Research data:

Finding homologs between sequences for chr8 700,001..795,000

Chr8 sequence Annotations

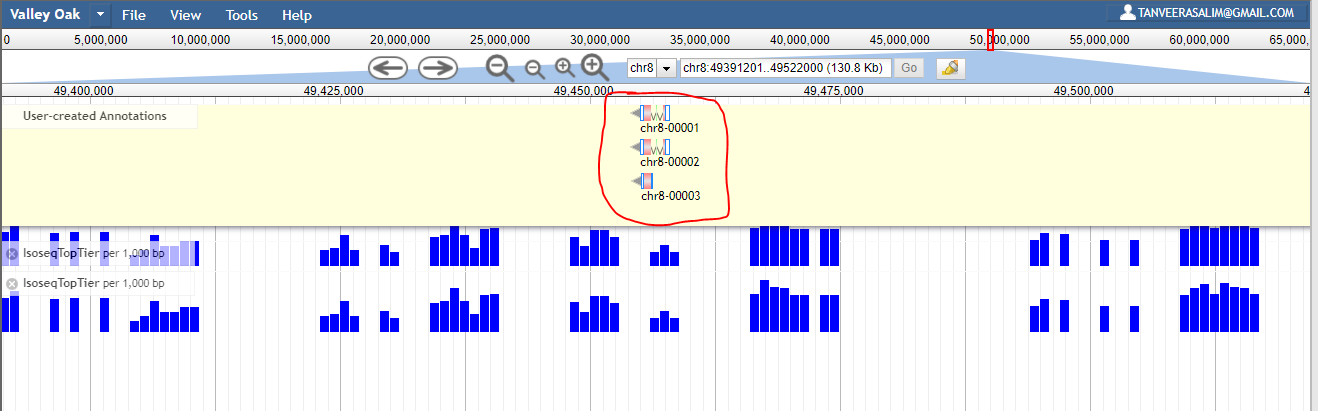
Annotation: chr8

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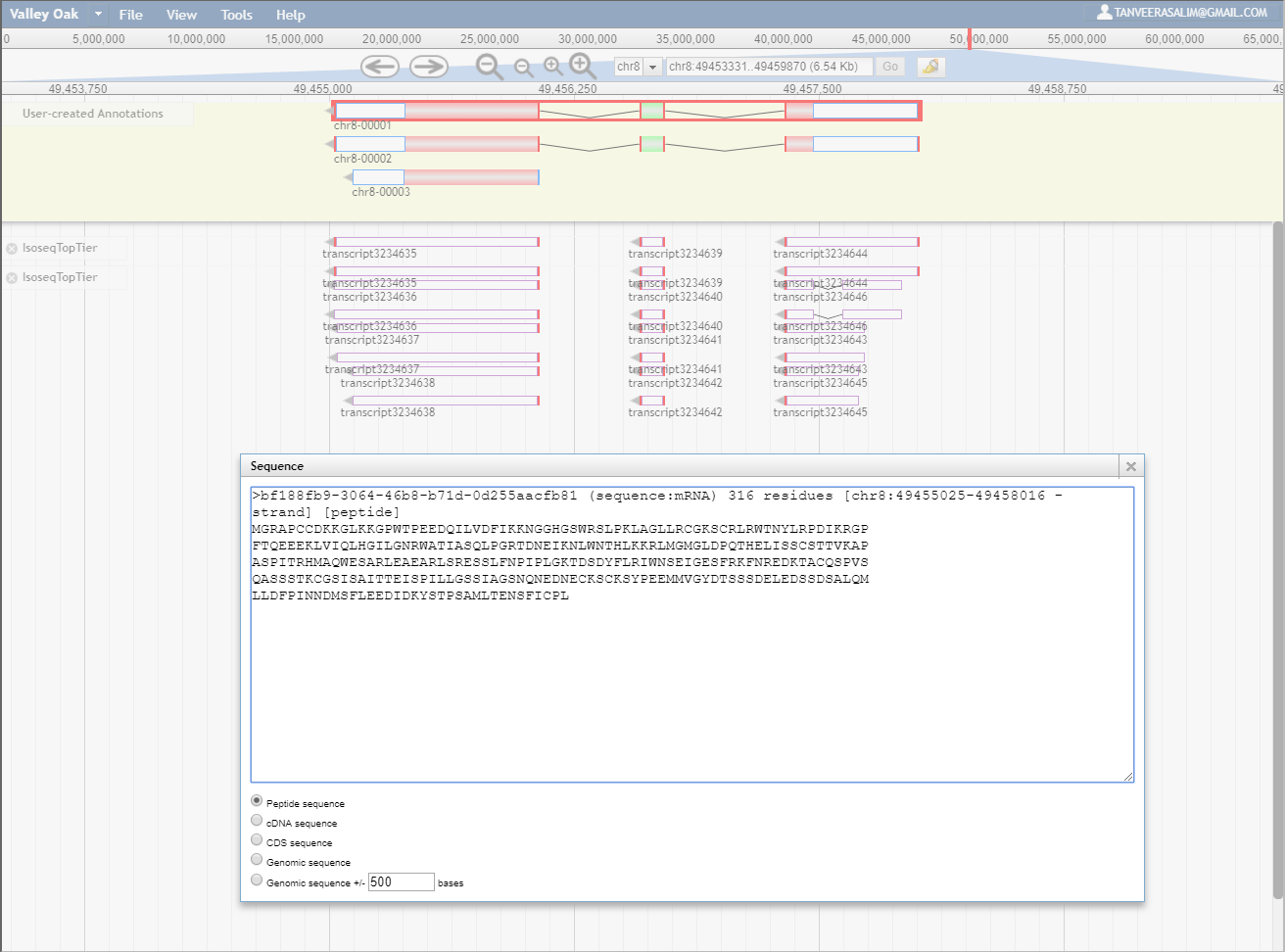


[chr8:49455025-49458016 - strand] [peptide]

IsoSeq Top Tier Results



IsoSeq Top Tier Results Close-Up



Peptide Sequences being Compared:

>bf188fb9-3064-46b8-b71d-0d255aacfb81 (sequence:mRNA) 316 residues [chr8:49455025-49458016 - strand] [peptide]

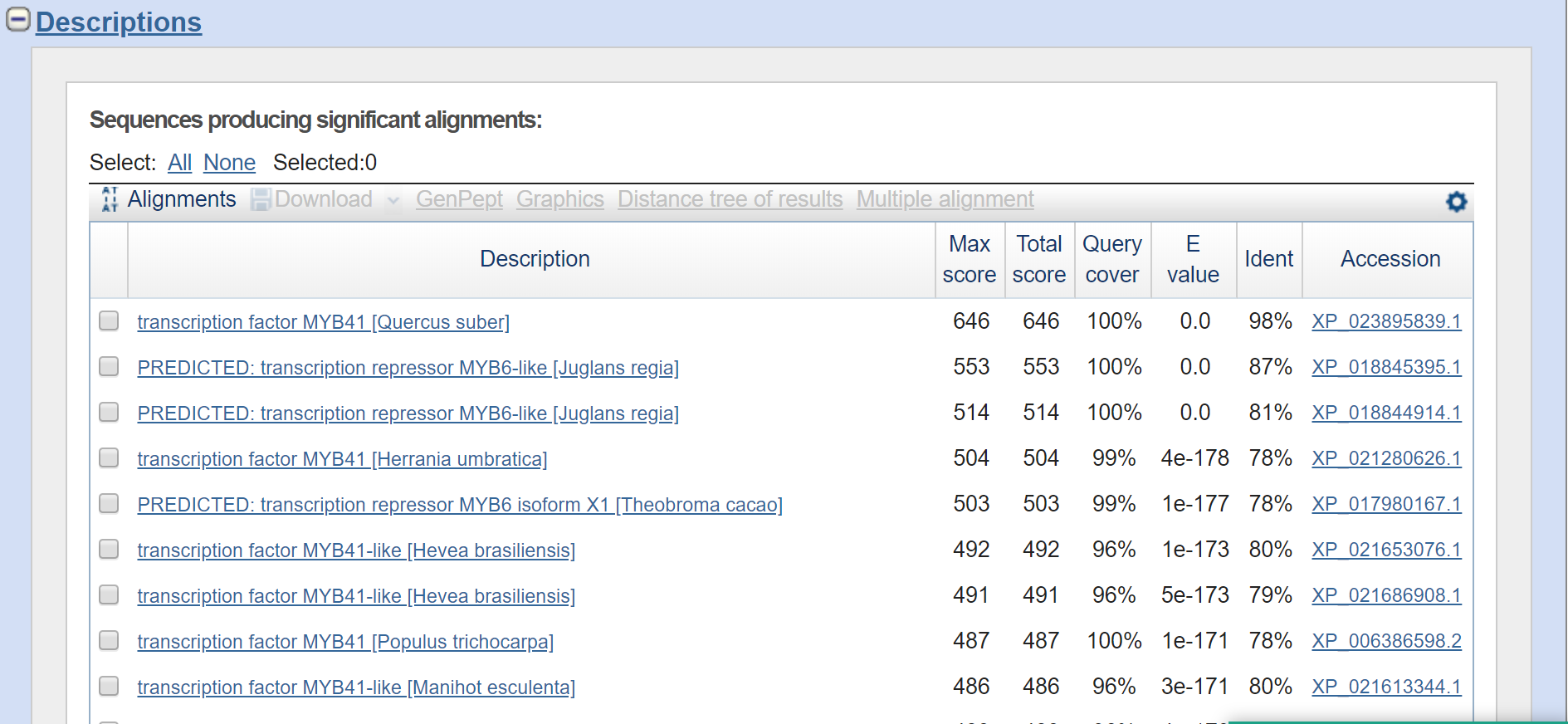
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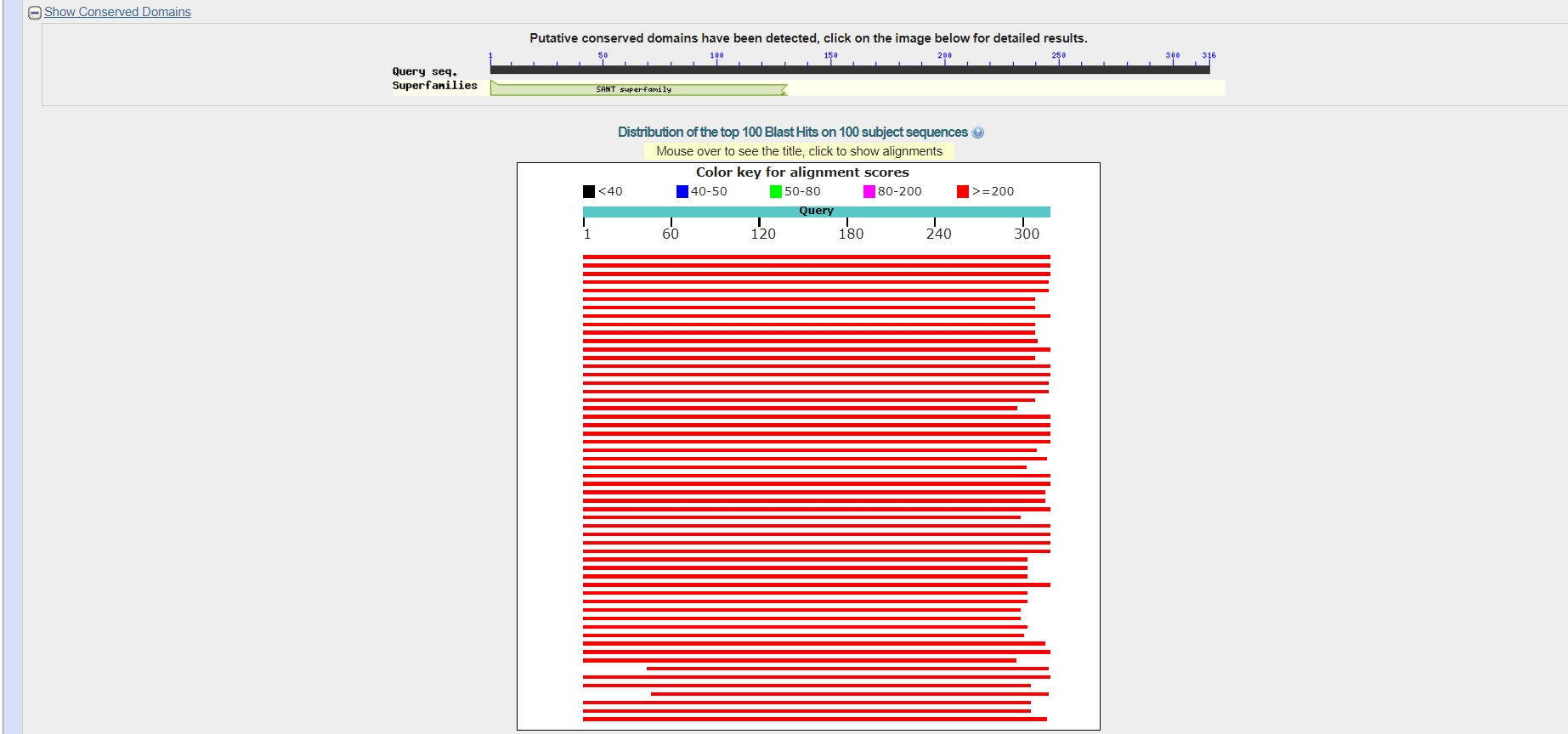
FTQEEEKLVIQLHGILGNRWATIASQLPGRTDNEIKNLWNTHLKKRLMGMGLDPQTHELISSCSTTVKAP

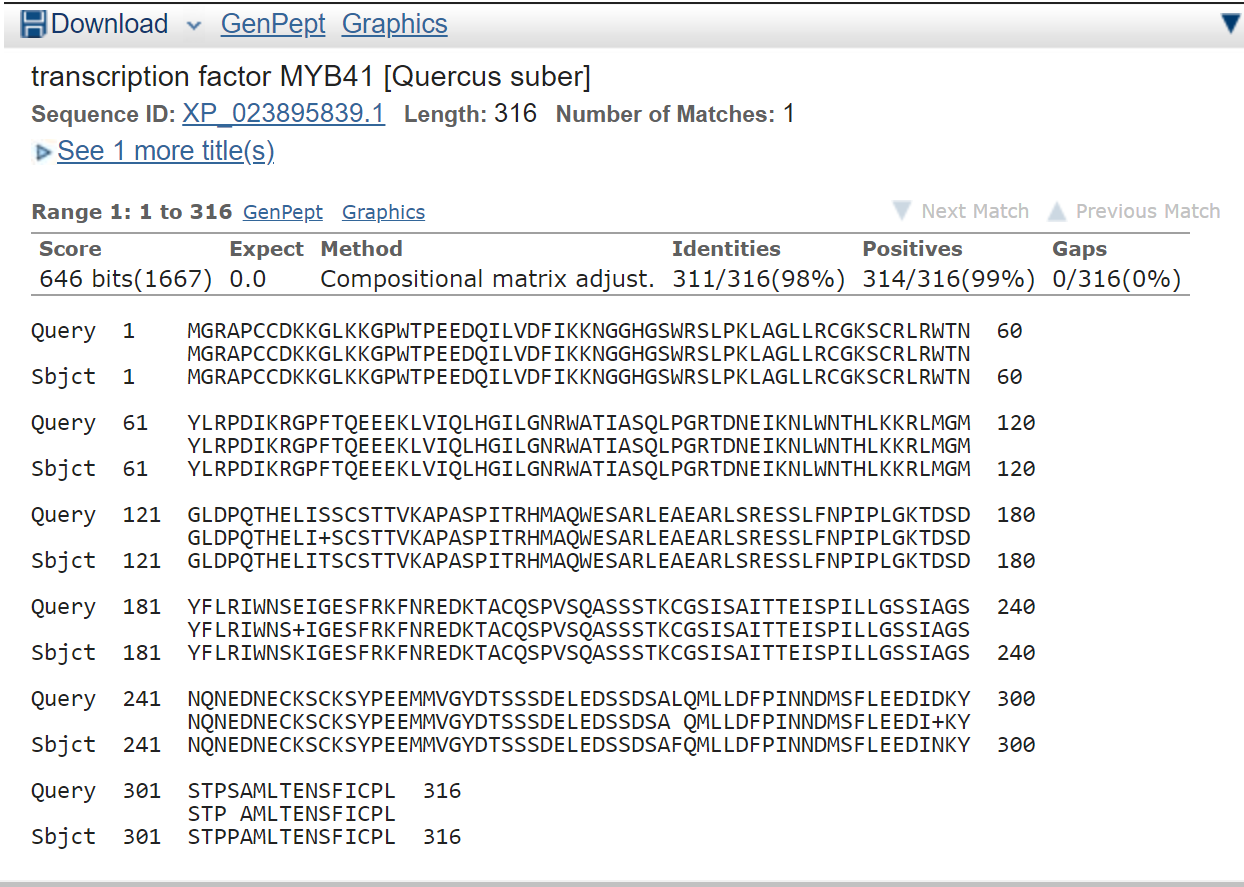
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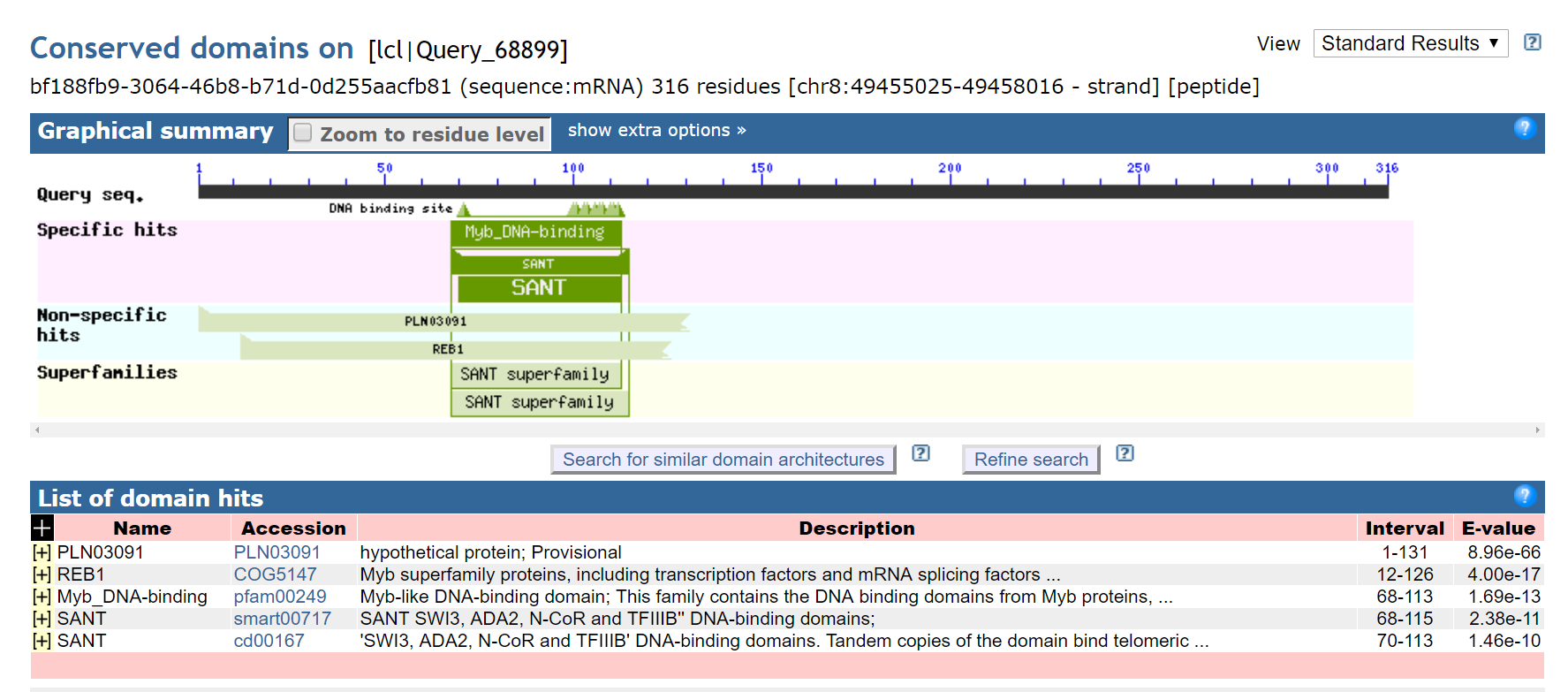
QASSSTKCGSISAITTEISPILLGSSIAGSNQNEDNECKSCKSYPEEMMVGYDTSSSDELEDSSDSALQM

LLDFPINNDMSFLEEDIDKYSTPSAMLTENSFICPL









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**transcription factor MYB41 [Quercus suber]**

**NCBI Reference Sequence: XP\_023895839.1**

>XP\_023895839.1 transcription factor MYB41 [Quercus suber]

MGRAPCCDKKGLKKGPWTPEEDQILVDFIKKNGGHGSWRSLPKLAGLLRCGKSCRLRWTNYLRPDIKRGP

FTQEEEKLVIQLHGILGNRWATIASQLPGRTDNEIKNLWNTHLKKRLMGMGLDPQTHELITSCSTTVKAP

ASPITRHMAQWESARLEAEARLSRESSLFNPIPLGKTDSDYFLRIWNSKIGESFRKFNREDKTACQSPVS

QASSSTKCGSISAITTEISPILLGSSIAGSNQNEDNECKSCKSYPEEMMVGYDTSSSDELEDSSDSAFQM

LLDFPINNDMSFLEEDINKYSTPPAMLTENSFICPL

# PREDICTED: transcription repressor MYB6-like [Juglans regia]

NCBI Reference Sequence: XP\_018845395.1

>XP\_018845395.1 PREDICTED: transcription repressor MYB6-like [Juglans regia]

MGRAPCCDKRGLKKGPWTPEEDEILVEYIKKNGGHGSWRSLPKLAGLLRCGKSCRLRWTNYLRPDIKRGP

FTQEEEKLVVQLHGILGNRWASIAAQLPGRTDNEIKNLWNTHLKKRLVCMGLDPQTHEPVNSCSTTIKAP

ASPTTRHMAQWESARLEAEARLSRESSLFHPNPVGGTDSDYFLRIWNSEVGESFRKFSMGDKTLCQSPVS

QASSSTKCGSMSAITTEICPILGGSSIAGSNQNEDTECKSCKSYTEEMMAASDCSSSDELEDSSENALQL

LLDFPINNDMSFLEEDLDMYALPPAMLTESSFICHL

# transcription factor MYB41 [Herrania umbratica]

NCBI Reference Sequence: XP\_021280626.1

>XP\_021280626.1 transcription factor MYB41 [Herrania umbratica]

MGRTPCCDRKGLKKGPWAPEEDEILVNYIKKHGHGSWRSLPKLAGLLRCGKSCRLRWTNYLRPDIKRGPF

TLEEEKLVIQLHGILGNRWAAIASQLPGRTDNEIKNLWNTHLKKRLVCMGLDPQTHEPFTPCGPTTAAPT

SPATRHMAQWESARLEAEARLSRESLLFSSPPLGKPDSDYFLRLWNSEVGESFRKLNREDKTACQSPISQ

ASSSTKCGSVSAVTIDICPNIAGSSTPASNQIEDTACKSFKSCTEDPVDASDSSCSNESEDSSDTALQLL

LDFPINNDMSFLENVDAYATSAAMLTDTSFISPSEGYLKA

# PREDICTED: transcription repressor MYB6 isoform X1 [Theobroma cacao]

NCBI Reference Sequence: XP\_017980167.1

[GenPept](https://www.ncbi.nlm.nih.gov/protein/XP_017980167.1?report=genpept) [Identical Proteins](https://www.ncbi.nlm.nih.gov/ipg/XP_017980167.1) [Graphics](https://www.ncbi.nlm.nih.gov/protein/XP_017980167.1?report=graph)

>XP\_017980167.1 PREDICTED: transcription repressor MYB6 isoform X1 [Theobroma cacao]

MGRTPCCDRKGLKKGPWAPEEDEILVNYIKKHGHGSWRSLPKLAGLLRCGKSCRLRWTNYLRPDIKRGPF

TLEEEKLVIQLHGILGNRWAAIASQLPGRTDNEIKNLWNTHLKKRLVCMGLDPQTHEPFTPCGPTTAAPT

SPATRHMAQWESARLEAEARLSRESLLFSSPPLGKPDSDYFLRLWNSEVGESFRKLNREDKTACQSPISQ

ASSSTKCGSVSAVTIDICPNIAGSSTPASNQIEDTACKSFKSCTEDPVDASDSSCSNESEDSSDTALQLL

LDFPINNDMSFLENVDTYATSHAMLTDTSFISPSEGYLKA

# transcription factor MYB41-like [Hevea brasiliensis]

NCBI Reference Sequence: XP\_021653076.1

[GenPept](https://www.ncbi.nlm.nih.gov/protein/XP_021653076.1?report=genpept) [Identical Proteins](https://www.ncbi.nlm.nih.gov/ipg/XP_021653076.1) [Graphics](https://www.ncbi.nlm.nih.gov/protein/XP_021653076.1?report=graph)

>XP\_021653076.1 transcription factor MYB41-like [Hevea brasiliensis]

MGRTPCCDKKGLKKGPWTPEEDEILVRYINKNGHGSWRSLPKLAGLLRCGKSCRLRWTNYLRPDIKRGPF

TLEEEKLVIQLHGILGNRWAAIASQLPGRTDNEVKNLWNTHLKKRLLCMGLDPQTHEPFTSCGPAIKTPA

SPATRHMAQWESARLEAEARLSRESSLFNPPTPGKTDSDYFLRMWNSEVGESFRKFNRGDKTTCQSPASA

SQASSSTKCGSFSAVTADISPNLAGYSTTASNQNEDTECKSFKSYAEDVNAGSDSSSSVELEDSSDSTLQ

LLLDFPINNDMSFLEENVDSIASYSAMQ

# transcription factor MYB41 [Populus trichocarpa]

NCBI Reference Sequence: XP\_006386598.2

[GenPept](https://www.ncbi.nlm.nih.gov/protein/XP_006386598.2?report=genpept) [Identical Proteins](https://www.ncbi.nlm.nih.gov/ipg/XP_006386598.2) [Graphics](https://www.ncbi.nlm.nih.gov/protein/XP_006386598.2?report=graph)

>XP\_006386598.2 transcription factor MYB41 [Populus trichocarpa]

MGRTPCCDKKGLKKGPWTPEEDDLLVTYIKKNGHGSWRSLPKLAGLLRCGKSCRLRWTNYLRPDIKRGPF

TLEEEKLVIQLHGILGNRWAAIASQLPGRTDNEIKNLWNTHLKKRLLCLGLDPQTHEPFSSRGPVNKGPA

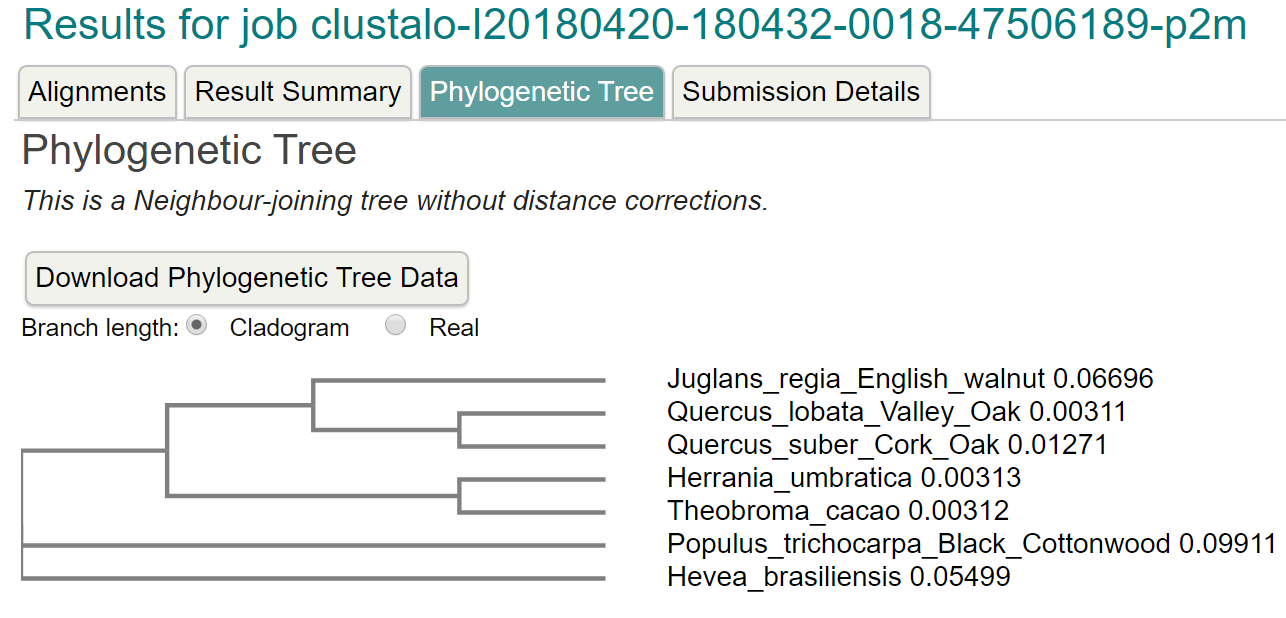
SPATRHMAQWESARLEAEQRLSRESSLFLPPMVEKIDCDHFLRIWNSEVGESFRRINMGDNKTACQSPVS

QASSSTKCGSISAITADIIPNLSRSPATASNQNEDMEWKSPKSYAEDVLAGSDSSSAELEDLTDSTLQLL

LDFPINNDMSFLDKNIDSYATSSAMLTGPSMICPL

Chr8 Phylogenetic Tree

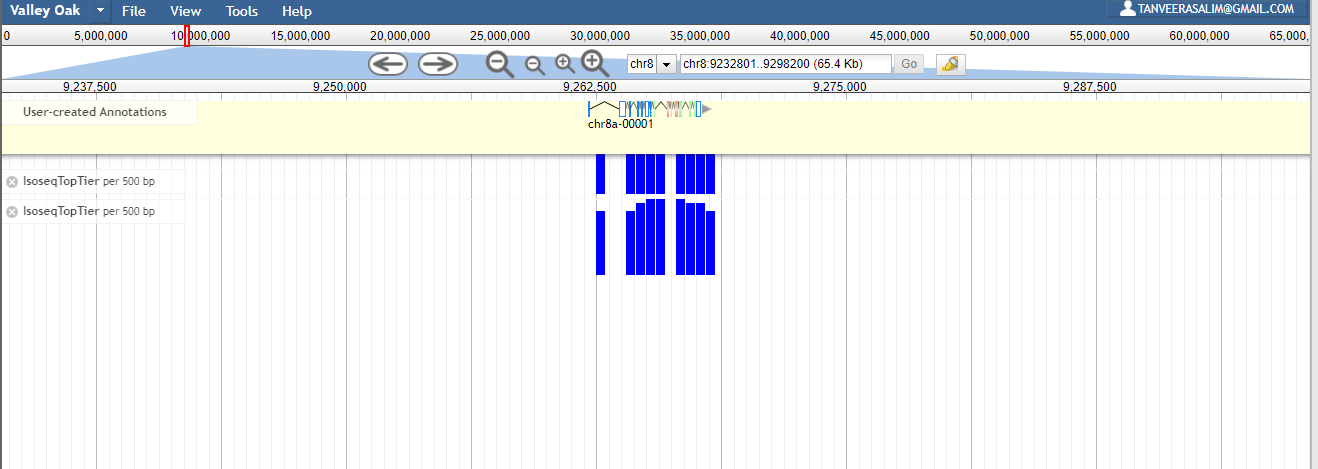
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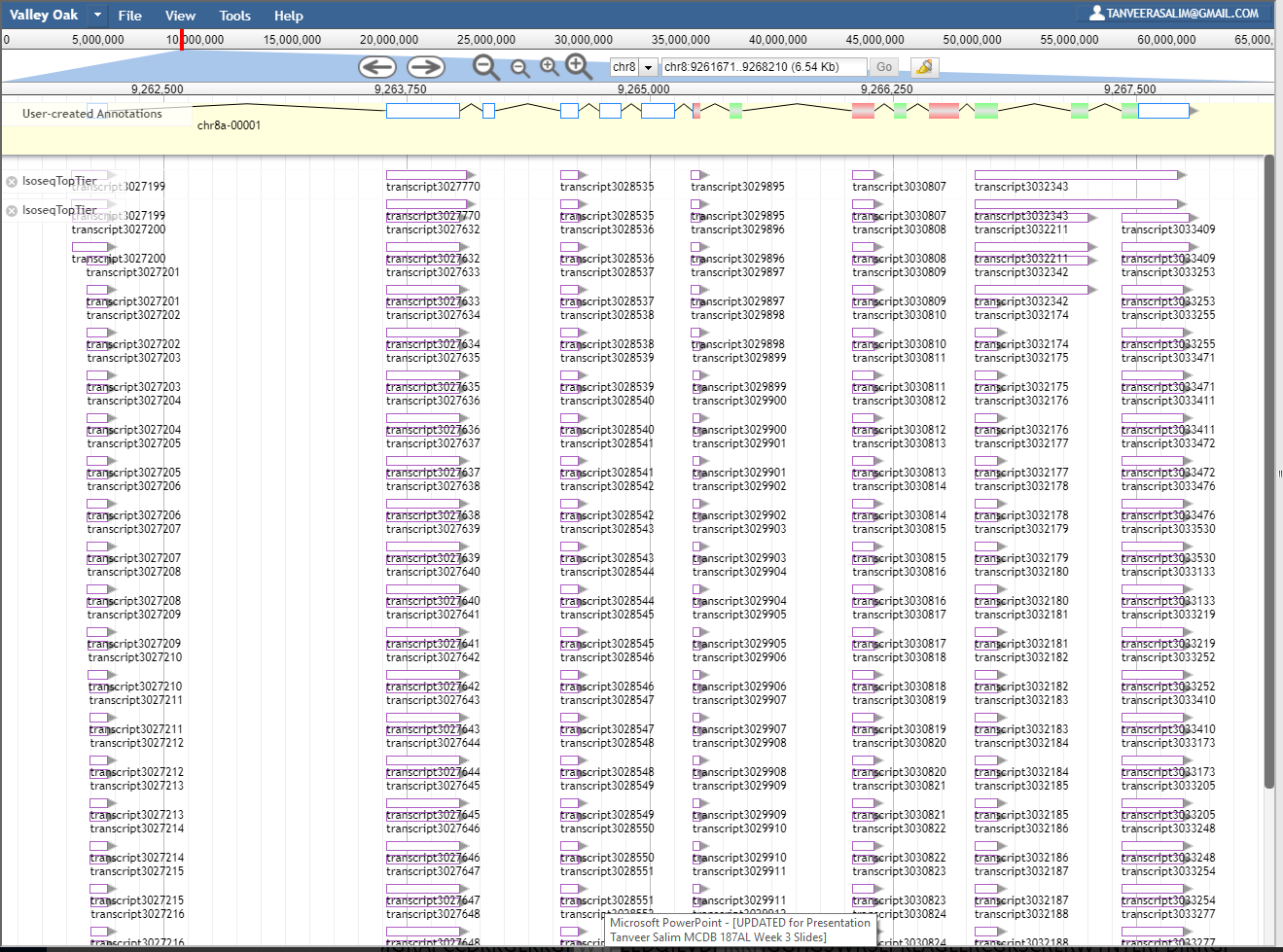


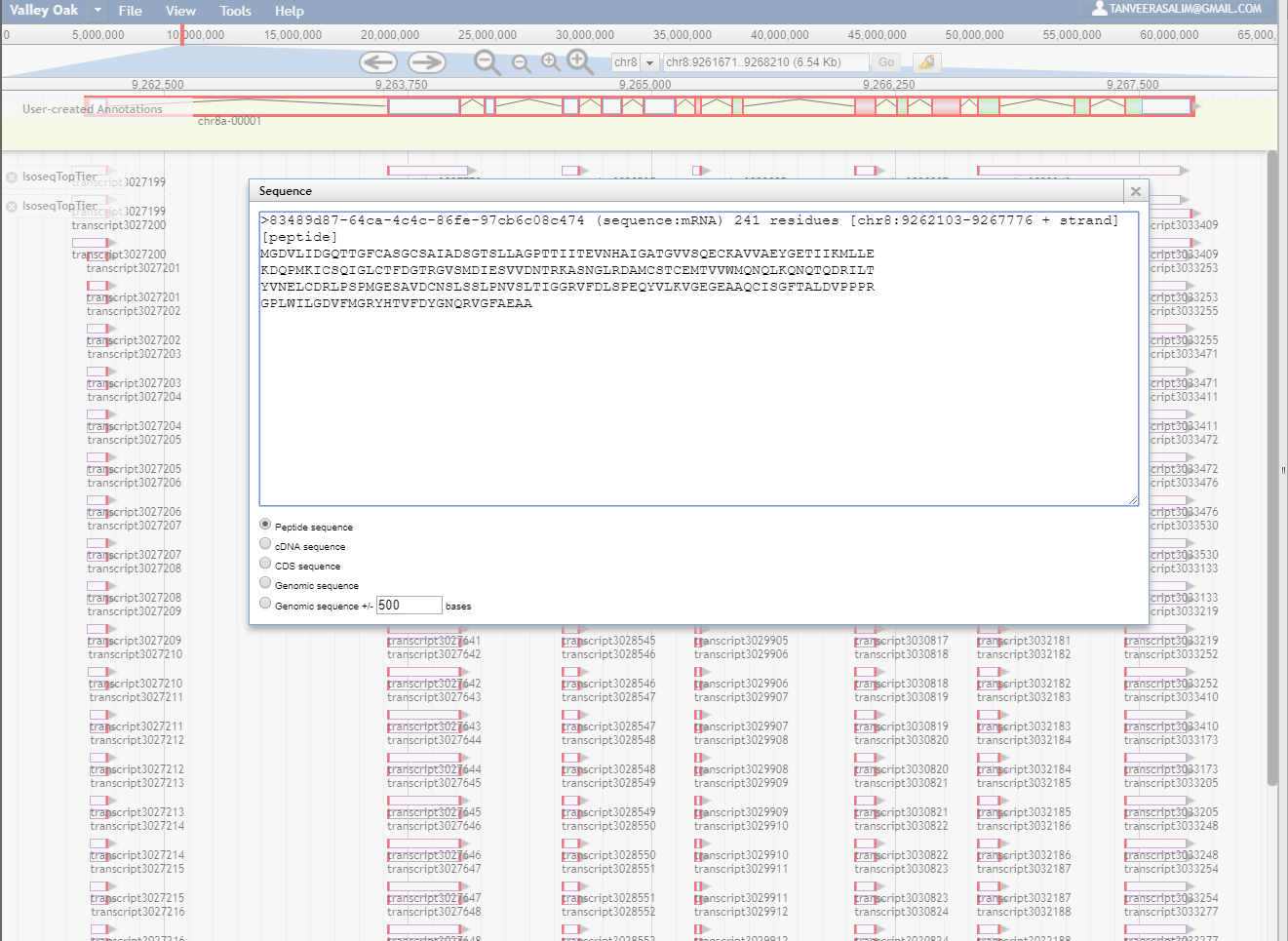
\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

Annotation: chr8a

Chr8a: [9262103-9267776 + strand] [peptide]







Peptide Sequences Being Compared:

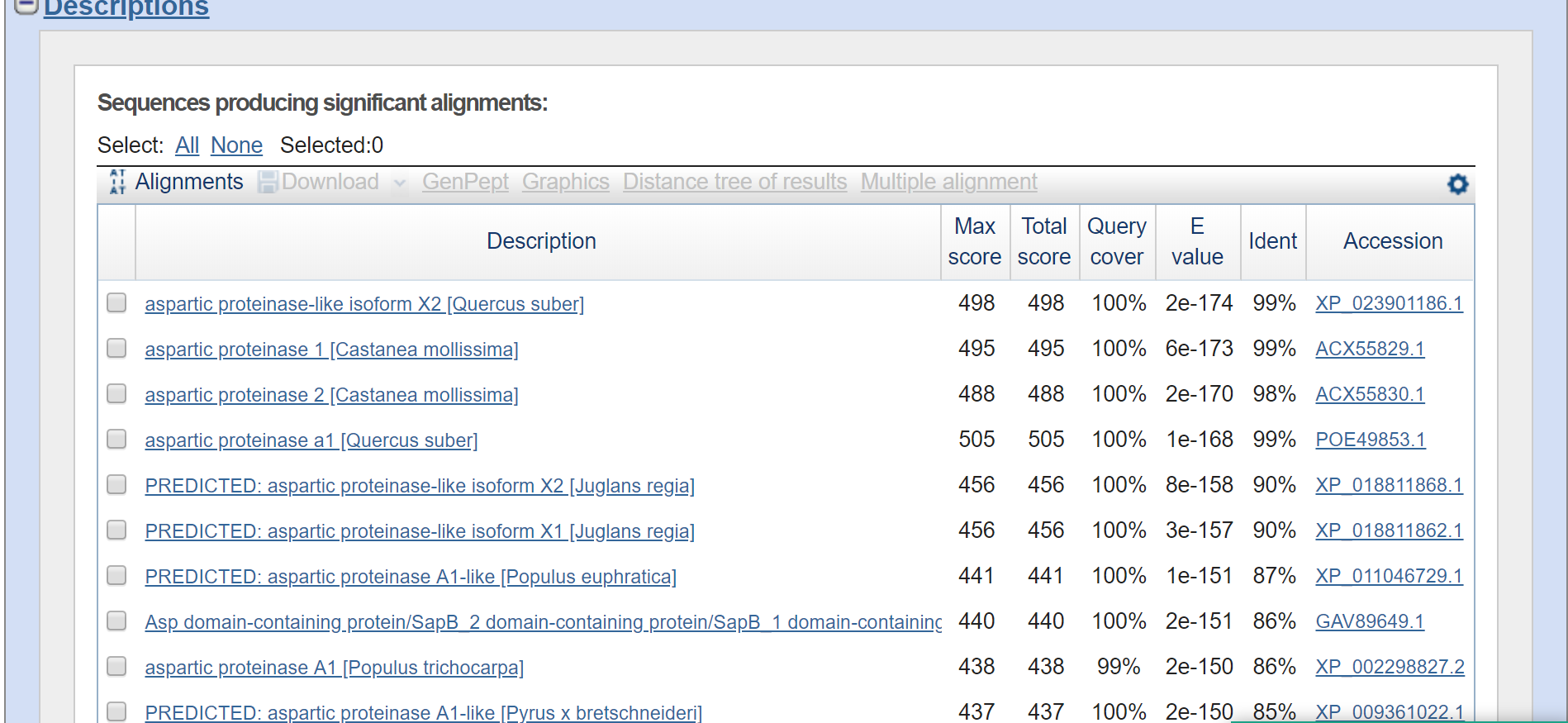
>83489d87-64ca-4c4c-86fe-97cb6c08c474 (sequence:mRNA) 241 residues [chr8:9262103-9267776 + strand] [peptide]

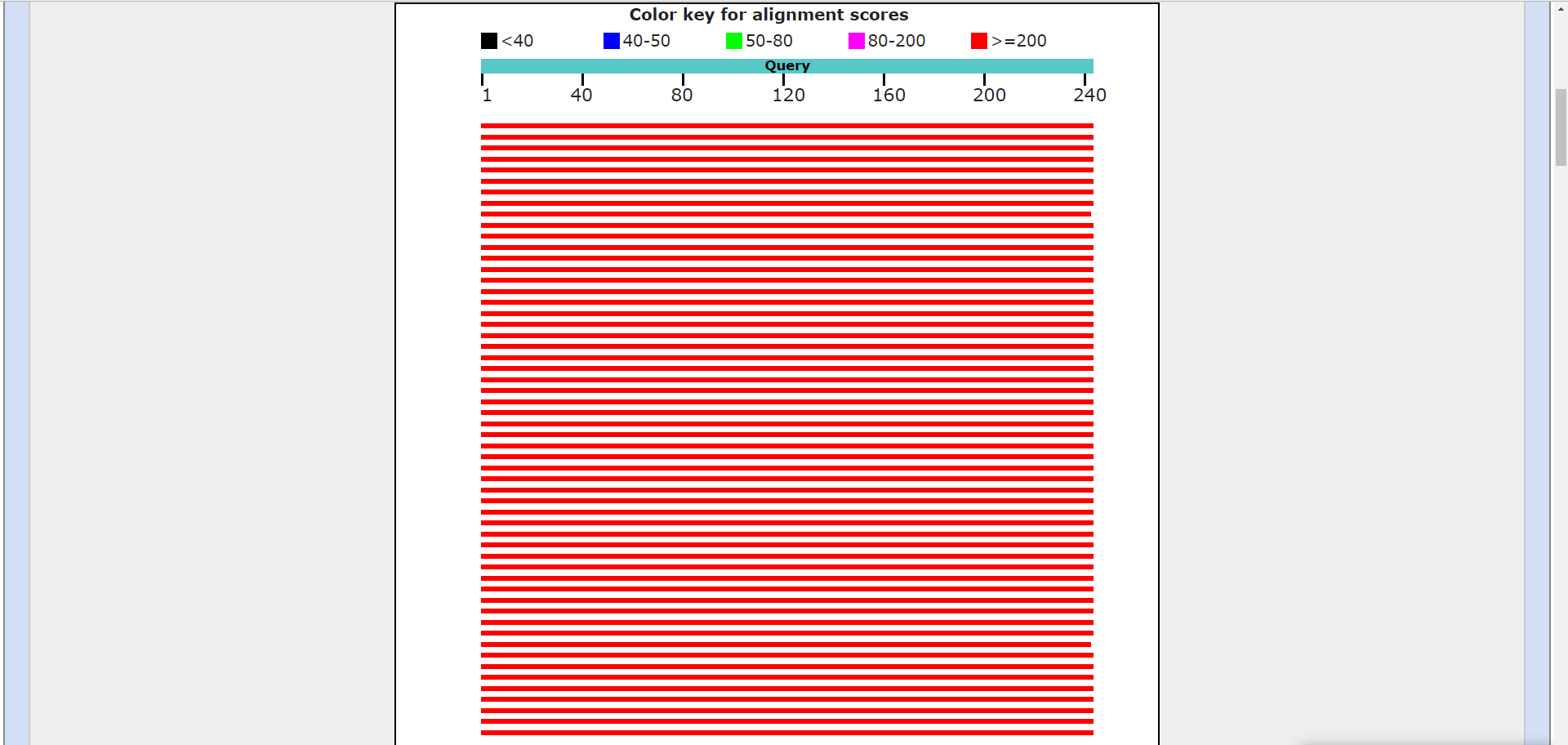
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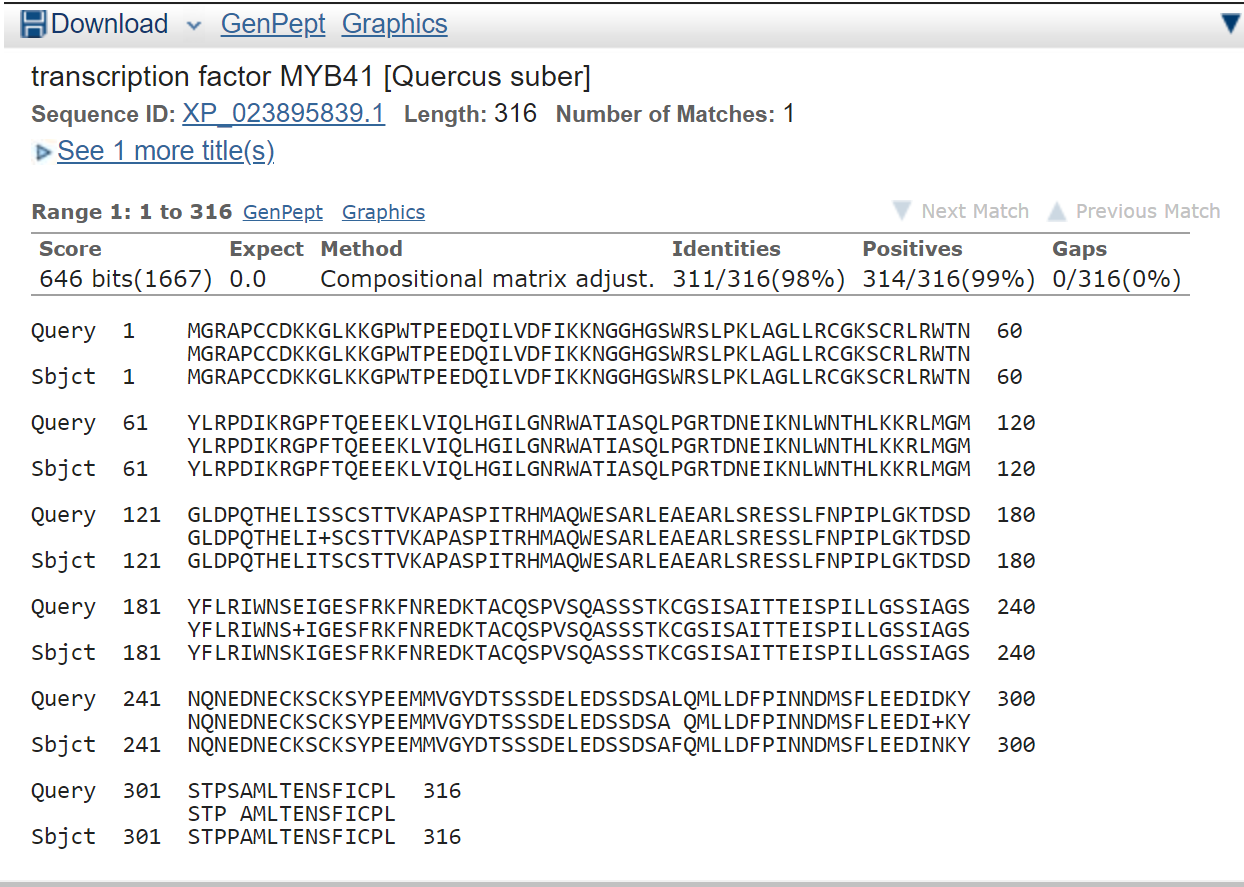
KDQPMKICSQIGLCTFDGTRGVSMDIESVVDNTRKASNGLRDAMCSTCEMTVVWMQNQLKQNQTQDRILT

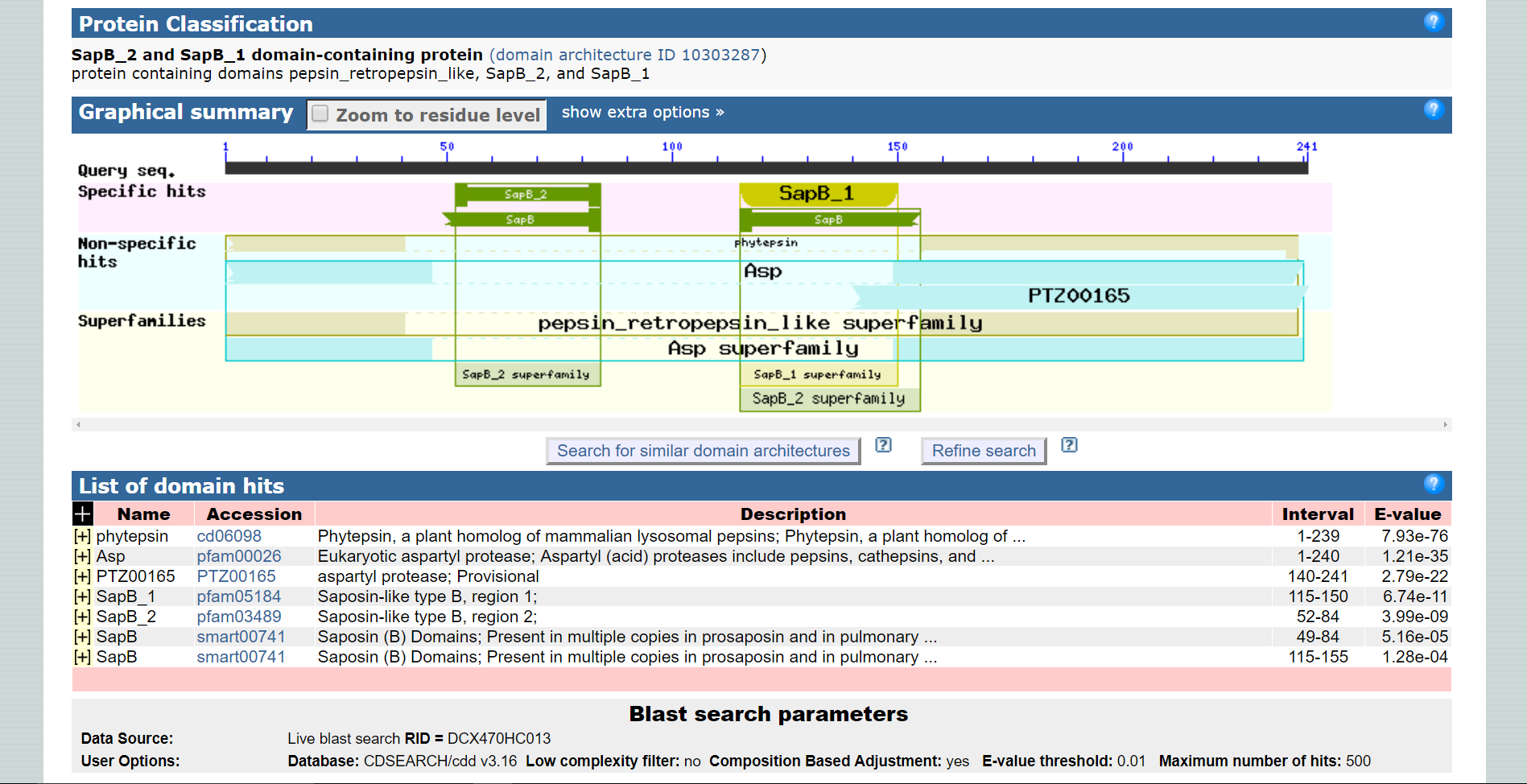
YVNELCDRLPSPMGESAVDCNSLSSLPNVSLTIGGRVFDLSPEQYVLKVGEGEAAQCISGFTALDVPPPR

GPLWILGDVFMGRYHTVFDYGNQRVGFAEAA









Homologous Sequences found on BLASTp

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1. **aspartic proteinase-like isoform X2 [Quercus suber]**

>XP\_023901186.1 aspartic proteinase-like isoform X2 [Quercus suber]

MGNKLKTVVATFFLCFLLFPLVFSASNGGLVRIGLKKTKLDKNNRVAAQLESKDGEVRSASIRKYYLRGN

SGDPEDIDIVSLKNYMDAQYFGEIGVGTPPQKFTVIFDTGSSNLWVPSSKCYFSVACYFHSKYKSSSSST

YKKNGKPADIHYGTGAISGYFSQDHVKVGDLVVKNQEFIEATREPSITFLVAKFDGILGLGFKEISVGNA

VPLWYNMVKQGLVKEPVFSFWFNRNTDEEEGGEIVFGGVDPNHYKGKHTYVPVTQKGYWQFDMGDVLIDG

QTTGFCASGCSAIADSGTSLLAGPTTIITEVNHAIGATGVVSQECKAVVAEYGETIIKMLLEKDQPMKIC

SQIGLCTFDGTRGVSMDIESVVDNTRKASNGLRDAMCSTCEMTVVWMQNQLKQNQTQDRILTYVNELCDR

LPSPMGESAVDCGSLSSLPNVSLTIGGRVFDLSPEQYVLKVGEGEAAQCISGFTALDVPPPRGPLWILGD

VFMGRYHTVFDYGNQRVGFAEAA

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# 2. aspartic proteinase 1 [Castanea mollissima]

GenBank: ACX55829.1

[GenPept](https://www.ncbi.nlm.nih.gov/protein/ACX55829.1?report=genpept) [Identical Proteins](https://www.ncbi.nlm.nih.gov/ipg/ACX55829.1) [Graphics](https://www.ncbi.nlm.nih.gov/protein/ACX55829.1?report=graph)

>ACX55829.1 aspartic proteinase 1 [Castanea mollissima]

MGTKLKTVVATFFLCFLLFPLVFSASNGGLVRIGLKKMKLDKNNRVAAQLESKDGEVRSASIRKYYLRGN

SGDPEDIDIVSLKNYMDAQYFGEIGVGTPPQKFTVIFDTGSSNLWVPSSKCYFSVACYFHSKYKSSSSST

YKKNGKPADIHYGTGAISGYFSQDHVKVGDLVVKNQEFIEATREPSITFLVAKFDGILGLGFKEISVGNA

VPVWYNMVKQGLVKEPVFSFWFNRNTDEEEGGEIVFGGVDPNHYKGKHTYVPVTQKGYWQFDMGDVLIDG

QTTGFCARGCSAIADSGTSLLAGPTTIITEVNHAIGATGVVSQECKAVVAEYGETIIKMLLEKDQPMKIC

SQIGLCTFDGVRGVSMDIESVVDNTRKASNGLRDAMCSTCEMTVVWMQNQLKQNQTQDRILTYVNELCDR

LPSPMGESAVDCGSLSSLPNVSLTIGGRVFDLSPEQYVLKVGEGEAAQCISGFTALDVPPPRGPLWILGD

VFMGRYHTVFDYGNQRVGFAEAA

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# 3. PREDICTED: aspartic proteinase-like isoform X2 [Juglans regia]

NCBI Reference Sequence: XP\_018811868.1

[GenPept](https://www.ncbi.nlm.nih.gov/protein/XP_018811868.1?report=genpept) [Identical Proteins](https://www.ncbi.nlm.nih.gov/ipg/XP_018811868.1) [Graphics](https://www.ncbi.nlm.nih.gov/protein/XP_018811868.1?report=graph)

>XP\_018811868.1 PREDICTED: aspartic proteinase-like isoform X2 [Juglans regia]

MGTKLKPVVASFFFCLLLFPLVFSASNGGLVRVGLKKRKFDQNDRIAAQLESKEGKAWKASIRKYHLRGN

SGDPEDTDIVALKNYMDAQYFGEIGIGTPPQKFTVIFDTGSSNLWVPSSKCYFSVACYFHSKYKSSSSST

YKKNGKPADIHYGTGAISGYFSQDHVKVGDLVVEGQEFIEATREPSITFLVAKFDGILGLGFQEISVGNA

VPVWYNMVNQGLVKEPVFSFWFNRNADEEEGGEIVFGGVDPNHYKGEHTYVPVTQKGYWQFDMGDVMIDG

ETTGFCGSGCSAIADSGTSLLAGPTTIITQVNHAIGATGVVSQECKAVVAEYGETIIKMLLEKDQPQKIC

AQIGLCTFDGTRDVSIGIESVVDDDTRKASGGLRDTMCSTCEMAVVWMQNQLKQNQTQDRIINYANDLCD

RLPSPMGESAVDCASLSSMPNVSFTIGGRVFDLRPEQYVLKVGEGDAAQCISGFTALDVPPPRGPLWILG

DVFMGRYHTVFDYGNQRIGFAEAA

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# 4. PREDICTED: aspartic proteinase A1-like [Populus euphratica]

NCBI Reference Sequence: XP\_011046729.1

[GenPept](https://www.ncbi.nlm.nih.gov/protein/XP_011046729.1?report=genpept) [Identical Proteins](https://www.ncbi.nlm.nih.gov/ipg/XP_011046729.1) [Graphics](https://www.ncbi.nlm.nih.gov/protein/XP_011046729.1?report=graph)

>XP\_011046729.1 PREDICTED: aspartic proteinase A1-like [Populus euphratica]

MGTILKPVAAATLFLCFLLLPMISSTLSPPNDGLIRIGLKKRKYERNNRLAAKLESKEGDSIKKYHLLRN

LGGDAEDTDIVSLKNYMDAQYFGEIGIGTPPQKFTVIFDTGSSNLWVPSSKCYFSVACYFHSKYKSSHSR

TYKENGKSAEIHYGTGAISGFFSQDHVKVGDLVVKNQEFIEATREPSVTFLVAKFDGILGLGFQEISVGK

AVPVWYNMVDQGLVKEPVFSFWFNRNADEKEGGEIVFGGVDPDHYKGEHTYVPVTQKGYWQFDMGDVLIG

GQTSGFCASGCAAIADSGTSLLAGPTTIITEVNHAIGATGVVSQECKEVVAQYGDTIIEMLLAKDQPQKI

CSQIGLCTFDGTRGVSVGIESVVNEHAQKASDGFHDAMCSTCEMAVVWMQNQLKQNQTQERILDYVNELC

ERLPSPMGESAVDCDGLSSMPNVSFTIGGRVFDLSPEQYVLKVGEGDVAQCISGFTALDVPPPRGPLWIL

GDVFMGRFHTVFDYGNMRVGFAEAS

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# 5. aspartic proteinase A1 [Populus trichocarpa]

NCBI Reference Sequence: XP\_002298827.2

[GenPept](https://www.ncbi.nlm.nih.gov/protein/XP_002298827.2?report=genpept) [Identical Proteins](https://www.ncbi.nlm.nih.gov/ipg/XP_002298827.2) [Graphics](https://www.ncbi.nlm.nih.gov/protein/XP_002298827.2?report=graph)

>XP\_002298827.2 aspartic proteinase A1 [Populus trichocarpa]

MGTILKPVAAATLFLCFLLLPMISSALSPPNDGLIRIGLKKRKYERNNRLAAKLESKEGESIKKYHLLRN

LGGDAEDTDIVSLKNYMDAQYFGEIGIGTPPQKFTVIFDTGSSNLWVPSSKCYFSVACYFHSKYKSSHSR

TYKENGKSAEIHYGTGAISGFFSQDHVKVGDLVVKNQEFIEATREPSVTFLVAKFDGILGLGFQEISVGK

AVPVWYNMVEQGLVKEPVFSFWFNRNADEKEGGEIVFGGVDPDHYKGEHTYVPVTQKGYWQFDMGDVLIG

GQTSGFCASGCAAIADSGTSLLAGPTTIITEVNHAIGATGVVSQECKAVVAQYGDTIMEMLLAKDQPQKI

CAQIGLCTFDGTRGVSMGIESVVNEHAQKASDGFHDAMCSTCEMAVVWMQNQLKQNQTQERILDYVNELC

ERLPSPMGESAVDCDGLSSMPNVSFTIGGRVFELSPEQYVLKVGEGDVAQCISGFTALDVPPPRGPLWIL

GDVFMGSFHTVFDYGNMRVGFAEAT

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# 6. PREDICTED: aspartic proteinase A1-like [Pyrus x bretschneideri]

NCBI Reference Sequence: XP\_009361022.1

[GenPept](https://www.ncbi.nlm.nih.gov/protein/XP_009361022.1?report=genpept) [Identical Proteins](https://www.ncbi.nlm.nih.gov/ipg/XP_009361022.1) [Graphics](https://www.ncbi.nlm.nih.gov/protein/XP_009361022.1?report=graph)

>XP\_009361022.1 PREDICTED: aspartic proteinase A1-like [Pyrus x bretschneideri]

METKLKSVTAMLFLCFLLFPLVFCESNDGLLRIGLKKRKLDQNNRVAAQIDSKEGESLRAVLQKYRLGGN

LADSQDIDIVSLKNYMDAQYFGEIGIGTPPQKFTVIFDTGSANLWVPSSKCYFSIACYLHPKYKSSSSST

YNKNGKPAAIQYGTGAISGFFSEDHVTVGDLVVKDQEFIEATKEPGVTFVVAKFDGILGLGFQEISVGNA

VPVWYNMVNQGLLKEPVFSFWFNRNADEEEGGEIVFGGVDPNHYKGEHTYVPVTQKGYWQFDMGDVMIDG

QTTGFCASGCSAIADSGTSLLVGPTTIITELNHAIGASGIVSQECKTVVAEYGETIIERILAKDQPAKIC

SQIGLCSFDGTHGVSIGIKSVVENTHKVSGDLSDATCSACEMTVVWMQNQLKQNQTQERILDYVNQLCDR

LPSPMGESAVDCAGLSSMPNVSFTIGGRTFDLTPEQYVLKVGEGDAAQCISGFTALDVPPPRGPLWILGD

VFMGRYHTVFDYGNERIGFAEAA

