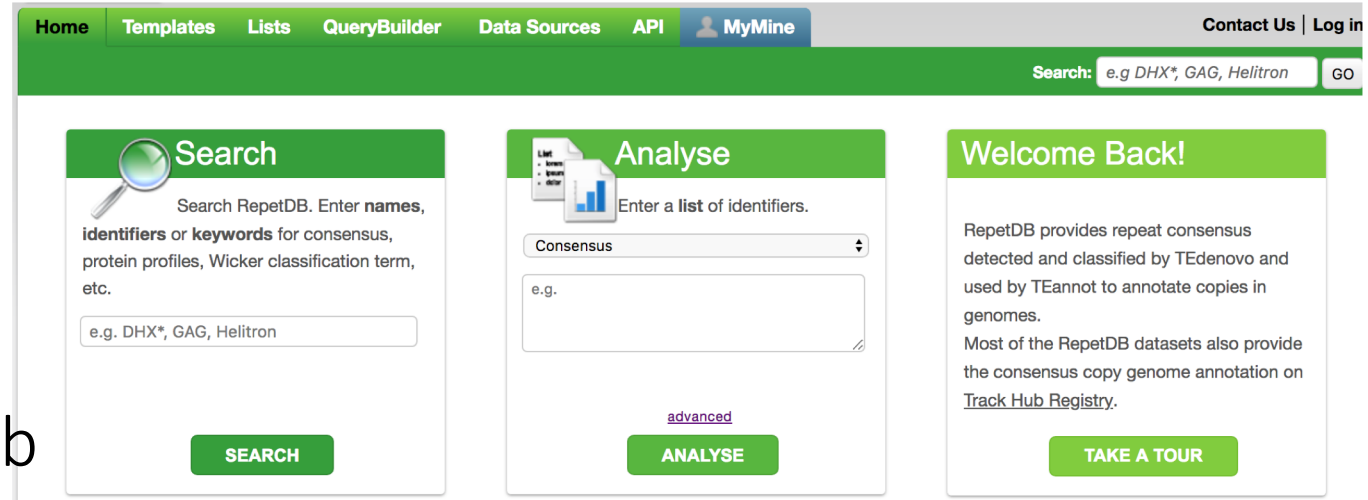
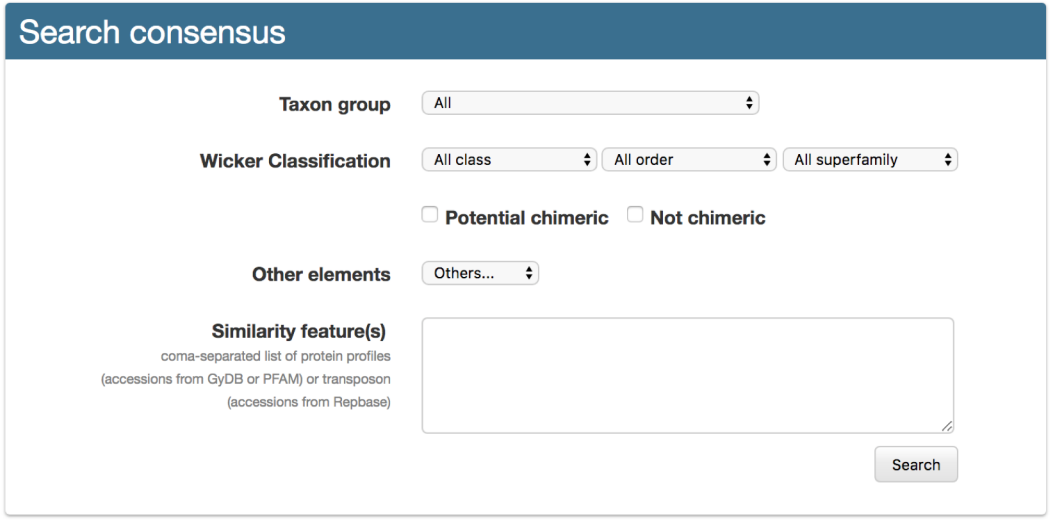
How to get consensus fasta sequences from a table or a list

https://urgi.versailles.inra.fr/repetdb

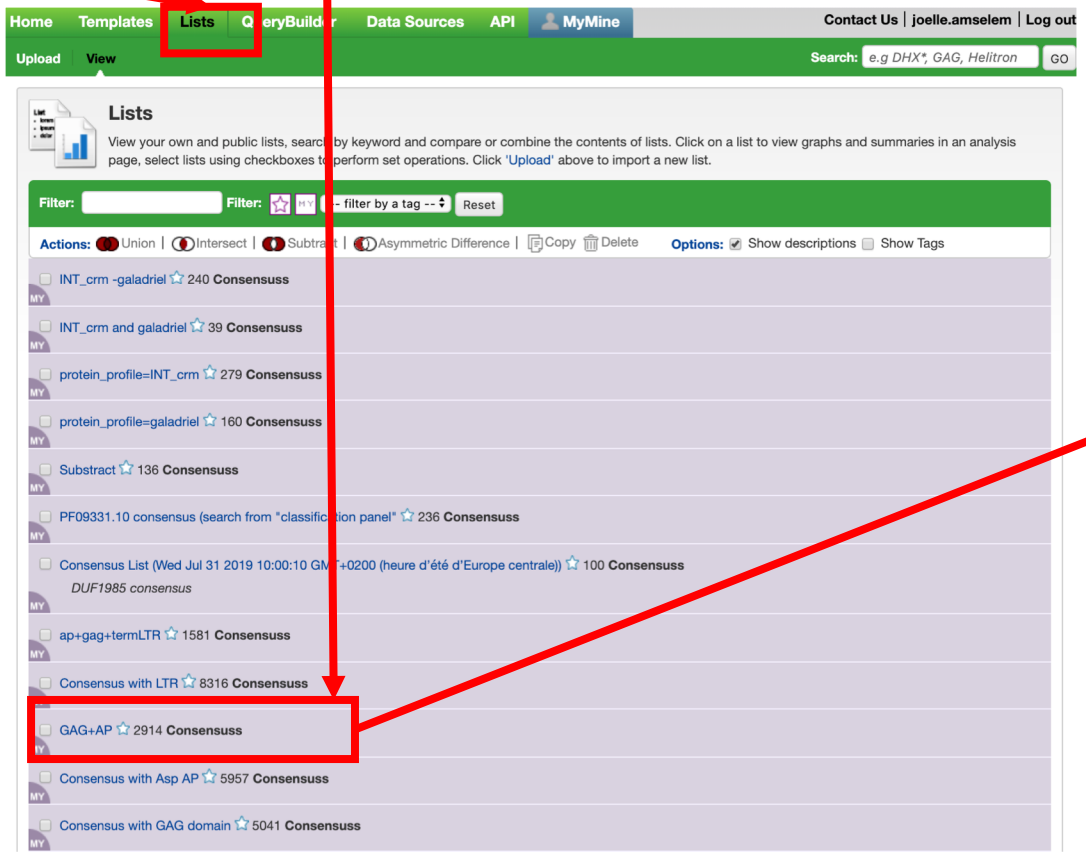


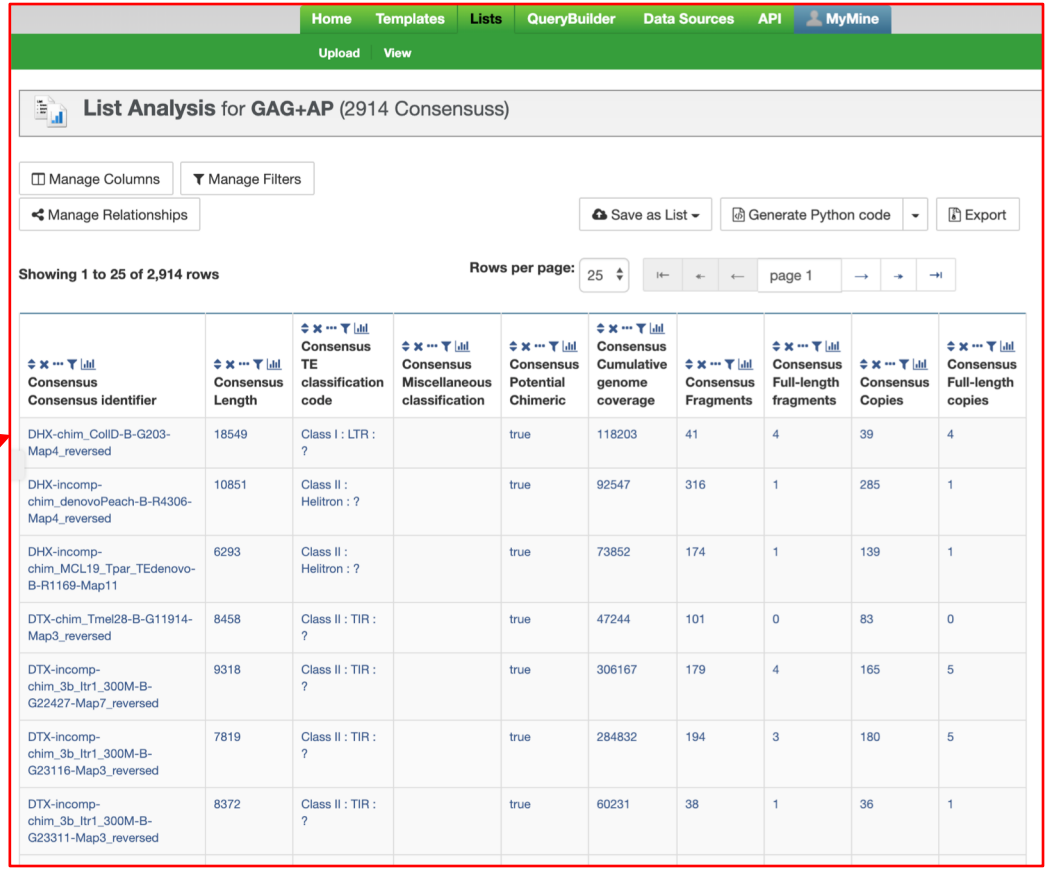


Amselem J, et al. RepetDB: a unified resource for transposable element references. Mobile DNA. 2019;10:6.

How to get consensus sequence from a table or a list

Example : from a
list you have previously saved



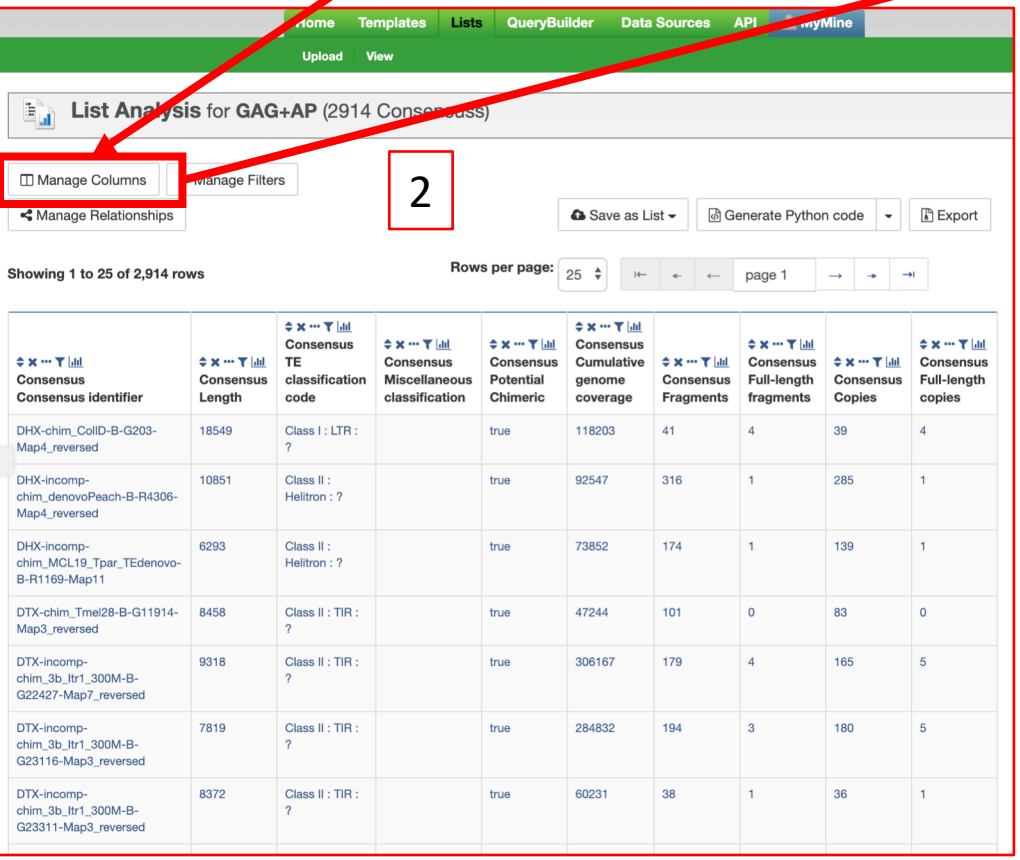


Consensus Consensus identifier	Consensus Length	Consensus TE classification code	Consensus Miscellaneous classification	Consensus Potential Chimeric	Consensus Cumulative genome coverage	Consensus Fragments	Consensus Full-length fragments	Consensus Copies	Consensus Full-length copies
DHX-chim_CollD-B-G203-Map4_reversed	18549	Class I : LTR : ?		true	118203	41	4	39	4
DHX-incomp-chim_denovoPeach-B-R4306-Map4_reversed	10851	Class II : Helitron : ?		true	92547	316	1	285	1
DHX-incomp-chim_MCL19_Tpar_TEdenovo-B-R1169-Map11	6293	Class II : Helitron : ?		true	73852	174	1	139	1
DTX-chim_Tmel28-B-G11914-Map3_reversed	8458	Class II : TIR : ?		true	47244	101	0	83	0
DTX-incomp-chim_3b_ltr1_300M-B-G22427-Map7_reversed	9318	Class II : TIR : ?		true	306167	179	4	165	5
DTX-incomp-chim_3b_ltr1_300M-B-G23116-Map3_reversed	7819	Class II : TIR : ?		true	284832	194	3	180	5
DTX-incomp-chim_3b_ltr1_300M-B-G23311-Map3_reversed	8372	Class II : TIR : ?		true	60231	38	1	36	1

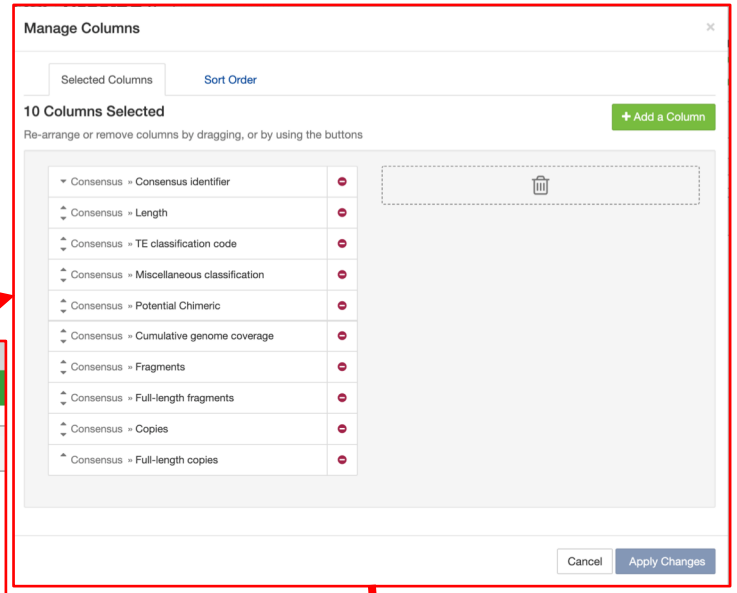
Manage columns

1

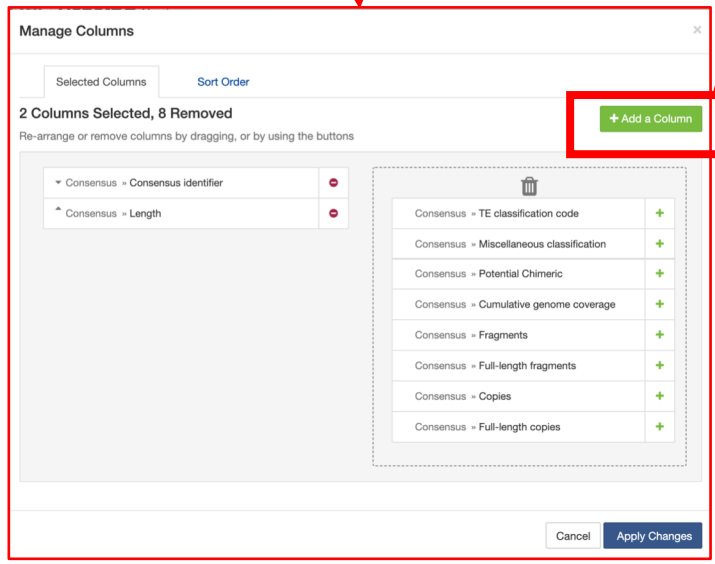
2

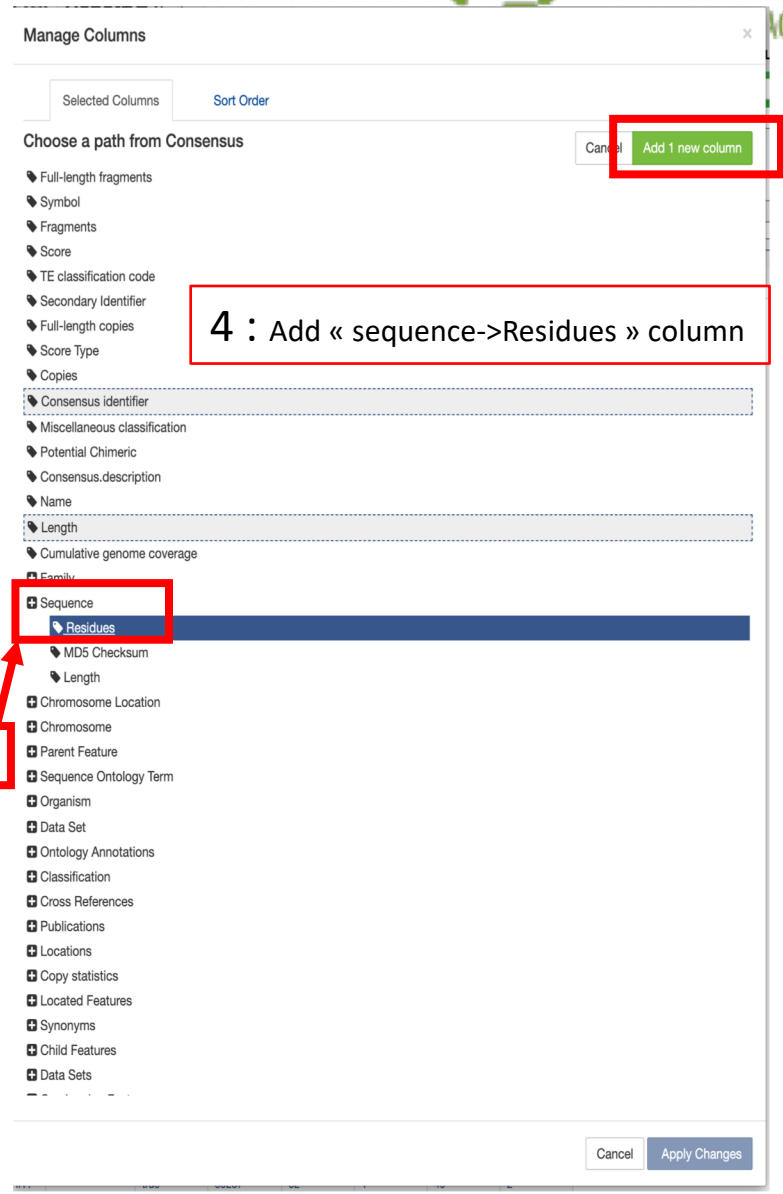


Consensus Consensus identifier	Consensus Length	Consensus TE classification code	Consensus Miscellaneous classification	Consensus Potential Chimeric	Consensus Cumulative genome coverage	Consensus Fragments	Consensus Full-length fragments	Consensus Copies	Consensus Full-length copies
DHX-chim_ColID-B-G203-Map4_reversed	18549	Class I : LTR : ?		true	118203	41	4	39	4
DHX-incomp-chim_denovoPeach-B-R4306-Map4_reversed	10851	Class II : Helitron : ?		true	92547	316	1	285	1
DHX-incomp-chim_MCL19_Tpar_TEdenovo-B-R1169-Map11	6293	Class II : Helitron : ?		true	73852	174	1	139	1
DTX-chim_Tmel28-B-G11914-Map3_reversed	8458	Class II : TIR : ?		true	47244	101	0	83	0
DTX-incomp-chim_3b_ltr1_300M-B-G22427-Map7_reversed	9318	Class II : TIR : ?		true	306167	179	4	165	5
DTX-incomp-chim_3b_ltr1_300M-B-G23116-Map3_reversed	7819	Class II : TIR : ?		true	284832	194	3	180	5
DTX-incomp-chim_3b_ltr1_300M-B-G23311-Map3_reversed	8372	Class II : TIR : ?		true	60231	38	1	36	1

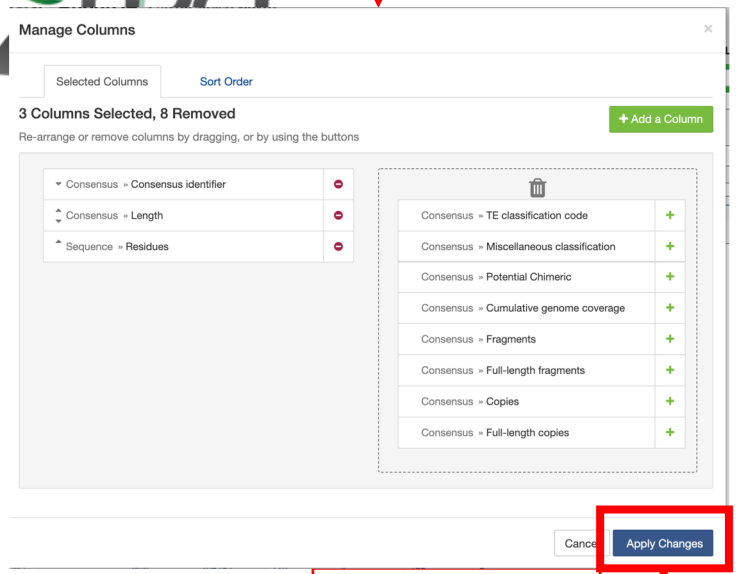


3 : delete all columns not needed



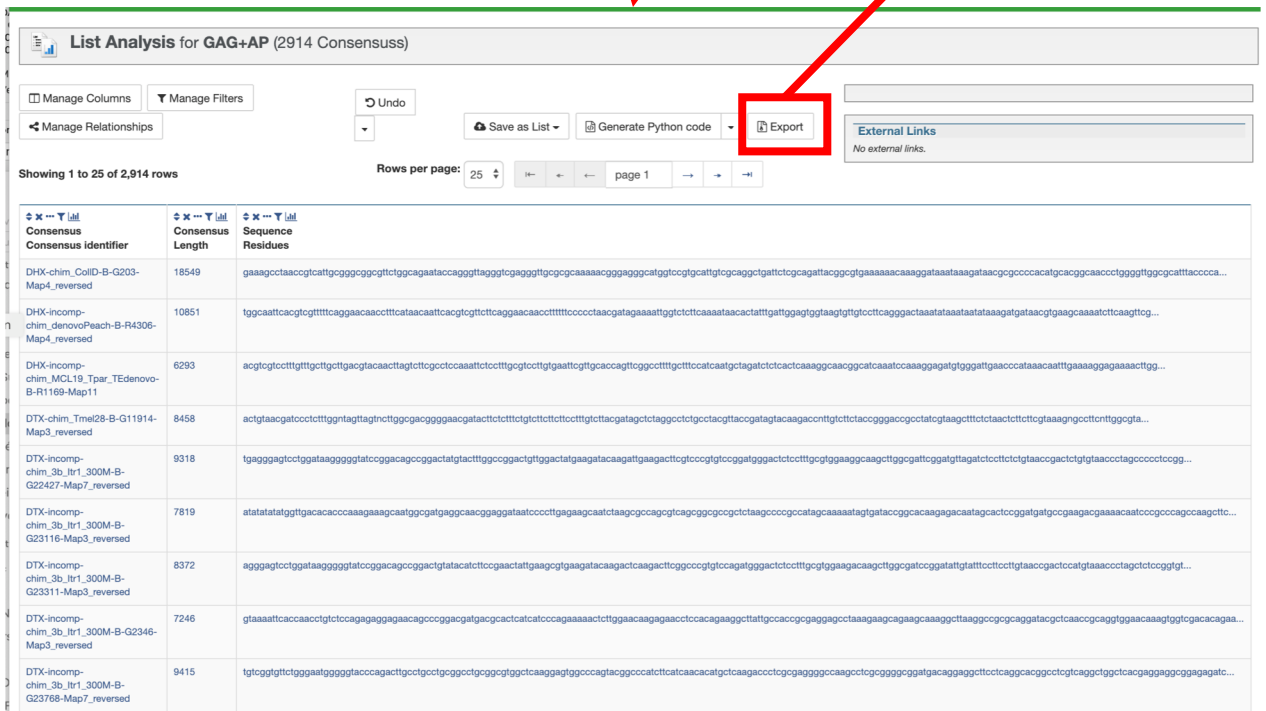


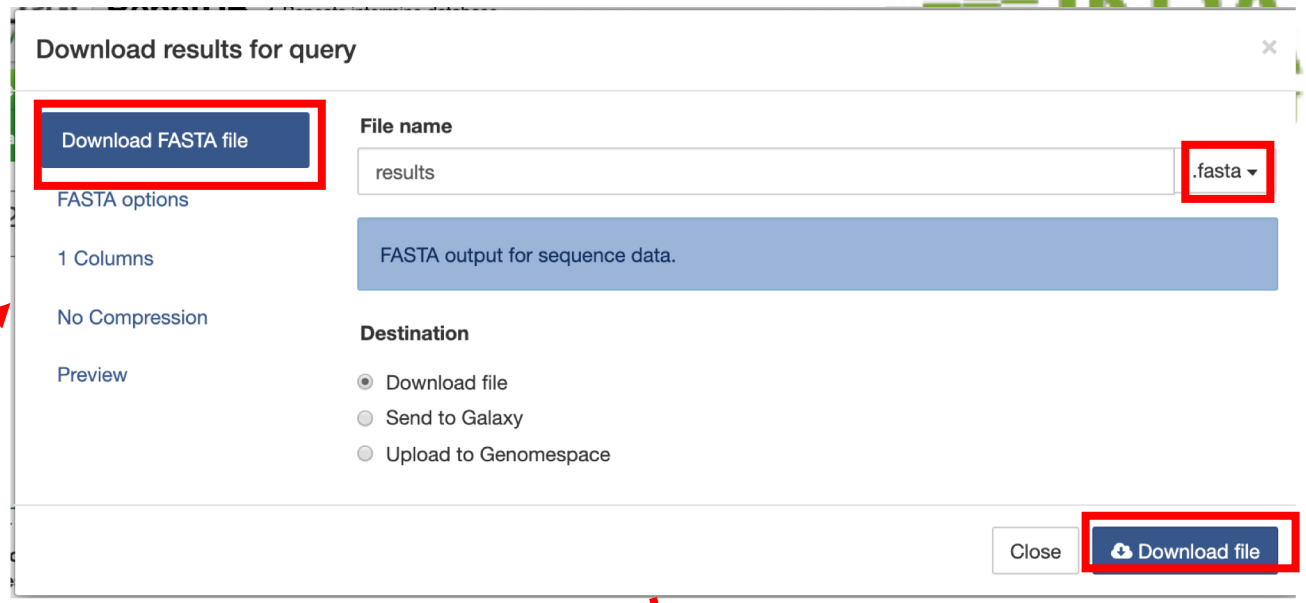
4 : Add « sequence->Residues » column

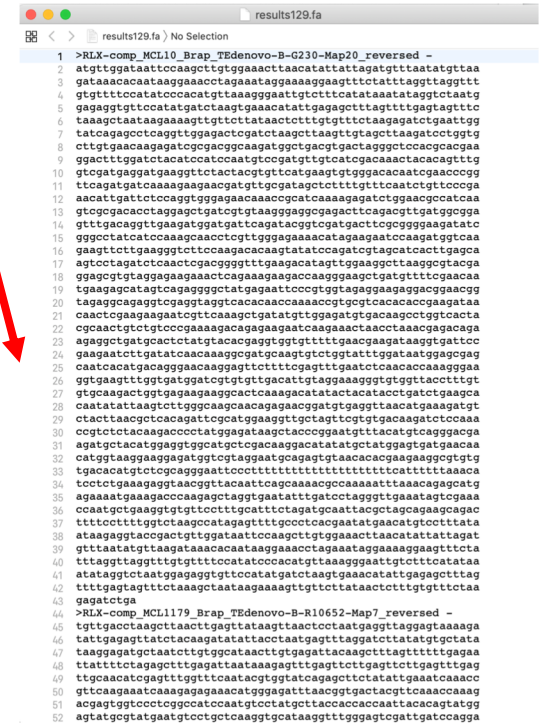


5：Apply changes

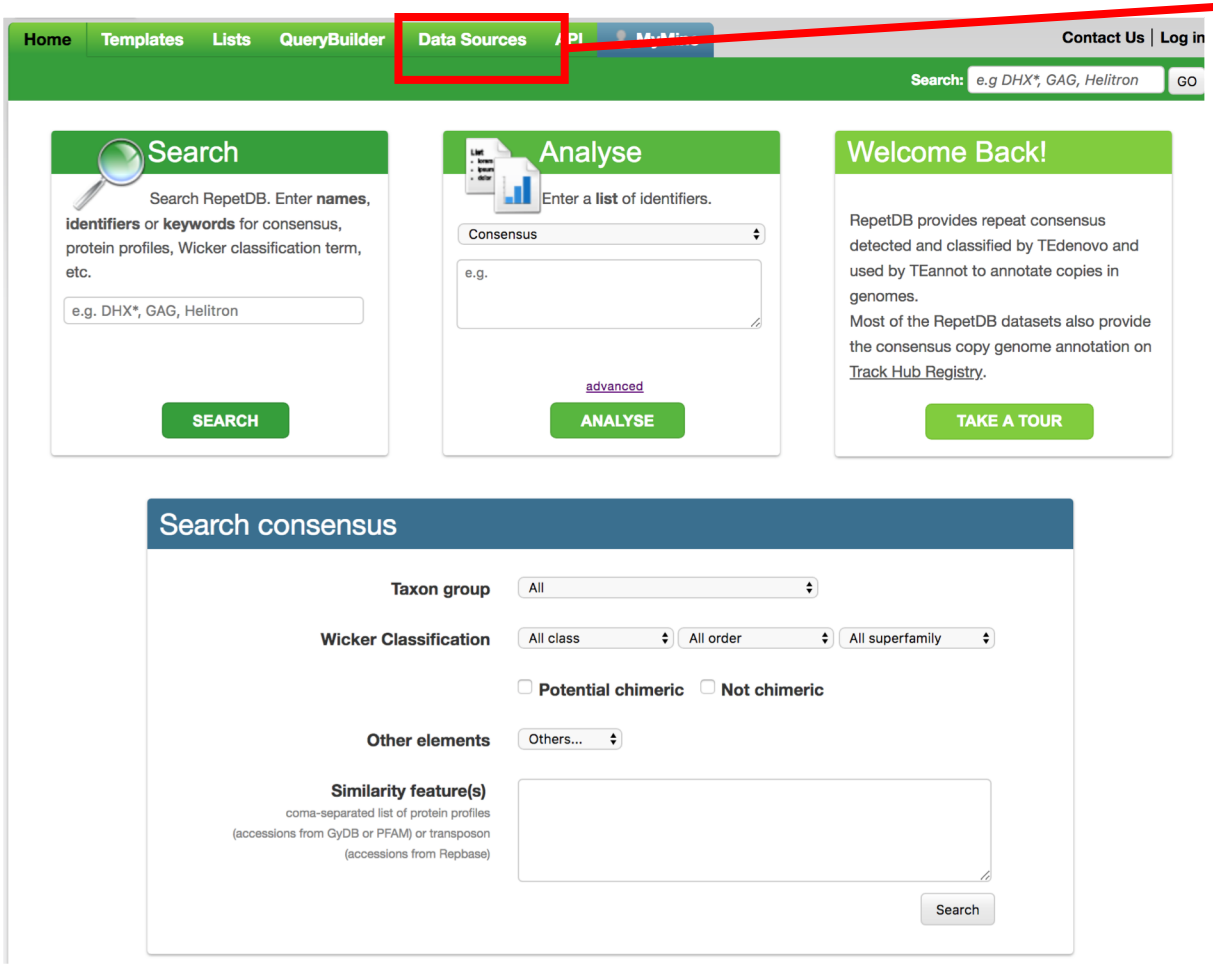
5：Export
all the consensus
in fasta format

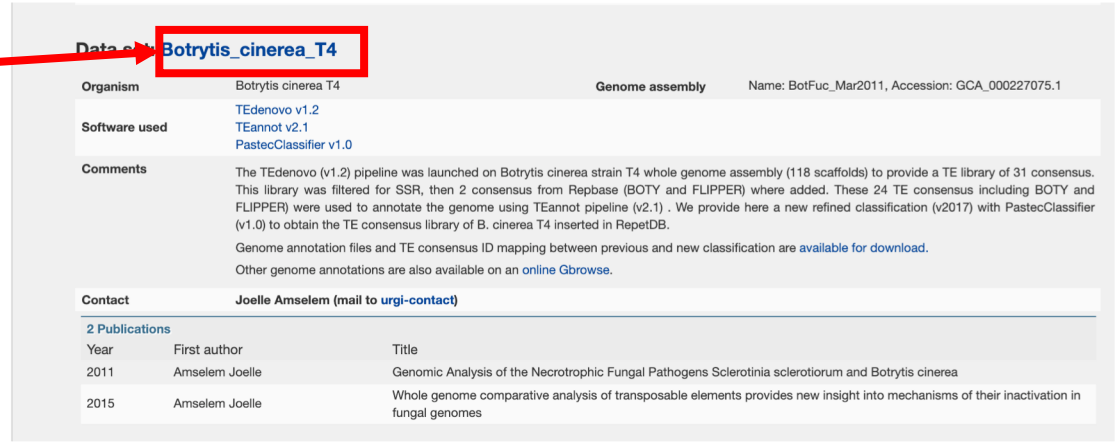






Fasta sequences of consensus could also be obtained from a particular data source, following the same steps in slides 2 - 3 - 4





- ✓ Select one of the dataset
- ✓ Manage columns
  - Consensus >> Consensus Identifier
  - Sequence >> Residues
- ✓ Export the consensus in fasta format