



The Centre for Applied Genomics DNA Sequencing Facility

Retrieving Results in GSLE

The account holder will receive an email from TCAG Sequencing when the order data is ready to be reviewed and downloaded. Please add this email (tcag_sequencing@sickkids.ca) to your contacts to be sure you receive our notifications (so that the message is not directed to your junk folder or deleted as spam). Also note that this email is meant for out-going notifications only and is not monitored.

Finding Results

- All orders, folders and individual data can be found by clicking on the appropriate link in the left-hand navigation panel or in the central panel on the homepage.

The screenshot shows the GeneSifter Lab Edition interface for the TCAG Sequencing Server. The left-hand navigation panel is visible, with 'Orders' and 'Data' highlighted by red circles. The main content area displays a 'Welcome to GeneSifter Lab Edition' message and two summary tables. The 'My Orders' table shows counts for New, Submitted, Processing, and All Completed orders. The 'My Data' table, also highlighted with a red circle, shows counts for Projects, Folders, Folders with New Data, Chromatograms, Fragment Analysis Files, and Other Files.

My Orders	
New	0
Submitted	0
Processing	0
All Completed	0

My Data	
Projects	0
Folders	0
Folders with New Data	0
Chromatograms	0
Fragment Analysis Files	0
Other Files	0

- In 'View Data' or 'View Folders', click on the desired order number.

Note: 'View Data' is a consolidated list of all orders and all samples – the list may continue onto multiple pages.

Viewing results

All data for a particular order can be viewed by clicking on the folder name, and individual samples can be examined by clicking on their name.

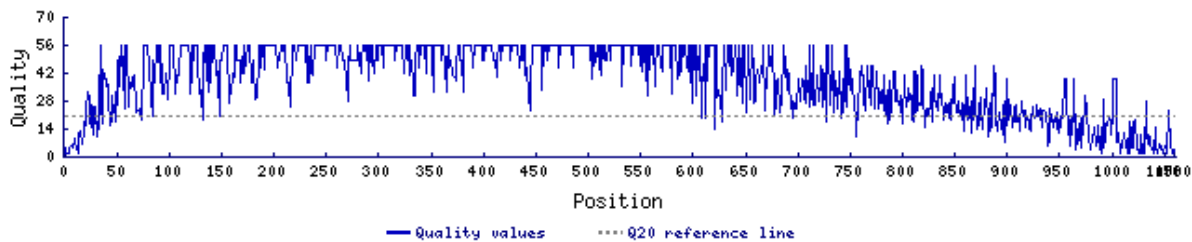
- **Chromatogram Read** summarizes the attributes of the sample (eg. name, run plate, signal strength)

Chromatogram Read

PDF Download Chromat Data Delete Chromat View Chromat Trace Open in FinchTV Edit Details			
▼ General Information for MT25-17			
Label	MT25-T7	Format	ABIF
Folder	100048	Plate Label	NOV20-BA-2013-1-GS-1
Instr Sample Name	257	Reaction ID	257
Instr. Model	3730	Instr. Name	3730XL-1-16108-004
Run Start	2013-11-20 12:35:40	Run Stop	2013-11-20 14:23:20
Lane	77	# Lanes	96
Spacing	15.00	Signal Strs	A=829, C=554, G=761, T=772
Mobility	KB_3730_POP7_BDTV3.mob	Matrix	n/a
Comment	<ID:257>		
Description	n/a		

- **Quality Graph** shows the quality score (Q) versus the position of each base in the sequence read. At Q20, the probability of miscalling a base is 1%. Above Q20, the probability of miscalling a base is lower than 1%; below Q20, the probability of a miscall increases. The read length, trimmed length (after vector and poor sequence have been trimmed), and the number of bases with a Q value >20 are given below the graph.

Quality Graph



Read Length	1061 b	Trimmed Length	850 b	Pos.	22-871
Q20	872 b	Q20/len	0.82		
Q40	564 b	Q40/len	0.53		

Please contact Tara Paton (tpaton@sickkids.ca) or Beverly Apresto (bapresto@sickkids.ca) with questions (416) 813-8643

- The nucleotide **Sequence** can be viewed. Low-quality sequence is trimmed from the final text (strikethrough text). Vector sequences (if present in the sequence) are denoted in light blue text.

▼ Sequence

Previous Revision	n/a	Current Revision	1	Next Revision	n/a	Latest Revision	1
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Links: [View Revision History](#)

>MT25-T7 CHROMAT_ID=213

```

arrccccccgggatctctggagtggtggctgcataattgcagaaatgtttcgtaga 60
aagcctcttttctggaagttcagatggtgatcaactaggaaaaatcttggcgtgatt 120
ggactcccaggagaagaagactggcctagagatgttggccttcccaggcaggctttcat 180
tcaaaatctgcccaaccaattgagaagtttgtaacagatatcgatgaactaggcaaaagac 240
ctactctgaaagtgtttgacatttaaccagccaaaagaatatctgcctacagtgccctg 300
tctcaccatacttccaggacctggaaaggtgcaaaagaaacctggattcccacctgccg 360
cccagccagaacacctcggagctgaatacagccggttaagcctatccctaacctctctc 420
ggtctcgtattctcagtgagacccagcttcttgtacaaagtggttgatccagcacagt 480
ggcggccgctcagcttagagggcccgcggttcgaaggttaagcctatccctaacctctc 540
ctcggctcgtattctacgcgtaccgggttagtaatgaggagaaagagtaaatgaaatggca 600
tcgactgcagtaggtaactgaggatccaatgtaactgtattcagcgtgacgaaattctt 660
agctattgtaataactctagaggatcttctggaaggaaccttactctcgtggtgtgacata 720
attggacaaactacctacagagatttaaagctctaaggtaaaatataaaattttaagtgt 780
ataatgtgttaaactactgattctaattggttggatatttagattccaacctatggaac 840
tgatgaatggggcagtggtggaatgcctttaatgaggaaaaacctgttttgctcagaaga 900
aatgccatctagtgatgatgaggctactgctgactctcacattctactctccaaaaaga 960
gagaaagttagagaccccaagacttccctcarattgctaagtttttgragtcatsckkgg 1020
ggtaarwwawaraacctcksgcksgctgsgcawtaaaaaca

```

~~æeg~~ trimmed region(s) [acgt](#) vector region(s)

Action buttons at the top of the page allow the user to delete, download, view or generate a PDF report for the sample.

Chromatogram Read

[PDF](#)
[Download Chromat Data](#)
[Delete Chromat](#)
[View Chromat Trace](#)
[Open in FinchTV](#)
[Edit Details](#)

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Viewing chromatograms

Electropherogram viewers are freely available for Microsoft Windows, MacOS Classic, and MacOSX from these sites. Users may be required to register to access the freeware. TCAG does not endorse or support any of this software.

- [Applied Biosystems Sanger Analysis Tools](#) - cloud-based data analysis
- [CHROMAS LITE CHROMATOGRAM VIEWER](#) - Microsoft Windows
- [4Peaks](#) - MacOS 10.7+
- [Sequence Scanner \(Applied Biosystems Genetic Analyzer\)](#)

Other useful tools. TCAG does not endorse or support these tools.

- [UCSC In-Silico PCR](#)
- [Primer3 for design of PCR Primers](#)
- [BioEdit Sequence Alignment Editor for Windows](#)

Downloading multiple files

In the folder view, choose samples to be downloaded by checking the empty box to the left of the sample name or click on the 'Download all Chromats' button at the top of the page.

Contents of folder 100005

Edit Folder
 Relabel all Chromats
 Move all Chromats
 Download all Chromats
 Folder Report

Chromatograms (19) FSA Next Gen Other

Find: Label CONTAINS Go Reset ?

Items 1-19 of 19

	Label	Start Time	Rev	Len	Trim	Q20	Q20/len	Q40	Q40/len	A sig	C sig	G sig	T sig	Description
<input checked="" type="checkbox"/>	DNA1-M13F -20 Invitrogen	2013-11-18 15:16:58	1	510	492	478	0.94	316	0.62	293	242	342	292	n/a
<input checked="" type="checkbox"/>	DNA2-M13F -20 Invitrogen	2013-11-18 15:16:58	1	513	486	474	0.92	419	0.82	368	255	380	348	n/a
<input checked="" type="checkbox"/>	DNA3-M13F -20 Invitrogen	2013-11-18 15:16:58	1	515	494	482	0.94	457	0.89	422	260	408	339	n/a
<input type="checkbox"/>	DNA4-M13F -20 Invitrogen	2013-11-18 15:16:58	1	542	479	471	0.87	369	0.68	633	672	361	326	n/a
<input type="checkbox"/>	DNA5-M13F -20 Invitrogen	2013-11-18 15:16:58	1	516	471	468	0.91	426	0.83	398	358	421	419	n/a
<input type="checkbox"/>	DNA6-M13F -20 Invitrogen	2013-11-18 15:16:58	1	516	491	477	0.92	417	0.81	424	270	365	430	n/a
<input checked="" type="checkbox"/>	DNA7-M13F -20 Invitrogen	2013-11-18 15:16:58	1	508	493	481	0.95	458	0.90	473	294	497	404	n/a
<input type="checkbox"/>	DNA8-M13F -20 Invitrogen	2013-11-18 15:16:58	1	535	467	455	0.85	384	0.72	539	597	383	333	n/a
<input type="checkbox"/>	DNA9-M13F -20 Invitrogen	2013-11-18 15:16:58	1	510	485	470	0.92	212	0.42	323	200	343	321	n/a
<input type="checkbox"/>	DNA10-M13F -20 Invitrogen	2013-11-18 15:16:58	1	515	491	473	0.92	367	0.71	233	230	332	262	n/a
<input type="checkbox"/>	DNA11-M13F -20 Invitrogen	2013-11-18 15:16:58	1	517	497	484	0.94	423	0.82	309	183	357	293	n/a
<input type="checkbox"/>	DNA12-M13F -20 Invitrogen	2013-11-18 15:16:58	1	546	495	483	0.88	356	0.65	433	424	375	326	n/a
<input checked="" type="checkbox"/>	DNA13-M13F -20 Invitrogen	2013-11-18 15:16:58	1	516	497	484	0.94	449	0.87	2929	2146	2545	2672	n/a
<input type="checkbox"/>	DNA14-M13F -20 Invitrogen	2013-11-18 15:16:58	1	341	0	37	0.11	0	0.00	47	48	40	62	n/a
<input type="checkbox"/>	DNA15-M13F -20 Invitrogen	2013-11-18 15:16:58	1	274	172	167	0.61	96	0.35	701	713	1120	814	n/a
<input type="checkbox"/>	DNA16-M13F -20 Invitrogen	2013-11-18 15:16:58	1	509	489	477	0.94	436	0.86	2628	1919	2158	2140	n/a
<input type="checkbox"/>	DNA17-M13F -20 Invitrogen	2013-11-18 15:16:58	1	512	0	128	0.25	0	0.00	114	95	107	124	n/a
<input type="checkbox"/>	DNA18-M13F -20 Invitrogen	2013-11-18 15:16:58	1	516	500	484	0.94	336	0.65	2156	1600	1807	1983	n/a
<input type="checkbox"/>	DNA19-M13F -20 Invitrogen	2013-11-18 15:16:58	1	521	504	491	0.94	390	0.75	2176	1601	1830	1864	n/a

-- Choose Action --
 Move chromat...
 Relabel chromat...
 Download chromat...
 Delete chromat...
 -- Choose Action --

Go

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Chromat Data Download

Chromatograms in Zip File

All Chromatograms with trace data ▾

Convert ABI to SCF format

Download Chromats

Sequences

Type Nucleotides Quality Scores Amino Acid Translations *Sequence type*

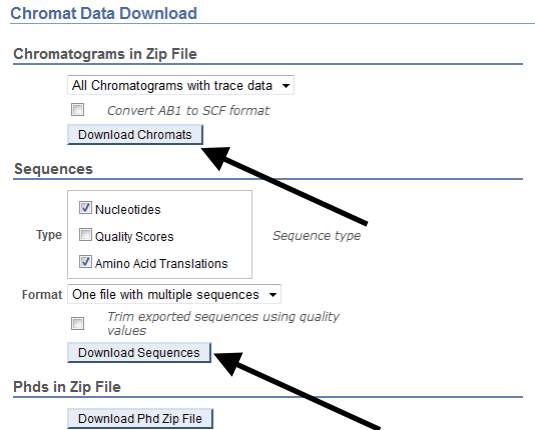
Format One file with multiple sequences ▾

Trim exported sequences using quality values

Download Sequences

Phds in Zip File

Download Phd Zip File

The image shows a web interface for downloading chromatogram and sequence data. It is divided into three main sections: 'Chromatograms in Zip File', 'Sequences', and 'Phds in Zip File'. The 'Chromatograms in Zip File' section has a dropdown menu set to 'All Chromatograms with trace data', a checkbox for 'Convert ABI to SCF format', and a 'Download Chromats' button. The 'Sequences' section has a 'Type' section with checkboxes for 'Nucleotides' (checked), 'Quality Scores', and 'Amino Acid Translations' (checked), and a 'Format' section with a dropdown set to 'One file with multiple sequences' and a checkbox for 'Trim exported sequences using quality values'. There is a 'Download Sequences' button. The 'Phds in Zip File' section has a 'Download Phd Zip File' button. Two black arrows point from the text below to the 'Download Chromats' and 'Download Sequences' buttons.

Choose to download **Sequence Text Files** or **Chromatograms** from this window. If you are downloading an entire folder, the chromat files will be saved as a .tar file and will need to be extracted (unzipped) to view the individual files. There are several free programs (e.g. [7-Zip](#) or [JustZIPit](#)) available to do this extraction step.