have necessary resources.

**[Question 02].** *Who should I contact with, if I have technical questions?*

For all technical questions, you can send emails to [conifergdb\\_support@muohio.edu](mailto:conifergdb_support@muohio.edu)  
For other general questions, you can send emails to [conifergdb\\_info@muohio.edu](mailto:conifergdb_info@muohio.edu)

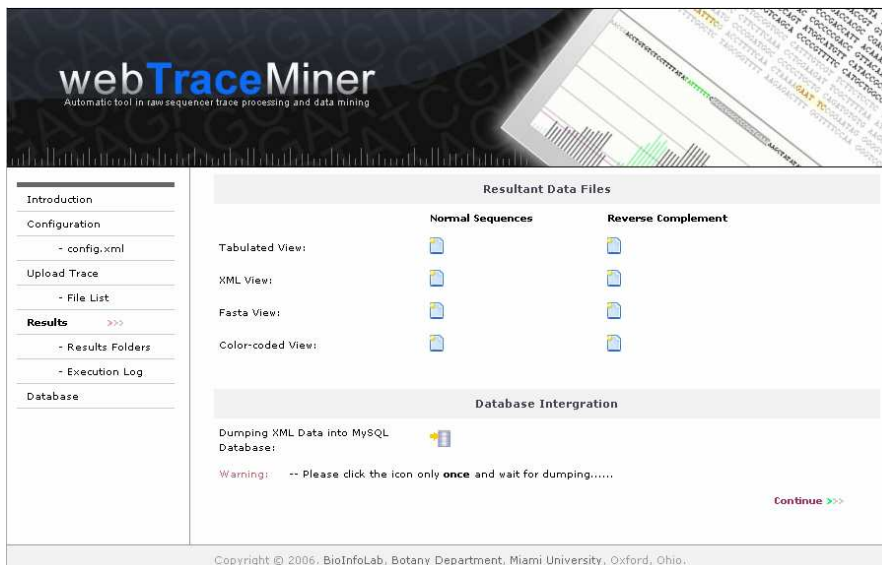
**[Question 03].** *Who can use the WebTraceMiner web service?*

A general user can utilize our server anonymously. All anonymous input and output data are store in our server with a unique identifier, which consists of a uniform guest email address plus a given date and time stamp (e.g., guest@email.com\_070328\_111250, EmailAddress\_YYMMDD\_HHMMSS). For registered users, data are identified similarly but with users' own email address.

**[Question 04].** *How many trace files I can upload at one time?*

Currently, we allow the maximum 50 MB trace files to be uploaded into our server. This should be enough for all trace files from a single sequencing 96-/384 plate. If you have multiple plates, you can use WebTraceMiner multiple times to process relevant data.


**[Question 05].** *How to download and save data locally?*



All raw traces files as well as derived files are stored in a specific folder created for a given trace processing event. As shown in the above figure, all the data displayed in four views (i.e., *Tabulated View*, *XML View*, *Fasta View* and *Color-coded View* can be saved locally for future exploration.

### (1) Tabulated View

After a user clicks “Sequence Filter”, then a link named “Save to file” will be available to save tab-delimited data.

Sequence Filter Help: ?  Here

No	Sequence	seqType	dir	rLen	qTag	GC	qStart	qStop	qLen	vNum
1	COLD1_10_A08.b1_A029	est	3	1329	1	42%	32	909	878	1
2	COLD1_12_A07.b1_A029	est	3	1357	1	51%	40	820	781	1
3	COLD1_12_B04.b1_A029	est	3	1342	1	42%	39	774	736	1
4	COLD1_12_G07.b1_A029	est	3	1355	1	51%	38	892	855	1
5	COLD1_14_B10.b1_A029	est	3	1405	1	51%	25	774	750	1
6	COLD1_15_A10.b1_A029	est	3	1420	1	43%	25	643	619	1
7	COLD1_17_H01.b1_A029	est	3	1354	1	44%	28	930	903	1
8	COLD1_19_G01.b1_A029	est	3	1413	1	51%	25	723	699	1

Sequence Filter Help: ?

SeqName:

Direction:  qTag:

Filter Vector: vNum:  ≤ vNum ≤

PolyT: ptNum:   Match:


PolyA: paNum:   Match:

Adaptor1: a1Num:   Match:

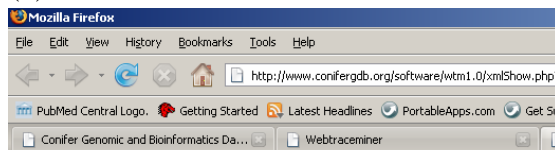
Adaptor2: a2Num:   Match:

Enzyme1: e1Num:   Match:

Enzyme2: e2Num:   Match:

 Here

### (2) XML View



A user can copy-and-paste to save the entire XML page displayed after XML View is selected.

```
<?xml version="1.0"?>
<xml>
<seq_read>
<config_uid>guest@muohio.edu_070330_020300</config_uid>
<seq_name>COLD1_10_A08.b1_A029</seq_name>
<seq_type>est</seq_type>
<est_dir>3</est_dir>
<reverse_complement>No</reverse_complement>
<raw_length>1329</raw_length>
<n_content>4</n_content>
<a_content>423</a_content>
<t_content>346</t_content>
<g_content>260</g_content>
<c_content>296</c_content>
<gc_content>42%</gc_content>
```

### (3) Fasta View

There are two different links for “Download Fasta Files”. One is “Individual Files” and the other is “Combined File” (see the left Figure). Using these two options, a user can download all individual fasta files or a combined fasta file.

**Fasta Files :**

Raw Sequences Fasta	<a href="#">All Seqs</a>	<a href="#">Passed</a>	<a href="#">Failed</a>
High Quality Seq Fasta	<a href="#">All Seqs</a>	<a href="#">Passed</a>	<a href="#">Failed</a>
Final Sequence Fasta	<a href="#">All Seqs</a>	<a href="#">Passed</a>	<a href="#">Failed</a>

Total 8 sequences. | Page 1 |

Download Fasta Files [Individual Files](#) [Combined File](#) [Help](#)

```
> COLD1_10_A08.b1_A029
ATAGGNMNGGACCGCTGACGATACCCTANACTTCTCGAGTTTTTTTTTTTT
TTTTTTTTTTCACAAATACACAGCATTAACTCGTGATTTTATCATAAATGT
AAAACCATACATCGTTGTCTACAGATAATGATACTTGATTAATAAATCACAA
AAAATAATCAGAAATCTGTAATACTCGGCAAAATCGATTTTAAAGAATATC
ACACCGTAACTTCGACAAATTTGCTTGGACCAAATTTATTTCTTGGCAGGAA
AAATGCGAAAGACCAGGATTTAAATGAATGTAACATATAGCTCTAAGGAAG
GCAGATATTGACCTGTTATTGCGCATCTAACCTTCCCAGCTTGGATAACA
AACTATCAAATTTTTTCCGAAACAGTGCAAAAGAATACAGCCACAATTACG
ATTTCCCAGGAAGACTATAGGACACTTCAATATCAAAGAGTCCAGAATGC
TGCAC TGAAAGAGATAAACAACTCGCAATCATTATGATAAACATTTGGA
TTTGC TTTACAGAAAAAAACCCCTCTTCACTGATCTGTTATGTAATAATCA
AACAACTGAAAGCCGACTGAATTGTTGATGAAACATGCGAAGCAATAG
TCTGAGATGC AAAATTTTGAACCTGTTTCTTTGCACTTTTTCGGCATTTT
GTAATCCAAACAAATGTTTGC AATGCTTAAAGCCAAACAACTCCAACCAC
TAGAAGATAATCAATGTTGAGCTTGATTAAGGCTACAATCCCCAATGCCA
```

### (4) Color-coded View

A user can use Browser save function to save the whole file as a HTML document.

Good quality	ATCG ... ATCG	Low quality	ATCG ... ATCG
Poly T tail	TTTTTTTT	Poly A tail:	AAAAAAA
Vector high quality	ATCG ... ATCG	Vector low quality	ATCG ... ATCG
Adaptor 1	GGCAAGG	Adaptor 2	NO_INFO
Enzyme 1: EcoRI	GAATTC	Enzyme 2: XhoI	CTCGAG

Back

```
> COLD1_10_A08.b1_A029
1 11 21 31 41 51 61 71 81 91
0 ATAGGNMNGGACCGCTGACGATACCCTANACTTCTCGAGTTTTTTTTTTTT CACAATACAG AGCATTAACT CGTGATTTTA TCATAAATGT
1 AAAACCATACATCGTTGTCTACAGATAATGATACTTGATTAATAAATCACAA GAATCTGTAA TCTGGCAAA AATCGAATTT AAAGATATG
2 AACCCGTAAC TTGCAAAATT TCTTTGACCC AAATTAATTC TTGCGAGAA AAATCGAAA GACCGAATTT TAATGAAAT TAACATATAG TCTAAGGAAG
3 CGAGATATG AACTTATAT GGCATCTAAA CTTTCCGAGC TTGCAATACA AACTATGAAA TTTTTCGGA ACATGCAAA AGATAACAG CACAATTAGG
4 ATTTCCGAGG AAGACTATAG GACACTTCAA TATCAAAGAG TCCGAATGCG TGCATGAGC AGATAAACA ACTCGCAAT CATTATGATA AACATTGGA
5 TTTGCTTAC AAAAATAAAC CCTTTTCACT GATCTGTTAT CTAATATACA AACAACTG AAAGCCGACT GAATGTTTGA TCAAAATATG GAAGCAATAG
6 TTGAGATGCG AAAATTTTGA ACTGTTTGT TTGCTCTTT TTGGGATTC GTAAATGAAA GATGTTTGC AATGCTTAA CCGAAGAAA CTCGACAGC
7 TAGAAGATAA TCAATCTTGA CTTTGAATTA GGTATAAAT CCAATGCA CCAACAAAG ACCTGTGAGA TAAAGCTCC ACCAAAGAG CCATGATCC
8 TTTTGTAAA TCGGGATAA TGACTCTGCG CTGCTGCGCA ATTCGTAATC ATGCTATAGC TGTTCCTGT GTGAATTTT TATCCGCTCA CAATTCCACA
9 CAACATAGC GCGCGAAGCA TAAAGTATA AGCCTGGGT CCTAAGAG TGAGCTAAT CACAATAAT GCTTGGCTT CACTGCGCC ITTCCAGTCC
10 GGAAGACTGT CTTGCAAGCT GATTAATGTA ATGCGCAAG CCGCGGAGA GCGGTTTGC TAAAGGCGC CTTTTCCTT CTTGCTAAT GACTGCTGC
11 CTTCCGCGCT TGGCTGCGG CCGCGGAT CACTCACTA AGGGGGTAA TACGTTTCC CCAAAATCCG GGAATAACD CAGAAAAAAA TCGTAGCAA
12 AGCCCGGAAA AGCCGAGAC CTTAAAGG CCGTTTTG GTTTTTTC AGGGCCCCC CCGAAGAAA TCAAAAATG CCGCTTAAT AAAGTGGAA
13 AACCCGAAA CATAAACC AGGTTTTCC
```