

1/18

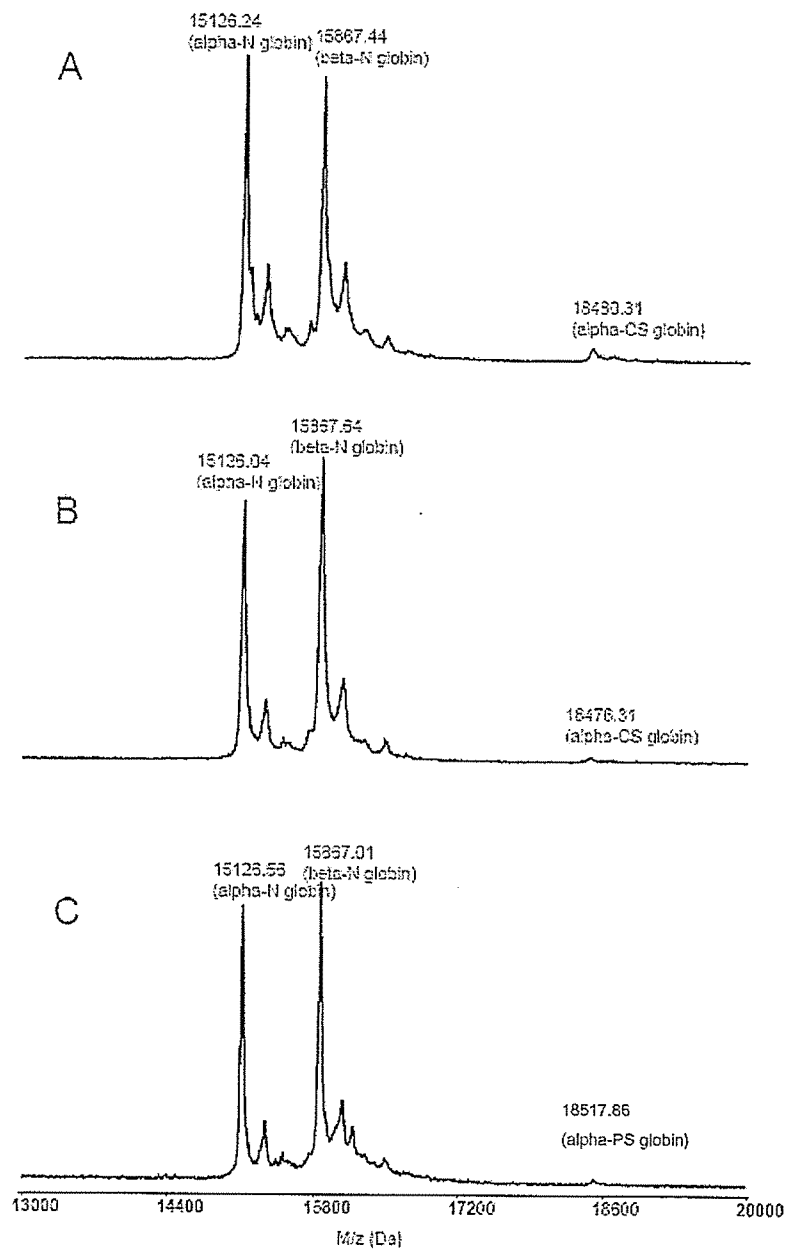


FIGURE 1

2/18

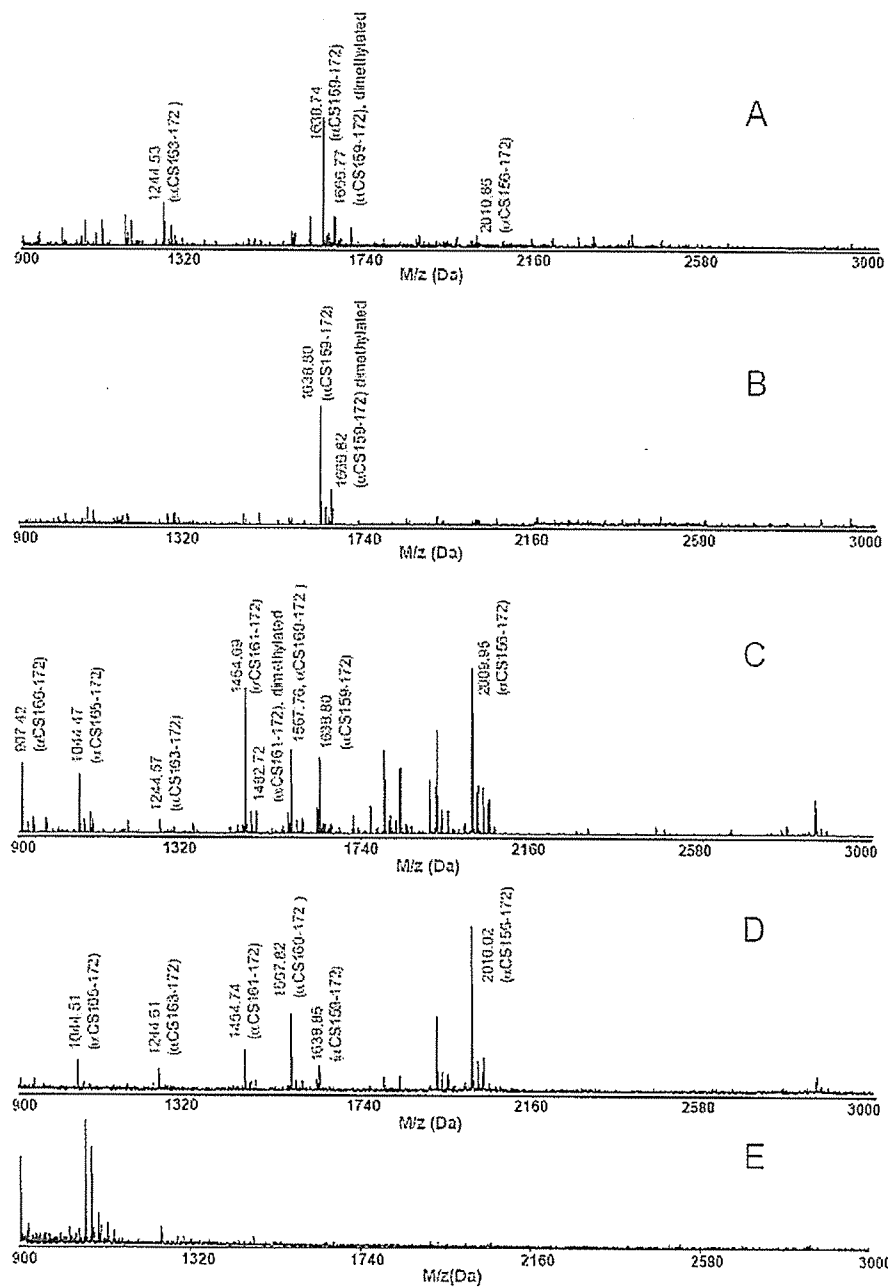


FIGURE 2

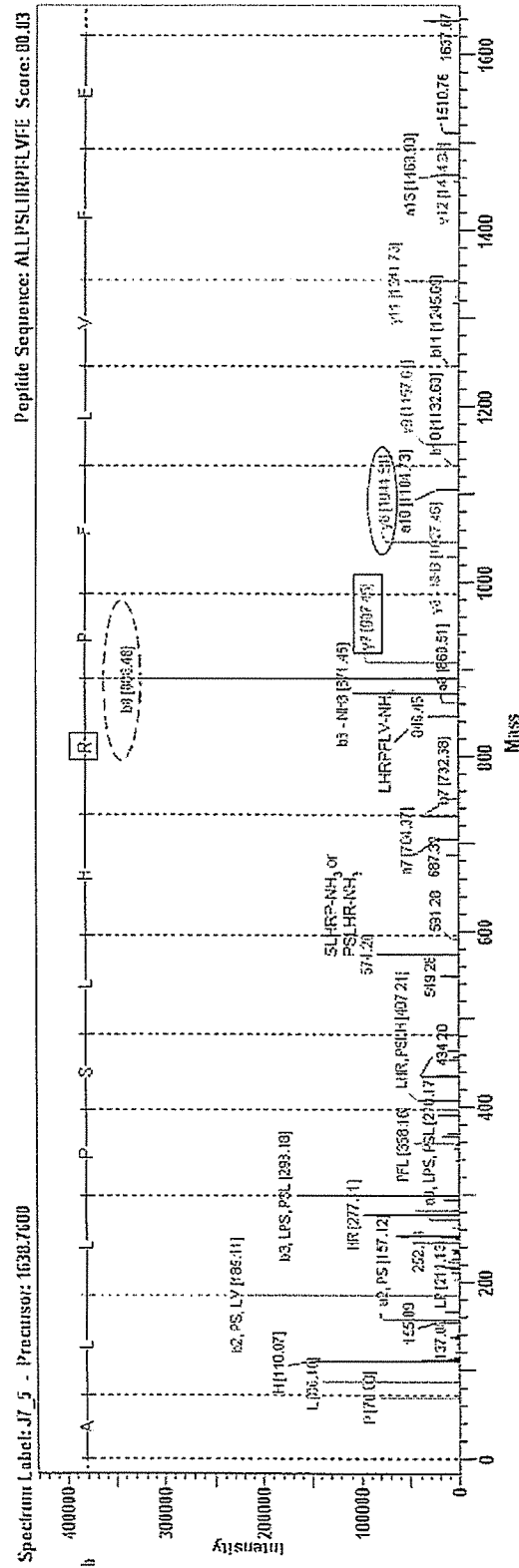


FIGURE 3A

4/18

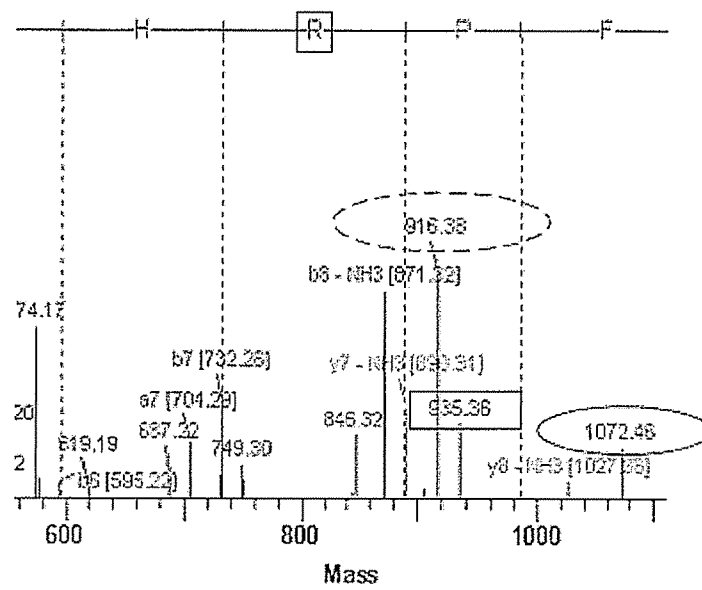


FIGURE 3B

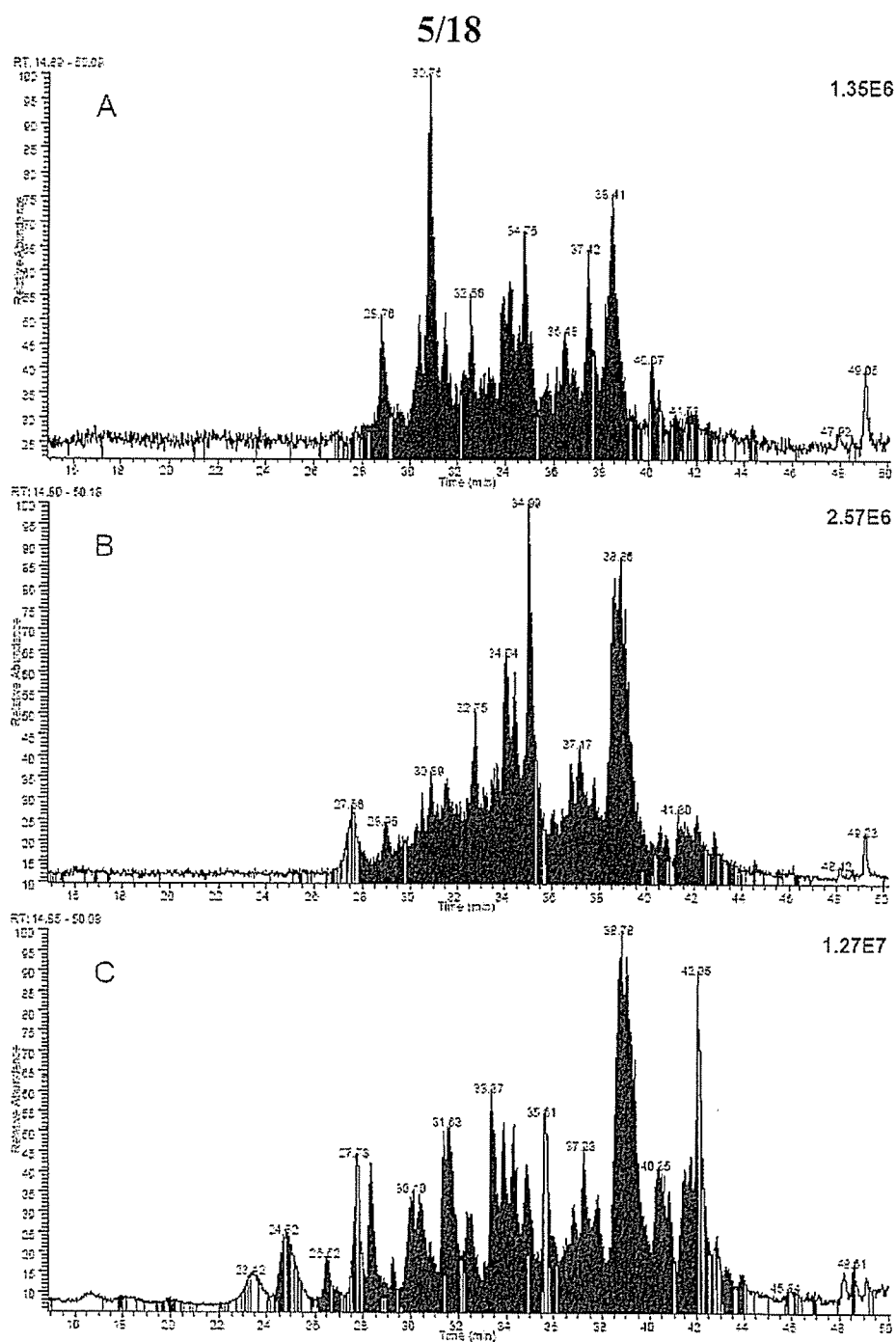
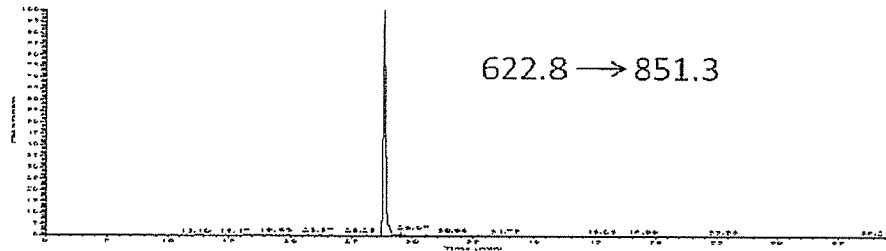


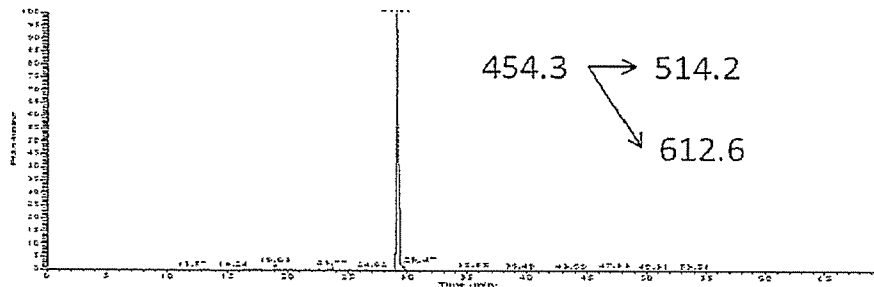
FIGURE 4

6/18

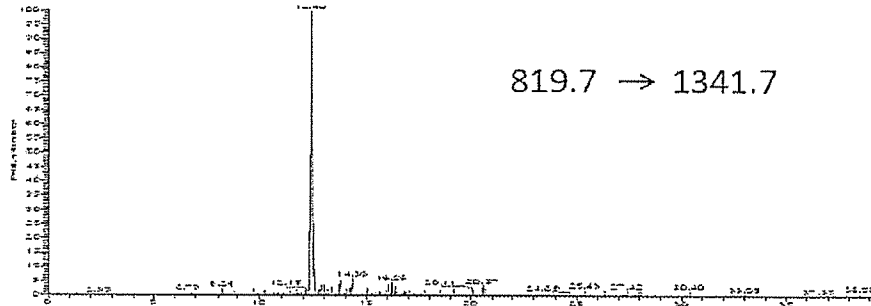
MRM Transition for peptide sequence: SLHRPFLVFE, 622.8 m/z



MRM Transition for peptide sequence: 454.26 RPFLVFE, 454.26 m/z



MRM Transition for peptide sequence: ALLPSLHRPFLVFE, 819.97 m/z



MRM Transition for peptide sequence: LPSLHRPFLVFE 727.9

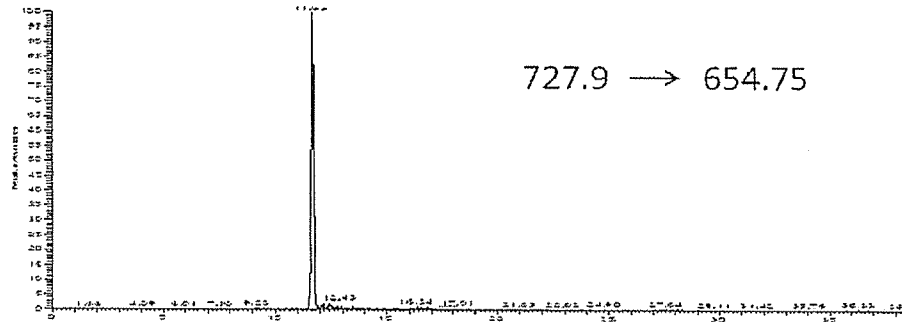
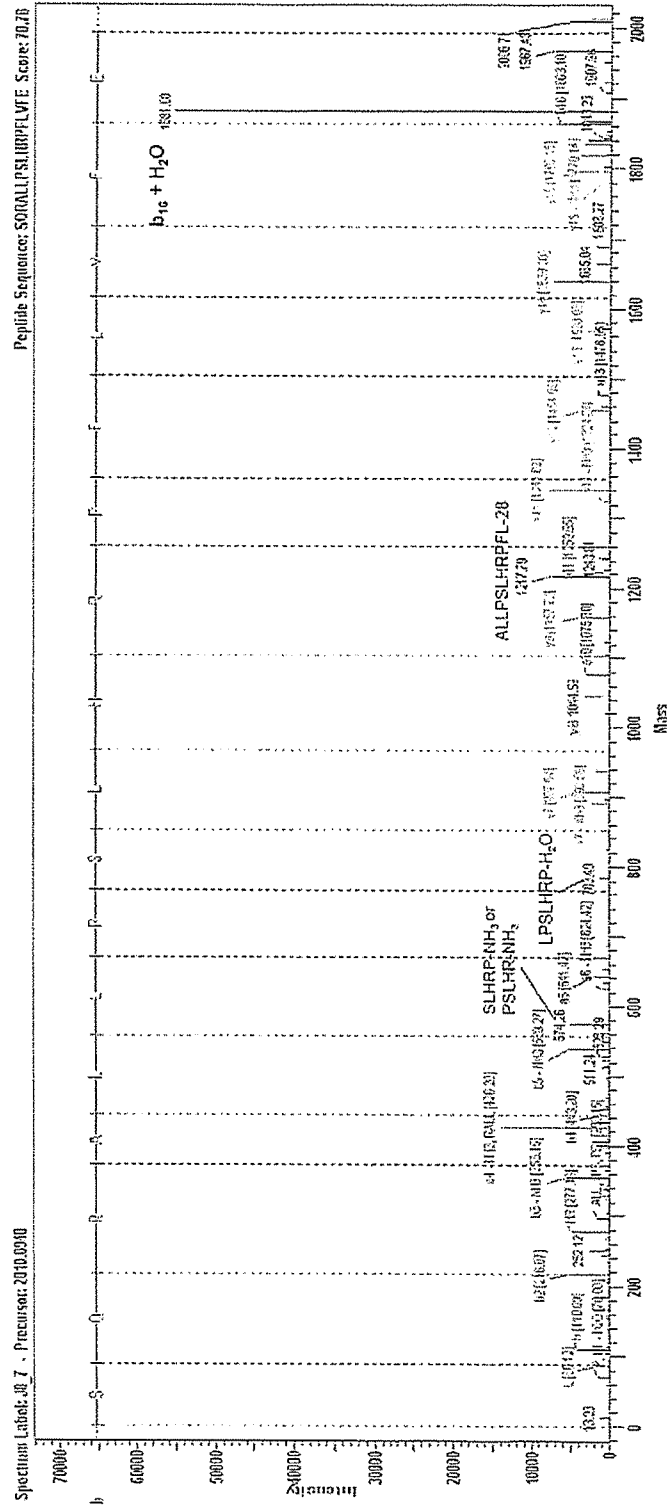


FIGURE 5



Supporting Table 1. Peptides identified by MALDI-TOF/TOF in hemolysates from various thalassemic genotypes

Genotype	Sample code	Ionized CS	1044 (g/mol)	1244 (g/mol)	1263 (g/mol)	1452 (g/mol)	1638 (g/mol)	1666 (g/mol)	1794 (g/mol)	1912 (g/mol)	2010 (g/mol)
α ⁺ α ⁺	15A1 (WB)	im	-	-	-	-	-	-	-	-	-
	25A2 (WB)	im	-	-	-	-	-	-	-	-	-
	40A2 (PRC)	im	-	-	-	-	-	-	-	-	-
α ⁺ α ⁺	21A1 (PRC)	im	-	-	-	-	-	-	-	-	-
	Hemo C31 (PRC)	im	-	-	-	-	-	-	-	-	-
	Hemo C32 (PRC)	im	-	-	-	-	-	-	-	-	-
α ⁺ α ⁺	Hemo C33 (WB)	im	-	-	-	-	-	-	-	-	-
	Hemo C34 (PRC)	im	-	-	-	-	-	-	-	-	-
	Hemo C34 (WB)	im	-	-	-	-	-	-	-	-	-
α ⁺ α ⁺	Hemo C34 - P (PRC)	im	-	-	-	-	-	-	-	-	-
	Hemo C34 - P (WB)	im	-	-	-	-	-	-	-	-	-
	17 HCS (WB) aged	im	-	-	-	-	-	-	-	-	-
α ⁺ α ⁺	117 HCS (PRC)	im	-	-	-	-	-	-	-	-	-
	117 HCS (WB)	im	-	-	-	-	-	-	-	-	-
	117 HCS - P (PRC)	im	-	-	-	-	-	-	-	-	-
α ⁺ α ⁺	117 HCS - P (WB)	im	-	-	-	-	-	-	-	-	-
	19 HCS (WB)	im	-	-	-	-	-	-	-	-	-
	21 HCS (WB)	im	-	-	-	-	-	-	-	-	-
α ⁺ α ⁺	25 HCS (PRC)	im	-	-	-	-	-	-	-	-	-
	14HPS (WB)	im	-	-	-	-	-	-	-	-	-
	15HPS (WB)	im	-	-	-	-	-	-	-	-	-
α ⁺ α ⁺	23 HCS (PRC)	im	-	-	-	-	-	-	-	-	-
	216 HCS (PRC)	im	-	-	-	-	-	-	-	-	-
	216 HCS (WB)	im	-	-	-	-	-	-	-	-	-
α ⁺ α ⁺	216 HCS - P (PRC)	im	-	-	-	-	-	-	-	-	-
	216 HCS - P (WB)	im	-	-	-	-	-	-	-	-	-
	10M (PRC)	im	-	-	-	-	-	-	-	-	-
α ⁺ α ⁺	N (PRC)	im	-	-	-	-	-	-	-	-	-
	N (WB)	im	-	-	-	-	-	-	-	-	-
	N (PRC - P)	im	-	-	-	-	-	-	-	-	-
α ⁺ α ⁺	Number = 4	im	-	-	-	-	-	-	-	-	-
	Number = 2	im	-	-	-	-	-	-	-	-	-
	Number = 2	im	-	-	-	-	-	-	-	-	-

im = small peak detected
 n/s = not tested, due to complete consumption of sample for other test.
 WB = whole blood, PRC = packed red cell, P = protease inhibitors

TABLE 1

Supporting Table 2. Origin of the proteolytic peptides found in α^S heterozygous, homozygous and Hb H CS disease samples

Reference	Peptide	DeltaM	z	P (ppm)	SI	Score	Coverage	DeltaCn	SP	Accession	RSP	Peptide (HIS)	Count
1	HBA_HUMAN Hemoglobin subunit alpha=Constant Spring					150.17			18600.8			19 (17 1 0 0 1)	1
33.30	A SCRALPSLHRPFL	1521.35496	0.00043	9.95E-07	6.77	3.34	0.16		1312.5		1	24/72	1
33.32	S GRALLPSLHRPFL	1434.83283	0.00115	7.49E-02	0.87	3.24	0.19		533.6		3	16/44	1
36.65	LLPSLHRPFLVE-	1454.81645	0.00198	9.95E-07	0.81	3.14	0.42		429.0		1	12/22	1
32.21	ASVAVFPARWASQ.R	1339.71171	0.00111	4.82E-04	0.76	3.08	0.26		354.7		1	15/24	1
33.28	A SCRALPSLHRPFL	1521.35496	0.00011	5.89E-02	0.81	2.79	0.05		1450.8		1	25/48	1
33.28	A SCRALPSLHRPFL	1374.75644	0.00153	3.36E-02	0.21	2.77	0.02		314.8		7	14/44	1
36.02	P SLHRPFLVE-	1244.57862	0.00039	1.30E-04	0.74	2.48	0.33		414.7		1	12/18	1
38.08	S GRALLPSLHRPFLVE-	1823.05831	-0.00055	1.88E-01	0.41	2.41	0.35		232.0		2	21/50	1
37.99	A SCRALPSLHRPFLVE-	2010.12834	0.00186	1.39E-01	0.40	2.31	0.15		459.2		1	28/96	1
38.07	A SCRALPSLHRPFLVE-	2010.12834	0.00342	8.01E-03	0.28	2.29	0.21		213.1		1	19/64	1
32.55	LLPSLHRPFL	906.55196	0.00300	6.21E-02	0.75	2.11	0.24		528.5		1	11/14	1
34.62	LLHRPFLVE-	1044.55253	0.00068	1.17E-02	0.60	2.07	0.02		589.0		1	11/14	1
32.04	ASVAVFPARWAS.Q	1140.91682	0.00254	1.58E-01	0.12	1.87	0.02		244.3		2	10/20	1
36.78	SLHRPFLVE-	1157.54059	0.00151	1.10E-01	0.37	1.81	0.25		296.4		1	9/16	1
34.09	LLPSLHRPFLV	1079.63693	0.00059	5.70E-02	0.15	1.78	0.04		199.1		9	15/32	1
36.16	S GRALLPSLHRPFLVE-	1823.05831	0.00010	1.58E-01	0.14	1.68	0.21		194.2		1	17/50	1
38.22	Q RALLPSLHRPFLVE-	1795.03774	0.00277	6.78E-02	0.05	1.48	0.10		191.7		1	14/55	1
40.84	RALLPSLHRPFLVE-	1638.92662	0.00059	8.63E-02	0.10	1.41	0.12		292.1		1	17/52	1
36.75	VAVFPARWASQ RALLPSLH	1833.04036	0.00050	1.49E-02	0.00	1.10	0.16		64.5		152	10/54	1
2	ANK1_HUMAN Ankyrin-1 - Homo sapiens					130.21			208136.2			14 (14 0 0 0 0)	1
3	SYUA_HUMAN Alpha-synuclein - Homo sapiens					120.20			14451.2			13 (13 0 0 0 0)	1
4	HBB_HUMAN Hemoglobin subunit beta - Homo sapiens					88.22			15088.3			10 (9 1 0 0 0)	1
5	B3AT_HUMAN Band 3 anion transport protein - Homo sapiens					78.21			101727.8			8 (7 1 0 0 0)	1
6	41_HUMAN Protein 4.1 - Homo sapiens					70.19			90957.3			7 (7 0 0 0 0)	1
7	DENA_HUMAN Denatin - Homo sapiens					50.20			45486.3			6 (6 0 0 0 0)	1
8	GLPA_HUMAN Glycophorin-A precursor - Homo sapiens					50.18			16283.4			5 (5 0 0 0 0)	1
9	TYB4_HUMAN Thymosin beta-4 - Homo sapiens					50.13			5049.5			5 (5 0 0 0 0)	1
10	GLPC_HUMAN Glycophorin-C - Homo sapiens					30.28			13801.7			3 (3 0 0 0 0)	1
11	GTR1_HUMAN Solute carrier family 2, facilitated glucose transporter member 1 - Homo sapiens					30.13			54046.7			3 (3 0 0 0 0)	1
12	RD3A_HUMAN UV excision repair protein RAD23 homolog A - Homo sapiens					26.20			39584.7			2 (2 0 1 0 0)	1
13	NPTL4_HUMAN Nucleosome assembly protein 1-like 4 - Homo sapiens					20.19			42797.0			2 (2 0 0 0 0)	1
14	HSPB1_HUMAN Heat shock protein beta-1 - Homo sapiens					10.25			22768.5			1 (1 0 0 0 0)	1
15	QXSR1_HUMAN Serine/threonine-protein kinase OSR1 - Homo sapiens					10.18			57986.2			1 (1 0 0 0 0)	1
16	TCPI_HUMAN T-complex protein 1 subunit eta - Homo sapiens					10.14			59320.0			1 (1 0 0 0 0)	1
17	ICAL_HUMAN Calpastatin - Homo sapiens					10.13			78526.3			1 (1 0 0 0 0)	1

R_S
+
Tail

TABLE 2

1 HBA_HUMAN Hemoglobin subunit alpha=Constant Spring										30 (25 3 1 0)									
5.89	A.VPPARWASQ.RA	1167.63815	0.00079	5.43E-06	12.75	210.20	18600.8	0.20	157.1	11/18	1								
15.17 - 16.40	A.VPPARWASQ.R	883.47846	0.00030	1.53E-01	0.45	2.27	0.20	0.20	157.1	11/18	3								
15.50	A.VPPARWASQ.R	1011.53704	0.00106	2.41E-03	0.71	2.40	0.22	0.22	157.1	11/18	1								
16.90	L.PSLHRP.F	819.49355	-0.00022	1.28E-01	0.78	2.23	0.11	0.11	558.5	11/12	1								
30.33	A.SCRALLPSLHRP.F	1374.79644	-0.00285	5.16E-03	0.82	3.06	0.02	0.02	736.8	21/84	1								
30.33	A.SCRALLPSLHRP.F	1374.79644	-0.00091	1.57E-02	0.87	3.20	0.25	0.25	921.7	21/84	1								
31.65	S.VAVPPARWASQ.R	1181.64257	0.00133	2.73E-02	0.29	1.83	0.05	0.05	178.6	13/20	1								
32.04	A.SVAVPPARWASQ.R	1265.67460	0.00177	1.93E-04	0.91	3.02	0.40	0.40	707.3	18/22	1								
32.36	G.SVAVPPARWASQ.R	1339.71171	0.00095	6.63E-03	0.77	2.47	0.29	0.29	457.8	17/24	1								
32.59	L.PSLHRP.F	965.55196	0.00100	7.94E-02	0.11	1.67	0.03	0.03	182.1	13/28	1								
32.59	A.GASVAVPPARWASQ.R	1395.73317	0.00106	8.27E-02	0.78	3.04	0.39	0.39	357.9	15/26	1								
32.86	L.PSLHRP.F	965.55196	0.00039	5.76E-02	0.76	2.48	0.21	0.21	457.0	11/14	1								
32.86	S.SCRALLPSLHRP.F	1434.83283	0.00166	3.95E-02	0.88	3.02	0.22	0.22	1032.9	22/44	1								
33.40	A.SCRALLPSLHRP.F	1521.85468	0.00129	9.97E-02	0.89	3.67	0.14	0.14	1446.8	35/72	1								
33.40	S.SCRALLPSLHRP.F	1434.83283	0.00109	4.74E-02	0.53	2.44	0.15	0.15	480.2	28/66	1								
33.41	A.SCRALLPSLHRP.F	1521.85468	0.00234	6.55E-02	0.56	3.40	0.07	0.07	1350.1	26/48	1								
34.81	A.SCRALLPSLHRP.F	1634.94892	-0.00349	1.37E-01	0.58	2.37	0.63	0.63	892.6	32/78	1								
35.42	R.ALLPSLHRP.F	1159.67314	0.00067	1.21E-02	0.07	1.44	0.12	0.12	197.6	15/36	1								
36.00	S.LHRP.F	1157.54659	0.00133	3.60E-02	0.82	2.55	0.29	0.29	688.2	12/16	1								
36.06	P.SLHRP.F	1244.67862	0.00192	2.46E-04	0.36	2.13	0.07	0.07	270.3	11/18	1								
39.23	A.SCRALLPSLHRP.F	2010.12834	0.00002	7.75E-02	0.10	1.55	0.13	0.13	342.5	24/56	1								
39.35 - 38.46	Q.SCRALLPSLHRP.F	1795.03774	-0.00015	2.91E-03	0.59	2.29	0.32	0.32	400.0	31/90	1								
39.45	L.PSLHRP.F	1454.81645	0.00074	1.21E-05	0.73	3.03	0.37	0.37	392.0	12/22	1								
39.79	S.SCRALLPSLHRP.F	1923.03631	0.00470	3.86E-04	0.16	1.49	0.21	0.21	248.3	19/60	1								
39.94	A.SCRALLPSLHRP.F	2010.12834	0.00327	6.49E-03	0.05	1.30	0.17	0.17	249.7	18/64	1								
40.05	L.PSLHRP.F	1454.81645	0.00131	2.50E-02	0.08	1.26	0.11	0.11	297.4	18/44	1								
40.25	A.LLPSLHRP.F	1597.89951	0.00391	4.40E-04	0.83	3.17	0.37	0.37	311.4	15/24	1								
41.16	R.ALLPSLHRP.F	1638.93662	0.00090	8.73E-04	0.11	1.94	0.13	0.13	212.0	14/53	1								
41.25 - 41.27	R.ALLPSLHRP.F	1638.93662	0.00202	5.43E-05	0.79	3.13	0.45	0.45	355.7	13/26	1								
2 HBB_HUMAN Hemoglobin subunit beta - Homo sapiens			2	3.55E-08	13.00	200.22	15988.3		15988.3	22 (22 0 0 0 0)									
3 ANK1_HUMAN Ankyrin-1 - Homo sapiens			7.01E-06	6.94	110.23		206136.2		206136.2	11 (11 0 0 0 0)									
4 SYUA_HUMAN Alpha-synuclein - Homo sapiens			2.79E-06	6.10	80.24		14451.2		14451.2	8 (8 0 0 0 0)									
5 HSPB1_HUMAN Heat shock protein beta-1 - Homo sapiens			1.15E-10	4.95	66.33		22768.5		22768.5	10 (9 0 1 0 0)									
6 B3AT_HUMAN Band 3 anion transport protein - Homo sapiens			1.19E-04	2.44	66.21		101727.8		101727.8	7 (6 0 1 0 0)									
7 41_HUMAN Protein 4.1 - Homo sapiens			1.18E-04	2.65	56.23		96857.3		96857.3	6 (5 0 1 0 0)									
8 G3P_HUMAN Glyceraldehyde-3-phosphate dehydrogenase - Homo sapiens			3.80E-04	4.10	50.25		36030.4		36030.4	5 (5 0 0 0 0)									
9 GLPC_HUMAN Glycophorin-C - Homo sapiens			1.44E-09	1.92	30.25		13801.7		13801.7	3 (3 0 0 0 0)									
11 TCPW_HUMAN T-complex protein 1 subunit zeta-2 - Homo sapiens			6.44E-04	2.43	30.18		4510.4		4510.4	3 (3 0 0 0 0)									
12 SYSC_HUMAN Seryl-tRNA synthetase, cytoplasmic - Homo sapiens			1.17E-04	1.39	28.21		57728.6		57728.6	3 (2 1 0 0 0)									
13 RLAD_HUMAN 60S acidic ribosomal protein P0 - Homo sapiens			9.46E-05	1.54	20.17		58740.1		58740.1	2 (2 0 0 0 0)									
14 OXSR1_HUMAN Serine/threonine-protein kinase OSR1 - Homo sapiens			3.37E-04	1.61	20.16		34251.8		34251.8	2 (2 0 0 0 0)									
15 DBPA_HUMAN DNA-binding protein A - Homo sapiens			2.50E-05	0.91	10.20		57986.2		57986.2	1 (1 0 0 0 0)									
16 CHMB_HUMAN Charged multivesicular body protein 4b - Homo sapiens			2.89E-04	0.94	10.20		40066.1		40066.1	1 (1 0 0 0 0)									
17 SOCBI_HUMAN Synectin-1 - Homo sapiens			8.09E-04	0.65	10.18		24934.6		24934.6	1 (1 0 0 0 0)									
18 TCPH_HUMAN T-complex protein 1 subunit eta - Homo sapiens			1.18E-04	0.83	10.18		32423.9		32423.9	1 (1 0 0 0 0)									
19 ACTA_HUMAN Actin, aortic smooth muscle - Homo sapiens			2.07E-07	0.91	10.17		59329.0		59329.0	1 (1 0 0 0 0)									
20 NP1L_HUMAN Nucleosome assembly protein 1-like 4 - Homo sapiens			2.53E-04	0.68	10.17		41981.8		41981.8	1 (1 0 0 0 0)									
21 ICAL_HUMAN Calpastatin - Homo sapiens			1.91E-04	0.80	10.17		42797.0		42797.0	1 (1 0 0 0 0)									
22 ALG1_HUMAN Chitinobiosylidiphosphoridic acid beta-mannosyltransferase - Homo sapiens			5.17E-04	0.63	10.15		76526.3		76526.3	1 (1 0 0 0 0)									
			1.30E-05	0.04	8.08		52484.0		52484.0	1 (0 1 0 0 0)									

TABLE 2 (Continued)

HB H-C	1 HBA_HUMAN Hemoglobin subunit alpha=Constant Spring	2.51E-08	14.17	254.21	18600.8	35 (28 3 1 2 1)
25.92	A VPPARWASQ	1.62E-02	0.83	2.13	0.16	1
27.41	A VPPARWASQR	5.26E-03	0.82	2.68	0.21	1
29.97	ALLPSLRPF	3.48E-02	0.30	2.01	0.17	1
30.00	SORALLPSLRPF	6.86E-02	0.43	2.75	0.12	1
30.04	A SORALLPSLRPF	6.34E-03	0.83	3.60	0.12	1
31.47	S VAVPPARWASQR	2.72E-04	0.89	2.21	0.26	1
32.60	A S VAVPPARWASQ	9.36E-03	0.62	2.38	0.15	1
32.61	LLPSLRPF	1.51E-01	0.10	1.45	0.11	1
32.68	GASVAVPPARWASQR	1.46E-02	0.72	2.60	0.26	1
32.69	LLPSLRPF	7.09E-02	0.75	2.37	0.20	1
33.25	ORALLPSLRPF	1.90E-03	0.82	2.99	0.21	1
33.95	ALLPSLRPF	7.35E-03	0.26	1.58	0.12	1
34.65	LLPSLRPF	1.21E-01	0.09	1.36	0.13	1
35.39	LHRPFLVFE-	3.09E-02	0.85	2.21	0.17	1
35.49	RALLPSLRPF	8.01E-03	0.77	2.34	0.23	1
35.77	ALLPSLRPF	5.51E-02	0.44	2.34	0.33	1
35.93	S LHRPFLVFE-	2.50E-02	0.64	2.26	0.16	1
36.32	P LHRPFLVFE-	1.26E-04	0.58	2.60	0.20	1
36.82	V VPPARWASORALLPSLH	8.54E-02	0.12	2.13	0.29	1
38.04	V VPPARWASORALLPSLH	3.09E-02	0.00	1.13	0.15	1
38.37	A SORALLPSLRPF	4.84E-02	0.27	1.85	0.12	1
38.44	SORALLPSLRPF	2.08E-04	0.12	1.66	0.08	1
38.45	Q RALLPSLRPF	4.36E-05	0.20	1.65	0.11	1
38.46	A SORALLPSLRPF	1.70E-03	0.88	3.93	0.35	1
38.50	SORALLPSLRPF	4.69E-03	0.48	2.47	0.26	1
38.59	Q RALLPSLRPF	3.15E-04	0.09	1.14	0.08	1
38.79	LLPSLRPF	7.77E-02	0.19	1.50	0.10	1
39.10	A SORALLPSLRPF	2.14E-04	0.48	2.61	0.34	1
39.86	LLPSLRPF	2.48E-06	0.43	2.02	0.14	1
40.11	ALLPSLRPF	4.48E-02	0.08	1.59	0.01	1
40.14	ALLPSLRPF	9.53E-05	0.87	3.17	0.43	1
40.22	LLPSLRPF	2.53E-03	0.88	3.01	0.39	1
41.14	ALLPSLRPF	2.77E-02	0.01	0.94	0.19	1
41.15	RALLPSLRPF	7.85E-02	0.05	1.54	0.16	1
41.24	RALLPSLRPF	4.24E-07	0.90	3.52	0.46	1
2 HBB_HUMAN Hemoglobin subunit beta - Homo sapiens		2.17E-11	18.19	240.31	15988.3	37 (36 0 0 1 0)
3 SYUA_HUMAN Alpha-synuclein - Homo sapiens		6.27E-07	10.94	144.21	14451.2	17 (16 0 0 1 0)
4 HSPB1_HUMAN Heat shock protein beta-1 - Homo sapiens		7.92E-10	0.85	80.37	22768.5	11 (10 1 0 0 0)
5 47_HUMAN Protein 4.1 - Homo sapiens		1.30E-06	2.68	50.20	96957.3	5 (5 0 0 0 0)
6 EFT1_HUMAN Elongation factor 1-alpha 1 - Homo sapiens		1.96E-04	2.98	44.15	50109.2	5 (2 3 0 0 0)
7 G6VFQ6_HUMAN Hemoglobin beta chain (fragment) - Homo sapiens		2.28E-06	1.87	20.30	4510.4	4 (4 0 0 0 0)
8 B3AT_HUMAN Band 3 anion transport protein - Homo sapiens		5.90E-06	1.48	20.22	101727.8	2 (2 0 0 0 0)
9 TCFP_HUMAN T-complex protein 1 subunit epsilon - Homo sapiens		5.30E-08	1.67	20.21	59329.0	2 (2 0 0 0 0)
10 ANK1_HUMAN Ankyrin-1 - Homo sapiens		4.10E-06	1.74	20.18	206136.2	2 (2 0 0 0 0)
11 Q8IZ0_HUMAN Hemoglobin beta chain variant Hb-L_Toulouse (Fragment) - Homo sapiens		1.14E-06	0.92	10.28	11497.8	1 (1 0 0 0 0)
12 GLPC_HUMAN Glycophorin-C - Homo sapiens		6.10E-07	0.95	10.25	138071.7	1 (1 0 0 0 0)
13 DD12_HUMAN Protein DD1 homolog 2 - Homo sapiens		2.59E-04	0.87	10.24	44494.6	2 (2 0 0 0 0)
14 DEMA_HUMAN Densin - Homo sapiens		9.93E-07	0.87	10.23	45486.3	1 (1 0 0 0 0)
15 LASP1_HUMAN LIM and SH3 domain protein 1 - Homo sapiens		2.67E-05	0.87	10.19	29698.2	1 (1 0 0 0 0)
16 PRDX2_HUMAN Peroxisomal protein 2 - Homo sapiens		5.63E-05	0.25	10.16	21878.2	3 (3 0 0 0 0)
17 TCPE_HUMAN T-complex protein 1 subunit epsilon - Homo sapiens		9.97E-05	0.10	10.11	59632.9	1 (1 0 0 0 0)

TABLE 2 (Continued)

M / Z (mass to charge ratio)			Hb CS peptides
[M+H] ⁺	[M+2H] ²⁺	[M+3H] ³⁺	
1396.7332	698.8702		¹⁴⁴ GASVAVPPARWASQ ¹⁵⁷
1268.6746	634.8409		¹⁴⁴ GASVAVPPARWAS ¹⁵⁶
1181.6426	591.3249		¹⁴⁴ GASVAVPPARWA ¹⁵⁵
1110.6055	555.8064		¹⁴⁴ GASVAVPPARW ¹⁵⁴
1339.7117	670.3595		¹⁴⁵ ASVAVPPARWASQ ¹⁵⁷
1906.0657	953.5365	635.0268	¹⁴⁵ SVAVPPARWASQRALLPS ¹⁶¹
1268.6746	634.8409		¹⁴⁵ SVAVPPARWASQ ¹⁵⁷
1140.6160	570.6116		¹⁴⁵ SVAVPPARWAS ¹⁵⁶
982.5469	491.7771		¹⁴⁵ SVAVPPARW ¹⁵⁴
1181.6426	591.3249		¹⁴⁵ VAVPPARWASQ ¹⁵⁷
2858.5940	1429.8007	953.5362	¹⁴⁶ AVPPARWASQRALLPSLHRPFLVFE ¹⁷²
1833.0494	917.0283	611.6880	¹⁴⁶ AVPPARWASQRALLPSL ¹⁶⁵
1719.9653	860.4863	573.9993	¹⁴⁶ AVPPARWASQRALLPS ¹⁶²
1762.0122	881.5098	588.0089	¹⁴⁶ VPPARWASQRALLPSL ¹⁶²
1648.9282	824.9677	550.3142	¹⁴⁶ VPPARWASQRALLPS ¹⁶³
1167.6382	584.3227	389.8842	¹⁴⁶ VPPARWASQR ¹⁵⁶
1011.5370	506.2722		¹⁴⁶ VPPARWASQ ¹⁵⁷
883.4785	442.2429		¹⁴⁶ VPPARWAS ¹⁵⁵
2081.1655	1041.0864	694.3933	¹⁵⁵ ASQRALLPSLHRPFLVFE ¹⁷²
1705.9860	853.4967	569.3335	¹⁵⁵ ASQRALLPSLHRPFL ¹⁶⁹
1592.9020	796.9546	531.6388	¹⁵⁵ ASQRALLPSLHRPFL ¹⁶⁵
2010.1283	1005.5678	670.7143	¹⁵⁵ SQRALLPSLHRPFLVFE ¹⁷²
1634.9489	817.9781	545.6545	¹⁵⁵ SQRALLPSLHRPFL ¹⁶⁹
1521.8649	761.4361	507.9598	¹⁵⁵ SQRALLPSLHRPFL ¹⁶⁵
1374.7964	687.9019	458.9370	¹⁵⁵ SQRALLPSLHRP ¹⁶⁷
984.5837	492.7955		¹⁵⁵ SQRALLPSL ¹⁶⁴
1923.0963	962.0518	641.7036	¹⁵⁷ QRALLPSLHRPFLVFE ¹⁷²
1547.9169	774.4621	516.6438	¹⁵⁷ QRALLPSLHRPFL ¹⁶⁹
1434.8328	717.9201	478.9491	¹⁵⁷ QRALLPSLHRPFL ¹⁶⁵
1287.7644	644.3858	429.9263	¹⁵⁷ QRALLPSLHRP ¹⁶⁷
1795.0377	898.0225	599.0174	¹⁵⁹ RALLPSLHRPFLVFE ¹⁷²
1419.8583	710.4328	473.9576	¹⁵⁹ RALLPSLHRPFL ¹⁶⁹
1306.7743	653.8908	436.2629	¹⁵⁹ RALLPSLHRPFL ¹⁶⁵
1159.7058	580.3566	387.2401	¹⁵⁹ RALLPSLHRP ¹⁶⁷
1638.9366	819.9720	546.9837	¹⁵⁹ ALLPSLHRPFLVFE ¹⁷²
1263.7572	632.3822	421.9239	¹⁵⁹ ALLPSLHRPFL ¹⁶⁵
1150.6731	575.8402	384.2292	¹⁵⁹ ALLPSLHRPFL ¹⁶⁹
1003.6047	502.3060	335.2064	¹⁵⁹ ALLPSLHRP ¹⁶⁷

TABLE 3

1567.8995	784.4534	523.3047	¹⁶⁰ LLPSLHRPFLVFE ¹⁷²
1438.8569	719.9321	480.2905	¹⁶⁰ LLPSLHRPFLVF ¹⁷¹
1150.6731	575.8402	384.2292	¹⁶² LLPSLHRPF ¹⁶⁹
1454.8154	727.9114	485.6100	¹⁶¹ LPSLHRPFLVFE ¹⁷³
1325.7729	663.3901	442.5958	¹⁶¹ LPSLHRPFLVF ¹⁷¹
1178.7044	589.8559	393.5730	¹⁶¹ LPSLHRPFLV ¹⁷⁰
1079.6360	540.3217	360.5502	¹⁶¹ LPSLHRPFL ¹⁶⁹
966.5520	483.7796	322.8555	¹⁶¹ LPSLHRPF ¹⁶⁰
819.4835	410.2454	273.8327	¹⁶¹ LPSLHRP ¹⁶⁷
1341.7314	671.3693	447.9153	¹⁶² PSLHRPFLVFE ¹⁷¹
853.4679	427.2376	285.1608	¹⁶² PSLHRPF ¹⁶⁸
1244.6786	622.8429	415.5644	¹⁶⁵ SLHRPFLVFE ¹⁷²
1157.6466	579.3269	386.5537	¹⁶⁴ LHRPFLVFE ¹⁷¹
1044.5625	522.7849	348.8590	¹⁶⁵ HRPFLVFE ¹⁷²
915.5199	458.2636	305.8448	¹⁶⁵ HRPFLVF ¹⁷¹
907.5036	454.2554		¹⁶⁶ RPFLVFE ¹⁷²
3044.6945	1522.8309	1015.569	¹⁴⁶ SVAVPPARWASQRALLPSLHRPFLVFE ¹⁷²
971.5170	486.2621	324.5105	¹⁵¹ PARWA SQR ¹⁵⁶
906.5520	453.7796	302.8555	¹⁵⁵ ALLPSL HR ¹⁵⁸

TABLE 3 (Continued)

M / Z (Mass to Charge Ratio)			Hb E Peptides
[M+H] ⁺	[M-2H] ²⁺	[M-3H] ³⁺	
4568.4875	2282.2436	1521.8291	⁴⁴ VHLTPEEKSAVTALWGKVNDEVGGKALGRLLVYPWTQRF ⁴⁴
4260.818	2130.659	1420.7726	⁴² VHLTPEEKSAVTALWGKVNDEVGGKALGRLLVYPWTQ ⁴²
3585.016	1793.008	1195.672	⁴² VHLTPEEKSAVTALWGKVNDEVGGKALGRLLV ⁴²
3485.9478	1743.4776	1162.6541	⁴² VHLTPEEKSAVTALWGKVNDEVGGKALGRLLV ⁴²
3386.8794	1693.9397	1129.6264	⁴² VHLTPEEKSAVTALWGKVNDEVGGKALGRLL ⁴²
3273.7954	1637.3977	1091.9318	⁴² VHLTPEEKSAVTALWGKVNDEVGGKALGR ⁴²
3004.61	1502.8087	1002.2083	⁴² VHLTPEEKSAVTALWGKVNDEVGGKALG ⁴²
2634.5046	1317.7523	945.50153	⁴² VHLTPEEKSAVTALWGKVNDEVGGKA ⁴²
2768.495	1384.7415	923.4843	⁴³ LTPEEKSAVTALWGKVNDEVGGKALG ⁴³
3136.7565	1568.8681	1046.2454	⁴⁴ TPEEKSAVTALWGKVNDEVGGKALGRLLV ⁴⁴
2355.8142	1178.1573	785.7716	⁴² KSAVTALWGKVNDEVGGKALGR ⁴²
2199.2152	1100.1102	733.7426	⁴² KSAVTALWGKVNDEVGGKALG ⁴²
2552.4558	1276.7316	851.4901	⁴⁵ SAVTALWGKVNDEVGGKALGRLLV ⁴⁵
2071.1182	1036.0628	691.0445	⁴⁵ SAVTALWGKVNDEVGGKALG ⁴⁵
3372.858	1686.9326	1124.9575	⁴² TALWGKVNDEVGGKALGRLLVYPWTQRF ⁴²
2968.6407	1484.824	990.2124	⁴² TALWGKVNDEVGGKALGRLLVYPWTQ ⁴²
2654.5027	1327.7551	885.5058	⁴² TALWGKVNDEVGGKALGRLLVYP ⁴²
2394.3867	1197.6933	798.7955	⁴² TALWGKVNDEVGGKALGRLLV ⁴²
2295.5184	1148.1628	765.7776	⁴² TALWGKVNDEVGGKALGRLLV ⁴²
2196.25	1098.6286	732.7548	⁴² TALWGKVNDEVGGKALGRLL ⁴²
2083.1658	1042.0666	695.0501	⁴² TALWGKVNDEVGGKALGR ⁴²
1970.0818	985.5445	657.3654	⁴² TALWGKVNDEVGGKALGR ⁴²
1818.9907	907.494	605.3317	⁴² TALWGKVNDEVGGKALG ⁴²

TABLE 4

M / Z (Mass to Charge Ratio)			Hb E Peptides
[M+H] ⁺	[M-2H] ²⁺	[M-3H] ³⁺	
1756.9592	878.9832	586.3246	²² TALWGKVNVDVEGGKAL ²⁵
1643.8751	822.4412	548.6299	²² TALWGKVNVDVEGGKA ²⁷
1572.838	786.919	524.946	²² TALWGKVNVDVEGGK ²⁸
2194.2705	1097.639	732.0951	²³ ALWGKVNVDVEGGKALGRLLV ²⁵
2095.2021	1048.1048	699.0723	²³ ALWGKVNVDVEGGKALGRLL ³²
1869.054	935.0174	623.6782	²³ ALWGKVNVDVEGGKALGR ³²
1712.958	856.9701	571.6492	²³ ALWGKVNVDVEGGKALG ²⁸
1635.9115	828.4594	552.642	²³ ALWGKVNVDVEGGKAL ²⁸
1542.8274	771.9137	514.9424	²³ ALWGKVNVDVEGGKA ²⁷
1471.7904	736.3965	491.2623	²³ ALWGKVNVDVEGGK ²⁸
3200.7752	1600.6866	1067.5910	²⁴ LWGKVNVDVEGGKALGRLLVVYPWTQRF ⁴¹
2897.6055	1449.3054	966.5394	²⁴ LWGKVNVDVEGGKALGRLLVVYPWTQ ²⁸
2482.418	1241.709	828.1395	²⁴ LWGKVNVDVEGGKALGRLLVVYP ²⁵
2123.2534	1062.1204	708.416	²⁴ LWGKVNVDVEGGKALGRLLV ²⁵
1911.081	956.0442	637.6985	²⁴ LWGKVNVDVEGGKALGRLL ³¹
1797.997	899.5021	600.0058	²⁴ LWGKVNVDVEGGKALGR ³²
1641.8959	821.4516	547.9701	²⁴ LWGKVNVDVEGGKALG ²⁸
1584.8744	792.9408	528.963	²⁴ LWGKVNVDVEGGKAL ²⁸
1400.7532	700.8803	467.5893	²⁴ LWGKVNVDVEGGK ²⁵
2784.5195	1392.7624	928.8447	²⁵ WSKVNVDVEGGKALGRLLVVYPWTQ ²⁵
2369.834	1185.167	790.4446	²⁵ WSKVNVDVEGGKALGRLLVVYP ²⁵
2010.1494	1005.5784	670.7213	²⁵ WSKVNVDVEGGKALGRLLV ²⁵
1911.081	956.0405	637.6956	²⁵ WSKVNVDVEGGKALGRLL ³¹

TABLE 4 (Continued)

M / Z (Mass to Charge Ratio)			Hb E Peptides
[M+H] ⁺	[M-2H] ²⁺	[M-3H] ³⁺	
1797.997	899.5021	600.0038	²⁵ WGKVNVDDEVGGKALGRL ³¹
1684.915	842.9601	562.3032	²⁵ WGKVNVDDEVGGKALGR ³²
1538.8118	764.9095	510.2755	²⁵ WGKVNVDDEVGGKALG ³⁵
1471.7903	736.3986	491.2685	²⁵ WGKVNVDDEVGGKAL ³⁸
1287.6592	644.3381	429.8946	²⁵ WGKVNVDDEVGGK ³⁸
2598.4402	1299.7238	866.8185	²⁶ GKVNVDDEVGGKALGRLLVYPWTQ ³³
2183.2546	1092.131	728.4231	²⁶ GKVNVDDEVGGKALGRLLVYP ³⁵
1824.0702	912.5387	608.6949	²⁶ GKVNVDDEVGGKALGRLLV ³³
1725.0037	863.0045	573.6721	²⁶ GKVNVDDEVGGKALGRLL ³²
1611.9176	806.4625	537.9774	²⁶ GKVNVDDEVGGKALGR ³¹
1498.8535	749.9204	500.2827	²⁶ GKVNVDDEVGGKALGR ³⁰
1342.7535	671.8689	448.249	²⁶ GKVNVDDEVGGKALG ²⁸
1285.711	643.3592	429.2419	²⁶ GKVNVDDEVGGKAL ²⁸
1172.627	586.8171	391.5472	²⁶ GKVNVDDEVGGKA ²⁷
1101.5893	551.2986	367.8681	²⁶ GKVNVDDEVGGK ²⁶
1767.0437	884.025	589.6877	²⁷ KVNVDDEVGGKALGRLLV ³³
1667.9902	834.4986	556.6649	²⁷ KVNVDDEVGGKALGRLL ³²
1554.8952	777.9517	518.9703	²⁷ KVNVDDEVGGKALGR ³¹
1441.8121	721.4097	481.2756	²⁷ KVNVDDEVGGKALGR ³⁰
1285.721	643.3592	429.2419	²⁷ KVNVDDEVGGKALG ²⁸
1228.6896	614.8464	410.2347	²⁷ KVNVDDEVGGKAL ²⁸
1115.6055	558.3064	372.54	²⁷ KVNVDDEVGGKA ²⁷
1044.5694	522.7878	348.861	²⁷ KVNVDDEVGGK ²⁶

TABLE 4 (Continued)

M / Z (Mass to Charge Ratio)			Hb E Peptides
[M+H] ⁺	[M-2H] ²⁺	[M-3H] ³⁺	
2413.8237	1207.1653	805.1128	¹⁶ VNVDEVGGKALGRLLVYPWTQ ³⁵
1998.1532	999.5728	666.7176	¹⁶ VNVDEVGGKALGRLLVYP ³⁶
1638.9537	819.9768	546.9845	¹⁶ VNVDEVGGKALGRLLV ³³
1426.8013	713.9043	476.2719	¹⁶ VNVDEVGGKALGRLL ³²
1313.7172	657.3622	438.5772	¹⁶ VNVDEVGGKALGR ³⁰
1157.6161	579.3117		¹⁶ VNVDEVGGKALG ²⁹
1100.5946	550.2009		¹⁶ VNVDEVGGKAL ²⁸
967.51056	494.2569		¹⁶ VNVDEVGGKA ²⁷
916.47345	458.7404		¹⁶ VNVDEVGGK ²⁶
2617.4248	1309.2161	873.1455	¹⁶ NVDEVGGKALGRLLVYPWTQRF ³⁴
2314.2554	1157.6277	772.0851	¹⁶ NVDEVGGKALGRLLVYPWTQ ³²
1539.8253	770.4463	513.9566	¹⁶ NVDEVGGKALGRLLV ³¹
1440.8269	720.9064	480.9589	¹⁶ NVDEVGGKALGRLL ³¹
1214.6493	607.823	405.3544	¹⁶ NVDEVGGKALGR ³⁰
1058.5476	529.7775		¹⁶ NVDEVGGKALG ²⁹
1001.5262	501.2667		¹⁶ NVDEVGGKAL ²⁸
2503.882	1252.1946	835.1322	²⁰ VDEVGGKALGRLLVYPWTQRF ⁴¹
2200.3124	1100.6062	734.0703	²⁰ VDEVGGKALGRLLVYPWTQ ³⁸
1425.8424	713.4248	475.9523	²⁰ VDEVGGKALGRLLV ³³
1326.7759	663.8873	442.9243	²⁰ VDEVGGKALGRLL ³²
1100.6053	550.8066	367.5401	²⁰ VDEVGGKALGR ³⁰
944.5047	472.756		²⁰ VDEVGGKALG ²⁹
867.4853	444.2453		²⁰ VDEVGGKAL ²⁸

TABLE 4 (Continued)

M / Z (Mass to Charge Ratio)			Hb E Peptides
[M+H] ⁺	[M-2H] ²⁺	[M-3H] ³⁺	
774.3932	587.6996		²⁰ VDEVGGKA ²⁷
1404.3135	1202.6604	602.1034	²¹ DEVGGKALGRLLVVPWTQRF ²⁵
2101.144	1051.072	701.048	²¹ DEVGGKALGRLLVVPWTQ ²⁶
1326.7739	663.8869	442.9246	²¹ DEVGGKALGRLLV ³³
1227.7056	614.3528	409.9018	²¹ DEVGGKALGRLL ³²
1001.5574	501.2687	334.5124	²¹ DEVGGKALGR ³¹
2289.2866	1145.1433	763.7622	²² EVGGKALGRLLVVPWTQRF ²¹
1986.1171	993.5622	662.7105	²² EVGGKALGRLLVVPWTQ ³⁵
1211.7471	606.37355	404.5825	²² EVGGKALGRLLV ³¹
1112.6786	556.8429	371.5644	²² EVGGKALGRLL ³²
866.5105	443.7552	296.1701	²² EVGGKALGR ³⁰
601.36675	301.187		²³ VGGKALG ²⁵
2061.1756	1031.0915	687.7301	²⁴ GKALGRLLVVPWTQRF ⁴¹
1758.0061	879.50305	586.6687	²⁴ GKALGRLLVVPWTQ ³⁶
1245.7677	623.3841	415.9228	²⁴ GKALGRLLVVY ³²
983.636	492.3217	328.5502	²⁴ GKALGRLLV ³⁵
664.5676	442.7828	295.5225	²⁴ GKALGRLL ³²

TABLE 4 (Continued)