

SUPPLEMENTARY INFORMATION

Targeted expression of TGFB β peptides in mouse and human tissue by MALDI-Mass Spectrometry Imaging

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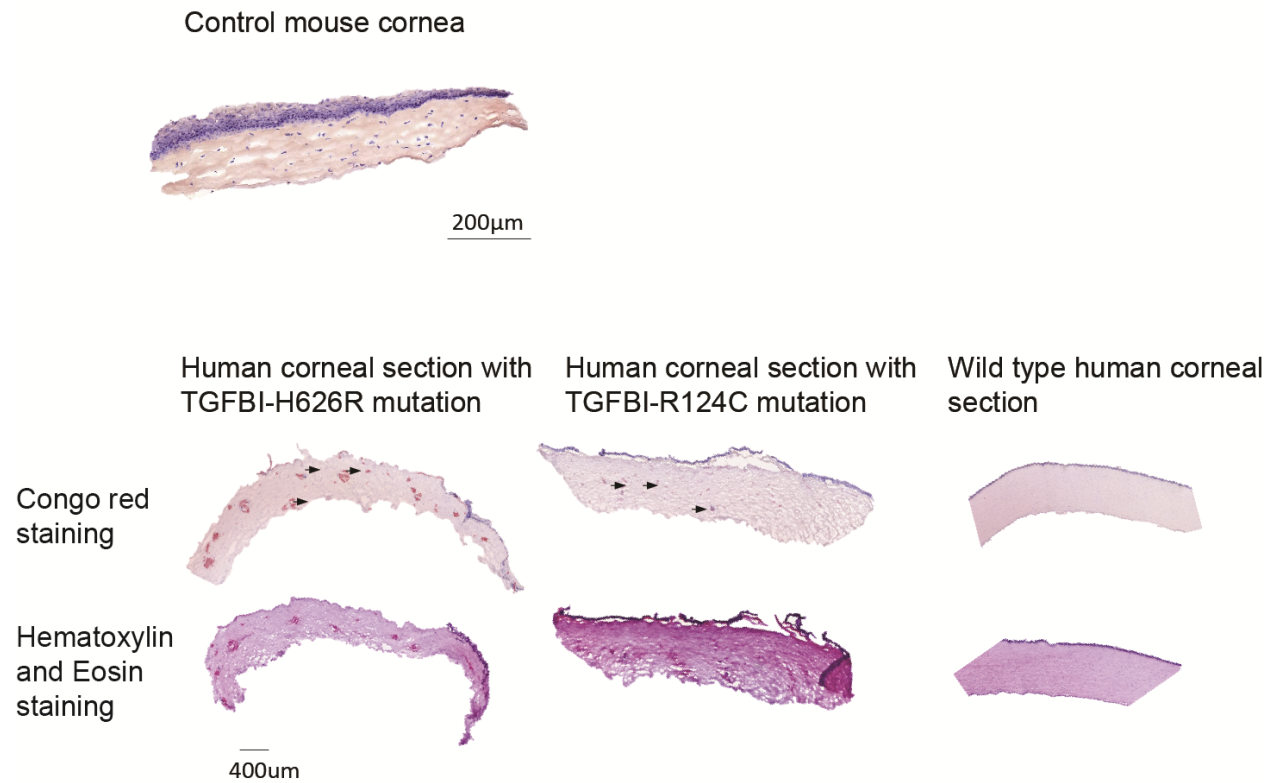
⁶Singapore National Eye Centre, 11 Third Hospital Avenue, Singapore 168751

* Both authors (VA and GH) contributed equally towards the publication.

Supplementary Table S1: *TGFBI* mouse digests in solution matching with in silico digestion (2 missed cleavages allowed). 21 peptide digests from *TGFBI* were obtained.

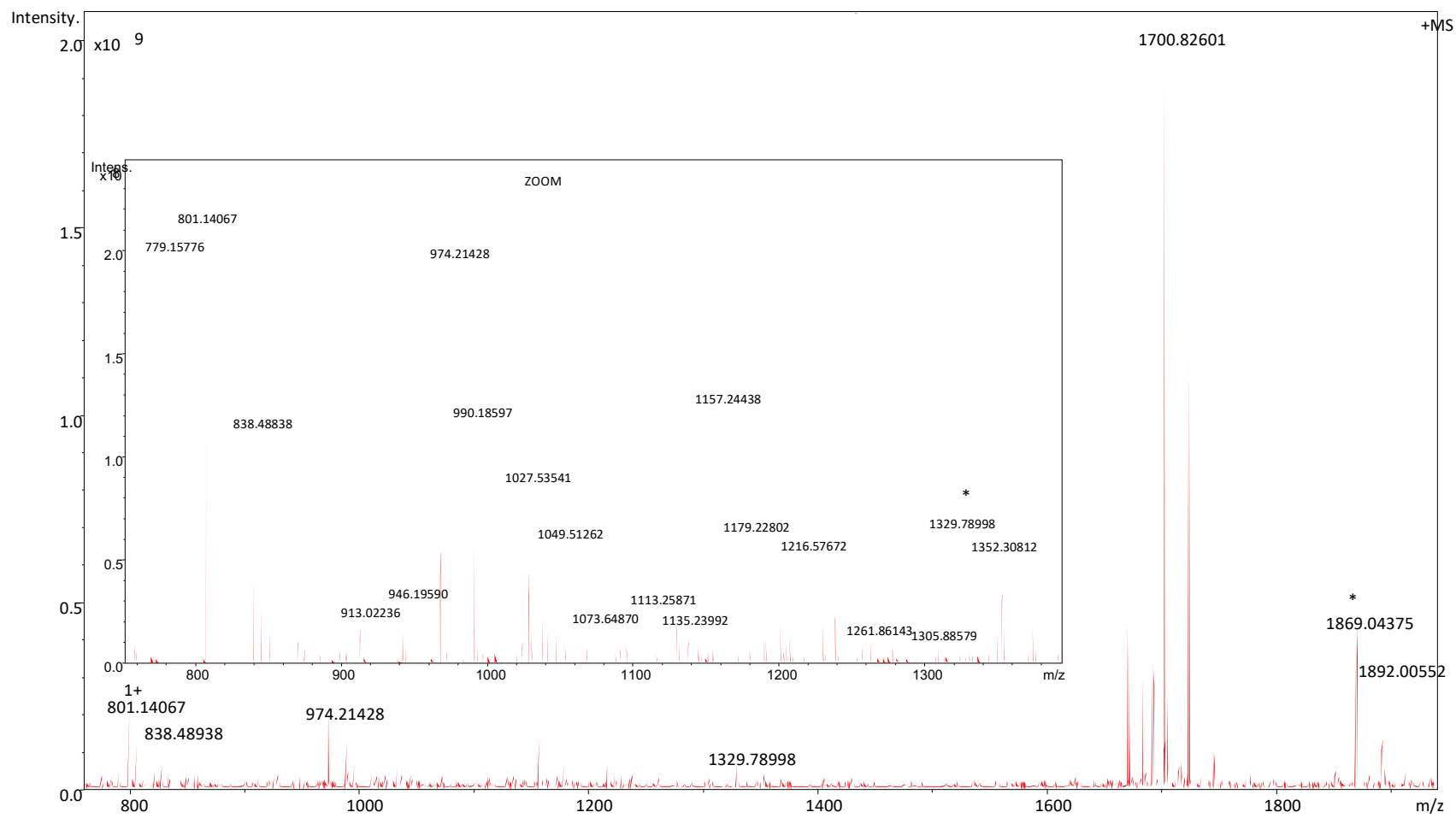
Range	Miscleavages	Theoretical [M+H] ⁺	Experimental [M+H] ⁺	Mass accuracy (ppm)	Sequence
[462-464]	1	416.298	416.29775	2.5	KLR
[663-666]	0	445.2518	445.251666	2.3	AAQR
[91-95]	0	529.298	529.298371	2.1	VPGEK
[677-680]	0	530.3297	530.330071	1.9	LLER
[422-426]	0	543.2885	543.287468	1.5	DGVPR
[54-59]	0	631.3774	631.377337	1.3	VIGTNK
[350-355]	0	631.3774	631.377337	1.2	AVISNK
[465-469]	0	683.3875	683.386065	0.6	VFVYR
[67-71]	0	780.3787	780.3787	0.4	QWYQR
[656-662]	0	782.3791	782.379335	0.3	QASAYSR
[180-186]	0	817.4666	817.467336	0.1	VLTDELK
[173-178]	0	820.377	820.37741	0.1	YHMOVDR
[564-570]	0	830.4982	830.496124	0	ELTNILK
[670-676]	0	846.4832	846.483454	-0.3	LAPVYQR
[603-610]	0	873.4789	873.479686	-0.3	NNVSVNKK
[288-295]	0	913.5102	913.509012	-0.5	IPAETLNR
[173-179]	1	976.4781	976.479467	-0.7	YHMOVDRR
[296-304]	0	983.552	983.549738	-0.7	ILGDPEALR
[305-313]	0	1079.6208	1079.6195	-0.9	DLLNNHILK
[488-496]	0	1087.5241	1087.5253	-0.9	FGLFTMDR
[591-602]	1	1290.69	1290.68948	-1.1	SLQGDKLEVSSK
[497-510]	0	1532.7885	1532.7862	-1.4	MLTPPMGTVM DVLK

Supplementary Figure S1: H&E and Congo red staining for mouse, human samples as adopted from [1](control and diseased)



Supplementary Figure S2: 7T-MALDI-FTICR spectrum of TGFBIp digest in solution matching (A) with in silico digestion (2 missed cleavages allowed). 17 peptide digests from TGFBIp were obtained. Each * in the spectrum corresponds to unique m/z digest of TGFBIp matching with the in-silico approach and thus reported in the study. Other major peaks may correspond to the trypsin only or non-reported peptides in the reaction mixture.

Mass spectrum of digested TGFBI from m/z 300 to m/z 2000.



Supplementary Table S2: 7T-MALDI-FTICR spectrum of TGFBIp digest in solution matching. The major peaks may correspond to the trypsin only or non-reported peptides in the reaction mixture.

Range	[M+H] ⁺	Miscleavages	Sequence
[73- 76]	420.228	0	ICGK
[656-662]	766.384	0	QASAFSR
[670-676]	818.477	0	LAPVYQK
[549-555]	838.489	1	ALPPRER
[556-563]	859.5	1	SRLLGDAK
[667-676]	1160.679	1	SVRLAPVYQK
[422-432]	1179.575	0	DGTPPIDAHTR
[670-680]	1329.789	1	LAPVYQKLLER
[41- 53]	1393.712	1	GRQHGPNVCAVQK
[643-655]	1407.7	0	GDELADSALEIFK
[656-669]	1550.815	2	QASAFSRASQRSVR
[589-602]	1557.921	2	LKSLQGDKLEVSLK
[448-461]	1579.811	0	YLYHGQTLETGGK
[220-234]	1626.835	0	ADHHATNGVVHLIDK
[556-570]	1640.969	2	SRLLGDAKELANILK
[534-548]	1700.828	0	EGVYTVFAPTNEAFR
[571-588]	1869.023	0	YHIGDEILVSGGIGALVR

Supplementary Figure S3: Search parameters used for TFGBlp as adopted from [1] to match PMF obtained from the control and treated tissue sections.

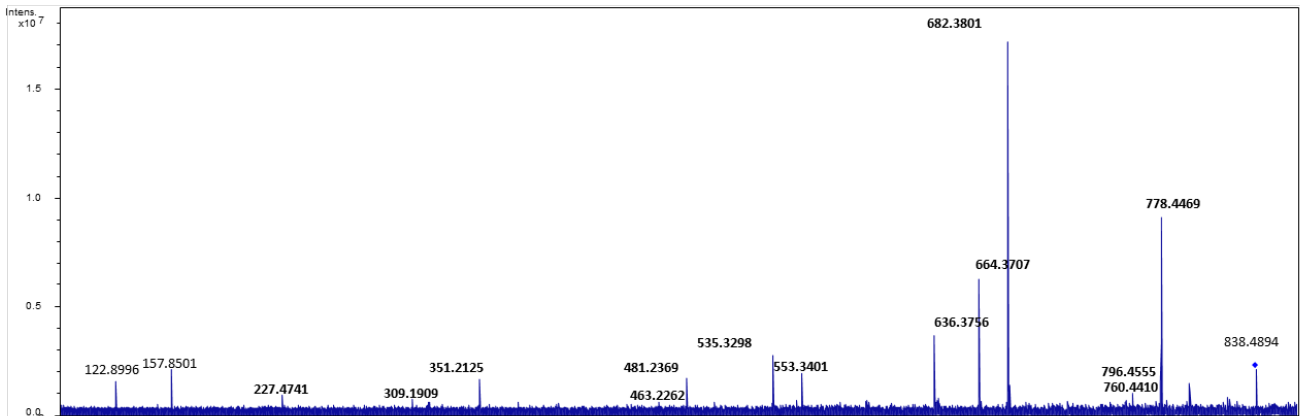
Search Parameters

Type of search : Peptide Mass Fingerprint
 Enzyme : Trypsin
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 0.1 ppm
 Peptide Charge State : 1+
 Max Missed Cleavages : 2
 Number of queries : 1

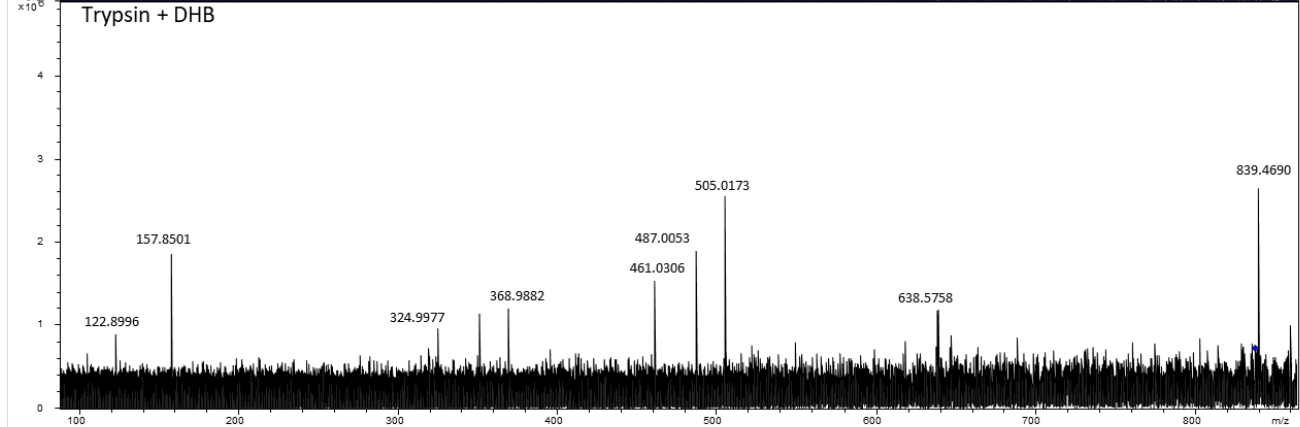
TISD_HUMAN	Mass: 51031	Score: 16	Expect: 5e+02	Matches: 1
mRNA decay activator protein ZFP36L2 OS=Homo sapiens OX=9606 GN=ZFP36L2 PE=1 SV=3				
GDF5_HUMAN	Mass: 55376	Score: 16	Expect: 5e+02	Matches: 1
Growth/differentiation factor 5 OS=Homo sapiens OX=9606 GN=GDF5 PE=1 SV=3				
APEX2_HUMAN	Mass: 57364	Score: 16	Expect: 5.1e+02	Matches: 1
DNA-(apurinic or apyrimidinic site) lyase 2 OS=Homo sapiens OX=9606 GN=APEX2 PE=1 SV=1				
ZNF695_HUMAN	Mass: 60109	Score: 16	Expect: 5.2e+02	Matches: 1
Zinc finger protein 695 OS=Homo sapiens OX=9606 GN=ZNF695 PE=1 SV=4				
KCNN2_HUMAN	Mass: 63719	Score: 16	Expect: 5.7e+02	Matches: 1
Small conductance calcium-activated potassium channel protein 2 OS=Homo sapiens OX=9606 GN=KCNN2 PE=1 SV=2				
CRT3_HUMAN	Mass: 66918	Score: 15	Expect: 6.2e+02	Matches: 1
CREB-regulated transcription coactivator 3 OS=Homo sapiens OX=9606 GN=CRT3 PE=1 SV=2				
PALM3_HUMAN	Mass: 71652	Score: 15	Expect: 6.7e+02	Matches: 1
Paralemmin-3 OS=Homo sapiens OX=9606 GN=PALM3 PE=1 SV=2				
BGH3_HUMAN	Mass: 74634	Score: 15	Expect: 6.7e+02	Matches: 1
Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens OX=9606 GN=TGFB1 PE=1 SV=1				
SETMR_HUMAN	Mass: 77984	Score: 15	Expect: 6.7e+02	Matches: 1
Histone-lysine N-methyltransferase SETMAR OS=Homo sapiens OX=9606 GN=SETMAR PE=1 SV=2				
PPP3R3_HUMAN	Mass: 74721	Score: 15	Expect: 6.9e+02	Matches: 1
Protein phosphatase 1 regulatory subunit 37 OS=Homo sapiens OX=9606 GN=PPP1R37 PE=1 SV=4				
TGM6_HUMAN	Mass: 79263	Score: 15	Expect: 7.1e+02	Matches: 1
Protein-glutamine gamma-glutamyltransferase 6 OS=Homo sapiens OX=9606 GN=TGM6 PE=1 SV=3				
KCNN3_HUMAN	Mass: 81334	Score: 14	Expect: 7.2e+02	Matches: 1
Small conductance calcium-activated potassium channel protein 3 OS=Homo sapiens OX=9606 GN=KCNN3 PE=2 SV=2				
ZNF585B_HUMAN	Mass: 88009	Score: 14	Expect: 7.6e+02	Matches: 1
Zinc finger protein 585B OS=Homo sapiens OX=9606 GN=ZNF585B PE=2 SV=1				
RRF2M_HUMAN	Mass: 86546	Score: 14	Expect: 7.7e+02	Matches: 1
Ribosome-releasing factor 2, mitochondrial OS=Homo sapiens OX=9606 GN=GFM2 PE=1 SV=1				
ZNF629_HUMAN	Mass: 96559	Score: 14	Expect: 8.5e+02	Matches: 1
Zinc finger protein 629 OS=Homo sapiens OX=9606 GN=ZNF629 PE=1 SV=2				

Supplementary Figure S4 as adopted from [1]: MS/MS fragmentation of *m/z* 838.489 in (a) Digested human cornea, (b) Control trypsin only and (c) Query of the MS/MS in Mascot database

A



B



c)

Search Parameters	
Type of search	: MS/MS Ion Search
Enzyme	: Trypsin
Mass values	: Monoisotopic
Protein Mass	: Unrestricted
Peptide Mass Tolerance	: ± 0.015 Da
Fragment Mass Tolerance	: ± 0.03 Da
Max Missed Cleavages	: 2
Instrument type	: Default
Number of queries	: 1

1. [BGH3 HUMAN](#) Mass: 74634 Score: 3 Matches: 1(0) Sequences: 1(0)
Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=IGFBI PE=1 SV=1
☐ Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	838.5026	837.4953	837.4821	0.0133	1	3	2.7	1	U	R.ALPPRER.S

2. [FOXNB HUMAN](#) Mass: 18613 Score: 2 Matches: 1(0) Sequences: 1(0)
FOXNL2 neighbor protein OS=Homo sapiens GN=FOXNL2NB PE=2 SV=1
☐ Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	838.5026	837.4953	837.4821	0.0133	1	2	3.5	2	U	R.RLPAPER.E

3. [ZNF695 HUMAN](#) Mass: 60109 Score: 2 Matches: 1(0) Sequences: 1(0)
Zinc finger protein 695 OS=Homo sapiens GN=ZNF695 PE=1 SV=4
☐ Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	838.5026	837.4953	837.4821	0.0133	1	2	3.6	3	U	K.RIHVGKEK.H

4. [TGM3L HUMAN](#) Mass: 79263 Score: 2 Matches: 1(0) Sequences: 1(0)
Protein-glutamine gamma-glutamyltransferase 6 OS=Homo sapiens GN=TGM6 PE=1 SV=3
☐ Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	838.5026	837.4953	837.4821	0.0133	1	2	3.6	4	U	R.GVEKHIR.A






Supplementary Figure S5:

BLAST Results of the peptides showing TGFB1p to be the best hit protein. This shows the specificity of the peptide to TGFB1p

Blast queries Parameters
Non-redundant UniProtKB/Swissprot sequences
Humans taxid:9605

Sequence	Experimental <i>m/z</i>	First Blast result
ALPPRER	838.489	TGFB1-p Big-h3
VIGTNRK	787.474	TGFB1-p Big-h3
IPSETLNR	929.508	TGFB1-p Big-h3
DGTPPIDAHTR	1179.579	TGFB1-p Big-h3
LTLLAPLNSVFK	1315.802	TGFB1-p Big-h3

Peptide ALPPRER (m/z 838.489)

ALPPRER	838.4894	-0.923	549-555	1
Job Title	Protein Sequence			
RID	ZUSC47SN013	Search expires on 01-13 15:44 pm		Download All 
Program	BLASTP 	Citation 		
Database	swissprot	See details 		
Query ID	Ic Query_45689			
Description	None			
Molecule type	amino acid			
Query Length	7			
Other reports	Distance tree of results Multiple alignment MSA viewer 			

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Percent Identity

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Query Coverage

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Descriptions	Graphic Summary	Alignments	Taxonomy					
Sequences producing significant alignments								
Download ▼ New Select columns ▼ Show 100 ▼ ?								
<input checked="" type="checkbox"/> select all 100 sequences selected								
GenPept Graphics Distance tree of results Multiple alignment New MSA Viewer								
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> RecName: Full=Transforming growth factor-beta-induced protein Ig-h3; Short=Beta Ig-h3; AltName: Full=Kerato-epitheli... Homo sapiens	Homo sapiens	25.7	25.7	100%	0.075	100.00%	683	Q15582.1
<input checked="" type="checkbox"/> RecName: Full=AP-5 complex subunit zeta-1; AltName: Full=Adaptor-related protein complex 5 zeta subunit; Short=Zet... Homo sapiens	Homo sapiens	23.1	23.1	85%	0.62	100.00%	807	Q43299.2
<input checked="" type="checkbox"/> RecName: Full=BTB/POZ domain-containing protein KCID7 [Homo sapiens]	Homo sapiens	23.1	23.1	85%	0.62	100.00%	289	Q96MP8.1
<input checked="" type="checkbox"/> RecName: Full=Vertnin [Homo sapiens]	Homo sapiens	22.3	22.3	85%	1.2	100.00%	702	Q9H8Y1.1
<input checked="" type="checkbox"/> RecName: Full=Endoplasmic reticulum-Golgi intermediate compartment protein 2 [Homo sapiens]	Homo sapiens	22.3	22.3	85%	1.2	100.00%	377	Q96RQ1.2
<input checked="" type="checkbox"/> RecName: Full=Forkhead box protein D4-like 3; Short=FOXO4-like 3 [Homo sapiens]	Homo sapiens	21.4	33.9	100%	2.5	85.71%	417	Q6VB84.2
<input checked="" type="checkbox"/> RecName: Full=Forkhead box protein D4-like 6; Short=FOXO4-like 6 [Homo sapiens]	Homo sapiens	21.4	33.9	100%	2.5	85.71%	417	Q3SYB3.2
<input checked="" type="checkbox"/> RecName: Full=Forkhead box protein D4-like 5; Short=FOXO4-like 5 [Homo sapiens]	Homo sapiens	21.4	33.9	100%	2.5	85.71%	416	Q5VV16.1
<input checked="" type="checkbox"/> RecName: Full=Forkhead box protein D4-like 4; Short=FOXO4-like 4; AltName: Full=Forkhead box protein D4-like 2; Alt... Homo sapiens	Homo sapiens	21.4	33.9	100%	2.5	85.71%	416	Q8WXT5.2

Peptide VIGTNRK (m/z 787.474)

VIGTNRK 787.478 787.474 0.004 5.07 TGFB1*

Job Title	Protein Sequence
RID	ZUSBCXSS016 <small>Search expires on 01-13 15:44 pm</small> Download All ▼
Program	BLASTP Citation ▼
Database	swissprot See details ▼
Query ID	lcl Query_21095
Description	None
Molecule type	amino acid
Query Length	7
Other reports	Distance tree of results Multiple alignment MSA viewer ?

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Query Coverage to

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Descriptions	Graphic Summary	Alignments	Taxonomy					
Sequences producing significant alignments								
Download New Select columns Show 100 ?								
<input checked="" type="checkbox"/> select all 100 sequences selected GenPept Graphics Distance tree of results Multiple alignment New MSA Viewer								
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> RecName: Full=Transforming growth factor-beta-induced protein ig-h3; Short=Beta ig-h3; AltName: Full=Kerato-s...	Homo sapiens	24.8	24.8	100%	0.15	100.00%	683	Q15582.1
<input checked="" type="checkbox"/> RecName: Full=Kinesin-like protein KIFC1; AltName: Full=Kinesin-like protein 2; AltName: Full=Kinesin-related pr...	Homo sapiens	19.7	19.7	100%	10	70.00%	673	Q9BW19.2
<input checked="" type="checkbox"/> RecName: Full=Ankyrin repeat domain-containing protein 10 [Homo sapiens]	Homo sapiens	19.3	19.3	85%	15	83.33%	420	Q9NXR5.2
<input checked="" type="checkbox"/> RecName: Full=Coiled-coil domain-containing protein 168 [Homo sapiens]	Homo sapiens	18.9	18.9	71%	21	100.00%	2452	Q8NDH2.2
<input checked="" type="checkbox"/> RecName: Full=Clathrin heavy chain 1; AltName: Full=Clathrin heavy chain on chromosome 17; Short=CLH-17 [H...	Homo sapiens	18.5	18.5	100%	30	71.43%	1675	Q00610.5
<input checked="" type="checkbox"/> RecName: Full=DDP1- and CUL4-associated factor 1; AltName: Full=HIV-1 Vpr-binding protein; Short=VprBP; Alt...	Homo sapiens	18.5	33.5	71%	30	100.00%	1507	Q9Y4B6.3
<input checked="" type="checkbox"/> RecName: Full=Disintegrin and metalloproteinase domain-containing protein 12; Short=ADAM 12; AltName: Full=...	Homo sapiens	18.5	18.5	71%	30	100.00%	909	Q43184.3
<input checked="" type="checkbox"/> RecName: Full=Cytochrome P450 2U1; AltName: Full=Long-chain fatty acid omega-monooxygenase [Homo sapie...	Homo sapiens	18.5	18.5	85%	30	83.33%	544	Q7Z449.1
<input checked="" type="checkbox"/> RecName: Full=Lysophosphatidic acid receptor 4; Short=LPA receptor 4; Short=LPA-4; AltName: Full=G-protein c...	Homo sapiens	18.5	18.5	85%	30	83.33%	370	Q99677.1

Peptide IPSETLNR (m/z= 929.508)

IPSETLNR 929.505 929.508 0.003 3.23 TGFB1

Job Title	Protein Sequence
RID	ZUS2E8DX013 <small>Search expires on 01-13 15:39 pm</small> Download All ▼
Program	BLASTP Citation ▼
Database	swissprot See details ▼
Query ID	lcl Query_54440
Description	None
Molecule type	amino acid
Query Length	7
Other reports	Distance tree of results Multiple alignment MSA viewer ?

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Descriptions	Graphic Summary	Alignments	Taxonomy					
Sequences producing significant alignments								
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<input checked="" type="checkbox"/> select all 100 sequences selected GenPept Graphics Distance tree of results Multiple alignment New MSA Viewer								
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> RecName: Full=Transforming growth factor-beta-induced protein ig-h3; Short=Beta ig-h3; AltName: Full=Kerato-epitheli... Homo sapiens	Homo sapiens	25.7	25.7	100%	0.075	100.00%	683	Q15582.1
<input checked="" type="checkbox"/> RecName: Full=AP-5 complex subunit zeta-1; AltName: Full=Adaptor-related protein complex 5 zeta subunit; Short=Zet... Homo sapiens	Homo sapiens	23.1	23.1	85%	0.62	100.00%	807	Q43299.2
<input checked="" type="checkbox"/> RecName: Full=BTB/POZ domain-containing protein KCTD7 [Homo sapiens] Homo sapiens	Homo sapiens	23.1	23.1	85%	0.62	100.00%	289	Q96MP8.1
<input checked="" type="checkbox"/> RecName: Full=Vertnin [Homo sapiens] Homo sapiens	Homo sapiens	22.3	22.3	85%	1.2	100.00%	702	Q9H8Y1.1
<input checked="" type="checkbox"/> RecName: Full=Endoplasmic reticulum-Golgi intermediate compartment protein 2 [Homo sapiens] Homo sapiens	Homo sapiens	22.3	22.3	85%	1.2	100.00%	377	Q96RQ1.2
<input checked="" type="checkbox"/> RecName: Full=Forkhead box protein D4-like 3; Short=FOXD4-like 3 [Homo sapiens] Homo sapiens	Homo sapiens	21.4	33.9	100%	2.5	85.71%	417	Q6VB84.2
<input checked="" type="checkbox"/> RecName: Full=Forkhead box protein D4-like 6; Short=FOXD4-like 6 [Homo sapiens] Homo sapiens	Homo sapiens	21.4	33.9	100%	2.5	85.71%	417	Q3SYB3.2
<input checked="" type="checkbox"/> RecName: Full=Forkhead box protein D4-like 5; Short=FOXD4-like 5 [Homo sapiens] Homo sapiens	Homo sapiens	21.4	33.9	100%	2.5	85.71%	416	Q5VY16.1
<input checked="" type="checkbox"/> RecName: Full=Forkhead box protein D4-like 4; Short=FOXD4-like 4; AltName: Full=Forkhead box protein D4-like 2; Alt... Homo sapiens	Homo sapiens	21.4	33.9	100%	2.5	85.71%	416	Q8WXT5.2
<input checked="" type="checkbox"/> RecName: Full=SH3 domain-containing kinase-binding protein 1; AltName: Full=CD2-binding protein 3; Short=CD2BP3... Homo sapiens	Homo sapiens	21.0	21.0	100%	3.6	77.78%	665	Q96B97.2
<input checked="" type="checkbox"/> RecName: Full=Exocyst complex component 3-like protein 4 [Homo sapiens] Homo sapiens	Homo sapiens	20.6	20.6	100%	5.1	85.71%	722	Q17RC7.2

Peptide DGTTPIDAHTR (m/z = 1179.579)

DGTTPIDAHTR 1179.575 1179.579 0.004 3.39

TGFBI

Job Title	Protein Sequence
RID	ZUS6RYW8013 Search expires on 01-13 15:41 pm Download All ▼
Program	BLASTP ? Citation ▼
Database	swissprot See details ▼
Query ID	lcl Query_59003
Description	None
Molecule type	amino acid
Query Length	11
Other reports	Distance tree of results Multiple alignment MSA viewer ?

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Sequences producing significant alignments									
Download ▼ New Select columns ▼ Show 100 ▼ ?									
<input checked="" type="checkbox"/> select all 100 sequences selected GenPept Graphics Distance tree of results Multiple alignment New MSA Viewer									
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	RecName: Full=Transforming growth factor-beta-induced protein ig-h3; Short=Beta ig-h3; AltName: Full=Kerato-epith...	Homo sapiens	38.4	38.4	100%	5e-06	100.00%	683	Q15582.1
<input checked="" type="checkbox"/>	RecName: Full=Nesprin-2; AltName: Full=KASH domain-containing protein 2; Short=KASH2; AltName: Full=Nuclear...	Homo sapiens	21.0	21.0	72%	8.7	75.00%	6885	Q8WXH0.3
<input checked="" type="checkbox"/>	RecName: Full=Zinc finger protein 469 [Homo sapiens]	Homo sapiens	21.0	30.5	90%	8.7	75.00%	3925	Q96JG9.3
<input checked="" type="checkbox"/>	RecName: Full=Protocadherin-16; AltName: Full=Cadherin-19; AltName: Full=Cadherin-25; AltName: Full=Fibroblast...	Homo sapiens	21.0	98.0	90%	8.7	70.00%	3298	Q96JQ0.1
<input checked="" type="checkbox"/>	RecName: Full=Hermansky-Pudlak syndrome 1 protein [Homo sapiens]	Homo sapiens	21.0	21.0	63%	8.7	85.71%	700	Q92902.2
<input checked="" type="checkbox"/>	RecName: Full=NACHT domain- and WD repeat-containing protein 1 [Homo sapiens]	Homo sapiens	20.6	30.1	72%	12	63.64%	1564	Q149M9.3
<input checked="" type="checkbox"/>	RecName: Full=Transmembrane protein 232 [Homo sapiens]	Homo sapiens	20.6	20.6	54%	12	83.33%	657	C9JQI7.2
<input checked="" type="checkbox"/>	RecName: Full=P antigen family member 4; Short=PAGE-4; AltName: Full=G antigen family C member 1; AltName: ...	Homo sapiens	20.6	20.6	63%	12	71.43%	102	Q60829.1
<input checked="" type="checkbox"/>	RecName: Full=Tubulinyl-Tyr carboxypeptidase 2; AltName: Full=Vasohibin-2; AltName: Full=Vasohibin-like protein [...]	Homo sapiens	20.2	20.2	54%	18	83.33%	355	Q86V25.2

Peptide LTLLAPLNSVFK (m/z= 1315.802)

LTLLAPLNSVFK 1315.798 1315.802 0.004 3.04

TGFBI

Job Title	Protein Sequence
RID	ZUS6B3EG013 Search expires on 01-13 15:41 pm Download All ▼
Program	BLASTP ? Citation ▼
Database	swissprot See details ▼
Query ID	lcl Query_49253
Description	None
Molecule type	amino acid
Query Length	12
Other reports	Distance tree of results Multiple alignment MSA viewer ?

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Organism

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Percent Identity

to

E value

to

Query Coverage

to

Filter

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- Descriptions
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- Alignments
- Taxonomy

Sequences producing significant alignments									
Download ▼ New Select columns ▼ Show 100 ▼ ?									
<input checked="" type="checkbox"/> select all 100 sequences selected GenPept Graphics Distance tree of results Multiple alignment New MSA Viewer									
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	RecName: Full=Transforming growth factor-beta-induced protein ig-h3; Short=Beta ig-h3; AltName: Full=Kerato-epithell...	Homo sapiens	39.7	59.4	100%	2e-06	100.00%	683	Q15582.1
<input checked="" type="checkbox"/>	RecName: Full=Perlestin; Short=PN; AltName: Full=Osteoblast-specific factor 2; Short=OSF-2; Flags: Precursor (Homo...	Homo sapiens	23.5	65.3	91%	1.3	70.00%	836	Q15063.2
<input checked="" type="checkbox"/>	RecName: Full=Monocarboxylate transporter 1; Short=MCT1; AltName: Full=Solute carrier family 16 member 1 (Homo...	Homo sapiens	23.1	51.5	75%	1.8	87.50%	500	P53985.3
<input checked="" type="checkbox"/>	RecName: Full=Protein BANP; AltName: Full=BEN domain-containing protein 1; AltName: Full=Btg3-associated nuclea...	Homo sapiens	22.7	37.8	100%	2.6	80.00%	519	Q8N9N5.3
<input checked="" type="checkbox"/>	RecName: Full=Zinc finger CCH domain-containing protein 7B; AltName: Full=Rotavirus 'X'-associated non-structural...	Homo sapiens	22.3	22.3	75%	3.7	77.78%	977	Q9UGR2.2
<input checked="" type="checkbox"/>	RecName: Full=Fc receptor-like protein 2; Short=FcR-like protein 2; Short=FcRL2; AltName: Full=Fc receptor homolog...	Homo sapiens	22.3	37.8	100%	3.7	72.73%	508	Q96LA5.1
<input checked="" type="checkbox"/>	RecName: Full=Vitamin K-dependent protein C; AltName: Full=Anticoagulant protein C; AltName: Full=Autoproteohrombin...	Homo sapiens	22.3	22.3	58%	3.7	85.71%	461	P04070.1
<input checked="" type="checkbox"/>	RecName: Full=Vasoactive intestinal polypeptide receptor 2; Short=VIP-R-2; AltName: Full=Helodermin-preferring VIP r...	Homo sapiens	22.3	35.6	83%	3.7	66.67%	438	P41587.2
<input checked="" type="checkbox"/>	RecName: Full=Serine/arginine-rich splicing factor 11; AltName: Full=Arginine-rich 54 kDa nuclear protein; Short=p54...	Homo sapiens	21.8	21.8	83%	5.2	70.00%	484	Q05519.1
<input checked="" type="checkbox"/>	RecName: Full=Alpha-2-HS-glycoprotein; AltName: Full=Alpha-2-Z-globulin; AltName: Full=Ba-alpha-2-glycoprotein; Alt...	Homo sapiens	21.4	21.4	50%	7.5	100.00%	367	P02765.2
<input checked="" type="checkbox"/>	RecName: Full=Keratin_type II cytoskeletal 72; AltName: Full=Cytokeratin-72; Short=CK-72; AltName: Full=Keratin-72...	Homo sapiens	21.4	21.4	50%	7.5	100.00%	511	Q14CN4.2

1. Venkatraman, A., et al., *Matrix-Assisted Laser Desorption Ionization Mass Spectrometry Imaging of Key Proteins in Corneal Samples from Lattice Dystrophy Patients with TGFBI-H626R and TGFBI-R124C Mutations*. *Proteomics Clin Appl*, 2019. **13**(1): p. e1800053.