

## 7 Appendix

### 7.1 Genetic classification of human mitochondrial disorders

Type of disorder	Inheritance pattern
<b>Mitochondrial genetic disorders*</b>	
Rearrangements (large scale partial deletions and duplications)	
Chronic progressive external ophthalmoplegia (CPEO)	S
Kearns-Sayre syndrome	S
Diabetes and deafness	S
Pearson marrow-pancreas syndrome	S
Sporadic tubulopathy	S
Point mutations	
Protein encoding genes	
• LHON (G11778A, T14484C, G3460A)	M
• NARP/Leigh syndrome (T8993G/C)	M
tRNA genes	
• MELAS (A3243G, T3271C, A3251G)	M
• MERRF (A8344G, T8356C)	M
• CPEO (A3243G, T4274C)	M
• Myopathy (T14709C, A12320G)	M
• Cardiomyopathy (A3243G, A4269G, A4300G)	M
• Diabetes and deafness (A3243G, C12258A)	M
• Encephalomyopathy (G1606A, T10010C)	M
rRNA genes	
• Non-syndromic sensorineural deafness (A7445G)	M
• Aminoglycoside induced non-syndromic deafness (A1555G)	M
<b>Nuclear genetic disorders</b>	
<b>Disorders of mtDNA maintenance</b>	
Autosomal dominant progressive external ophthalmoplegia (with 2° multiple mtDNA deletions)	
• Mutations in adenine nucleotide translocator (ANT1)	AD
• Mutations in DNA polymerase g (POLG)	AD or AR
• Mutations in Twinkle helicase (C10orf2)	AD
Mitochondrial neuro-gastrointestinal encephalomyopathy (with 2° multiple mtDNA deletions)	
• Mutations in thymidine phosphorylase (TP)	AR
Myopathy with mtDNA depletion	
• Mutations in thymidine kinase (TK2)	AR
Encephalopathy with liver failure	
• Mutations in deoxyguanosine kinase (DGK)	AR
<b>Primary disorders of the respiratory chain</b>	
Leigh syndrome	
• Complex I deficiency: mutations in complex I subunits (NDUFS2, 4, 7, 8, and NDUFV1)	AR
• Complex II deficiency: mutations in complex II flavoprotein subunit (SDH)	AR
Leukodystrophy and myoclonic epilepsy	
• Complex I deficiency: mutations in complex I subunit (NDUFV1)	AR
Cardioencephalomyopathy	
• Complex I deficiency: mutations in complex I subunit (NDUFS2)	AR
Optic atrophy and ataxia	
• Complex II deficiency: mutations in complex II flavoprotein subunit (SDH)	AD
<b>Disorders of mitochondrial protein import</b>	
Dystonia-deafness	
• Mutations in deafness-dystonia protein DDP1 (TIMM8A)	XLR
<b>Disorders of assembly of the respiratory chain</b>	
Leigh syndrome	
• Complex IV deficiency: mutations in COX assembly protein (SURF1)	AR
• Complex IV deficiency: mutations in COX assembly protein (COX10)	AR
Cardioencephalomyopathy	
• Complex IV deficiency: mutations in COX assembly protein (SCO2)	AR
Hepatic failure and encephalopathy	
• Complex IV deficiency: mutations in COX assembly protein (SCO1)	AR
• Complex IV deficiency: mutations in protein affecting COX mRNA stability (LRPPRC)	AR
Tubulopathy, encephalopathy, and liver failure	
• Complex III deficiency: mutations in complex III assembly (BCS1L)	AR

\*mtDNA nucleotide positions refer to the L-chain, and are taken from the standard Cambridge reference sequence. AD, autosomal dominant; AR, autosomal recessive; M, maternal; S, sporadic; XLR, X linked recessive.

## 7.2 Details of the clones generated for Y2H screening.

Clone	Forward Primer	Reverse primer	Y2H Vectors	Restriction sites
OPA1: 80-187	5' ggc <b>tcg agt</b> ggc tac cag cct cgc agg aat 3'	5' cta aga acc tgaggt aaa aaa gtc c 3'	pBTM118b, pGAD427b	Xho I/ Not I
OPA1: 80-290	5' ggc <b>tcg agt</b> ggc tac cag cct cgc agg aat 3'	5' caa caa cct gtg gca gat gat 3'	pBTM118b, pGAD427b	Xho I/ Not I
OPA1: 80-520	5' ggc <b>tcg agt</b> ggc tac cag cct cgc agg aat 3'	5' ggc <b>ccg ggt</b> tat ttc tcc tga tga aga gct tc 3'	pBTM118b, pGAD427b	Xho I/ Not I
OPA1: 520-905	5' <b>gtc gac</b> ata aga gaa tat gaa gaa gag 3'	5' ctc taa tca cct aac ttc 3'	pBTM118c, pGAD428c	Sal I/ Not I
OPA1: 520-960	5' <b>gtc gac</b> ata aga gaa tat gaa gaa gag 3'	5' ggc <b>ccg ggt</b> tat ttc tcc tga tga aga gct tc 3'	pBTM118c, pGAD428c	Sal I/ Not I
OPA1: 880-960	5' <b>gtc gac</b> cgt ata cag cgc atg ctt gct 3'	5' ggc <b>ccg ggt</b> tat ttc tcc tga tga aga gct tc 3'	pBTM118c, pGAD428c	Sal I/ Not I

## 7.3 Details of the clones generated for prokaryotic expression

Clone	Forward Primer	Reverse primer	Expression Vectors	Restriction sites
OPA1: 111-960	5' <b>cgg atc</b> cgg cta cac agc caa aaa gac 3'	5' gcc <b>cgg gct</b> att ctt cat att etc tta tag 3'	pGEX-2T	Bam HI/ Sma I
OPA1: 111-520	5' <b>cgg atc</b> cgg cta cac agc caa aaa gac 3'	5' ggc <b>ccg ggt</b> tat ttc tcc tga tga aga gct tc 3'	pGEX-2T	Bam HI/ Sma I
OPA1: 880-960	5' <b>cgg atc</b> ccg tat aca gcg cat gct tgc 3'	5' ggc <b>ccg ggt</b> tat ttc tcc tga tga aga gct tc 3'	pET-43.1a	Bam HI/ Sma I

## 7.4 Peptides identified by MS/MS analysis

### Band 1

#### Heart -Trypsin digest

Start-End	Observed	Mr (expt)	Mr (Calc)	Delta in mass	Miss	Sequence
102 - 116	735.36	1468.7	1468.79	-0.1	0	R.YIILGSAVGGGYTAK.K (Ions score 63)
181 - 194	751.8	1501.59	1501.68	-0.1	0	K.DFFTAGSPGETAFR.A (Ions score 41)
231 - 243	701.78	1401.54	1401.65	-0.11	0	R.AAGQYSTSYAQK.R (Ions score 49)
532 - 542	563.28	1124.55	1124.62	-0.07	0	K.ALGYFAVVTGK.G (Ions score 51)
595 - 605	634.26	1266.5	1266.57	-0.07	0	R.ESVEQQADSFK.A (Ions score 59)
609 - 616	533.73	1065.45	1065.51	-0.07	0	R.FNLETEWK.N (Ions score 31)
624 - 633	646.78	1291.56	1291.64	-0.09	1	R.ELDRNELFEK.A (Ions score 19)
751 - 760	626.74	1251.47	1251.55	-0.09	0	K.WNDFAEEDSLR.V (Ions score 61)
761 - 770	597.77	1193.53	1193.62	-0.08	0	R.VIQHNALED.R.S (Ions score 73)
872 - 879	552.73	1103.44	1103.51	-0.08	0	K.DTWHQVYR.R (Ions score 39)
949 - 960	690.77	1379.52	1379.61	-0.09	0	K.EVLEDFAEEDGK.K (Ions score 65)

#### Kidney -Trypsin digest

181 - 194	751.93	1501.85	1501.68	0.16	0	K.DFFTAGSPGETAFR.A ( 53)
195 - 207	501.63	1501.88	1501.65	0.22	1	R.ATDHGSESDKHYR.K ( 38)
209 - 229	816.49	2446.46	2446.27	0.19	0	K.GLLGELILLQQIQEHEEEAR.R De (NQ) ( 39)
231 - 243	702.02	1402.03	1401.65	0.38	0	R.AAGQYSTSYAQK.R ( 61)
252 - 265	855.11	1708.21	1707.9	0.3	0	K.IDQLQEELLHTQLK.Y De (NQ) ( 54)
328 - 338	529.93	1057.85	1057.58	0.27	0	R.VVVVGDQSAGK.T ( 49)
339 - 349	617.99	1233.97	1233.64	0.33	0	K.TSVLEMIAQAR.I (M) ( 58)
354 - 361	434.77	867.52	867.36	0.17	0	R.GSGEMMTR.S ( 45)
410 - 424	824.61	1647.21	1646.82	0.39	0	K.EGCTVSPETISLNVK.G (C) ( 37)
431 - 452	753.84	2258.51	2258.15	0.35	0	R.MVLVDLPGVINTVTSGMAPDTK.E De (NQ) ( 58)
483 - 497	828.1	1654.19	1653.81	0.37	0	R.SIVTDLVSQMDPHGR.R ( 75)
532 - 542	563.46	1124.9	1124.62	0.28	0	K.ALGYFAVVTGK.G ( 79)
543 - 553	581.95	1161.89	1161.56	0.33	0	K.GNSSESIEAIR.E ( 65)
595 - 605	634.37	1266.73	1266.57	0.16	0	R.ESVEQQADSFK.A ( 64)
609 - 616	534.35	1066.69	1066.5	0.19	0	R.FNLETEWK.N De (NQ) ( 25)
636 - 651	595.86	1784.55	1784.94	-0.39	0	K.NEILDEVISLSQVTPK.H De (NQ) ( 31)
652 - 664	585.37	1753.09	1752.86	0.24	0	K.HWEEILQQLWER.V ( 23)
706 - 720	598.73	1793.18	1792.86	0.32	0	K.AVEVAVETLQEEFSR.F ( 37)
739 - 747	516.85	1031.68	1031.55	0.13	1	K.EAVKEESIK.R ( 28)
751 - 760	626.91	1251.8	1251.55	0.25	0	K.WNDFAEEDSLR.V ( 58)
761 - 770	597.98	1193.95	1193.62	0.34	0	R.VIQHNALED.R.S ( 82)
771 - 792	862.98	2585.92	2586.21	-0.29	1	R.SISDKQQWDAIYFMEEALQGR.L De (NQ) ( 65)
793 - 809	987.66	1973.3	1972.96	0.34	1	R.LKDTENAIENMIGPDWK.K ( 47)
819 - 829	687.34	1372.67	1372.6	0.06	0	R.TQEQCVHNETK.N (C) ( 43)
838 - 855	677.76	2030.26	2029.96	0.3	0	K.VNDEHPAYLASDEITTVR.K De (NQ) ( 45)
872 - 879	552.89	1103.77	1103.51	0.25	0	K.DTWHQVYR.R ( 40)
903 - 919	727.47	2179.38	2179	0.38	0	R.HFIDSELECNDVVLFWR.I (C); De (NQ) ( 57)

Start-End	Observed	Mr (expt)	Mr (Calc)	Delta in mass	Miss	Sequence
949 - 961	755.04	1508.07	1507.7	0.36	1	K.EVLEDFEAEDGEKK.V ( 22)
970 - 978	522.41	1042.8	1042.6	0.2	1	R.VQLAEDLKK.V ( 31)
979 - 985	451.43	900.85	900.5	0.34	1	K.VREIQEK.L ( 21)

**Band-2****Brain -Trypsin digest**

102 - 116	735.39	1468.76	1468.79	-0.03	0	R.YIILGSAVGGGYTAK.K (Ions score 23)
155 - 171	871.41	1740.81	1740.88	-0.07	0	K.ALPSSEDLASLAPDLK.I (Ions score 80)
155 - 180	909.51	2725.51	2725.46	0.04	0	K.ALPSSEDLASLAPDLKITESLSLLK.D (Ions score 43)
157 - 180	848.1	2541.29	2541.34	-0.06	0	L.PSSEDLASLAPDLKITESLSLLK.D (Ions score 65)
181 - 194	751.83	1501.64	1501.68	-0.04	0	K.DFFTAGSPGETAFR.A (Ions score 42)
215 - 228	854.4	1706.79	1706.92	-0.13	0	K.IDQLQEELLHTQLK.Y (Ions score 80)
302 - 312	609.82	1217.63	1217.64	-0.02	0	K.TSVLEMIAQAR.I (Ions score 74)
347 - 360	825.39	1648.78	1648.83	-0.06	0	R.EFDLTKEEDLAALR.H (Ions score 80)
349 - 360	687.35	1372.68	1372.72	-0.03	0	F.DLTKEEDLAALR.H (Ions score 86)
446 - 460	827.89	1653.76	1653.81	-0.05	0	R.SIVTDLVSQMDPHGR.R (Ions score 73)
506 - 516	581.78	1161.54	1161.56	-0.02	0	K.GNSSESIEAIR.E (Ions score 83)
517 - 527	725.3	1448.59	1448.61	-0.02	0	R.EYEEFFQNSK.L (Ions score 67)
558 - 568	634.28	1266.55	1266.57	-0.03	0	R.ESVEQQADSFK.A (Ions score 67)
587 - 596	646.81	1291.61	1291.64	-0.03	0	R.ELDRNELFEK.A (Ions score 41)
597 - 614	992.51	1983	1983.09	-0.09	0	K.AKNEILDEVISLSQVTPK.H (Ions score 101)
599 - 614	892.95	1783.88	1783.96	-0.07	0	K.NEILDEVISLSQVTPK.H (Ions score 113)
615 - 627	877.41	1752.8	1752.86	-0.05	0	K.HWEEILQQSLWER.V (Ions score 72)
628 - 645	1000.98	1999.94	2000	-0.06	0	R.VSTHVIENIYLPAAQTMN.S (Ions score 49)
669 - 683	897.41	1792.81	1792.86	-0.05	0	K.AVEVAWETLQEEFSR.F (Ions score 53)
714 - 723	626.78	1251.54	1251.55	-0.01	0	K.WNDFEAEDSLR.V (Ions score 45)
724 - 733	597.81	1193.61	1193.62	-0.01	0	R.VIQHNALED.R.S (Ions score 83)
739 - 755	1028.43	2054.84	2054.95	-0.11	0	K.QQWDAAIYFMEEALQGR.L (Ions score 16)
756 - 772	987.46	1972.9	1972.96	-0.06	0	R.LKDTENAIENMIGPDWK.K (Ions score 76)
758 - 772	866.86	1731.71	1731.78	-0.07	0	K.DTENAIENMIGPDWK.K (Ions score 78)
801 - 818	677.32	2028.93	2028.98	-0.05	0	K.VNDEHPAYLASDEITTVR.K (Ions score 71)
835 - 842	552.76	1103.51	1103.51	-0.01	0	K.DTWHQVYR.R (Ions score 37)
912 - 923	690.82	1379.62	1379.61	0.01	0	K.EVLEDFEAEDGEK.K (Ions score 68)
949 - 960	707.35	1412.69	1412.73	-0.04	0	K.LDAFIEALHQEK.- (Ions score 79)

**Brain -Glu-C digest**

175 - 190	834.83	1667.65	1667.84	-0.19	1	E.SLSLLKDFFTAGSPGE.T (Ions score 43)
307 - 320	511.54	1531.59	1531.79	-0.21	0	E.MIAQARIFPRGSGE.M (Ions score 10)
348 - 355	498.66	995.31	995.44	-0.14	3	E.FDLTKEED.L (Ions score 30)
559 - 575	657.24	1968.71	1968.95	-0.24	2	E.SVEQQADSFKATRFNLE.T (Ions score 38)
576 - 587	535.86	1604.57	1604.81	-0.24	1	E.TEWKNNYPRLE.L (Ions score 15)
588 - 595	518.18	1034.35	1034.5	-0.15	2	E.LDRNELFEK.K (Ions score 33)
605 - 618	551.54	1651.59	1651.86	-0.27	1	E.VISLSQVTPKHWEI.I (Ions score 25)
627 - 634	470.7	939.38	939.51	-0.14	0	E.RVSTHVIE.N (Ions score 30)
814 - 822	537.24	1072.47	1072.62	-0.16	0	E.ITTVRKNLE.S (Ions score 35)

Start-End	Observed	Mr (expt)	Mr (Calc)	Delta in mass	Miss	Sequence
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**Heart -Trypsin digest**

102 - 116	735.37	1468.73	1468.79	-0.06	0	R.YIILGSAVGGGYTAK.K (Ions score 52)
181 - 194	751.82	1501.62	1501.68	-0.06	0	K.DFFTAGSPGETAFR.A (Ions score 63)
291 - 301	529.77	1057.53	1057.58	-0.05	0	R.VVVVGDQSAGK.T (Ions score 56)
495 - 505	563.29	1124.57	1124.62	-0.05	0	K.ALGYFAVVTGK.G (Ions score 51)
558 - 568	634.26	1266.51	1266.57	-0.07	0	R.ESVEQQADSFK.A (Ions score 71)
572 - 579	533.74	1065.47	1065.51	-0.04	0	R.FNLETEWK.N (Ions score 45)
712 - 723	506.55	1516.64	1516.71	-0.07	1	R.HKWNDFAEDSLR.V (Ions score 42)
714 - 723	626.76	1251.5	1251.55	-0.05	0	K.WNDFAEDSLR.V (Ions score 54)
724 - 733	597.79	1193.56	1193.62	-0.06	0	R.VIQHNALED.R.S (Ions score 65)
801 - 819	719.98	2156.93	2157.07	-0.14	1	K.VNDEHPAYLASDEITTVRK.N (score 61)
835 - 842	552.74	1103.46	1103.51	-0.06	0	K.DTWHQVYR.R (Ions score 26)
858 - 865	576.75	1151.49	1151.55	-0.06	1	R.RGFYYYQR.H (Ions score 29)
949 - 960	707.34	1412.66	1412.73	-0.07	0	K.LDAFIEALHQEK.- (Ions score 47)

**Liver -Trypsin digest**

102 - 116	735.38	1468.75	1468.79	-0.04	0	R.YIILGSAVGGGYTAK.K (Ions score 55)
181 - 194	751.81	1501.61	1501.68	-0.08	0	K.DFFTAGSPGETAFR.A (Ions score 58)
495 - 505	563.3	1124.58	1124.62	-0.04	0	K.ALGYFAVVTGK.G (Ions score 50)
558 - 568	634.27	1266.52	1266.57	-0.05	0	R.ESVEQQADSFK.A (Ions score 69)
572 - 579	533.75	1065.48	1065.51	-0.03	0	R.FNLETEWK.N (Ions score 35)
714 - 723	626.76	1251.52	1251.55	-0.04	0	K.WNDFAEDSLR.V (Ions score 54)
801 - 818	677.31	2028.92	2028.98	-0.06	0	K.VNDEHPAYLASDEITTVR.K (Ions score 77)
825 - 834	528.78	1055.55	1055.59	-0.04	0	R.GVEVDPSLIK.D (Ions score 44)
835 - 842	552.75	1103.48	1103.51	-0.03	0	K.DTWHQVYR.R (Ions score 28)
858 - 865	576.77	1151.52	1151.55	-0.03	1	R.RGFYYYQR.H (Ions score 25)
859 - 865	498.72	995.43	995.45	-0.02	0	R.GFYFYQR.H (Ions score 9)
912 - 923	690.79	1379.56	1379.61	-0.05	0	K.EVLEDFEAEDGEK.K (Ions score 68)

**Kidney -Glu-C digest**

175 - 190	834.88	1667.75	1667.84	-0.09	1	E.SLSLLKDFFTAGSPGE.T (Ions score 49)
605 - 618	551.59	1651.75	1651.86	-0.1	1	E.VISLSQVTPKHWEI.I (Ions score 17)

**Kidney -Trypsin digest**

159 - 171	751.94	1501.86	1501.65	0.21	1	R.ATDHGSESDKHYR.K ( 61)
216 - 229	570.09	1707.25	1706.92	0.33	0	K.IDQLQEELLHTQLK.Y ( 35)
292 - 302	529.96	1057.9	1057.58	0.32	0	R.VVVVGDQSAGK.T ( 46)
303 - 313	610.01	1218.01	1217.64	0.36	0	K.TSVLEMIAQAR.I ( 74)
318 - 325	434.8	867.58	867.36	0.22	0	R.GSGEMMTR.S ( 45)
354 - 361	458.68	915.35	915.47	-0.12	0	K.EEDLAALR.H ( 55)
395 - 416	1137.74	2273.47	2273.16	0.3	0	R.MVLVDLPGVINTVTSGMAPDTK.E (M) ( 21)
425 - 446	832.62	2494.84	2495.13	-0.29	0	K.AYMQNPNAIILCIQDGSVDAER.S (C); 2 De (NQ); (M) ( 89)
447 - 461	828.27	1654.52	1654.8	-0.28	0	R.SIVTDLVSQMDPHGR.R De (NQ) ( 26)
483 - 490	464.63	927.24	927.54	-0.3	0	R.IQIIEGK.L ( 28)
544 - 555	727.43	1452.84	1452.71	0.13	0	R.NLSLAVSDCFWK.M (C) ( 46)

Start-End	Observed	Mr (expt)	Mr (Calc)	Delta in mass	Miss	Sequence
559 - 569	634.2	1266.38	1266.57	-0.19	0	R.ESVEQQADSFK.A (46)
573 - 580	534.12	1066.23	1066.5	-0.27	0	R.FNLETEWK.N De (NQ) (21)
598 - 615	993.18	1984.36	1984.07	0.28	1	K.AKNEILDEVISLSQVTPK.H De (NQ) (65)
600 - 615	893.64	1785.27	1784.94	0.33	0	K.NEILDEVISLSQVTPK.H De (NQ) (69)
616 - 628	877.62	1753.23	1752.86	0.37	0	K.HWEEILQQSLWER.V (54)
658 - 664	459.92	917.83	917.5	0.33	1	K.LKQWTDK.Q (32)
670 - 684	897.93	1793.84	1793.85	0	0	K.AVEVAVETLQEEFSR.F De (NQ) (23)
691 - 700	602.43	1202.84	1202.56	0.28	1	K.GKEHDDIFDK.L (56)
703 - 711	516.88	1031.75	1031.55	0.2	1	K.EAVKEESIK.R (44)
725 - 734	597.93	1193.84	1193.62	0.23	0	R.VIQHNALED.R.S (24)
735 - 756	863.27	2586.79	2587.19	-0.4	1	R.SISDKQQWDAAIYFMEEALQGR.L 2 De (NQ) (76)
740 - 756	686.1	2055.29	2054.95	0.34	0	K.QQWDAAIYFMEEALQGR.L (73)
757 - 773	659.01	1974.01	1973.94	0.07	1	R.LKDTENAIENMIGPDWK.K De (NQ) (35)
783 - 793	687.43	1372.84	1372.6	0.23	0	R.TQEQCVHNETK.N (C) (49)
802 - 819	1016.08	2030.15	2029.96	0.19	0	K.VNDEHPAYLASDEITTVR.K De (NQ) (44)
836 - 843	552.95	1103.88	1103.51	0.37	0	K.DTWHQVYR.R (37)
897 - 905	544.93	1087.85	1087.56	0.29	0	R.QQLTNTEVR.R (44)
913 - 925	755.05	1508.08	1507.7	0.37	1	K.EVLEDFEAEDGEKK.V (62)
934 - 942	522.46	1042.9	1042.6	0.29	1	R.VQLAEDLKK.V (40)
943 - 949	451.38	900.74	900.5	0.24	1	K.VREIQEK.L (28)
950 - 961	472.05	1413.13	1412.73	0.4	0	K.LDAFIEALHQEK. (21)

**Band-3****Heart -Trypsin digest**

195 - 207	701.8	1401.58	1401.65	-0.07	0	R.AAGQYSTSYAQQK.R (Ions score 60)
348 - 361	825.39	1648.76	1648.83	-0.07	1	R.EFDLTKEEDLAALR.H (Ions score 70)
496 - 506	563.3	1124.58	1124.62	-0.05	0	K.ALGYFAVVVTGK.G (Ions score 44)
559 - 569	634.26	1266.5	1266.57	-0.07	0	R.ESVEQQADSFK.A (Ions score 65)
573 - 580	533.74	1065.47	1065.51	-0.04	0	R.FNLETEWK.N (Ions score 38)
588 - 597	646.8	1291.58	1291.64	-0.06	1	R.ELDRNELFEK.A (Ions score 35)
670 - 684	897.41	1792.8	1792.86	-0.07	0	K.AVEVAVETLQEEFSR.F (Ions score 67)
715 - 724	626.75	1251.5	1251.55	-0.06	0	K.WNDFAEDSLR.V (Ions score 59)
725 - 734	597.79	1193.56	1193.62	-0.05	0	R.VIQHNALED.R.S (Ions score 60)
802 - 820	719.99	2156.96	2157.07	-0.11	1	K.VNDEHPAYLASDEITTVR.K.N (score 71)
826 - 835	528.78	1055.54	1055.59	-0.05	0	R.GVEVDPSLIK.D (Ions score 23)
836 - 843	552.74	1103.46	1103.51	-0.05	0	K.DTWHQVYR.R (Ions score 39)
859 - 866	576.76	1151.5	1151.55	-0.05	1	R.RGFYYYYQR.H (Ions score 29)
897 - 905	544.77	1087.52	1087.56	-0.04	0	R.QQLTNTEVR.R (Ions score 51)
913 - 924	690.77	1379.53	1379.61	-0.08	0	K.EVLEDFEAEDGEK.K (Ions score 82)
950 - 961	707.34	1412.66	1412.73	-0.07	0	K.LDAFIEALHQEK.- (Ions score 55)

**Liver -Trypsin digest**

291 - 301	529.78	1057.55	1057.58	-0.03	0	R.VVVVGDQSAGK.T (Ions score 64)
558 - 568	634.27	1266.52	1266.57	-0.05	0	R.ESVEQQADSFK.A (Ions score 39)
572 - 579	533.75	1065.49	1065.51	-0.02	0	R.FNLETEWK.N (Ions score 23)

Start-End	Observed	Mr (expt)	Mr (Calc)	Delta in mass	Miss	Sequence
714 - 723	626.77	1251.53	1251.55	-0.02	0	K.WNDFEAEDSLR.V (Ions score 39)
858 - 865	576.77	1151.53	1151.55	-0.02	1	R.RGFYYYQR.H (Ions score 12)
896 - 904	544.77	1087.53	1087.56	-0.03	0	R.QQLTNTTEVR.R (Ions score 57)
912 - 923	690.79	1379.56	1379.61	-0.04	0	K.EVLEDFEAEDGEK.K (Ions score 58)

**Kidney -Glu-C digest**

178 - 191	875.47	1748.92	1748.89	0.03	3	E.LILLQQQIQEHEEE.A (Ions score 86)
349 - 363	596.3	1785.88	1785.89	-0.01	4	E.FDLTKEEDLAALRHE.I (Ions score 63)
560 - 576	657.32	1968.95	1968.95	0	2	E.SVEQQADSFKATRFNLE.T (Ions score 36)
606 - 619	551.63	1651.86	1651.86	0	1	E.VISLSQVTPKHWEI.I (Ions score 46)
815 - 823	537.32	1072.63	1072.62	0	0	E.ITTVRKNLE.S (Ions score 26)

**Kidney -Trypsin digest**

195 - 207	751.82	1501.62	1501.65	-0.03	1	R.ATDHGSESDKHRYR.K ( 53)
209 - 229	816.1	2445.29	2445.29	0.01	0	K.GLLGELILLQQQIQEHEEEAR.R ( 45)
230 - 243	520.32	1557.95	1557.75	0.19	1	R.RAAGQYSTSYAQQR.R ( 40)
231 - 243	701.92	1401.82	1401.65	0.17	0	R.AAGQYSTSYAQQR.R ( 57)
250 - 265	655.69	1964.06	1964.06	0	1	K.EKIDQLQEELLHTQLK.Y ( 33)
252 - 265	854.49	1706.97	1706.92	0.05	0	K.IDQLQEELLHTQLK.Y ( 42)
300 - 327	1092.55	3274.63	3274.5	0.14	0	K.SLIDMYSEVLDVLSYDASYNTQDHLPR.V (M) ( 58)
328 - 338	529.81	1057.61	1057.58	0.04	0	R.VVVVGDQSAGK.T ( 66)
339 - 349	609.84	1217.67	1217.64	0.02	0	K.TSVLEMIAQARI.I ( 62)
354 - 361	434.77	867.52	867.36	0.16	0	R.GSGEMMTR.S ( 45)
366 - 379	767.92	1533.83	1533.83	0	0	K.VTLSEGP HHVALFK.D ( 78)
384 - 397	825.44	1648.87	1648.83	0.04	1	R.EFDLTKEEDLAALR.H ( 77)
410 - 424	824.43	1646.84	1646.82	0.02	0	K.EGCTVSPETISLNVK.G (C) ( 70)
431 - 452	764.07	2289.18	2289.16	0.03	0	R.MVLVDLPGVINTVTSGMAPDTK.E 2 (M) ( 68)
453 - 460	462.75	923.49	923.5	-0.01	0	K.ETIFSISK.A ( 37)
461 - 482	832.03	2493.08	2493.16	-0.09	0	K.AYMQNPNAIILCIQDGSVDAER.S (C); (M) ( 94)
483 - 497	552.27	1653.79	1653.81	-0.02	0	R.SIVTDLVSQMDPHGR.R ( 66)
499 - 505	411.28	820.55	820.51	0.05	0	R.TIFVLTK.V ( 22)
519 - 526	464.78	927.55	927.54	0.01	0	R.IQQIIEGK.L ( 29)
532 - 542	563.35	1124.68	1124.62	0.06	0	K.ALGYFAVVTGK.G ( 78)
543 - 553	581.76	1161.51	1161.56	-0.05	0	K.GNSSESIEAIR.E ( 43)
554 - 564	725.29	1448.56	1448.61	-0.05	0	R.EYEEFFQNSK.L ( 38)
580 - 591	720.36	1438.71	1438.69	0.02	0	R.NLSLAVSDCFWK.M (C) ( 63)
595 - 605	634.32	1266.62	1266.57	0.05	0	R.ESVEQQADSFK.A ( 80)
609 - 616	533.77	1065.52	1065.51	0	0	R.FNLETEWK.N ( 38)
624 - 633	646.82	1291.62	1291.64	-0.02	1	R.ELDRNELFEK.A ( 38)
634 - 651	992.56	1983.11	1983.09	0.02	1	K.AKNEILDEVISLSQVTPK.H ( 66)
636 - 651	893.01	1784	1783.96	0.04	0	K.NEILDEVISLSQVTPK.H ( 71)
652 - 664	585.36	1753.05	1752.86	0.19	0	K.HWEEILQQLWER.V ( 68)
665 - 693	1055.56	3163.65	3163.59	0.07	0	R.VSTHVIENIYLPAAQTMNSGTFNTTVDIK.L ( 49)
694 - 700	459.83	917.64	917.5	0.14	1	K.LKQWTDK.Q ( 32)
706 - 720	598.64	1792.91	1792.86	0.04	0	K.AVEVAVETLQEEFSR.F ( 76)
727 - 736	602.28	1202.55	1202.56	0	1	K.GKEHDDIFDK.L ( 72)

Start-End	Observed	Mr (expt)	Mr (Calc)	Delta in mass	Miss	Sequence
729 - 736	509.75	1017.49	1017.44	0.05	0	K.EHDDIFDK.L ( 26)
739 - 747	516.83	1031.65	1031.55	0.1	1	K.EAVKEESIK.R ( 33)
749 - 760	506.89	1517.65	1517.69	-0.04	1	R.HKWNDFAEDSLR.V De (NQ) ( 56)
751 - 760	626.8	1251.59	1251.55	0.04	0	K.WNDFAEDSLR.V ( 47)
761 - 770	597.83	1193.64	1193.62	0.02	0	R.VIQHNALEDR.S ( 56)
771 - 792	862.83	2585.45	2585.22	0.23	1	R.SISDKQQWDAAIYFMEEALQGR.L ( 85)
776 - 792	686.02	2055.02	2054.95	0.07	0	K.QQWDAAIYFMEEALQGR.L ( 73)
793 - 809	987.49	1972.96	1972.96	0.01	1	R.LKDTENAIENMIGPDWK.K ( 60)
819 - 829	687.34	1372.67	1372.6	0.06	0	R.TQEQC VHNETK.N (C) ( 48)
838 - 855	1015.49	2028.96	2028.98	-0.01	0	K.VNDEHPAYLASDEITTVR.K ( 95)
862 - 871	528.8	1055.59	1055.59	0	0	R.GVEVDPSLIK.D ( 37)
862 - 879	714.73	2141.16	2141.09	0.07	1	R.GVEVDPSLIKDTWHQVYR.R ( 48)
872 - 879	552.76	1103.51	1103.51	0	0	K.DTWHQVYR.R ( 40)
885 - 894	629.79	1257.57	1257.57	0	0	K.TALNHCNLCR.R 2 (C) ( 46)
896 - 902	498.73	995.45	995.45	0	0	R.GFYYYQR.H ( 24)
903 - 919	727.02	2178.03	2178.02	0.01	0	R.HFIDSELECNVVLFWR.I (C) ( 85)
923 - 932	552.33	1102.64	1102.62	0.02	0	R.MLAITANTLR.Q ( 44)
933 - 941	545.3	1088.58	1088.55	0.03	0	R.QQLTNTTEVR.R De (NQ) ( 53)
949 - 960	690.83	1379.65	1379.61	0.04	0	K.EVLEDFEAEDGEK.K ( 57)
970 - 977	458.3	914.59	914.51	0.08	0	R.VQLAEDLK.K ( 30)
970 - 978	522.32	1042.63	1042.6	0.02	1	R.VQLAEDLKK.V ( 30)
979 - 985	451.33	900.64	900.5	0.14	1	K.VREIQEK.L ( 26)
986 - 997	707.41	1412.8	1412.73	0.07	0	K.LDAFIEALHQEK.- ( 53)

**Band-4****Heart -Trypsin digest**

195 - 207	701.8	1401.59	1401.65	-0.06	0	R.AAGQYSTSYAQK.R (Ions score 64)
216 - 229	854.43	1706.85	1706.92	-0.07	0	K.IDQLQEELLHTQLK.Y (Ions score 73)
303 - 313	609.8	1217.59	1217.64	-0.06	0	K.TSVLEMIAQAR.I (Ions score 73)
330 - 343	767.89	1533.77	1533.83	-0.06	0	K.VTLSEGGPHHVALFK.D (Ions score 73)
348 - 361	825.39	1648.77	1648.83	-0.06	1	R.EFDLTKEEDLAALR.H (Ions score 83)
559 - 569	634.27	1266.52	1266.57	-0.05	0	R.ESVEQQADSFK.A (Ions score 87)
573 - 580	533.75	1065.48	1065.51	-0.04	0	R.FNLETEWKN (Ions score 37)
588 - 597	646.81	1291.6	1291.64	-0.04	1	R.ELDRNELFEK.A (Ions score 38)
598 - 615	992.51	1983.01	1983.09	-0.08	1	K.AKNEILDEVISLSQVTPK.H (Ions score 123)
616 - 628	877.41	1752.8	1752.86	-0.06	0	K.HWEEILQQLWER.V (Ions score 34)
670 - 684	897.4	1792.79	1792.86	-0.07	0	K.AVEVAWETLQEEFSR.F (Ions score 61)
691 - 700	602.26	1202.51	1202.56	-0.05	1	K.GKEHDDIFDK.L (Ions score 47)
725 - 734	597.79	1193.57	1193.62	-0.05	0	R.VIQHNALEDR.S (Ions score 41)
802 - 819	1015.46	2028.91	2028.98	-0.07	0	K.VNDEHPAYLASDEITTVR.K (score 44)
826 - 835	528.78	1055.55	1055.59	-0.03	0	R.GVEVDPSLIK.D (Ions score 37)
836 - 843	552.74	1103.47	1103.51	-0.04	0	K.DTWHQVYR.R (Ions score 29)
859 - 866	576.76	1151.51	1151.55	-0.04	1	R.RGFYYYQR.H (Ions score 29)
897 - 905	544.77	1087.52	1087.56	-0.04	0	R.QQLTNTTEVR.R (Ions score 84)
913 - 924	690.78	1379.55	1379.61	-0.06	0	K.EVLEDFEAEDGEK.K (Ions score 58)



Start-End	Observed	Mr (expt)	Mr (Calc)	Delta in mass	Miss	Sequence
934 - 942	522.29	1042.56	1042.6	-0.04	1	R.VQLAEDLKK.V (Ions score 42)
950 - 961	471.9	1412.67	1412.73	-0.06	0	K.LDAFIEALHQEK.- (Ions score 36)

**Liver -Trypsin digest**

195 - 207	701.82	1401.62	1401.65	-0.04	0	R.AAGQYSTSYAQQK.R (Ions score 50)
292 - 302	529.78	1057.56	1057.58	-0.02	0	R.VVVVGDQSAGK.T (Ions score 57)
330 - 343	512.27	1533.8	1533.83	-0.03	0	K.VTLSEGP HHVALFK.D (Ions score 60)
348 - 361	550.61	1648.81	1648.83	-0.02	1	R.EFDLTKEEDLAALR.H (Ions score 34)
417 - 424	462.75	923.49	923.5	-0.01	0	K.ETIFSISK.A (Ions score 28)
483 - 490	464.77	927.53	927.54	-0.01	0	R.IQQIIEGK.L (Ions score 43)
496 - 506	563.31	1124.6	1124.62	-0.02	0	K.ALGYFAVVTGK.G (Ions score 61)
559 - 569	634.28	1266.56	1266.57	-0.02	0	R.ESVEQQADSFK.A (Ions score 69)
573 - 580	533.76	1065.51	1065.51	0	0	R.FNLETEWK.N (Ions score 42)
588 - 597	646.82	1291.62	1291.64	-0.02	1	R.ELDRNELFEK.A (Ions score 20)
691 - 702	482.25	1443.73	1443.74	-0.01	2	K.GKEHDDIFDKLKE (Ions score 43)
703 - 712	594.82	1187.62	1187.65	-0.03	2	K.EAVKEESIKR.H (Ions score 47)
802 - 819	677.32	2028.94	2028.98	-0.03	0	K.VNDEHPAYLASDEITTVR.K (Ions score 64)
826 - 835	528.8	1055.58	1055.59	0	0	R.GVEVDPSLIK.D (Ions score 42)
836 - 843	552.76	1103.5	1103.51	-0.01	0	K.DTWHQVYR.R (Ions score 39)
859 - 866	576.78	1151.54	1151.55	-0.01	1	R.RGFYYYQR.H (Ions score 30)
897 - 905	544.78	1087.54	1087.56	-0.02	0	R.QQLTNTVEVR.R (Ions score 84)
913 - 924	690.8	1379.59	1379.61	-0.02	0	K.EVLEDAEDGK.K (Ions score 82)
934 - 942	522.31	1042.6	1042.6	-0.01	1	R.VQLAEDLKK.V (Ions score 38)

**Kidney- Glu-C digestion**

307 - 320	511.6	1531.78	1531.79	-0.01	0	E.MIAQARIFPRGSGE.M (Ions score 18)
348 - 355	498.73	995.44	995.44	-0.01	3	E.FDLTKEED.L (Ions score 34)
348 - 362	596.3	1785.88	1785.89	-0.01	4	E.FDLTKEEDLAALRHE.I (Ions score 52)
559 - 575	657.32	1968.95	1968.95	0	2	E.SVEQQADSFKATRFNLE.T (Ions score 36)
605 - 618	551.62	1651.85	1651.86	-0.01	1	E.VISLSQVTPKHWEI.I (Ions score 47)
797 - 813	653.98	1958.93	1958.94	-0.01	3	E.KMLKVNDEHPAYLASDE.I (Ions score 22)
814 - 822	537.32	1072.62	1072.62	-0.01	0	E.ITTVRKNLE.S (Ions score 40)
945 - 954	603.32	1204.63	1204.63	-0.01	2	E.IQEKLDAFIE.A (Ions score 45)

**Kidney- Trypsin digestion**

194 - 207	520.48	1558.41	1558.74	-0.33	1	R.RAAGQYSTSYAQQK.R (NQ) ( 25)
195 - 207	701.77	1401.53	1401.65	-0.13	0	R.AAGQYSTSYAQQK.R ( 62)
216 - 229	570.37	1708.08	1707.9	0.18	0	K.IDQLQEELLHTQLK.Y (NQ) ( 35)
247 - 251	600.25	599.24	599.4	-0.16	0	K.LVLQK.D ( 25)
292 - 302	529.95	1057.89	1057.58	0.31	0	R.VVVVGDQSAGK.T ( 53)
303 - 313	609.98	1217.95	1217.64	0.31	0	K.TSVLEMIAQARI ( 33)
374 - 388	824.46	1646.91	1646.82	0.09	0	K.EGCTVSPETISLNVK.G (C) ( 48)
395 - 416	753.82	2258.43	2258.15	0.27	0	R.MVLVDLPGVINTVTSGMADPTK.E (NQ) ( 61)
417 - 424	462.63	923.24	923.5	-0.25	0	K.ETIFSISK.A ( 55)
425 - 446	832.98	2495.91	2496.11	-0.21	0	K.AYMQNPNAILCIQDGSVDAER.S (C); 3 (NQ); (M) ( 77)
496 - 506	563.5	1124.99	1124.62	0.37	0	K.ALGYFAVVTGK.G ( 65)

Start-End	Observed	Mr (expt)	Mr (Calc)	Delta in mass	Miss	Sequence
544 - 555	720.81	1439.61	1439.68	-0.06	0	R.NLSLAVSDCFWK.M (C); (NQ) (36)
559 - 569	634.26	1266.51	1266.57	-0.07	0	R.ESVEQQADSFK.A (63)
573 - 580	534.15	1066.29	1066.5	-0.21	0	R.FNLETEWK.N (NQ) (22)
598 - 615	992.85	1983.69	1984.07	-0.39	1	K.AKNEILDEVISLSQVTPK.H (NQ) (66)
600 - 615	595.94	1784.81	1784.94	-0.13	0	K.NEILDEVISLSQVTPK.H (NQ) (51)
616 - 628	585.9	1754.68	1754.83	-0.15	0	K.HWEEILQQSLWER.V 2 (NQ) (31)
670 - 684	897.79	1793.56	1793.85	-0.29	0	K.AVEVAWETLQEEFSR.F (NQ) (26)
691 - 700	602.45	1202.9	1202.56	0.34	1	K.GKEHDDIFDK.L (56)
725 - 734	597.7	1193.39	1193.62	-0.23	0	R.VIQHNALEDR.S (55)
757 - 773	988.05	1974.09	1973.94	0.15	1	R.LKDTENAIENMIGPDWK.K (NQ) (24)
759 - 773	867.54	1733.06	1732.76	0.3	0	K.DTENAIENMIGPDWK.K (NQ) (23)
783 - 793	694.43	1386.84	1386.62	0.22	0	R.TQEQCVHNETK.N (C) (50)
802 - 819	1016.13	2030.24	2029.96	0.28	0	K.VNDEHPAYLASDEITTVR.K (NQ) (55)
849 - 858	630.42	1258.83	1258.55	0.27	0	K.TALNHCNLCR.R 2 (C); (NQ) (31)
897 - 905	544.92	1087.83	1087.56	0.27	0	R.QQLTNTTEVR.R (77)
913 - 924	690.81	1379.6	1379.61	0	0	K.EVLEDFEAEDGEK.K (70)

**Band-5****Heart -Trypsin digest**

291 - 301	529.78	1057.54	1057.58	-0.04	0	R.VVVVGDQSAGK.T (Ions score 68)
416 - 423	462.74	923.46	923.5	-0.03	0	K.ETIFSISK.A (Ions score 26)
558 - 568	634.27	1266.52	1266.57	-0.05	0	R.ESVEQQADSFK.A (Ions score 69)
572 - 579	533.74	1065.47	1065.51	-0.05	0	R.FNLETEWK.N (Ions score 33)
587 - 596	646.8	1291.59	1291.64	-0.05	1	R.ELDRNELFEK.A (Ions score 34)
690 - 699	602.27	1202.53	1202.56	-0.02	1	K.GKEHDDIFDK.L (Ions score 63)
724 - 733	597.79	1193.57	1193.62	-0.05	0	R.VIQHNALEDR.S (Ions score 75)
801 - 819	720	2156.98	2157.07	-0.09	1	K.VNDEHPAYLASDEITTVR.K (score 49)
825 - 834	528.78	1055.54	1055.59	-0.04	0	R.GVEVDPSLIK.D (Ions score 32)
835 - 842	552.74	1103.48	1103.51	-0.04	0	K.DTWHQVYR.R (Ions score 36)
858 - 865	576.76	1151.5	1151.55	-0.05	1	R.RGFYYYQR.H (Ions score 33)
859 - 865	498.72	995.42	995.45	-0.03	0	R.GFYYYQR.H (Ions score 14)
912 - 923	690.78	1379.54	1379.61	-0.07	0	K.EVLEDFEAEDGEK.K (Ions score 51)

**Liver- Trypsin digest**

291 - 301	529.76	1057.51	1057.58	-0.07	0	R.VVVVGDQSAGK.T (Ions score 60)
329 - 342	512.25	1533.72	1533.83	-0.11	0	K.VTLSEGP HHVALFK.D (Ions score 42)
347 - 360	550.58	1648.73	1648.83	-0.1	1	R.EFDLTKEEDLAALR.H (Ions score 30)
495 - 505	563.28	1124.55	1124.62	-0.07	0	K.ALGYFAVVTGK.G (Ions score 58)
558 - 568	634.25	1266.49	1266.57	-0.08	0	R.ESVEQQADSFK.A (Ions score 74)
572 - 579	533.73	1065.44	1065.51	-0.07	0	R.FNLETEWK.N (Ions score 45)
587 - 596	646.78	1291.55	1291.64	-0.09	1	R.ELDRNELFEK.A (Ions score 32)
702 - 711	594.79	1187.57	1187.65	-0.08	2	K.EAVKEESIKR.H (Ions score 42)
724 - 733	597.77	1193.53	1193.62	-0.09	0	R.VIQHNALEDR.S (Ions score 64)
801 - 818	677.28	2028.82	2028.98	-0.15	0	K.VNDEHPAYLASDEITTVR.K (Ions score 66)
825 - 834	528.76	1055.51	1055.59	-0.07	0	R.GVEVDPSLIK.D (Ions score 47)

Start-End	Observed	Mr (expt)	Mr (Calc)	Delta in mass	Miss	Sequence
835 - 842	552.73	1103.44	1103.51	-0.07	0	K.DTWHQVYR.R (Ions score 37)
896 - 904	544.75	1087.49	1087.56	-0.08	0	R.QQLTNTTEVR.R (Ions score 52)
949 - 960	707.32	1412.63	1412.73	-0.1	0	K.LDAFIEALHQEK.- (Ions score 79)

**Kidney- Glu-C digest**

559 - 575	657.32	1968.93	1968.95	-0.02	2	E.SVEQQADSFKATRFNLE.T (Ions score 40)
605 - 618	551.63	1651.85	1651.86	0	1	E.VISLSQVTPKHWEI.I (Ions score 34)
814 - 822	537.32	1072.62	1072.62	-0.01	0	E.ITTVRKNLE.S (Ions score 41)

**Kidney- Trypsin digest**

215 - 228	854.79	1707.57	1707.9	-0.33	0	K.IDQLQEELLHTQLK.Y (NQ) (40)
291 - 301	529.97	1057.93	1057.58	0.36	0	R.VVVVGDQSAGK.T (59)
424 - 445	832.8	2495.36	2495.13	0.23	0	K.AYMQNPNAIILCIQDGSVDAER.S (C); 2 (NQ); (M) (73)
446 - 460	552.72	1655.15	1654.8	0.35	0	R.SIVTDLVSQMDPHGR.R (NQ) (25)
482 - 489	464.74	927.47	927.54	-0.07	0	R.IQIHIEGK.L (37)
495 - 505	563.5	1124.99	1124.62	0.36	0	K.ALGYFAVVTGK.G (70)
543 - 554	720.87	1439.72	1439.68	0.04	0	R.NLSLAVSDCFWK.M (C); (NQ) (50)
558 - 568	634.2	1266.38	1266.57	-0.19	0	R.ESVEQQADSFK.A (96)
572 - 579	534.24	1066.46	1066.5	-0.04	0	R.FNLETEWK.N (NQ) (22)
615 - 627	585.56	1753.67	1753.84	-0.18	0	K.HWEEILQQSLWER.V (NQ) (44)
669 - 683	897.6	1793.19	1792.86	0.33	0	K.AVEVAWETLQEEFSR.F (72)
690 - 699	602.48	1202.95	1202.56	0.4	1	K.GKEHDDIFDK.L (56)
714 - 723	626.88	1251.74	1251.55	0.19	0	K.WNDFAEDSL.R.V (56)
739 - 755	686.52	2056.53	2056.92	-0.39	0	K.QQWDAAIYFMEEALQGR.L 2 (NQ) (84)
782 - 792	458.67	1373	1372.6	0.4	0	R.TQEQCVHNETK.N (C) (23)
801 - 818	677.53	2029.58	2029.96	-0.38	0	K.VNDEHPAYLASDEITTVR.K (NQ) (30)
848 - 857	630.41	1258.8	1258.55	0.24	0	K.TALNHCNLCR.R 2 (C); (NQ) (42)
886 - 895	552.24	1102.46	1102.62	-0.15	0	R.MLAITANTLR.Q (41)
896 - 904	544.98	1087.95	1087.56	0.39	0	R.QQLTNTTEVR.R (44)
912 - 923	691.01	1380	1379.61	0.39	0	K.EVLEDFAEEDGEK.K (53)
933 - 941	522.93	1043.84	1043.59	0.26	1	R.VQLAEDLKK.V (NQ) (38)

1 MWRAGRAAVA CEVCQSLVKH SSGIQRNVPL QKLHLVSRSI YRSHHPALKL QRPQLRTPFQ QFSSLTHLSL HKLKLSPIKY GYQPRRNFWP

91 ARLAARLLKL RYIILGSAVG GGYTAKKTFD EWKDMIPDLS DYKWIVPDFI WEIDEYIDLE KIRKALPSSE DLASLAPDLL KITESLSLLK

181 DFFTAGPKLV SEVLEVSEAL LLLGSPGETA FRATDHGSES DKHYRKGLLG ELILLQQQIQ EHEEEARRAA GOYSTSYAQQ KRKVSDEKI

Exon 4b Exon 5b

271 DQLQEELLHT QLKYQRILER LEKENKELRK LVLQKDDKGI HHRKLLKSLI DMYSEVLVLDV SDYDASYNTQ DHLPRVVVVG DQSAGKTSVL

361 EMIAQARIFP RGSSEMMTRS PVKVTLSEGP HHVALFKDSS REFDLTKKEED LAALRHEIEL RMRKNVKEGC TVSPETISLN VKGPGLQRMV

451 LVDLPGVINT VTSGMAPDTK ETIFSISKAY MQNPNAIILC IQDGSVDAER SIVTDLVSQM DPHGRRTIFV LTKVDLAEKN VASPSRIQQI

541 IEGKLFPMKA LGYFAVVTGK GNSSESIEAI REYEEFFQON SKLLKTSMLK AHQVTTNLS LAVSDCFWKM VRESVEQQAD SFKATRFNLE

631 TEWKNNYPRL RELDRNELFE KAKNEILDEV ISLSQVTPKH WEEILQOSLW ERVSTHVIEN IYLPAAQTMN SGTFNNTTVDI KLKQWTDKQL

721 PNKAVEVAWE TLQEEFSRFM TEPKGKEHDD IFDKLKEAVK EESIKRHKWN DFAEDSLRVI QHNALEDRSI SDKQQWDAAI YFMEEALQGR

811 LKDTENAIEN MIGPDWKKRW MYWKNRTQEQ CVHNETKNEL EKMLKVNDEH PAYLASDEIT TVRKNLESRG VEVDPSLIKD TWHQVYRRHF

901 LKTALNHCNL CRRGFYYQOR HFIDSELECN DVVLFWRIQR MLAITANTLR QQLTNTTEVRR LEKNVKEVLE DFAEDGKQV KLLTGKRVQL

991 AEDLKKVREI QEKLDAFIEA LHQEK

Summary of alignment of the peptides detected in MS/MS analysis to OPA1 isoform 8 ( — Band-1; — Band-2; — Band-3; — Band-4; — Band-5).

## 7.5 Abbreviations

°C	Celcius
A	Ampere
aa	Amino acid
ATP	Adenosine triphosphate
BSA	Bovine serum albumin
bp	base pairs
cDNA	complementary DNA
DEPC	Diethylene pyrocarbonate
DNA	Deoxyribonucleic acid
DNase	Deoxyribonuclease
DTT	Dithiothreitol
dNTP	Deoxy-nucleoside triphosphate
EDTA	Ethylendiamine-N,N,N',N'-tetraacetate
EGTA	Ethylenglycol-N,N,N',N'-tetraacetate
FADH	Falvin adenine dinucleotide hydrogenase
e.g.	exempli gratia
g	Gram
GTP	Guanosine triphosphate
HEPES	4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid
hr	hour
i.e.	id est
kb	kilo bases
kDa	kilo Dalton
l	Litre
LB	Luria Bertani
LMP	low-melting point
M	Molar
m	Milli
μ	Micro
Min	Minute
NaCl	Sodiumchloride
NADH	Nicotinamide adenine dinucleotide hydrogenase
No.	Number
PCR	Polymerase chain reaction
pH	Logarithm of the reciprocal of the hydrogen ion concentration
PMSF	Phenyl-methyl-sulphonyl-fluoride
RNA	Ribonucleic acid
RNase	Ribonuclease
rpm	revolutions per minute
RT	Reverse transcriptase
s	second
SDS	Sodium dodecyl sulfate
Taq	Thermophilus aquaticus
Tris	Tris-(hydroxymethyl)-aminomethane
U	Unit
V	Volt

## 7.6 List of Figures

Figure 1.1:	A schematic image of a mitochondrion.....	2
Figure 1.2:	Mitochondrial Fusion and Fission.....	3
Figure 1.3:	Eye fundus photographs.....	9
Figure 1.4:	Splice variants of human OPA1.....	11
Figure 1.5a, b:	Domain structure of the human dynamin superfamily.....	12
Figure 1.6a, b, c:	Mutation spectrum of OPA1.....	14
Figure 3.1a, b:	Calibration of Superose-6 column.....	36
Figure 4.1:	Analysis of RT-PCR product obtained from primer pair 3-9.....	39
Figure 4.2:	Analysis of RT-PCR product obtained from primer pair 4-9.....	40
Figure 4.3:	Analysis of RT-PCR product obtained from primer pair 3-5b.....	42
Figure 4.4:	Analysis of RT-PCR product obtained from primer pair e3-e7.....	42
Figure 4.5:	Analysis of RT-PCR product obtained from primer pair 4-5b.....	43
Figure 4.6:	Schematic representation of the regions amplified for the antibody characterization.....	44
Figure 4.7a, b:	Epitope mapping of the hybridomas.....	45
Figure 4.8:	Mitochondrial localisation of OPA1 in HeLa cells.....	46
Figure 4.9:	Expression profile of various OPA1 protein forms from mouse and human.....	47
Figure 4.10a, b:	Immunoprecipitated OPA1 protein isoforms separated on SDS-PAGE.....	48
Figure 4.11:	Alignment of the peptides identified from different bands to mouse OPA1 isoforms.....	49
Figure 4.12a, b:	Edman sequencing of OPA1 isoform 1.....	52
Figure 4.13:	Membrane topology of mOPA1.....	53
Figure 4.14:	Elution profile of the mitochondrial lysates after gel filtration.....	54
Figure 4.15a, b:	Western blot analysis of the TCA precipitated fractions after gel filtration.....	55
Figure 4.16:	OPA1 isoforms build up different high molecular mass complexes.....	56
Figure 4.17:	Peptide array binding assay.....	57
Figure 4.18:	SE analytical ultracentrifugation.....	58
Figure 4.19:	Schematic representation of the OPA1 regions amplified for the Y2H screen.....	60
Figure 4.20a, b:	Identification of OPA1 interaction proteins by Y2H.....	60
Figure 4.21:	Confirmation of the interaction between OPA1 and selected proteins retrieved in Y2H screen by <i>in vitro</i> pull-down assay.....	61
Figure 5.1:	OPA1 splice variants found in mouse tissues.....	62
Figure 5.2:	OPA1 protein isoforms identified in steady state mitochondria in mouse tissues.....	65
Figure 5.3:	Model for OPA1 protein isoforms being processed in the mitochondria.....	66
Figure 5.4:	Cartoon depicting association of CC-0 and CC-I.....	71

## 7.7 List of tables

Table 1.1:	Mitochondrial shaping proteins in mammals and yeast .....	4
Table 1.2:	Mitochondrial proteins mutated in neurodegenerative diseases .....	8
Table 3.1:	Recalculated molecular mass of the standard proteins.....	37
Table 4.1a:	Details of the primers used for amplification of splice forms of OPA1 .....	41
Table 4.1b:	Details of the expected lengths of PCR products generated using specific primers.....	41
Table 4.2:	Expression profile of OPA1 splice forms.....	43
Table 4.3:	Epitope mapping of the hybridomas that recognised OPA1 .....	45
Table 4.4:	Expression profile of OPA1 protein forms .....	47
Table 4.5:	Calculated mass of the protein complexes eluted in different fractions.....	55
Table 4.6:	Details of the OPA1 interaction proteins.....	61
Table 5.1:	Complexity of OPA1 splicing in different species.....	65