

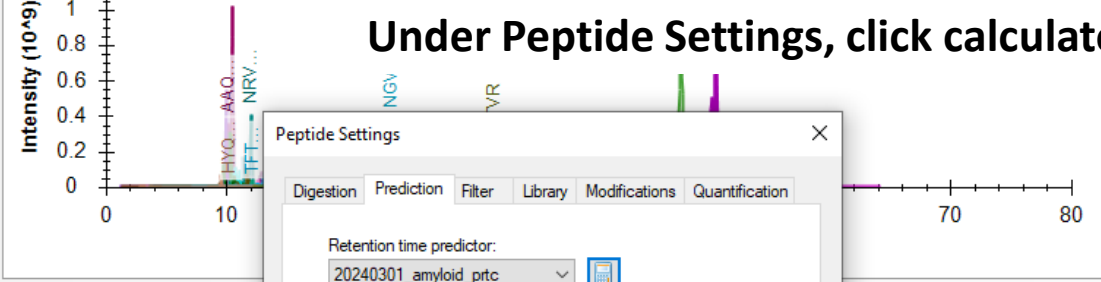
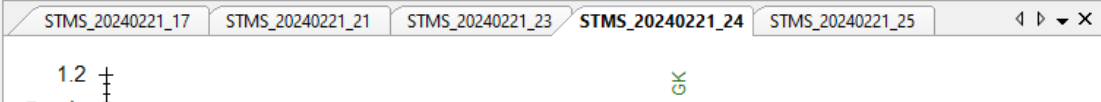
Targets

- Replicates: STMS\_20240221\_24
- Pierce standards
    - SSAAPPPPR
    - GISNEGQNASIK
    - HVLTSGEIK
    - DIPVPKPK
    - IGDYAGIK
    - TASEFDSAIAQDK
    - SAAGAFGPELSR
    - ELGQSGVDTYLQTK
    - SFANQPLEVVYSK
    - GLILVGGYGTTR
    - GILFVGGVSGGEEGAR
    - LTILEELR
    - ELASGLSPVGFVK
    - LSSEAPALFQFDLK
  - sp|P02743|SAMP\_HUMAN
    - .MKNKPLLWISVLTSLLEFAHTDLSGK.V [1, 26]
    - R.ESVTDHVNLTPEKPLQNFTLCFR.A [33, 57]
    - R.AYSDLSR.A [58, 64]
    - R.AYSLFSYNTQGR.D [65, 76]
    - R.DNELLYYK.E [77, 84]
    - R.VGEYSLYIGR.H [87, 96]
    - R.QGYFVEAQP.K [140, 149]
    - K.IVLGQEQDSYGGK.F [150, 162]
    - R.GYVIKPLVWV.- [213, 223]
  - sp|P02649|APOE\_HUMAN
    - K.VLWALLVTFLAGQAK.V [3, 19]
    - K.VEQAVETEPEPELR.Q [20, 33]
    - R.QQTEWQSGQR.W [34, 43]
    - R.WELALGR.F [44, 50]
    - R.FWDYLR.W [51, 56]
    - R.WVQTLSEQVQELLSSQVTQELR.A [57, 79]
    - R.ALMDETMK.E [80, 87]
    - K.SELEEQLTPEAEETR.A [94, 108]
    - K.ELQAAQAR.L [114, 121]
    - R.LGADMEDVQGR.L [122, 132]
    - R.GEVQAMLQGSTTEELR.V [138, 152]
    - R.DADDLQK.R [169, 175]
    - R.LAVYQAGAR.E [177, 185]

Results Grid

Reports 4 of 5

Replicate	Sample Type	Analyte Concentrat
<a href="#">STMS_20240221_17</a>	Unknown	
<a href="#">STMS_20240221_21</a>	Unknown	
<a href="#">STMS_20240221_23</a>	Unknown	
<a href="#">STMS_20240221_24</a>	Unknown	



Peptide Settings

Digestion Prediction Filter Library Modifications Quantification

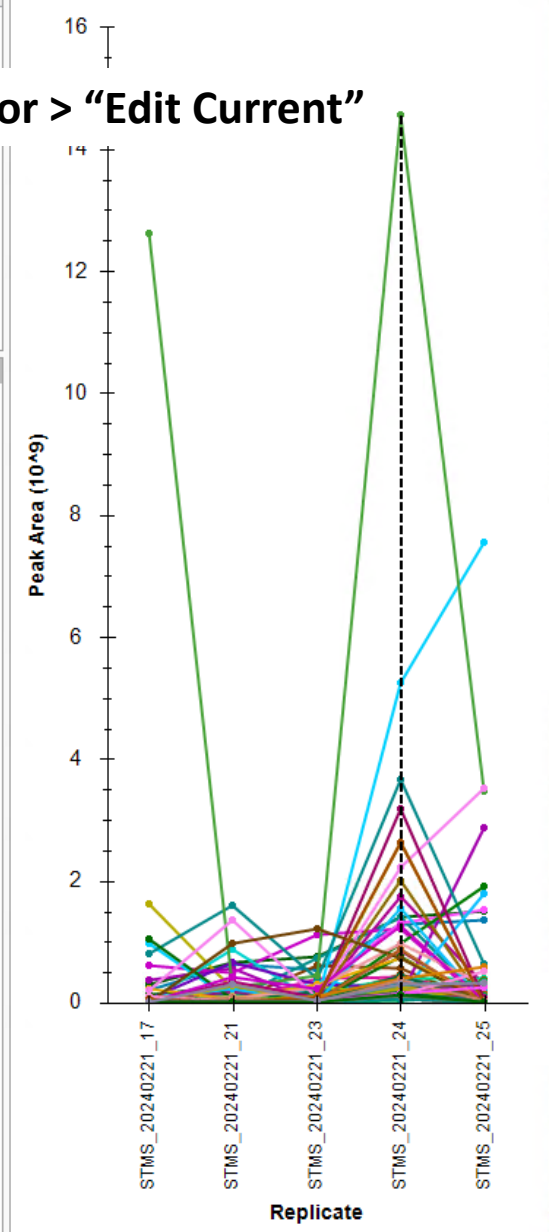
Retention time predictor: 20240301\_amyloid\_ptrc

Use measured retention times with

Time window: 2 min

Buttons: Add..., Edit Current..., Edit List..., OK, Cancel

Peak Areas - Replicate Comparison



Under Peptide Settings, click calculator > "Edit Current"

File Edit Refine View Settings Tools Help

**Targets**

Replicates: STMS\_20240221\_24

Pierce standards

- SSAAPPPPPR
- GISNEGQNASIK
- HVLTSIGEK
- DIPVPPPK
- IGDYAGIK
- TASEFDSAIAQDK
- SAAGAFGPESLR
- ELGQSGVDTYLQTK
- SFANQPLEVWYSK
- GLILVGGYGTR
- GILFVGSVSGGEEGAR
- LTILEELR
- ELASGLSFPVGFK
- LSSEAPALFQFDLK

sp|P02743|SAMP\_HUMAN

- .MNKPLLWISVLTSLLEAFAHTDLSGK.V [1, 26]
- R.ESVTDHVNLTIPLEKPLQNFTLCFR.A [33, 57]
- R.AYSDLSR.A [58, 64]
- R.AYSLFSYNTQGR.D [65, 76]
- R.DNELLYYK.E [77, 84]
- R.VGEYSLYIGR.H [87, 96]
- R.QGYFVEAQP.K.I [140, 149]
- K.IVLGQEQDSYGGK.F [150, 162]
- R.GYVIKPLVWV.- [213, 223]

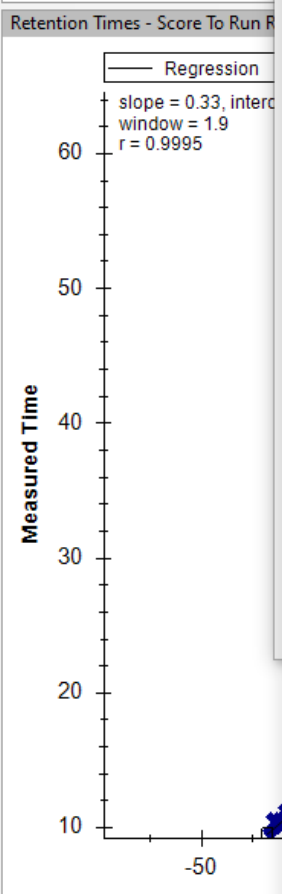
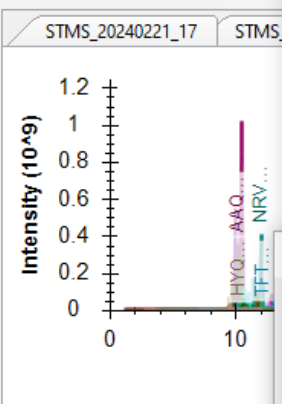
sp|P02649|APOE\_HUMAN

- K.VLWAAALLVTFLAGCQAK.V [3, 19]
- K.VEQAVETEPEPELR.Q [20, 33]
- R.QQTEWQSGQR.W [34, 43]
- R.WELALGR.F [44, 50]
- R.FWDYLR.W [51, 56]
- R.WVQTLSEQVQEEELLSSQVTQELR.A [57, 79]
- R.ALMDETMK.E [80, 87]
- K.SEEELQTPVAEETR.A [94, 108]
- K.ELQAAQAR.L [114, 121]
- R.LGADMEDVQGR.L [122, 132]
- R.GEVQAMLGQSTEELR.V [138, 152]
- R.DADDLQK.R [169, 175]
- R.LAVYQAGAR.E [177, 185]

**Results Grid**

Reports 4 of 5

Replicate	Sample Type	Analyte Concentrat
STMS_20240221_17	Unknown	
STMS_20240221_21	Unknown	
STMS_20240221_23	Unknown	
STMS_20240221_24	Unknown	



**Edit iRT Calculator**

Name: 20240301\_amyloid\_prtc

iRT database: D:\Skyline\prosit\20240301\_amyloid\_prtc.blib

Regression type: Linear

Store redundant iRT values

iRT standards: Pierce (iRT-C18)

Target	iRT Value
SSAAPPPPPR	-27.60
GISNEGQNASIK	-17.47
HVLTSIGEK	-9.98
DIPVPPPK	-3.88
IGDYAGIK	7.84
TASEFDSAIAQDK	18.42
SAAGAFGPESLR	26.22
ELGQSGVDTYLQTK	32.61
SFANQPLEVWYSK	51.41
GLILVGGYGTR	52.36
GILFVGSVSGGEEGAR	54.27
LTILEELR	71.78
ELASGLSFPVGFK	79.61
LSSEAPALFQFDLK	90.41

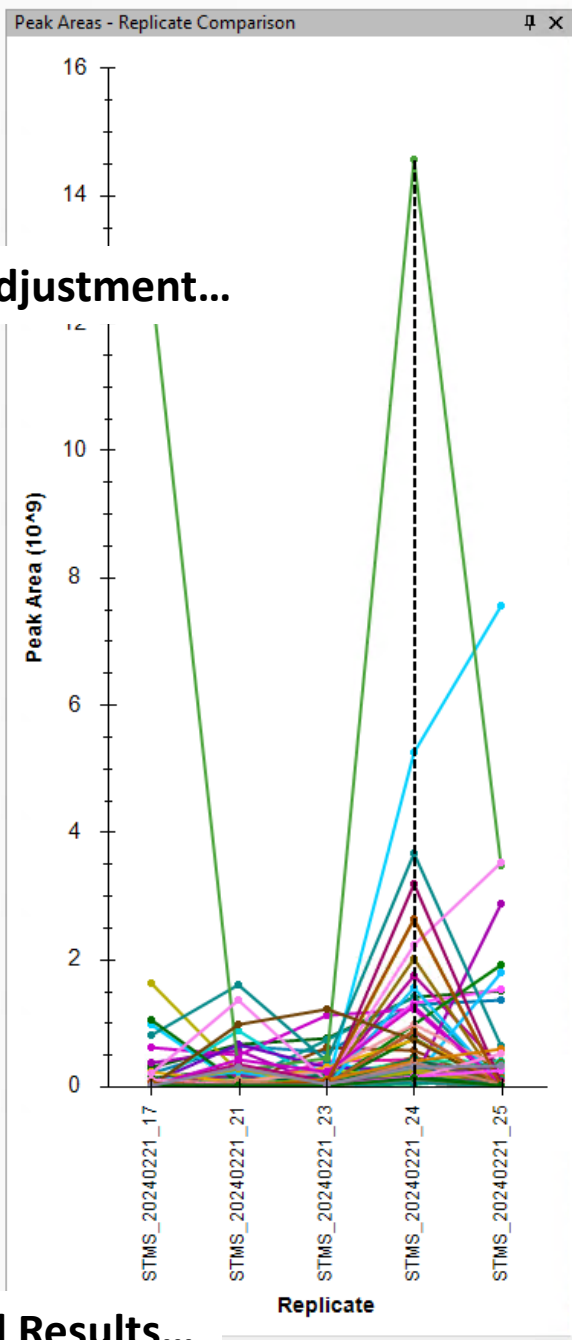
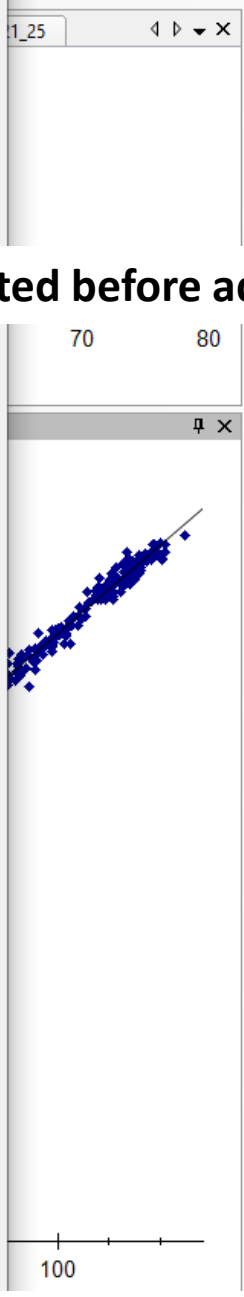
14 Standard peptides (11 required)

Other iRT values:

Target	iRT Value
HSNGSQSQHSR	-45.20
ASGKPVNHSTR	-43.92
GQHYSGQK	-41.95
GTQNPQDQGNPSPGK	-41.54

1119 Peptides

**iRT Values listed before adjustment...**



**< Select Add Results...**

Targets

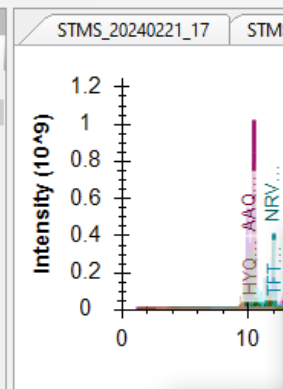
Replicates: STMS\_20240221\_24

- Pierce standards
  - SSAAPPPPR
  - GISNEGQNASIK
  - HVLTSIGEK
  - DIPVPKPK
  - IGDYAGIK
  - TASEFDSAIAQDK
  - SAAGAFGPESLR
  - ELGQSGVDTYLQTK
  - SFANQPLEVYSK
  - GLILVGGYGTR
  - GILFVGSVSGGEEGAR
  - LTILEELR
  - ELASGLSFPVGFK
  - LSSEAPALFQFDLK
- sp|P02743|SAMP\_HUMAN
  - MNNKPLLWISVLTSLLFAHTDLGK.V [1, 26]
  - R.ESVTDHVNLIPLKPLQNFLLCFR.A [33, 57]
  - R.AYSDLSR.A [58, 64]
  - R.AYSLFSYNTQGR.D [65, 76]
  - R.DNELLVYK.E [77, 84]
  - R.VGEYSLYGR.H [87, 96]
  - R.QGYFVEAQP.K [140, 149]
  - K.IVLGQEQDSYGGK.F [150, 162]
  - R.GYVIKPLVW.V [213, 223]
- sp|P02649|APOE\_HUMAN
  - K.VLWAALLVTFFLAGQAK.V [3, 19]
  - K.VEQAVETEPEPELR.Q [20, 33]
  - R.QQTEWQSGQR.W [34, 43]
  - R.WELALGR.F [44, 50]
  - R.FWDYLR.W [51, 56]
  - R.WVQTLSEQVQEELLSSQVTQELR.A [57, 79]
  - R.ALMDETMK.E [80, 87]
  - K.SELEEQLTPEAEETR.A [94, 108]
  - K.ELQAAQAR.L [114, 121]
  - R.LGADMEDVQGR.L [122, 132]
  - R.GEVQAMLGQSTEELR.V [138, 152]
  - R.DADDLQK.R [169, 175]
  - R.LAVYQAGAR.E [177, 185]

Results Grid

Reports 4 of 5

Replicate	Sample Type	Analyte Concentrat
STMS_20240221_17	Unknown	
STMS_20240221_21	Unknown	
STMS_20240221_23	Unknown	
STMS_20240221_24	Unknown	



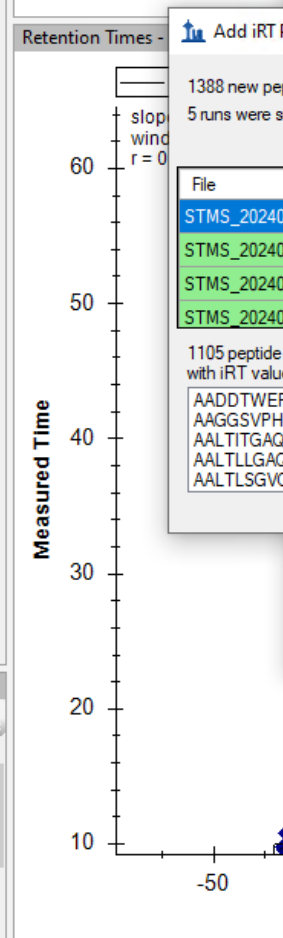
Edit iRT Calculator

Name: 20240301\_amyloid\_prtc

iRT database: D:\Skyline\prosit\20240301\_amyloid\_prtc.blib

Regression type: Linear

iRT standards: Pierce (iRT-C18)



Add iRT Peptides

1388 new peptides will be added to the iRT database.  
5 runs were successfully converted.

File	Points	Equation	R	Result
STMS_20240221_17.mzML	14	iRT = 2.963 * Measured RT - ...	0.998	Success
STMS_20240221_21.mzML	14	iRT = 2.978 * Measured RT - ...	0.997	Success
STMS_20240221_23.mzML	14	iRT = 2.977 * Measured RT - ...	0.997	Success
STMS_20240221_24.mzML	14	iRT = 2.981 * Measured RT - ...	0.998	Success

1105 peptide iRT values calculated from MS/MS scans will be replaced with iRT values calculated from chromatogram peaks:

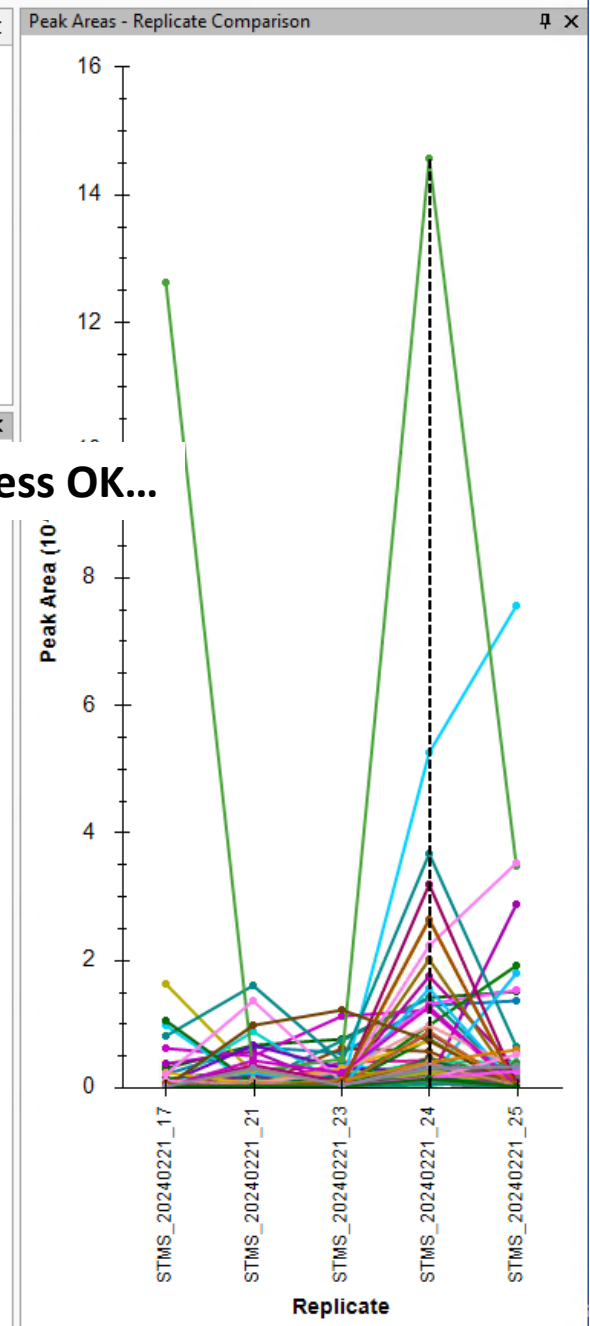
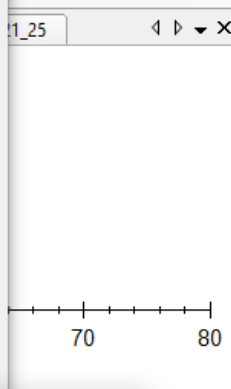
- AADDTWEPFASGK
- AAGGSVPHPR
- AALTITGAQADDESYYC[+57.021464]VLYMGSGI
- AALLTGAQPEDEAEYYC[+57.021464]LLSYSGAR
- AALLTSGVQPEDEAEYYC[+57.021464]LLYGGGAQ

14 Standard peptides (11 required)

Other iRT values:

Target	iRT Value
HSNGSQSQHSR	-45.20
ASGKPVNHSTR	-43.92
GQHYSQK	-41.95
GTONPSODQGNPSGK	-41.54

1119 Peptides



< Press OK...

Targets

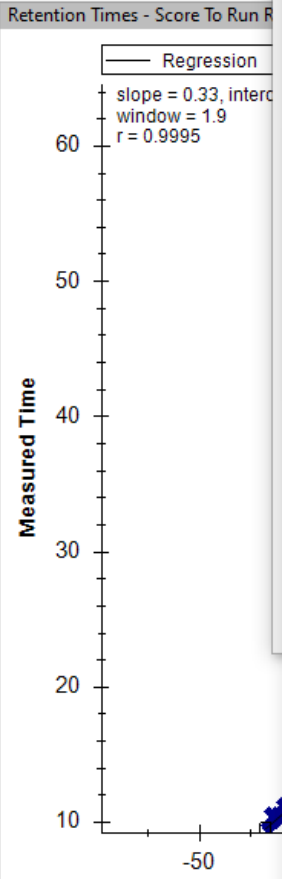
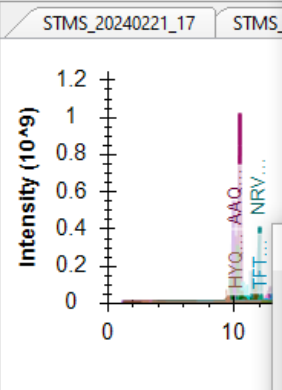
Replicates: STMS\_20240221\_24

- Pierce standards
  - SSAAPPPPR
  - GISNEGQNASIK
  - HVLTISIGEK
  - DIPVPPPK
  - IGDYAGIK
  - TASEFDSAIAQDK
  - SAAGAFGPESLR
  - ELGQSGVDTYLQTK
  - SFANQPLEVVYSK
  - GLILVGGYGTR
  - GILFVSGVSGGEEGAR
  - LTILEELR
  - ELASGLSFPVGFK
  - LSSEAPALFQFDLK
- sp|P02743|SAMP\_HUMAN
  - MKNPLLWISVLTSLLFAHTDLGK.V [1, 26]
  - R.ESVTDHVNLIPTLEKPLQNFQLCFR.A [33, 57]
  - R.AYSDLSR.A [58, 64]
  - R.AYSLFSYNTQGR.D [65, 76]
  - R.DNELLYYK.E [77, 84]
  - R.VGEYSLYIGR.H [87, 96]
  - R.QGYFVEAQP.K.I [140, 149]
  - K.IVLGQEQDSYGGK.F [150, 162]
  - R.GYVIKPLVWV.- [213, 223]
- sp|P02649|APOE\_HUMAN
  - K.VLWAALLVTFLLAGCQAK.V [3, 19]
  - K.VEQAVETEPEPELR.Q [20, 33]
  - R.QQTEWQSGQR.W [34, 43]
  - R.WELALGR.F [44, 50]
  - R.FWDYLR.W [51, 56]
  - R.WVQTLSEGVQEELLSSQVTQELR.A [57, 79]
  - R.ALMDETMK.E [80, 87]
  - K.SELEEQLTPVAEETR.A [94, 108]
  - K.ELQAAQAR.L [114, 121]
  - R.LGADMEDVCGR.L [122, 132]
  - R.GEVQAMLGQSTEELR.V [138, 152]
  - R.DADDLQK.R [169, 175]
  - R.LAVYQAGAR.E [177, 185]

Results Grid

Reports 4 of 5

Replicate	Sample Type	Analyte Concentrat
<a href="#">STMS_20240221_17</a>	Unknown	
<a href="#">STMS_20240221_21</a>	Unknown	
<a href="#">STMS_20240221_23</a>	Unknown	
<a href="#">STMS_20240221_24</a>	Unknown	



Edit iRT Calculator

Name: 20240301\_amyloid\_ptc

iRT database: D:\Skyline\prosit\20240301\_amyloid\_ptc.blib

Regression type: Linear

Store redundant iRT values

iRT standards: Pierce (iRT-C18)

Target	iRT Value
SSAAPPPPR	-27.60
GISNEGQNASIK	-17.47
HVLTISIGEK	-9.98
DIPVPPPK	2.88

Skyline

Do you want to recalibrate the iRT standard values relative to the peptides being added?  
This can improve retention time alignment under stable chromatographic conditions.

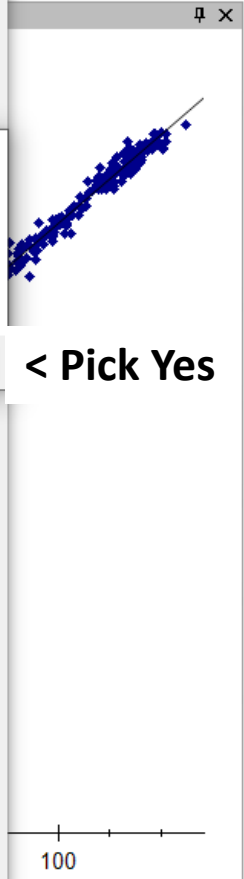
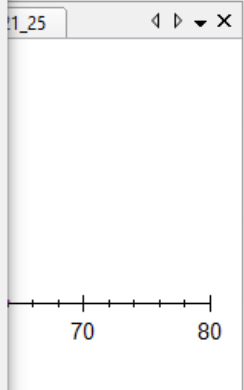
LTILEELR	71.78
ELASGLSFPVGFK	79.61
LSSEAPALFQFDLK	90.41

14 Standard peptides (11 required)

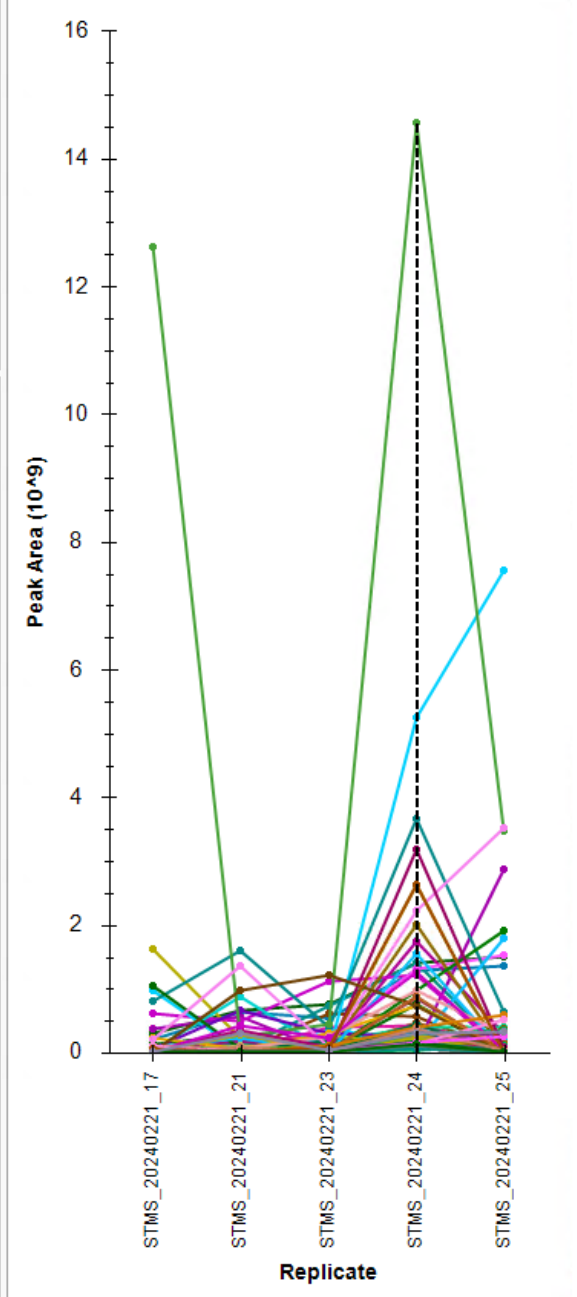
Other iRT values:

Target	iRT Value
HSNGSQSQHSR	-45.20
ASGKPVNHSTR	-43.92
GQHYSGQK	-41.95
GTNPSQDQGNPSGK	-41.54

1119 Peptides



Peak Areas - Replicate Comparison



File Edit Refine View Settings Tools Help

Targets

Replicates: STMS\_20240221\_24

Pierce standards

- SSAAPPPPPR
- GISNEGQNASIK
- HVLTSIGEK
- DIPVPPPK
- IGDYAGIK
- TASEFDSAIAQDK
- SAAGAFGPESLR
- ELGQSGVDTYLQTK
- SFANQPLEVYYSK
- GLILVGGYGTR
- GILFVGSVSGGEEGAR
- LTILEELR
- ELASGLSFPVGFK
- LSSEAPALFQFDLK

sp|P02743|SAMP\_HUMAN

- .MNKPLLWISVLTSLLEAFAHTDLSGK.V [1, 26]
- R.ESVTDHVNLTIPLEKPLNQFTLCFR.A [33, 57]
- R.AYSDLSR.A [58, 64]
- R.AYSLFSYNTQGR.D [65, 76]
- R.DNELLYK.E [77, 84]
- R.VGEYSLYGR.H [87, 96]
- R.QGYFVEAQPK.I [140, 149]
- K.IVLGQEQDSYGGK.F [150, 162]
- R.GYVIKPLVWV.- [213, 223]

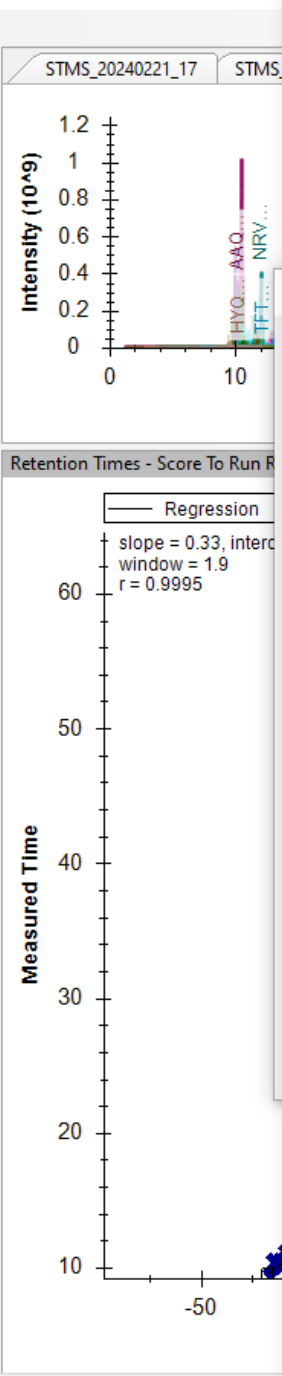
sp|P02649|APOE\_HUMAN

- K.VLWAALLVTFLAGCQAK.V [3, 19]
- K.VEQAVETEPEPELR.Q [20, 33]
- R.QQTEWQSGQR.W [34, 43]
- R.WELALGR.F [44, 50]
- R.FWDYLR.W [51, 56]
- R.WVQTLSEQVQELLSSQVTQELR.A [57, 79]
- R.ALMDETMK.E [80, 87]
- K.SELEEQLTPVAEETR.A [94, 108]
- K.ELQAAQAR.L [114, 121]
- R.LGADMEDVQGR.L [122, 132]
- R.GEVQAMLGQSTEELR.V [138, 152]
- R.DADDLQK.R [169, 175]
- R.LAVYQAGAR.E [177, 185]

Results Grid

Reports 4 of 5

Replicate	Sample Type	Analyte Concentrat
STMS_20240221_17	Unknown	
STMS_20240221_21	Unknown	
STMS_20240221_23	Unknown	
STMS_20240221_24	Unknown	



Edit iRT Calculator

Name: 20240301\_amyloid\_prtc

iRT database: D:\Skyline\prosit\20240301\_amyloid\_prtc.blib

Regression type: Linear

Store redundant iRT values

iRT standards: None

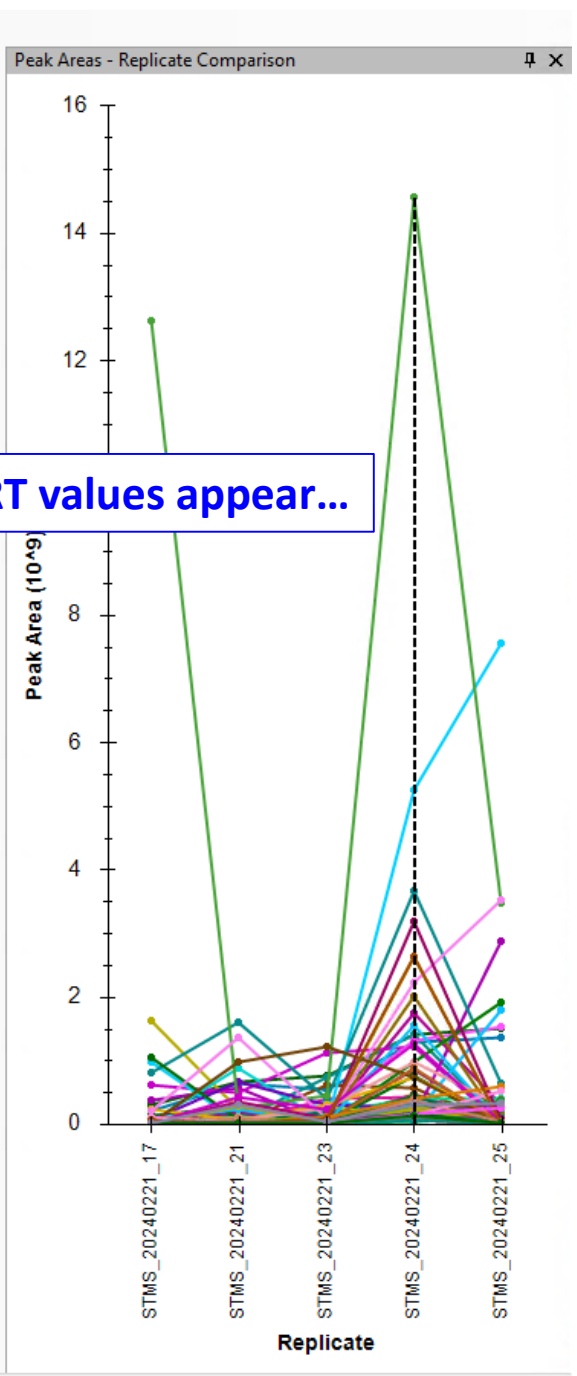
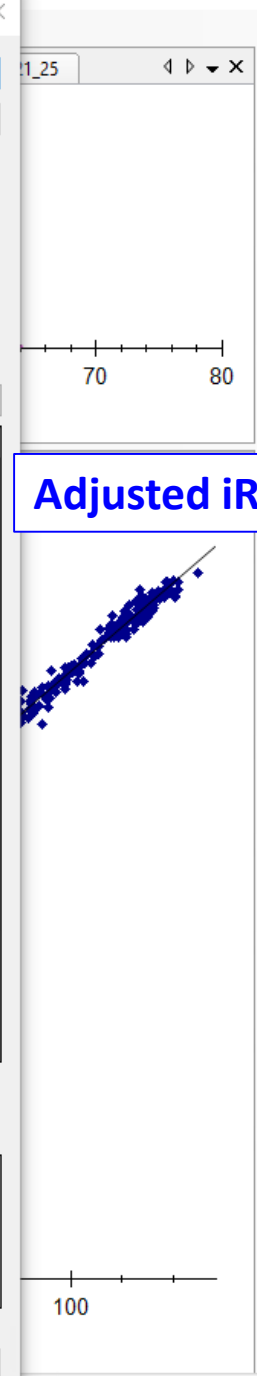
Target	iRT Value
SSAAPPPPPR	-27.60
GISNEGQNASIK	-22.56
HVLTSIGEK	-14.38
DIPVPPPK	-4.34
IGDYAGIK	-1.05
TASEFDSAIAQDK	12.11
SAAGAFGPESLR	19.56
ELGQSGVDTYLQTK	29.88
SFANQPLEVYYSK	49.95
GLILVGGYGTR	49.06
GILFVGSVSGGEEGAR	51.06
LTILEELR	66.56
ELASGLSFPVGFK	80.06
LSSEAPALFQFDLK	90.41

14 Standard peptides (11 required)

Other iRT values: Choose Standards... Recalibrate...

Target	iRT Value
HSNGSQSQHSR	-36.28
ASGKPVNHSTR	-36.27
GQHYSGQK	-35.27
GTQNSQDQGNSSPSGK	-35.04

2507 Peptides Add...



File Edit Refine View Settings Tools Help

Targets

Replicates: STMS\_20240221\_24

Pierce standards

- SSAAPPPPPR
- GISNEGQNASIK
- HVLTSIGEK
- DIPVPKPK
- IGDYAGIK
- TASEFDSAIAQDK
- SAAGAFGPESLR
- ELGQSGVDTYLQTK
- SFANQPLEVYYSK
- GLILVGGYGTR
- GILFVGGVSGGEEGAR
- LTILEELR
- ELASGLSFPVGFK
- LSSEAPALFQFDLK

sp|P02743|SAMP\_HUMAN

- .MNKPLLWISVLTSLLEAFAHTDLSGK.V [1, 26]
- R.ESVTDHVNLIPTLEKPLQNFTLCFR.A [33, 57]
- R.AYSDLSR.A [58, 64]
- R.AYSLFSYNTQGR.D [65, 76]
- R.DNELLVYK.E [77, 84]
- R.VGEYSLYGR.H [87, 96]
- R.QGYFVEAQPK.I [140, 149]
- K.IVLGQEQDSYGGK.F [150, 162]
- R.GYVIKPLVWV.- [213, 223]

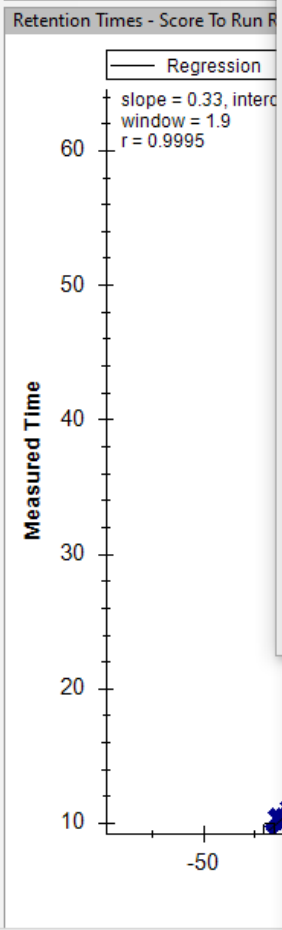
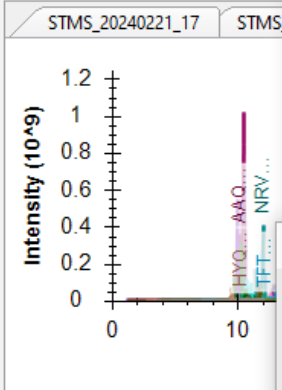
sp|P02649|APOE\_HUMAN

- K.VLWAALLVTFLAGCQAK.V [3, 19]
- K.VEQAVETEPEPELR.Q [20, 33]
- R.QQTEWQSGQR.W [34, 43]
- R.WELALGR.F [44, 50]
- R.FWDYLR.W [51, 56]
- R.WVQTLSEQVQEELLSSQVTQELR.A [57, 79]
- R.ALMDETMK.E [80, 87]
- K.SEEELQTPVAEETR.A [94, 108]
- K.ELQAAQAR.L [114, 121]
- R.LGADMEDVQGR.L [122, 132]
- R.GEVQAMLGQSTEELR.V [138, 152]
- R.DADDLQK.R [169, 175]
- R.LAVYQAGAR.E [177, 185]

Results Grid

Reports 4 of 5

Replicate	Sample Type	Analyte Concentrat
STMS_20240221_17	Unknown	
STMS_20240221_21	Unknown	
STMS_20240221_23	Unknown	
STMS_20240221_24	Unknown	



Edit iRT Calculator

Name: 20240301\_amyloid\_prtc

iRT database: D:\Skyline\prost\20240301\_amyloid\_prtc.blib

Regression type: Linear

Store redundant iRT values:

iRT standards: None

Target	iRT Value
SSAAPPPPPR	-27.60
GISNEGQNASIK	-22.56
HVLTSIGEK	-14.38
DIPVPKPK	-4.34

Skyline

Spectral libraries cannot be modified. You must save this iRT calculator as a new file.

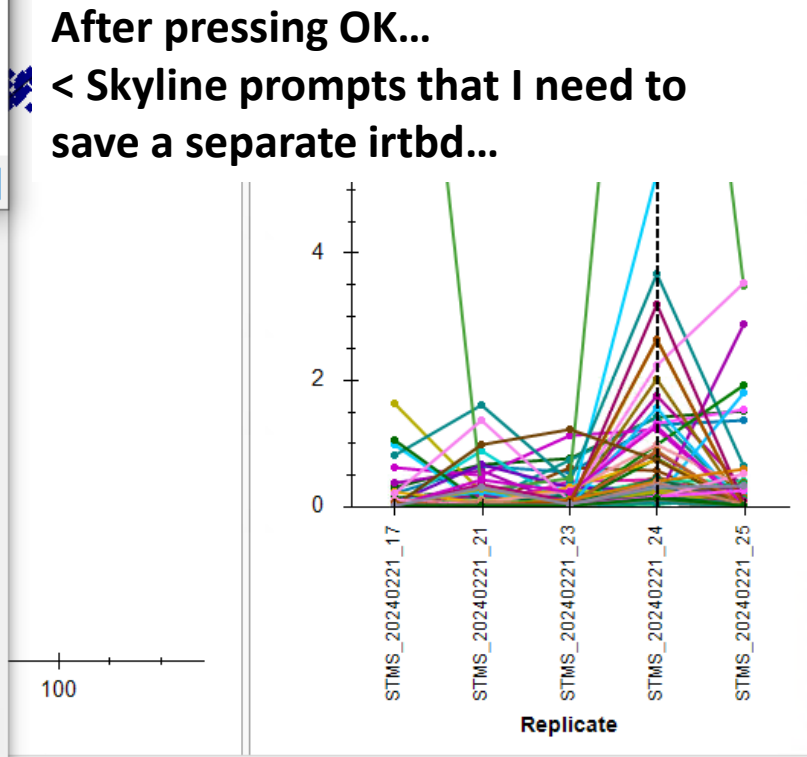
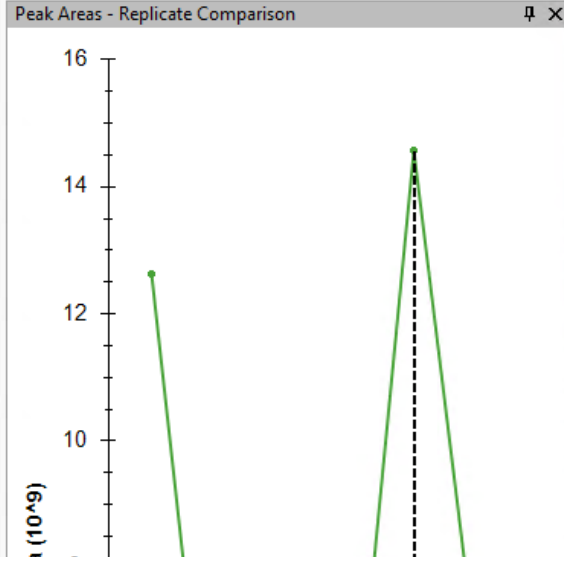
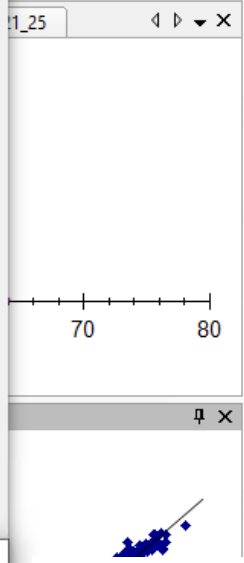
Target	iRT Value
LTILEELR	66.56
ELASGLSFPVGFK	80.06
LSSEAPALFQFDLK	90.41

14 Standard peptides (11 required)

Other iRT values: Choose Standards... Recalibrate...

Target	iRT Value
HSNGSQSQHSR	-36.28
ASGKPVNHSTR	-36.27
GQHYSGQK	-35.27
GTONPSQDQGNMSPSGK	-35.04

2507 Peptides



Skyline - Edit - 20240301\_Amyloid\_DIA\_03.sky \*

File Edit Refine View Settings Tools Help

Targets

Replicates: STMS\_20240221\_24

Pierce standards

- SSAAPPPPR
- GISNEGQNASIK
- HVLTSIGEK
- DIPVPKPK
- IGDYAGIK
- TASEFDSAIAQDK
- SAAGAFGPESLR
- ELGQSGVDTYLQTK
- SFANQPLEVYYSK
- GLILVGGYGTR
- GILFVSGVSGGEEGAR
- LTILEELR
- ELASGLSFPVGFK
- LSSEAPALFQFDLK

sp|P02743|SAMP\_HUMAN

- .MNKPLLWISVLTSLLEAFAHTDLSGK.V [1, 26]
- R.ESVTDHVNLIPTLEKPLQNTLCFR.A [33, 57]
- R.AYSDLSR.A [58, 64]
- R.AYSLFSYNTQGR.D [65, 76]
- R.DNELLVYK.E [77, 84]
- R.VGEYSLYIGR.H [87, 96]
- R.QGYFVEAQP.K [140, 149]
- K.IVLGQEQDSYGGK.F [150, 162]
- R.GYVIKPLVWV.- [213, 223]

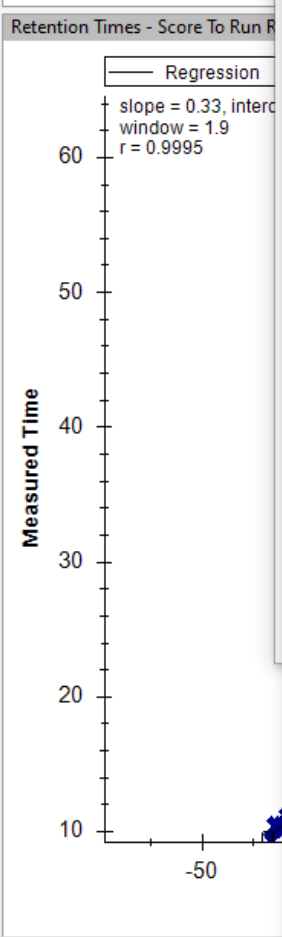
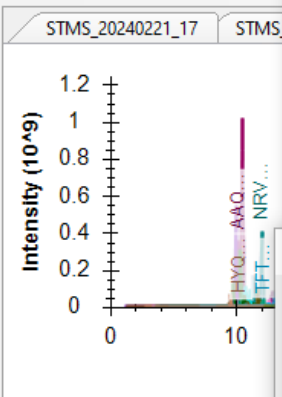
sp|P02649|APOE\_HUMAN

- K.VLWAALLVTFLAGCQAK.V [3, 19]
- K.VEQAVETEPEPELR.Q [20, 33]
- R.QQTEWQSGQR.W [34, 43]
- R.WELALGR.F [44, 50]
- R.FWDYLR.W [51, 56]
- R.WVQTLSEQVEELLSSQVTQELR.A [57, 79]
- R.ALMDETMK.E [80, 87]
- K.SELEEQLTVAEETR.A [94, 108]
- K.ELQAAQAR.L [114, 121]
- R.LGADMEDVCGR.L [122, 132]
- R.GEVQAMLGQSTEELR.V [138, 152]
- R.DADDLQK.R [169, 175]
- R.LAVYQAGAR.E [177, 185]

Results Grid

Reports 4 of 5

Replicate	Sample Type	Analyte Concentrat
STMS_20240221_17	Unknown	
STMS_20240221_21	Unknown	
STMS_20240221_23	Unknown	
STMS_20240221_24	Unknown	



Edit iRT Calculator

Save As

This PC > New Volume (D:) > Skyline > irtdb

Search irtdb

Organize New folder

Name	Date modified	Type	Size
data			
Desktop			
Downloads			
Documents			
Pictures			
fasta			
irtdb			
prosit			
Skyline			
OneDrive			
OneDrive			
This PC			
3D Objects			
Desktop			
Documents			
Downloads			
Music			
Pictures			
Videos			
Local Disk (C:)			
New Volume (D:)			
Divisions (\\amc			
uwlm-chemistry			
Network			

File name: 20240301\_irt\_04.irtdb

Save as type: iRT Database Files (\*.irtdb)

Save

2507 Peptides

Add...

188/188 prot 1,403/2,790 pep 2,000/3,976 prec 15,962/31,777 tran

I try to save one...

Targets

Replicates: STMS\_20240221\_24

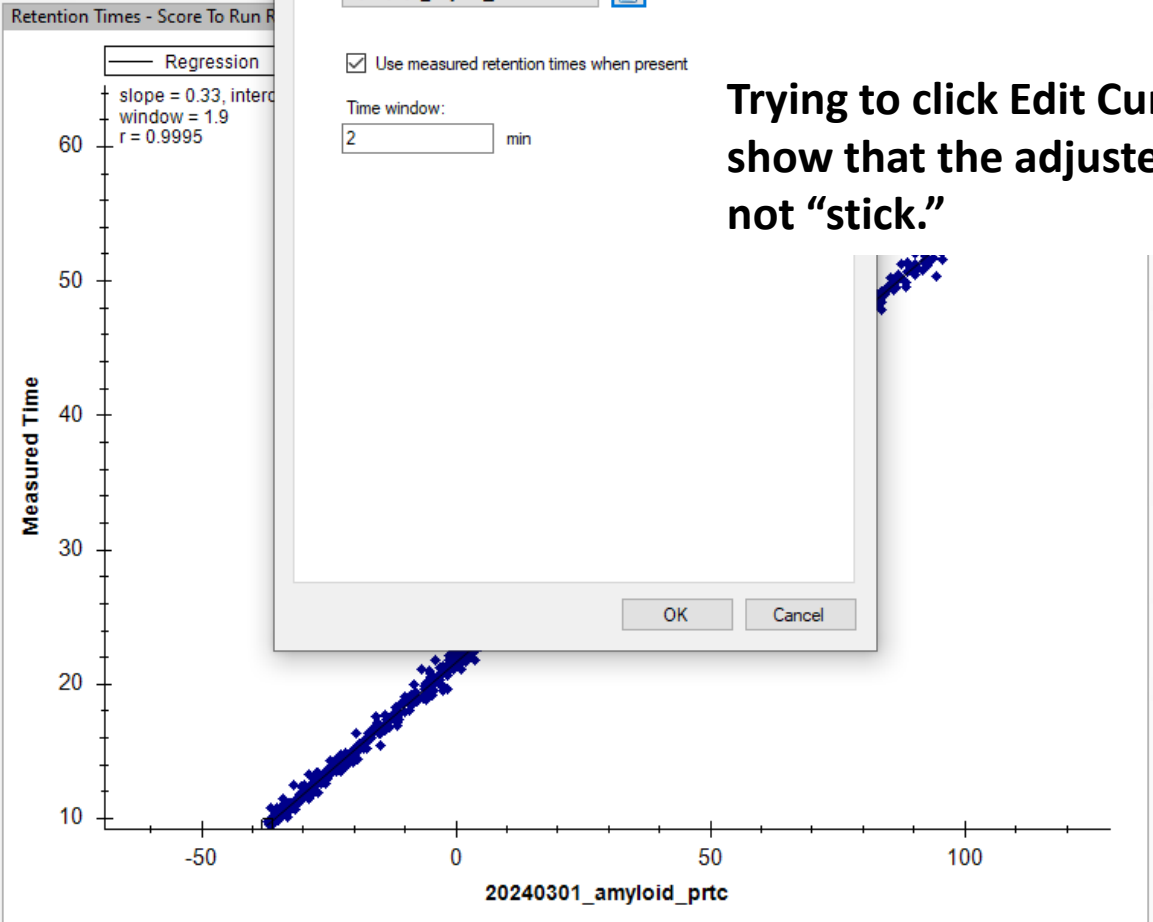
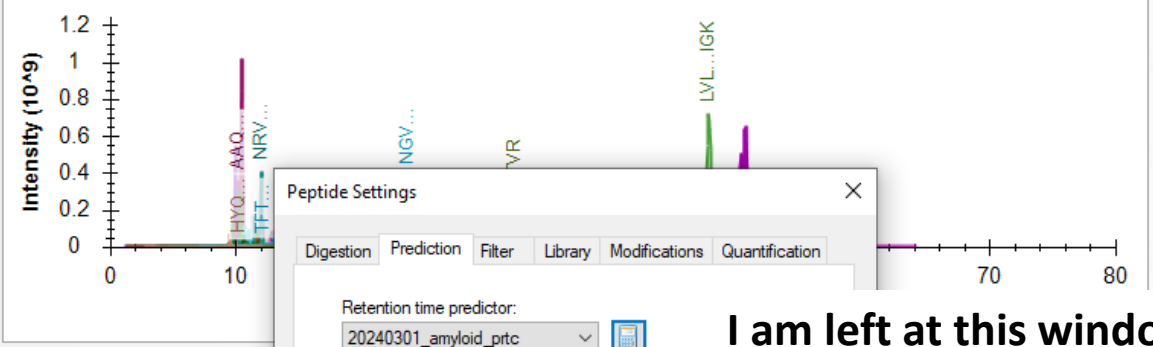
- Pierce standards
  - SSAAPPPPPR
  - GISNEGQNASIK
  - HVLTSIGEK
  - DIPVPPK
  - IGDYAGIK
  - TASEFDSAIAQDK
  - SAAGAFGPPELSR
  - ELGQSGVDTYLQTK
  - SFANGPLEVYYSK
  - GLILVGGYGTR
  - GILFVGSVSGGEEGAR
  - LTILEELR
  - ELASGLSFPVGFK
  - LSSEAPALFQDLK
- sp|P02743|SAMP\_HUMAN
  - .MNKPLLWISVLTSLLEAFAHTDLSGK.V [1, 26]
  - R.ESVTDHVNLTIPLEKPLQNFTLCFR.A [33, 57]
  - R.AYSDLSR.A [58, 64]
  - R.AYSLFSYNTQGR.D [65, 76]
  - R.DNELLVYK.E [77, 84]
  - R.VGEYSLYIGR.H [87, 96]
  - R.QGYFVEAQPK.I [140, 149]
  - K.IVLGQEQDSYGGK.F [150, 162]
  - R.GYVIKPLVWV.- [213, 223]
- sp|P02649|APOE\_HUMAN
  - K.VLWAALLVTFLAGCQAK.V [3, 19]
  - K.VEQAVETEPEPELR.Q [20, 33]
  - R.QQTEWQSGQR.W [34, 43]
  - R.WELALGR.F [44, 50]
  - R.FWDYLR.W [51, 56]
  - R.WVQTLSEQVQEELLSSQVTQELR.A [57, 79]
  - R.ALMDETMK.E [80, 87]
  - K.SELEEQLTVPAAEETR.A [94, 108]
  - K.ELQAAQAR.L [114, 121]
  - R.LGADMEDVQGR.L [122, 132]
  - R.GEVQAMLGQSTEELR.V [138, 152]
  - R.DADDLQK.R [169, 175]
  - R.LAVYQAGAR.E [177, 185]

Results Grid

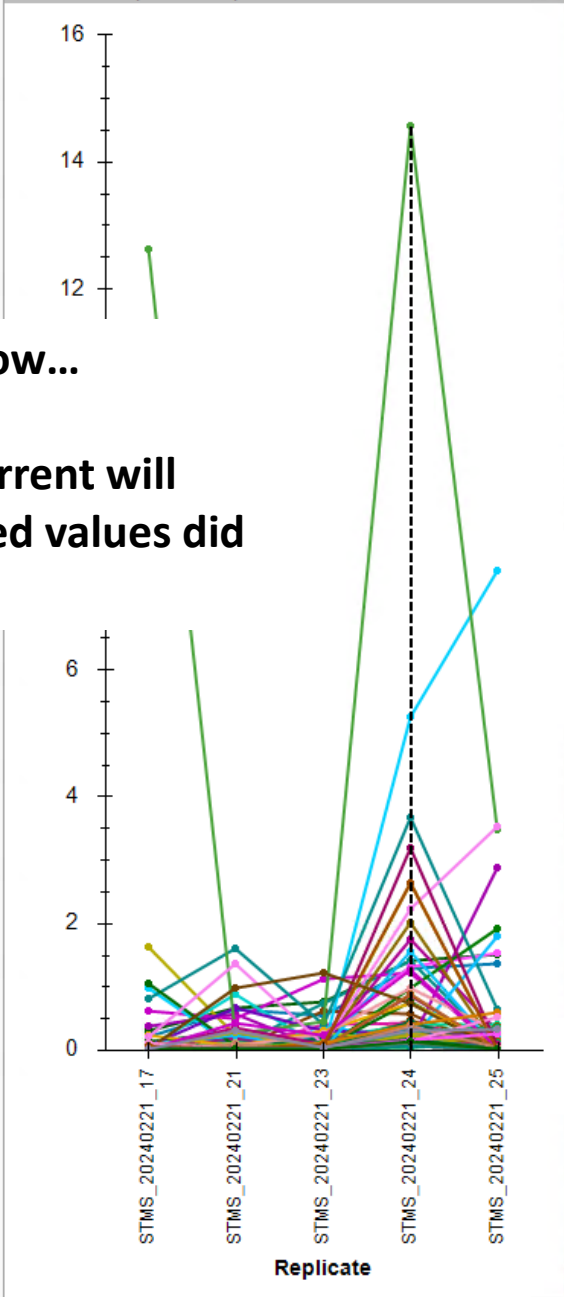
Reports 4 of 5

Replicate	Sample Type	Analyte Concentrat
STMS_20240221_17	Unknown	
STMS_20240221_21	Unknown	
STMS_20240221_23	Unknown	
STMS_20240221_24	Unknown	
STMS_20240221_25	Unknown	

STMS\_20240221\_17 STMS\_20240221\_21 STMS\_20240221\_23 STMS\_20240221\_24 STMS\_20240221\_25



Peak Areas - Replicate Comparison



I am left at this window...

Trying to click Edit Current will show that the adjusted values did not "stick."



File Edit Refine View Settings Tools Help

**Targets**

Replicates: STMS\_20240221\_24

Pierce standards

- SSAAPPPPPR
- GISNEGQNASIK
- HVLTSIGEK
- DIPVPPPK
- IGDYAGIK
- TASEFDSAIAQDK
- SAAGAFGPPELSR
- ELGQSGVDTYLQTK
- SFANQPLEVVYSK
- GLILVGGYGTR
- GILFVGSVSGGEEGAR
- LTILEELR
- ELASGLSFPVGFK
- LSSEAPALFQFDLK

sp|P02743|SAMP\_HUMAN

- .MKNPLLWISVLTSLLEAFAHTDLSGK.V [1, 26]
- R.ESVTDHVNLTPLEKPLQNFTLCFR.A [33, 57]
- R.AYSDLSR.A [58, 64]
- R.AYSLFSYNTQGR.D [65, 76]
- R.DNELLYK.E [77, 84]
- R.VGEYSLYGR.H [87, 96]
- R.QGYFVEAQP.K.I [140, 149]
- K.IVLGQEQDSYGGK.F [150, 162]
- R.GYVIKPLVWV.- [213, 223]

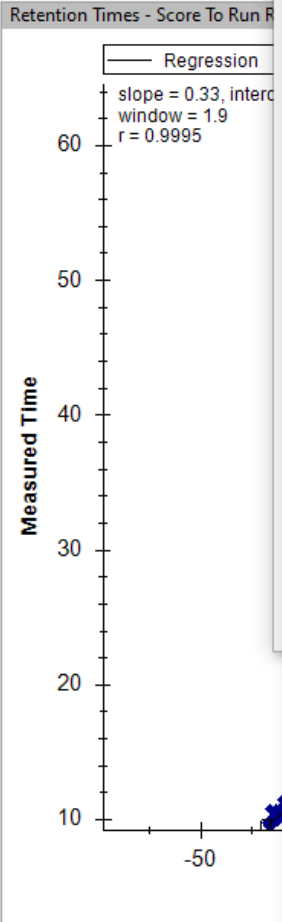
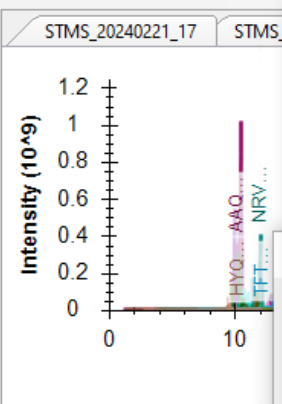
sp|P02649|APOE\_HUMAN

- K.VLWAALLVTLFLAGQQAQ.V [3, 19]
- K.VEQAVETEPEPELR.Q [20, 33]
- R.QQTEWQSGQR.W [34, 43]
- R.WELALGR.F [44, 50]
- R.FWDYLR.W [51, 56]
- R.WVQTLSEVQVEELLSSQVTQELR.A [57, 79]
- R.ALMDETM.K.E [80, 87]
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- K.ELQAAQAR.L [114, 121]
- R.LGADMEDVQGR.L [122, 132]
- R.GEVQAMLGQSTEELR.V [138, 152]
- R.DADDLQK.R [169, 175]
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**Results Grid**

Reports 4 of 5

Replicate	Sample Type	Analyte Concentrat
STMS_20240221_17	Unknown	
STMS_20240221_21	Unknown	
STMS_20240221_23	Unknown	
STMS_20240221_24	Unknown	



**Edit iRT Calculator**

Name: 20240301\_amyloid\_prtc

iRT database: D:\Skyline\prosit\20240301\_amyloid\_prtc.blib

Regression type: Linear

Store redundant iRT values

iRT standards: Pierce (iRT-C18)

Target	iRT Value
SSAAPPPPPR	-27.60
GISNEGQNASIK	-17.47
HVLTSIGEK	-9.98
DIPVPPPK	-3.88
IGDYAGIK	7.84
TASEFDSAIAQDK	18.42
SAAGAFGPPELSR	26.22
ELGQSGVDTYLQTK	32.61
SFANQPLEVVYSK	51.41
GLILVGGYGTR	52.36
GILFVGSVSGGEEGAR	54.27
LTILEELR	71.78
ELASGLSFPVGFK	79.61
LSSEAPALFQFDLK	90.41

14 Standard peptides (11 required)

Other iRT values:

Target	iRT Value
HSNGSQSQHSR	-45.20
ASGKPVNHSTR	-43.92
GQHYSQK	-41.95
GTQNPQQDQGNPSGK	-41.54

1119 Peptides

