

Supplementary DATA

Table 1. Identified peptides list to GABA_A receptor α 1 and β 3 subunits

GABA_A receptor $\alpha 1$
Condition 1: sequence coverage 73%

Sequence		Observed	Mr(expt)	Mr(calc)	Ions score	Charge state	Sequence (MS/MS)
Start	End						
27	43	968.70	1935.39	1934.93	18	2	Y.GQPSQDELKDNITVFTR.I
48	55	483.30	964.59	964.46	28	2	R.LLDGYDNR.L
56	63	449.32	896.62	896.52	24	2	R.LRPGLGER.V
57	63	392.78	783.55	783.44	41	2	L.RPGLGER.V
69	93	985.95	2954.82	2953.35	8	3	K.TDIFVTSFGPVSDHDMEYTDVFFR.Q
103	111	524.87	1047.73	1047.59	33	2	K.FKGPMTVLR.L
112	119	453.79	905.56	905.46	36	2	R.LNNLMASK.I
120	129	639.38	1276.75	1276.59	22	2	K.IWTPDTFFHN.G
122	131	582.36	1162.71	1162.54	37	2	W.TPDTFFHNGK.K
147	158	706.96	1411.91	1411.70	64	2	R.ITEDGTLTYMR.L
163	177	611.33	1830.96	1830.70	27	2	R.AECPMHLEDFPMDAH.A
163	182	801.12	2400.35	2400.00	29	3	R.AECPMHLEDFPMDAHACPLK.F
183	190	482.75	963.49	963.44	32	2	K.FGSYAYTR.A
191	199	576.85	1151.69	1151.56	50	2	R.AEVVYEWTR.E
191	203	536.01	1605.01	1604.79	27	3	R.AEVVYEWTR.E
193	199	476.80	951.59	951.48	33	2	E.VVYEWTR.E
204	213	509.82	1017.63	1017.51	63	2	R.SVVVAEDGSR.L
206	213	416.76	831.51	831.41	40	2	V.VVAEDGSR.L
282	300	1007.70	2013.38	2013.08	20	2	R.TVFGVTTVLTMTLSISAR.N
339	346	476.79	951.58	951.46	38	2	K.RGYAWDGK.S
340	346	398.74	795.46	795.36	27	2	R.GYAWDGK.S
347	354	442.32	882.62	882.52	31	2	K.SVVPEPK.K
356	362	406.82	811.63	811.52	37	2	K.VKDPLIK.K
357	362	357.28	712.54	712.45	35	2	V.KDPLIK.K
363	374	665.91	1329.81	1329.62	11	2	K.KNNTYAPTASY.T
363	380	661.76	1982.26	1981.99	27	3	K.KNNTYAPTASYTPNLR.G
364	377	757.96	1513.90	1513.67	16	2	K.NNTYAPTASYTPN.L
364	380	928.07	1854.13	1853.89	38	2	K.NNTYAPTASYTPNLR.G
371	380	547.36	1092.70	1092.56	32	2	T.ATSYTPNLR.G
373	380	461.30	920.58	920.47	26	2	T.SYTPNLR.G
381	390	471.82	941.62	941.52	47	2	R.GDPGLATIAK.S
383	390	385.80	769.58	769.47	54	2	D.PGLATIAK.S
398	409	460.31	1377.90	1377.75	42	3	K.EVKPETKPEPK.K
401	409	511.84	1021.67	1021.54	31	2	K.PETKPEPK.K
410	417	455.81	909.61	909.49	53	2	K.KTFNSVSK.I
410	420	768.00	1533.98	1533.60	10	2	K.KTFNSVSKIDR.L
424	444	844.58	2530.73	2530.38	24	3	R.IAFPLLFGINLVYWAYTLNR.E
436	444	593.39	1184.76	1184.60	28	2	L.VYWAYTLNR.E

GABA_A receptor $\alpha 1$
Condition 2: sequence coverage 64%

Sequence		Observed	Mr(expt)	Mr(calc)	Ions score	Charge state	Sequence (MS/MS)
Start	End						
27	43	968.70	1935.39	1934.93	20	2	Y.GQPSQDELKDNITVFTR.I
44	55	488.34	1461.98	1461.76	22	3	R.ILDRLLDGYDNR.L
45	55	675.44	1348.86	1348.67	13	2	I.LDRLLDGYDNR.L
46	55	618.89	1235.76	1235.59	17	2	L.DRLLDGYDNR.L
48	55	483.30	964.58	964.46	29	2	R.LLDGYDNR.L
56	63	449.32	896.62	896.52	27	2	R.LRPGLGER.V
56	68	485.36	1453.06	1452.84	7	3	R.LRPGLGERVTEVK.T
57	63	392.78	783.55	783.44	28	2	L.RPGLGER.V
94	102	397.27	1188.80	1188.63	24	3	R.OSWKDERLK.F
95	102	531.35	1060.69	1060.57	16	2	Q.SWKDERLK.F
101	111	435.98	1304.93	1304.76	29	3	R.LKFKGPMTVLR.L
103	111	524.88	1047.74	1047.59	51	2	K.FKGPMTVLR.L
105	111	387.29	772.56	772.43	17	2	K.GPMTVLR.L
112	119	453.79	905.57	905.46	15	2	R.LNNLMASK.I
120	131	488.32	1461.94	1461.70	15	3	K.IWTPDTFFHNGK.K
120	132	531.02	1590.03	1589.80	23	3	K.IWTPDTFFHNGK.K.S
125	132	489.82	977.63	977.51	23	2	D.TFFHNGK.K.S
133	143	481.95	958.07	957.93	12	2	K.SVAHNMTMPNK.L
147	158	706.95	1411.89	1411.70	52	2	R.ITEDGTLTYMRL.L
147	162	633.43	1897.28	1897.00	13	3	R.ITEDGTLTYMRLTVR.A
163	182	801.16	2400.45	2400.00	7	3	R.AECPMHLEDFPMDAHACPLK.F
191	199	576.87	1151.72	1151.56	49	2	R.AEVVYEWTR.E
191	203	536.02	1605.03	1604.79	38	3	R.AEVVYEWTR.EPAR.S
193	203	703.47	1404.92	1404.71	33	2	E.VVYEWTR.EPAR.S
194	203	653.92	1305.83	1305.65	13	2	V.VYEWTR.EPAR.S
195	203	604.39	1206.76	1206.58	13	2	V.YEWTR.EPAR.S
204	213	509.83	1017.64	1017.51	50	2	R.SVVAEDGSR.L
206	213	416.77	831.52	831.41	43	2	V.VVAEDGSR.L
276	300	885.28	2652.81	2652.42	12	3	R.ESVPARTVFGVTVLTMTTLSISAR.N
282	300	672.16	2013.46	2013.08	30	3	R.TVFGVTVLTMTTLSISAR.N
282	305	851.97	2552.89	2552.39	6	3	R.TVFGVTVLTMTTLSISARNSLPK.V
339	346	476.79	951.57	951.46	25	2	K.RGYAWDGK.S
340	346	398.74	795.46	795.36	28	2	R.GYAWDGK.S
356	362	406.82	811.63	811.52	32	2	K.VKDPLIK.K
363	380	661.76	1982.27	1981.99	34	3	K.KNNTYAPTATSYTPNLR.G
364	380	928.06	1854.11	1853.89	52	2	K.NNTYAPTATSYTPNLR.G
381	390	471.81	941.61	941.52	46	2	R.GDPGLATIAK.S
383	390	385.80	769.58	769.47	44	2	D.PGLATIAK.S
398	409	460.31	1377.92	1377.75	33	3	K.EVKPETKPPPEPK.K
401	409	511.85	1021.68	1021.54	41	2	K.PETKPPPEPK.K
410	420	432.30	1293.86	1293.70	52	3	K.KTFNSVSKIDR.L
411	423	508.35	1522.04	1521.83	33	3	K.TFNSVSKIDRLSR.I
412	423	474.66	1420.96	1420.78	40	3	T.FNSVSKIDRLSR.I
424	444	844.59	2530.75	2530.38	29	3	R.IAFPFLFGIFNLVYATYLNLR.E
424	444	844.64	2530.90	2530.38	7	3	R.IAFPFLFGIFNLVYATYLNLR.E
424	455	940.67	3758.63	3757.02	8	3	R.IAFPFLFGIFNLVYATYLNLR.EPQKAPTHQ.-

GABA_A receptor $\alpha 1$
Condition 3: sequence coverage 55%

Sequence		Observed	Mr(expt)	Mr(calc)	Ions score	Charge state	Sequence (MS/MS)
Start	End						
27	43	968.70	1935.39	1934.93	15	2	Y.GQPSODELKDNTTVFTR.I
44	55	488.33	1461.96	1461.76	31	3	R.ILDRLLDGYDNR.L
45	55	675.45	1348.89	1348.67	33	2	I.LDRLLDGYDNR.L
46	55	618.90	1235.78	1235.59	12	2	L.DRLLDGYDNR.L
48	55	483.30	964.58	964.46	23	2	R.LLDGYDNR.L
56	63	449.32	896.62	896.52	26	2	R.LRPGLGER.V
57	63	392.78	783.55	783.44	31	2	L.RPGLGER.V
103	111	532.87	1063.73	1063.58	49	2	K.FKGPMTVLR.L
104	111	459.31	916.61	916.52	47	2	F.KGPMTVLR.L
105	111	387.28	772.55	772.43	56	2	K.GPMTVLR.L
112	119	453.79	905.57	905.46	42	2	R.LNNLMASK.I
120	131	488.31	1461.90	1461.70	34	3	K.IWTPDTFFHNGK.K
120	132	531.02	1590.04	1589.80	19	3	K.IWTPDTFFHNGK.K
122	131	582.37	1162.73	1162.54	50	2	W.TPDTFFHNGK.K
125	132	489.82	977.63	977.51	19	2	D.TFFHNGK.K
126	132	439.29	876.57	876.46	19	2	T.TFFHNGK.K
147	158	706.97	1411.92	1411.70	53	2	R.ITEDGTLTYTMR.L
147	162	633.44	1897.31	1897.00	35	2	R.ITEDGTLTYMRLTVR.A
163	182	801.16	2400.45	2400.00	32	3	R.AECPMHLEDFPMDAHACPLK.F
183	190	482.80	963.58	963.44	35	2	K.FGSYAYTR.A
191	199	576.88	1151.74	1151.56	52	2	R.AEVVYEWTR.E
191	203	536.02	1605.03	1604.79	27	3	R.AEVVYEWTR.E
193	203	703.46	1404.91	1404.71	23	2	E.VVYEWTR.E
194	203	653.93	1305.84	1305.65	31	2	V.VYEWTR.E
195	203	604.38	1206.74	1206.58	16	2	V.YEWTR.E
204	213	509.83	1017.66	1017.51	48	2	R.SVVVAEDGSR.L
206	213	416.77	831.52	831.41	43	2	V.VVAEDGSR.L
282	300	672.16	2013.45	2013.08	35	3	R.TVFGVTTVLTMTLSISAR.N
339	346	476.79	951.57	951.46	35	2	K.RGYAWDGK.S
340	346	398.74	795.47	795.36	29	2	R.GYAWDGK.S
340	354	554.38	1660.12	1659.86	31	3	R.GYAWDGKSVPEKPK.K
347	354	442.32	882.63	882.52	33	2	K.SVPEKPK.K
356	362	406.82	811.63	811.52	32	2	K.VKDPLIK.K
357	362	357.28	712.55	712.45	30	2	V.KDPLIK.K
363	380	661.77	1982.29	1981.99	48	3	K.KNNTYAPTATSYTPNLR.G
364	380	928.07	1854.12	1853.89	38	2	K.NNTYAPTATSYTPNLR.G
381	390	471.82	941.63	941.52	46	2	R.GDPGLATIAK.S
383	390	385.80	769.58	769.47	63	2	D.PGLATIAK.S
398	409	460.31	1377.91	1377.75	42	3	K.EVKPETKPEPK.K
401	409	511.85	1021.68	1021.54	46	2	K.PETKPEPK.K
410	417	455.82	909.62	909.49	27	2	K.KTFNSVSK.I
410	420	432.30	1293.87	1293.70	32	3	K.KTFNSVSKIDR.L
411	420	583.90	1165.79	1165.61	20	2	K.TFNSVSKIDR.L
411	423	508.35	1522.03	1521.83	25	3	K.TFNSVSKIDRLSR.I
424	444	844.60	2530.78	2530.38	21	3	R.IAFPLLFIFNLVYVATYLN.R

GABA_A receptor $\alpha 1$

Condition 4: sequence coverage 66%

Sequence		Observed	Mr(expt)	Mr(calc)	Ions score	Charge state	Sequence (MS/MS)
Start	End						
42	52	667.98	1333.94	1333.74	11	2	F.TRILDRLLDGY.D
43	49	449.85	897.69	897.58	17	2	T.RILDRLL.D
57	72	606.44	1816.30	1815.98	8	3	L.RPGLGERVTEVKTDF.V
77	86	575.32	1148.62	1148.44	14	2	F.GPVSDHMEY.T
77	91	863.02	1724.02	1723.74	15	2	F.GPVSDHMEYTDV.F
92	96	362.24	722.47	722.35	12	2	F.FRQSW.K
97	103	468.33	934.65	934.52	15	2	W.KDERLKF.K
113	121	546.86	1091.70	1091.54	39	2	L.NNLMASKIW.T
114	121	489.82	977.62	977.50	24	2	N.NLMASKIW.T
116	121	376.25	750.49	750.37	19	2	L.MASKIW.T
116	127	730.48	1458.94	1458.69	6	2	L.MASKWTPDTFF.H
145	154	565.91	1129.81	1129.63	12	2	L.LRITEDGTL.LY
145	155	647.46	1292.91	1292.70	35	2	L.LRITEDGTL.LY.T
146	154	509.35	1016.69	1016.55	18	2	L.RITEDGTL.LY
146	155	590.91	1179.80	1179.61	44	2	L.RITEDGTL.LY.T
160	169	615.47	1228.93	1228.57	3	2	L.TVRAECPMHL.E
187	195	536.35	1070.68	1070.54	38	2	Y.AYTRAEVVY.E
187	197	693.95	1385.88	1385.66	41	2	Y.AYTRAEVVYEW.T
189	197	576.88	1151.74	1151.56	22	2	Y.TRAEVVYEW.T
196	214	719.83	2156.48	2156.10	30	3	Y.EWTREPARSVVAEDGSRL.N
198	214	614.77	1841.28	1840.98	28	3	W.TREPARSVVAEDGSRL.N
198	217	749.85	2246.51	2246.14	20	3	W.TREPARSVVAEDGSRLNQY.D
205	214	522.86	1043.71	1043.56	37	2	S.VVAEDGSRL.N
207	214	423.78	845.55	845.42	27	2	V.VAEDGSRL.N
207	217	626.40	1250.78	1250.59	30	2	V.VAEDGSRLNQY.D
218	230	672.96	1343.90	1343.69	27	2	Y.DLLGQTVDSGIVQ.S
231	243	737.95	1473.89	1473.64	51	2	Q.SSTGEYVMTTHF.H
237	243	417.77	833.53	833.41	40	2	Y.VVMTTHF.H
249	275	652.13	1301.11	1301.02	8	2	K.IGYFVIQTYLPCIMTVILSQVSWFLNR.E
258	266	538.38	1074.74	1074.58	32	2	Y.LPCIMTVIL.S
263	271	497.35	992.69	992.55	30	2	M.TVILSQVSF.W
263	272	590.45	1178.89	1178.63	14	2	M.TVILSQVSW.L
272	284	525.70	1574.07	1573.84	14	3	F.WLNRESVPARTVF.G
273	280	443.30	884.59	884.47	21	2	W.LNRESVPA.R
273	284	463.65	1387.93	1387.76	17	3	W.LNRESVPARTVF.G
274	284	638.45	1274.88	1274.67	17	2	L.NRESVPARTVF.G
302	308	389.29	776.57	776.44	15	2	N.SLPKVAY.A
309	320	732.45	1462.89	1462.63	5	2	Y.ATAMDWFIACVY.A
325	335	614.43	1226.84	1226.62	12	2	F.SALIEFATVNY.F
344	360	622.14	1863.40	1863.08	22	3	W.DGKSVVPEKPKVKDPLI
350	360	426.99	1277.95	1277.77	18	3	V.PEKKVKDPLI
350	362	507.40	1519.17	1518.95	30	3	V.PEKKVKDPLIK.K
375	385	555.88	1109.75	1109.58	25	2	Y.TPNLARGDPGLA
375	386	591.41	1180.80	1180.62	33	2	Y.TPNLARGDPGLA.T
375	387	641.93	1281.84	1281.67	28	2	Y.TPNLARGDPGLA.TI
375	388	698.50	1394.98	1394.75	20	2	Y.TPNLARGDPGLA.TIA
375	389	734.02	1466.03	1465.79	14	2	Y.TPNLARGDPGLA.TIA.K
375	390	532.38	1594.11	1593.88	33	3	Y.TPNLARGDPGLA.TIA.K.S
375	392	585.09	1752.23	1751.95	24	3	Y.TPNLARGDPGLA.TIA.K.SA.T

GABA_A receptor $\alpha 1$

Condition 5: sequence coverage 49%

Sequence		Observed	Mr(expt)	Mr(calc)	Ions score	Charge state	Sequence (MS/MS)
Start	End						
42	52	667.99	1333.97	1333.74	11	2	F.TRILDRLLDGY.D
73	86	800.47	1598.93	1598.66	1	2	F.VTSFGPVSDDHMEY.T
77	86	575.31	1148.61	1148.44	12	2	F.GPVSDDHMEY.T
77	91	871.02	1740.02	1739.73	5	2	F.GPVSDDHMEYTIDVF.F
92	96	362.25	722.48	722.35	14	2	F.FRQSW.K
97	103	468.33	934.64	934.52	24	2	W.KDERLKF.K
113	121	546.87	1091.72	1091.54	34	2	L.NNLMASKIW.T
114	121	489.83	977.64	977.50	25	2	N.NLMASKIW.T
116	121	376.26	750.50	750.37	19	2	L.MASKIW.T
116	126	656.93	1311.85	1311.62	26	2	L.MASKIWPTDF.F
117	126	583.40	1164.79	1164.58	30	2	M.ASKIWPTDF.F
146	155	590.92	1179.82	1179.61	8	2	L.RITEDGTLLY.T
146	154	509.36	1016.70	1016.55	18	2	L.RITEDGTLL.Y
160	167	482.29	962.56	962.43	17	2	L.TVRAECPM.H
168	181	557.00	1667.99	1667.71	12	3	M.HLEDFPMDAHACPL.K
187	195	536.36	1070.70	1070.54	29	2	Y.AYTRAEVVY.E
196	206	443.96	1328.87	1328.68	13	3	Y.EWTREPARSVV.V
198	214	614.76	1841.25	1840.98	28	3	W.TREPARSVVAEDGSRL.N
198	217	749.87	2246.58	2246.14	15	3	W.TREPARSVVAEDGSRLNQY.D
205	214	522.87	1043.72	1043.56	24	2	S.VVAEDGSRL.N
207	214	423.78	845.55	845.42	42	2	V.VAEDGSRL.N
207	217	626.40	1250.78	1250.59	22	2	V.VAEDGSRLNQY.D
218	230	672.96	1343.91	1343.69	44	2	Y.DLLGQTVDSGIVQ.S
231	243	737.95	1473.89	1473.64	53	2	Q.SSTGEYVVMTHF.H
237	243	425.77	849.52	849.41	37	2	Y.VVMTHF.H
244	252	387.97	1160.89	1160.68	4	3	F.HLKRKIGYF.V
272	284	525.70	1574.09	1573.84	25	3	F.WLNRESVPARTVF.G
273	280	443.30	884.59	884.47	20	2	W.LNRESVPA.R
273	284	694.99	1387.97	1387.76	28	2	W.LNRESVPARTVF.G
274	284	638.45	1274.89	1274.67	31	2	L.NRESVPARTVF.G
285	295	696.97	1391.92	1391.51	16	2	F.GVTTVLTMTL.S
344	354	592.42	1182.83	1182.66	34	2	W.DGKSVVPEKPK.K
344	358	552.08	1653.23	1652.95	17	3	W.DGKSVVPEKPKVKD.P
344	360	622.12	1863.35	1863.08	20	3	W.DGKSVVPEKPKVKDPL.I
350	360	640.01	1278.00	1277.77	24	2	V.PEKPKVKDPL.I
350	362	507.40	1519.17	1518.95	35	3	V.PEKPKVKDPLIK.K
359	367	545.90	1089.79	1089.62	22	2	D.PLIKNNTY.A
375	382	422.29	842.56	842.42	29	2	Y.TPNLARGD.P
375	385	555.89	1109.76	1109.58	22	2	Y.TPNLARGDPGLA
375	386	591.40	1180.78	1180.62	49	2	Y.TPNLARGDPGLA.T
375	387	641.95	1281.89	1281.67	36	2	Y.TPNLARGDPGLA.I
375	389	734.03	1466.04	1465.79	21	2	Y.TPNLARGDPGLATIA.K
375	390	532.39	1594.14	1593.88	29	3	Y.TPNLARGDPGLATIAK.S
375	392	585.09	1752.26	1751.95	15	3	Y.TPNLARGDPGLATIAKSA.T
381	390	471.83	941.85	941.52	13	2	R.GDPGLATIAK.S
388	397	529.40	1056.78	1056.62	30	2	T.IAKSATIEPK.E
389	397	472.84	943.66	943.53	24	2	I.AKSATIEPK.E
413	421	516.37	1030.73	1030.58	43	2	F.NSVSKIDRL.S
413	423	425.64	1273.91	1273.71	19	3	F.NSVSKIDRLSR.I

GABA_A receptor α 1
Condition 6: sequence coverage 52%

Sequence		Observed	Mr(expt)	Mr(calc)	Ions score	Charge state	Sequence (MS/MS)
Start	End						
42	49	500.39	998.77	998.62	24	2	F.TRILDRLL.D
42	52	667.99	1333.97	1333.74	17	2	F.TRILDRLLDGY.D
44	52	539.39	1076.77	1076.59	17	2	R.ILDRLLDGY.D
87	96	649.95	1297.89	1297.65	5	2	Y.TIDVFFRQSW.K
102	110	518.88	1035.74	1035.58	16	2	L.KFKGPMTVL.R
111	121	454.65	1360.92	1360.73	17	3	L.RLNNLMASKIW.T
111	126	641.78	1922.32	1921.97	20	3	L.RLNNLMASKIWTPTDF.F
113	121	546.88	1091.74	1091.54	15	2	L.NNLMASKIW.T
114	121	489.83	977.65	977.50	15	2	N.NLMASKIW.T
116	121	376.26	750.51	750.37	11	2	L.MASKIW.T
143	155	512.38	1534.12	1533.88	20	3	N.KLLRITEDGTLTY.T
145	155	647.47	1292.93	1292.70	15	2	L.LRITEDGTLTY.T
146	155	590.92	1179.82	1179.61	22	2	L.RITEDGTLTY.T
187	197	693.96	1385.91	1385.66	37	2	Y.AYTRAEVVYEW.T
198	214	614.78	1841.33	1840.98	16	3	W.TREPARSVVVAEDGSRL.N
198	217	749.86	2246.57	2246.14	19	3	W.TREPARSVVVAEDGSRLNQY.D
204	213	509.85	1017.68	1017.51	41	2	R.SVVVAEDGSRL.L
204	214	566.39	1130.77	1130.59	37	2	R.SVVVAEDGSRL.N
204	217	769.03	1536.04	1535.76	21	2	R.SVVVAEDGSRLNQY.D
207	217	626.42	1250.82	1250.59	17	2	V.VAEDGSRLNQY.D
231	243	737.96	1473.91	1473.64	34	2	Q.SSTGEYVVMTHF.H
237	243	425.78	849.54	849.41	42	2	Y.VVMTHF.H
272	284	525.71	1574.10	1573.84	16	3	F.WLNRESVPARTVF.G
273	284	463.66	1387.96	1387.76	20	3	W.LNRESVPARTVF.G
296	308	469.33	1404.98	1404.77	8	3	L.SISARNSLPKVAY.A
298	308	603.44	1204.87	1204.66	17	2	I.SARNSLPKVAY.A
337	343	441.30	880.58	880.46	7	2	F.TKRGYAW.D
349	362	540.44	1618.30	1618.02	19	3	V.VPEKPKVKVDPLIK.K
350	360	427.00	1277.98	1277.77	12	3	V.PEKPKVKVDPLI.I
350	362	507.41	1519.20	1518.95	33	3	V.PEKPKVKVDPLIK.K
350	363	550.12	1647.34	1647.04	39	3	V.PEKPKVKVDPLIKK.N
355	367	521.06	1560.17	1559.90	26	3	K.KVKDPLIKKNNTY.A
359	367	545.91	1089.80	1089.62	20	2	D.PLIKKNNTY.A
359	374	594.76	1781.26	1780.94	9	3	D.PLIKKNNTYAPTATSY.T
363	374	665.95	1329.88	1329.62	9	2	K.KNNTYAPTATSY.T
364	374	601.88	1201.74	1201.53	20	2	K.NNTYAPTATSY.T
375	386	591.41	1180.81	1180.62	41	2	Y.TPNLARGDPGLA.T
375	387	641.95	1281.88	1281.67	39	2	Y.TPNLARGDPGLA.T.I
375	389	734.04	1466.06	1465.79	13	2	Y.TPNLARGDPGLATIA.K
375	390	532.39	1594.15	1593.88	31	3	Y.TPNLARGDPGLATIAK.S
375	392	585.10	1752.27	1751.95	28	3	Y.TPNLARGDPGLATIAKSA.T
375	397	774.58	2320.73	2320.27	14	3	Y.TPNLARGDPGLATIAKSATIEPK.E
381	390	471.83	941.65	941.52	21	2	R.GDPGLATIAK.S
383	392	464.84	927.67	927.54	14	2	D.PGLATIAKSA.T
387	397	579.93	1157.85	1157.67	55	2	A.TIAKSATIEPK.E
389	397	472.84	943.68	943.53	25	2	I.AKSATIEPK.E
398	412	585.77	1754.30	1753.96	16	3	K.EVKPETKPEPKKTF.N
413	421	516.38	1030.75	1030.58	16	2	F.NSVSKIDRL.S
413	423	425.65	1273.92	1273.71	29	3	F.NSVSKIDRLSR.I

GABA_A receptor α 1
Condition 7: sequence coverage 53%

Sequence		Observed	Mr(expt)	Mr(calc)	Ions score	Charge state	Sequence (MS/MS)
Start	End						
42	49	500.36	998.70	998.62	24	2	F.TRILDRLL.D
42	52	668.01	1334.01	1333.74	15	2	F.TRILDRLLDGY.D
44	52	539.40	1076.78	1076.59	32	2	R.ILDRLLDGY.D
87	96	649.95	1297.89	1297.65	14	2	Y.TIDVFFRQSW.K
97	103	468.34	934.66	934.52	23	2	W.KDERLKF.K
97	110	560.08	1677.21	1676.93	1	3	W.KDERLKFPGPMTVL.R
111	121	454.65	1360.92	1360.73	19	3	L.RLNNLMASKIW.T
111	126	641.79	1922.34	1921.97	25	3	L.RLNNLMASKIWTPDTF.F
113	121	546.88	1091.74	1091.54	22	2	L.NNLMASKIW.T
114	121	489.83	977.65	977.50	15	2	N.NLMASKIW.T
116	121	376.26	750.51	750.37	20	2	L.MASKIW.T
146	154	509.36	1016.71	1016.55	16	2	L.RITEDGTLL.Y
187	195	536.36	1070.71	1070.54	41	2	Y.AYTRAEVVY.E
187	197	693.96	1385.90	1385.66	19	2	Y.AYTRAEVVYEW.T
198	217	749.88	2246.62	2246.14	16	3	W.TREPARSVVAEDGSRLNQY.D
204	214	566.39	1130.76	1130.59	39	2	R.SVVVAEDGSRL.N
204	217	769.03	1536.05	1535.76	23	2	R.SVVVAEDGSRLNQY.D
205	214	522.87	1043.72	1043.56	38	2	S.VVVAEDGSRL.N
207	214	423.79	845.56	845.42	21	2	V.VAEDGSRL.N
207	217	626.41	1250.81	1250.59	22	2	V.VAEDGSRLNQY.D
218	230	672.98	1343.94	1343.69	19	2	Y.DLLGQTVDSGIVQ.S
237	243	425.78	849.54	849.41	32	2	Y.VVMTHF.H
272	284	525.70	1574.09	1573.84	17	3	F.WLNRESVPARTVF.G
273	284	463.66	1387.96	1387.76	14	3	W.LNRESVPARTVF.G
296	308	469.33	1404.96	1404.77	13	3	L.SISARNSLPKVAY.A
337	343	441.30	880.59	880.46	11	2	F.TKRGYAW.D
342	354	481.00	1439.98	1439.78	47	3	Y.AWDGKSVVPEKPK.K
344	354	395.30	1182.89	1182.66	36	3	W.DGKSVVPEKPK.K
347	354	442.33	882.65	882.52	34	2	K.SVVPEKPK.K
347	358	452.01	1353.01	1352.80	21	3	K.SVVPEKPKVKD.P
349	362	540.44	1618.30	1618.02	15	3	V.VPEKPKVKDPLIK.K
350	358	534.91	1067.81	1067.63	28	2	V.PEKPKVKD.P
350	362	507.41	1519.20	1518.95	20	3	V.PEKPKVKDPLIK.K
350	363	550.12	1647.34	1647.04	19	3	V.PEKPKVKDPLIK.N
355	367	521.06	1560.16	1559.90	15	3	K.KVKDPLIKNNTY.A
356	367	478.35	1432.01	1431.81	19	3	K.VKDPLIKNNTY.A
359	367	545.91	1089.81	1089.62	24	2	D.PLIKNNTY.A
359	374	594.76	1781.25	1780.94	16	3	D.PLIKNNTYAPTATSY.T
375	382	422.29	842.57	842.42	18	2	Y.TPNLARGD.P
375	386	591.41	1180.81	1180.62	31	2	Y.TPNLARGDPGLA.T
375	387	641.96	1281.90	1281.67	32	2	Y.TPNLARGDPGLAT.I
375	389	734.04	1466.06	1465.79	7	2	Y.TPNLARGDPGLATI.A.K
375	390	532.39	1594.15	1593.88	32	3	Y.TPNLARGDPGLATI.A.K.S
375	392	585.10	1752.28	1751.95	17	3	Y.TPNLARGDPGLATI.A.K.S.A.T
375	397	774.57	2320.70	2320.27	24	3	Y.TPNLARGDPGLATI.A.K.SATIEPK.E
381	390	471.83	941.65	941.52	41	2	R.GDPGLATI.A.K.S
383	392	464.84	927.67	927.54	9	2	D.PGLATI.A.K.S.A.T
383	397	499.71	1496.11	1495.86	30	3	D.PGLATI.A.K.SATIEPK.E
387	397	579.95	1157.88	1157.67	19	2	A.TIAKSATIEPK.E

GABA_A receptor $\alpha 1$

Condition 8: sequence coverage 35%

Sequence		Observed	Mr(expt)	Mr(calc)	Ions score	Charge state	Sequence (MS/MS)
Start	End						
36	45	590.44	1178.86	1178.63	20	2	K.DNTTVFTRILD
46	52	426.29	850.56	850.42	33	2	L.DRLLDGY.D
53	69	647.47	1939.39	1939.06	1	3	Y.DNRLRPGLGERVTEVKT.D
70	80	584.91	1167.81	1167.58	34	2	T.DIFVTSFGPVSD.D
70	82	710.97	1419.93	1419.67	54	2	T.DIFVTSFGPVSDH.D
81	88	520.29	1038.57	1038.40	27	2	S.DHDMEYTI.D
89	97	606.93	1211.84	1211.61	27	2	I.DVFFRQSWK.D
91	97	499.85	997.68	997.51	25	2	V.FFRQSWK.D
192	209	707.19	2118.54	2118.07	10	3	A.EVVYEWTRPARSVVVAE.D
200	209	528.88	1055.74	1055.56	20	2	R.EPARSVVVAE.D
210	217	476.79	951.57	951.44	13	2	E.DGSRINQY.D
344	357	513.74	1538.19	1537.92	17	3	W.DGKSVPEKPKVKV.D
350	357	477.36	952.71	952.61	24	2	V.PEKKPKVKV.D
350	358	534.92	1067.82	1067.63	25	2	V.PEKKPKVKD.P
358	377	737.21	2208.60	2208.11	17	3	K.DPLIKKNNTYAPTATSYTPNL
358	381	869.61	2605.82	2605.35	7	3	K.DPLIKKNNTYAPTATSYTPNLARG.D
359	381	831.28	2490.82	2490.32	9	3	D.PLIKNNTYAPTATSYTPNLARG.D
365	381	899.60	1797.19	1796.87	31	2	N.NTYAPTATSYTPNLARG.D
368	381	710.51	1419.00	1418.72	10	2	Y.APTATSYTPNLARG.D
373	381	489.83	977.64	977.49	27	2	T.SYTPNLARG.D
375	386	591.42	1180.83	1180.62	7	2	Y.TPNLARGDPGLA.T
382	394	629.47	1256.92	1256.70	27	2	G.DPGLATIAKSATIE
382	397	538.07	1611.17	1610.89	36	3	G.DPGLATIAKSATIEPK.E
383	397	499.71	1496.11	1495.86	39	3	D.PGLATIAKSATIEPK.E
413	428	606.14	1815.41	1815.04	18	3	F.NSVSKIDRLSRIAFPL.L

GABA_A receptor $\alpha 1$
Condition 9: sequence coverage 33%

Sequence		Observed	Mr(expt)	Mr(calc)	Ions score	Charge state	Sequence (MS/MS)
Start	End						
36	45	590.43	1178.85	1178.63	25	2	K.DNTTVFTRIL.D
46	52	426.29	850.56	850.42	35	2	L.DRLLDGY.D
53	69	647.47	1939.38	1939.06	13	3	Y.DNRLRPGLGERVTEVKT.D
70	80	584.90	1167.79	1167.58	15	2	T.DIFVTSFGPV.S.D
70	82	710.96	1419.91	1419.67	15	2	T.DIFVTSFGPVSDH.D
81	88	520.29	1038.57	1038.40	18	2	S.DHDMEYTI.D
89	97	606.92	1211.83	1211.61	41	2	I.DVFFRQSWK.D
91	97	499.84	997.67	997.51	22	2	V.FFRQSWK.D
196	209	543.71	1628.11	1627.83	18	3	Y.EWTREPARSVVVAE.D
200	209	528.87	1055.72	1055.56	29	2	R.EPARSVVVAE.D
210	217	476.79	951.57	951.44	14	2	E.DGSRLNQY.D
287	297	638.91	1275.81	1275.60	8	2	V.TTVLTMITLSI.S
344	357	513.74	1538.19	1537.92	28	3	W.DGKSVVPEKPKVK.D
344	358	552.09	1653.25	1652.95	13	3	W.DGKSVVPEKPKVK.D.P
349	357	526.94	1051.86	1051.68	14	2	V.VPEKPKVK.D
350	358	534.92	1067.83	1067.63	20	2	V.PEKPKVK.D.P
358	381	869.59	2605.76	2605.35	15	3	K.DPLIKNNTYAPTATSYTPNLARG.D
365	381	899.59	1797.17	1796.87	7	2	N.NTYAPTATSYTPNLARG.D
368	381	710.49	1418.97	1418.72	15	2	Y.APTATSYTPNLARG.D
371	381	575.90	1149.79	1149.58	31	2	T.ATSYTPNLARG.D
382	394	629.48	1256.94	1256.70	30	2	G.DPGLATIAKSATIE
382	397	538.06	1611.16	1610.89	46	3	G.DPGLATIAKSATIEPK.E
383	397	499.71	1496.11	1495.86	26	3	D.PGLATIAKSATIEPK.E

GABA_A receptor $\alpha 1$
Condition 10: sequence coverage 33%

Sequence		Observed	Mr(expt)	Mr(calc)	Ions score	Charge state	Sequence (MS/MS)
Start	End						
36	45	590.42	1178.82	1178.63	35	2	K.DNTTVFTRILD
46	52	426.29	850.56	850.42	31	2	L.DRLLDGY.D
70	82	710.96	1419.91	1419.67	29	2	T.DIFVTSFGPVSDH.D
81	88	520.29	1038.57	1038.40	26	2	S.DHDMEYTI.D
89	97	606.92	1211.83	1211.61	29	2	I.DVFFRQSWK.D
91	97	499.84	997.67	997.51	24	2	V.FFRQSWK.D
192	199	541.37	1080.72	1080.52	41	2	A.EVVYEWTR.E
200	209	528.88	1055.74	1055.56	24	2	R.EPARSVVVAE.D
210	217	476.78	951.55	951.44	10	2	E.DGSRNLQY.D
218	224	373.28	744.54	744.40	19	2	Y.DLLGQTV.D
344	357	513.74	1538.19	1537.92	24	3	W.DGKSVVPEKPKVKV.D
344	358	552.09	1653.25	1652.95	12	3	W.DGKSVVPEKPKVKV.D.P
350	357	477.38	952.75	952.61	36	2	V.PEKPKVKV.D
350	358	534.92	1067.82	1067.63	22	2	V.PEKPKVKV.D.P
358	381	869.59	2605.75	2605.35	14	3	K.DPLIKNNTYAPTATSYTPNLARG.D
365	381	899.61	1797.20	1796.87	20	2	N.NTYAPTATSYTPNLARG.D
368	381	710.51	1419.00	1418.72	29	2	Y.APTATSYTPNLARG.D
369	375	450.05	899.09	899.27	5	2	A.PTATSYT.P
382	394	629.48	1256.94	1256.70	25	2	G.DPGLATIAKSATIE
382	397	538.07	1611.18	1610.89	38	3	G.DPGLATIAKSATIEPK.E
383	397	499.71	1496.12	1495.86	20	3	D.PGLATIAKSATIEPK.E
384	397	467.35	1399.02	1398.81	28	3	P.GLATIAKSATIEPK.E
386	397	615.47	1228.92	1228.70	19	2	L.ATIAKSATIEPK.E
445	455	623.45	1244.89	1244.65	12	2	R.EPQLKAPTPHQ.-

GABA_A receptor β3
Condition 1: sequence coverage 37%

Sequence		Observed	Mr(expt)	Mr(calc)	Ions score	Charge state	Sequence (MS/MS)
Start	End						
26	38	711.9383	1421.8620	1421.6609	56	2	A.QSVNDPGNMSFVK.E
26	38	719.9442	1437.8738	1437.6558	58	2	A.QSVNDPGNMSFVK.E
31	38	448.2585	894.5025	894.4269	26	2	D.PGNMSFVK.E
88	93	464.2641	926.5137	926.4398	25	2	Y.FQQYWR.D
112	122	653.9108	1305.8069	1305.6241	19	2	R.VADQLWVPDITY.F
112	127	642.0758	1923.2057	1922.9414	53	3	R.VADQLWVPDITYFLNDK.K
112	128	684.7938	2051.3596	2051.0363	29	3	R.VADQLWVPDITYFLNDK.K.S
118	127	606.3782	1210.7418	1210.5870	43	2	W.VPDITYFLNDK.K
119	127	556.8338	1111.6530	1111.5186	54	2	V.PDITYFLNDK.K
128	137	367.9380	1100.7920	1100.6342	31	3	K.KSFVHGVTVK.N
129	137	487.3232	972.6318	972.5392	50	2	K.SFVHGVTVK.N
131	137	370.2757	738.5369	738.4388	34	2	F.VHGVTVK.N
143	151	507.8181	1013.6217	1013.5182	16	2	R.LHPDGTLY.G
143	154	670.9577	1339.9009	1339.7248	57	2	R.LHPDGTLYGLR.I
155	166	708.4139	1414.8132	1414.6254	49	2	R.ITTTAACMMDLR.R
195	205	544.7589	1087.5033	1087.5621	35	2	R.GGDKAVTGVVER.I
199	205	366.2530	730.4914	730.3973	35	2	K.AVTGVVER.I
206	217	489.9816	1466.9230	1466.7881	46	3	R.IELPQFSIVEHR.L
208	217	613.4029	1224.7912	1224.6615	52	2	E.LPQFSIVEHR.L
209	217	556.8545	1111.6944	1111.5774	53	2	L.PQFSIVEHR.L
222	232	597.8810	1193.7474	1193.6192	68	2	R.NVVFATGAYPR.L
233	238	361.7563	721.4981	721.4122	32	2	R.LLSLFR.L
276	286	559.8984	1117.7823	1117.6416	17	2	R.VALGITTVLMT.T
276	292	596.0801	1785.2186	1784.9706	42	3	R.VALGITTVLMTTINTH.L
276	294	685.8281	2054.4625	2054.1558	54	3	R.VALGITTVLMTTINTHLR.E
287	294	478.3090	954.6035	954.5247	53	2	M.TTINTHLR.E
336	348	763.5199	1525.0253	1524.9099	15	2	G.PQRQKLAETAK.A
377	389	690.9023	1379.7901	1379.5986	36	2	N.EMNEVAGSVGDR.N
390	403	786.4744	1570.9342	1570.7375	72	2	R.NSAISFDNSGIQYR.K
396	403	476.7672	951.5198	951.4410	20	2	F.DNSGIQYR.K
437	450	528.3523	1582.0351	1581.8726	62	3	K.KIPDLTDVNAIDR.W
439	450	671.0204	1340.0263	1340.6936	74	2	K.IPDLTDVNAIDR.W

GABA_A receptor β3
Condition 2: sequence coverage 42%

Sequence		Observed	Mr(expt)	Mr(calc)	Ions score	Charge state	Sequence (MS/MS)
Start	End						
26	38	711.9312	1421.8478	1421.6609	46	2	A.QSVNDPGNMSFVK.E
26	43	671.0841	2010.2306	2009.9363	12	3	A.QSVNDPGNMSFVKETVDK.L
31	38	448.2608	894.5071	894.4269	19	2	D.PGNMSFVK.E
39	46	473.3191	944.6236	944.5542	51	2	K.ETVDKLLK.G
112	127	962.5657	1923.1169	1922.9414	44	2	R.VADQLWVPDITYFLNDK.K
112	128	684.7635	2051.2687	2051.0363	38	3	R.VADQLWVPDITYFLNDK.K.S
128	137	551.3919	1100.7693	1100.6342	43	2	K.KSFVHGVTVK.N
129	137	487.3141	972.6137	972.5392	53	2	K.SFVHGVTVK.N
130	137	443.7977	885.5808	885.5072	35	2	S.FVHGVTVK.N
131	137	370.2724	738.5303	738.4388	33	2	F.VHGVTVK.N
143	154	670.9617	1339.9089	1339.7248	18	2	R.LHPDGTLYGLR.I
155	166	692.4158	1382.8171	1382.6356	78	2	R.ITTTAACMMDLR.R
155	167	513.9746	1538.9019	1538.7367	32	3	R.ITTTAACMMDLR.Y
195	205	544.8572	1087.6998	1087.5621	42	2	R.GGDKAVTGVVER.I
206	217	489.9780	1466.9122	1466.7881	57	3	R.IELPQFSIVEHR.L
206	217	734.4866	1466.9586	1466.7881	41	2	R.IELPQFSIVEHR.L
208	217	613.4111	1224.8077	1224.6615	51	2	E.LPQFSIVEHR.L
209	217	556.8522	1111.6898	1111.5774	41	2	L.PQFSIVEHR.L
222	232	597.8898	1193.7650	1193.6192	60	2	R.NVVFATGAYPR.L
233	238	361.7579	721.5012	721.4122	33	2	R.LSLSFR.L
276	294	691.1452	2070.4137	2070.1507	68	3	R.VALGITTVLTMTINTHLR.E
361	389	1031.9365	3092.7876	3092.4290	37	3	R.VDAHGNILLAPMDVHNEMNEVAGSGDTR.N
374	389	577.6805	1730.0198	1729.7689	30	3	D.VHNEMNEVAGSGDTR.N
390	403	786.4599	1570.9053	1570.7375	56	2	R.NSAISFDNSGIQYR.K
390	404	567.3524	1699.0353	1698.8325	41	3	R.NSAISFDNSGIQYR.K.Q
394	404	657.9181	1313.8217	1313.6364	29	2	I.SFDNSGIQYR.K.Q
437	450	528.3561	1582.0464	1581.8726	57	3	K.IKIPDLTDVNAIDR.W
437	453	671.4541	2011.3405	2011.0850	44	3	K.IKIPDLTDVNAIDRWSR.I
439	450	671.4589	1340.9032	1340.6936	56	2	K.IPDLTDVNAIDR.W
439	453	591.0369	1770.0890	1769.9060	41	3	K.IPDLTDVNAIDRWSR.I
452	462	518.6362	1552.8869	1552.6169	13	3	W.SRIVFPFTFSL.F

GABA_A receptor β3
Condition 3: sequence coverage 50%

Sequence		Observed	Mr(expt)	Mr(calc)	Ions score	Charge state	Sequence (MS/MS)
Start	End						
26	38	711.9441	1421.8737	1421.6609	36	2	A.QSVNDPGNMSFVK.E
26	38	719.9429	1437.8712	1437.6558	39	2	A.QSVNDPGNMSFVK.E
31	38	448.2619	894.5092	894.4269	18	2	D.PGNMSFVK.E
39	46	473.3175	944.6205	944.5542	51	2	K.ETVDKLLK.G
44	51	489.3386	976.6627	976.5705	36	2	K.LLKGDIR.L
85	111	1121.6338	3361.8797	3361.7029	13	3	L.TMYFQQYWRDKRLAYSGIPLNLTLDNR.V
112	127	962.5639	1923.1133	1922.9414	38	2	R.VADQLWVPDITYFLNDK.K
112	128	684.7791	2051.3155	2051.0363	36	3	R.VADQLWVPDITYFLNDK.K
128	137	367.9458	1100.8157	1100.6342	27	3	K.KSFVHGVTVK.N
129	137	487.3201	972.6256	972.5392	52	2	K.SFVHGVTVK.N
129	139	415.2931	1242.8575	1242.6832	19	3	K.SFVHGVTVK.NR.M
130	137	443.8009	885.5873	885.5072	33	2	S.FVHGVTVK.N
131	137	370.2802	738.5458	738.4388	38	2	F.VHGVTVK.N
140	154	581.0662	1740.1767	1739.9504	45	3	R.MIRLHPDGTLYGLR.I
143	154	447.6195	1339.8367	1339.7248	50	3	R.LHPDGTLYGLR.I
155	166	692.4195	1382.8244	1382.6356	66	2	R.ITTTAACMMDLR.R
155	167	513.9692	1538.8858	1538.7367	26	3	R.ITTTAACMMDLRR.Y
157	167	671.4147	1340.8148	1340.5999	15	2	T.TTAACMMDLRR.Y
195	205	544.7526	1087.4906	1087.5621	34	2	R.GGDKAVTVER.I
199	205	366.2605	730.5065	730.3973	49	2	K.AVTGVER.I
206	217	489.9828	1466.9265	1466.7881	48	3	R.IELPQFSIVEHR.L
206	221	641.7858	1922.3355	1922.0737	52	3	R.IELPQFSIVEHRLVSR.N
208	217	613.4129	1224.8112	1224.6615	47	2	E.LPQFSIVEHR.L
209	217	556.8565	1111.6985	1111.5774	49	2	L.PQFSIVEHR.L
222	232	597.8787	1193.7428	1193.6192	62	3	R.NVVFATGAYPR.L
233	238	361.7596	721.5046	721.4122	33	2	R.LLSLFR.L
276	294	691.1483	2070.4232	2070.1507	54	3	R.VALGITTVLTMTTINTHLR.E
336	348	763.5213	1525.0281	1524.9099	12	2	G.PQRQKLAETAK.A
374	389	577.6702	1729.9888	1729.7689	42	3	D.VHNEMNEVAGSVGDTR.N
379	389	552.8409	1103.6673	1103.5206	23	2	M.NEVAGSVGDTR.N
390	403	786.4698	1570.9250	1570.7375	72	2	R.NSAISFDNSGIQYR.K
390	404	567.3516	1699.0330	1698.8325	47	3	R.NSAISFDNSGIQYR.Q
394	404	657.9245	1313.8345	1313.6364	30	2	I.SFDNSGIQYR.Q
437	450	528.3513	1582.0322	1581.8726	57	3	K.IKIPDLTDVNAIDR.W
437	453	671.4627	2011.3662	2011.0850	40	3	K.IKIPDLTDVNAIDRWSR.I
439	450	671.4376	1340.8606	1340.6936	62	2	K.IPDLTDVNAIDR.W
439	453	591.0589	1770.1547	1769.9060	45	3	K.IPDLTDVNAIDRWSR.I
452	462	518.6347	1552.8823	1552.6169	12	3	W.SRIVFPFTSL.F

GABA_A receptor β3
Condition 4: sequence coverage 69%

Sequence		Observed	Mr(expt)	Mr(calc)	Ions score	Charge state	Sequence (MS/MS)
Start	End						
34	44	464.9518	1391.8336	1391.6407	22	3	N.MSFVKETVDKLL
35	44	583.3931	1164.7717	1164.6390	38	2	M.SFVKETVDKLL
35	45	639.9540	1277.8934	1277.7230	40	2	M.SFVKETVDKLLK
35	48	543.0320	1626.0741	1625.9028	32	3	M.SFVKETVDKLLKGY.D
37	44	466.3120	930.6093	930.5385	34	2	F.VKETVDKLL
37	45	522.8701	1043.7256	1043.6226	23	2	F.VKETVDKLLK
37	48	464.9782	1391.9129	1391.8023	45	3	F.VKETVDKLLKGY.D
38	45	473.3199	944.6253	944.5542	18	2	V.KETVDKLLK
49	56	516.3385	1030.6625	1030.5559	15	2	Y.DIRLRPDF.G
49	65	634.7406	1901.2000	1900.9287	30	3	Y.DIRLRPDFGGPPVCVGM.N
66	82	973.0239	1944.0332	1943.8492	25	2	M.NIDIASIDMVSEVNDY.T
92	99	554.3670	1106.7194	1106.5985	15	2	Y.WRDKRLAY.S
107	122	636.0700	1905.1881	1904.9268	16	3	L.TLDRVADQLWVPDY.F
109	117	558.8422	1115.6699	1115.5359	30	2	L.DNRVADQLW.V
109	122	846.5222	1691.0298	1690.7951	31	2	L.DNRVADQLWVPDY.F
112	128	684.8114	2051.4124	2051.0363	17	3	R.VADQLWVPDYFLNDKK.S
123	130	499.8103	997.6061	997.5232	47	2	Y.FLNDKKS.F
124	130	426.2807	850.5469	850.4548	28	2	F.LNDKKS.F
131	140	570.8901	1139.7657	1139.6233	44	2	F.VHGVTVKNRM.I
133	140	452.7925	903.5705	903.4960	18	2	H.GVTVKNRM.I
139	151	524.3430	1570.0072	1569.8449	19	3	N.RMIRLHPDGTVLY.G
141	151	642.4420	1282.8695	1282.7033	45	2	M.IRLHPDGTVLY.G
142	151	585.8921	1169.7696	1169.6193	19	2	I.RLHPDGTVLY.G
152	158	381.2881	760.5617	760.4443	28	2	Y.GLRIITTT.A
152	161	532.3409	1062.6672	1062.5491	19	2	Y.GLRIITTTAAC.M
152	162	597.8713	1193.7281	1193.5896	22	2	Y.GLRIITTTAACM.M
152	163	663.4098	1324.8050	1324.6301	57	2	Y.GLRIITTTAACMM.D
183	191	530.7047	1059.3949	1059.4396	5	2	Y.GYTDDIEF.Y
193	201	495.3100	988.6055	988.5090	23	2	Y.WRGGDKAVT.G
202	211	594.3996	1186.7846	1186.6346	30	2	T.GVERIELPQF.S
202	216	585.0614	1752.1624	1751.9205	37	3	T.GVERIELPQFSIVEH.R
202	218	674.8098	2021.4076	2021.1057	43	3	T.GVERIELPQFSIVEHRL.V
206	217	489.9950	1466.9632	1466.7881	41	3	R.IELPQFSIVEHR.L
209	216	478.7836	955.5526	955.4763	37	2	L.PQFSIVEH.R
209	218	613.3914	1224.7682	1224.6615	7	2	L.PQFSIVEHRL.V
217	225	545.3832	1088.7519	1088.6454	17	2	H.RLVSRNVVF.A
222	232	597.9097	1193.8049	1193.6192	58	2	R.NVVFATGAYPR.L
226	235	524.8260	1047.6374	1047.5712	48	2	F.ATGAYPRLSL.S
226	237	641.9630	1281.9115	1281.6717	37	2	F.ATGAYPRLSLSF.R
240	246	449.2886	896.5626	896.4868	19	2	L.KRNIGYF.I
252	260	508.8606	1015.7067	1015.5987	36	2	Y.MPSILITIL.S
252	262	645.4644	1288.9142	1288.7101	24	2	Y.MPSILITILSW.V
267	278	632.4155	1262.8164	1262.6618	40	2	W.INYDASAARVAL.G
270	278	437.2775	872.5405	872.4715	40	2	Y.DASAARVAL.G
270	284	729.5208	1457.0270	1456.8249	14	2	Y.DASAARVALGITTTL.T
276	294	685.8424	2054.5055	2054.1558	54	3	R.VALGITTTLTMTTINTHLR.E
285	292	459.7600	917.5055	917.4277	42	2	L.TMTTINTH.L

GABA_A receptor β3

Condition 5: sequence coverage 68%

Sequence		Observed	Mr(expt)	Mr(calc)	Ions score	Charge state	Sequence (MS/MS)
Start	End						
34	44	464.9482	1391.8226	1391.6407	21	3	N.MSFVKETVDKLL
35	44	583.4019	1164.7892	1164.6390	42	2	M.SFVKETVDKLL
35	45	639.9647	1277.9149	1277.7230	29	2	M.SFVKETVDKLLK
35	48	543.0450	1626.1132	1625.9028	41	3	M.SFVKETVDKLLKGY.D
37	44	466.3115	930.6084	930.5385	38	2	F.VKETVDKLL
37	45	522.8725	1043.7304	1043.6226	24	2	F.VKETVDKLL.K
37	48	464.9709	1391.8909	1391.8023	39	3	F.VKETVDKLLKGY.D
38	45	473.3178	944.6211	944.5542	28	2	V.KETVDKLL.K
49	65	634.7443	1901.2112	1900.9287	28	3	Y.DIRLRPDFGGPPVCGM.N
92	99	369.9279	1106.7619	1106.5985	11	3	Y.WRDKRLAY.S
93	99	461.3072	920.5998	920.5191	8	2	W.RDKRLAY.S
107	122	636.0785	1905.2137	1904.9268	13	3	L.TLDNRVADQLWVPDLY.F
109	117	558.8480	1115.6815	1115.5359	31	2	L.DNRVADQLW.V
109	122	846.5351	1691.0556	1690.7951	31	2	L.DNRVADQLWVPDLY.F
123	130	499.8235	997.6324	997.5232	36	2	Y.FLNDKKS.F.V
124	130	426.2811	850.5476	850.4548	25	2	0 F.LNDKKS.F.V
131	140	380.9483	1139.8231	1139.6233	36	3	F.VHGVTVKNRM.I
139	151	524.3491	1570.0255	1569.8449	18	3	N.R.MIRLHPDGTVLY.G
141	151	642.4530	1282.8914	1282.7033	44	2	M.IRLHPDGTVLY.G
152	158	381.2916	760.5686	760.4443	30	2	Y.GLRITTT.A
152	161	532.3465	1062.6785	1062.5491	24	2	Y.GLRITTTAAC.M
152	162	605.8822	1209.7499	1209.5845	28	2	Y.GLRITTTAACM.M
152	163	663.4191	1324.8237	1324.6301	42	2	Y.GLRITTTAACM.D
183	192	612.2494	1222.4843	1222.5030	5	2	Y.GYTTDDIEFY.W
202	216	585.0660	1752.1761	1751.9205	47	3	T.GVERIELPQFSIVEH.R
202	218	674.8219	2021.4439	2021.1057	40	3	T.GVERIELPQFSIVEHRL.V
209	218	613.4082	1224.8018	1224.6615	9	2	L.PQFSIVEHRL.V
217	225	545.3870	1088.7595	1088.6454	19	2	H.RLVSRNVV.F.A
226	235	524.8888	1047.7630	1047.5712	41	2	F.ATGAYPRLSLS
226	237	641.9668	1281.9190	1281.6717	38	2	F.ATGAYPRLSLSF.R
238	245	510.3656	1018.7166	1018.6035	12	2	F.RLKRNI.GY.F
240	246	449.2902	896.5658	896.4868	17	2	L.KRNIGY.F.I
252	260	500.8705	999.7264	999.6038	30	2	Y.MPSILITIL.S
267	278	632.4292	1262.8439	1262.6618	28	2	W.INYDASAARVAL.G
270	278	437.2830	872.5515	872.4715	47	2	Y.DASAARVAL.G
270	284	729.5362	1457.0578	1456.8249	12	2	Y.DASAARVALGITT.VLT
276	294	685.8402	2054.4987	2054.1558	65	3	R.VALGITT.VLMTTINTHLR.E
285	292	459.7614	917.5082	917.4277	37	2	L.TMTTINTH.L
285	293	516.3179	1030.6212	1030.5117	43	2	L.TMTTINTHL.R
293	302	615.4542	1228.8939	1228.7179	26	2	H.LRETLPKIPY.V
303	309	428.2633	854.5121	854.4207	36	2	Y.VKAIMY.L
303	314	740.3318	1478.6491	1478.6607	13	2	Y.VKAIMYLMGCF.V
317	324	484.3400	966.6655	966.5426	17	2	F.VFLALLEY.A
320	330	658.4502	1314.8859	1314.6859	16	2	L.ALLEYAFVNYI.F
330	337	461.2852	920.5559	920.4868	25	2	Y.IFFGRGPQ.R
352	368	642.1011	1923.2813	1922.9922	8	3	N.DRSKSEINRVDAGHNILL
360	368	497.8228	993.6311	993.5355	22	2	N.RVDAHGNILL
369	395	965.0391	2892.0956	2892.3017	4	3	L.LAPMDVHNEMNEVAGSGDTRNSAIF.D

GABA_A receptor β3
Condition 6: sequence coverage 55%

Sequence		Observed	Mr(expt)	Mr(calc)	Ions score	Charge state	Sequence (MS/MS)
Start	End						
35	44	583.4177	1164.8208	1164.6390	11	2	M.SFVKETVDKLL
35	48	543.0524	1626.1354	1625.9028	40	3	M.SFVKETVDKLLKGY.D
37	44	466.3125	930.6104	930.5385	13	2	F.VKETVDKLL
37	48	464.9803	1391.9192	1391.8023	43	3	F.VKETVDKLLKGY.D
49	65	634.7667	1901.2783	1900.9287	37	3	Y.DIRLPDFGGPPVCVGM.N
92	99	369.9309	1106.7708	1106.5985	8	3	Y.WRDKRLAY.S
107	122	636.1026	1905.2861	1904.9268	11	3	L.TLDNRVADQLWVPDITY.F
109	122	846.5576	1691.1007	1690.7951	27	2	L.DNRVADQLWVPDITY.F
123	130	499.8250	997.6355	997.5232	42	2	Y.FLNDKKS.F
124	130	426.2931	850.5717	850.4548	25	2	F.LNDKKS.F
125	130	369.7542	737.4939	737.3708	19	2	L.LNDKKS.F
139	151	529.6931	1586.0574	1585.8398	13	3	N.RMIRLHPDGTVLY.G
141	151	642.4692	1282.9239	1282.7033	8	2	M.IRLHPDGTVLY.G
152	162	605.9007	1209.7868	1209.5845	7	2	Y.GLRITTTAACM.M
152	163	679.4322	1356.8499	1356.6199	6	2	Y.GLRITTTAACMM.D
183	192	612.2494	1222.4842	1222.5030	7	2	Y.GYTTDDIEFY.W
202	216	585.0717	1752.1932	1751.9205	32	3	T.GVERIELPQFSIVEH.R
217	225	545.4065	1088.7985	1088.6454	13	2	H.RLVSRRVVF.A
226	237	641.9397	1281.8648	1281.6717	33	2	F.ATGAYPRLSLSF.R
238	246	389.6357	1165.8852	1165.6719	11	3	F.RLKRNIQYF.I
240	246	449.2972	896.5798	896.4868	13	2	L.KRNIQYF.I
252	260	508.7617	1015.5088	1015.5987	10	2	Y.MPSILITL.S
303	309	428.2811	854.5477	854.4207	18	2	Y.VKAIMY.L
330	337	461.2992	920.5839	920.4868	24	2	Y.IFFGRGPQ.R
369	395	965.1980	2892.5721	2892.3017	11	3	L.LAPMDVHNMNEVAGSVGDRNSAISF.D
373	395	822.5459	2464.6159	2464.0924	34	3	M.DVHNMNEVAGSVGDRNSAISF.D
396	402	398.7421	795.4697	795.3399	14	2	F.DNSGIQY.R
403	415	551.9160	1652.7262	1652.7606	12	3	Y.RKQSMPEKGHGRY.M
406	415	387.9284	1160.7635	1160.5396	11	3	Q.SMPKEGHGRY.M
408	415	472.2993	942.5840	942.4671	18	2	M.PKEGHGRY.M
416	428	512.5898	1534.7474	1534.8038	12	3	Y.MGDRSIPHKKTHL.R
436	446	628.4525	1254.8905	1254.7183	22	2	L.KIKIPDLTDV.N.A
436	451	633.1231	1896.3476	1896.0468	38	3	L.KIKIPDLTDVNAIDRW.S
437	451	590.4180	1768.2321	1767.9519	30	3	K.IKIPDLTDVNAIDRW.S
439	451	764.5630	1527.1114	1526.7729	10	2	K.IPDLTDVNAIDRW.S
447	458	503.0113	1506.0122	1505.8143	15	3	N.AIDRWSRIVFPF.T
452	458	433.3052	864.5959	864.4857	20	2	W.SRIVFPF.T
452	460	557.3882	1112.7619	1112.6018	39	2	W.SRIVFPF.T.S
464	473	673.9695	1345.9245	1345.6706	12	2	F.NLYVWLYV.N.-

GABA_A receptor β3

Condition 7: sequence coverage 58%

Sequence		Observed	Mr(expt)	Mr(calc)	Ions score	Charge state	Sequence (MS/MS)
Start	End						
34	44	464.9716	1391.8928	1391.6407	18	3	N.MSFVKETVDKLL
35	44	583.4259	1164.8372	1164.6390	21	2	M.SFVKETVDKLL
35	48	543.0595	1626.1566	1625.9028	42	3	M.SFVKETVDKLLKGY.D
37	44	466.3190	930.6235	930.5385	26	2	F.VKETVDKLL
37	45	522.8911	1043.7676	1043.6226	25	2	F.VKETVDKLL.K
37	48	464.9807	1391.9202	1391.8023	40	3	F.VKETVDKLLKGY.D
49	61	480.3130	1437.9171	1437.7728	15	3	Y.DIRLRPDFGGPPV.C
49	65	634.7720	1901.2940	1900.9287	36	3	Y.DIRLRPDFGGPPVCVGM.N
88	99	558.7005	1673.0796	1672.8474	9	3	Y.FQYWRDKRLAY.S
92	99	369.9369	1106.7888	1106.5985	5	3	Y.WRDKRLAY.S
107	122	636.0905	1905.2498	1904.9268	11	3	L.TLDNRVADQLWVPDITY.F
109	122	846.5674	1691.1202	1690.7951	18	2	L.DNRVADQLWVPDITY.F
123	130	499.8316	997.6487	997.5232	25	2	Y.FLNDKKS.F.V
124	130	426.2882	850.5619	850.4548	28	2	F.LNDKKS.F.V
125	130	369.7616	737.5086	737.3708	22	2	L.NDKKS.F.V
131	140	380.9493	1139.8260	1139.6233	9	3	F.VHGVTVKNRM.I
152	162	605.9032	1209.7918	1209.5845	16	2	Y.GLRIITTAACM.M
152	163	679.4443	1356.8740	1356.6199	22	2	Y.GLRIITTAACM.M.D
183	192	612.2489	1222.4833	1222.5030	4	2	Y.GYTDDIEFY.W
217	225	545.4041	1088.7937	1088.6454	6	2	H.RLVSRNVV.F.A
226	237	641.9612	1281.9079	1281.6717	27	2	F.ATGAYPRLSLF.R
238	246	389.5640	1165.6702	1165.6719	17	3	F.RLKRNI.GY.F.I
276	294	685.8627	2054.5662	2054.1558	18	3	R.VALGITTVLMTINTHLR.E
293	302	615.4627	1228.9108	1228.7179	16	2	H.LRETLKIPY.V
303	309	428.2744	854.5342	854.4207	27	2	Y.VKAIMY.L
330	337	461.2955	920.5765	920.4868	22	2	Y.IFFGRGPQ.R
360	368	497.8306	993.6467	993.5355	30	2	N.RVDAHGNIL.L
369	395	965.0509	2892.1310	2892.3017	8	3	L.LAPMDVHNEMNEVAGSGDTRNSAIF.D
373	395	817.2096	2448.6068	2448.0975	28	3	M.DVHNEMNEVAGSGDTRNSAIF.D
403	415	525.2470	1572.7190	1572.7943	12	3	Y.RKQSMKPEGHGRY.M
406	415	387.9182	1160.7328	1160.5396	17	3	Q.SMPKEGHGRY.M
408	415	472.2653	942.5160	942.4671	16	2	M.PKEGHGRY.M
416	423	464.7640	927.5134	927.4232	11	2	Y.MGDRSIPH.K
416	428	507.2584	1518.7534	1518.8089	5	3	Y.MGDRSIPHKKTHL.R
436	446	628.4402	1254.8658	1254.7183	23	2	L.KIKIPDLTDVN.A
436	451	633.1328	1896.3765	1896.0468	30	3	L.KIKIPDLTDVNAIDRW.S
437	451	590.4237	1768.2492	1767.9519	26	3	K.KIKIPDLTDVNAIDRW.S
447	458	503.0114	1506.0123	1505.8143	11	3	N.AIDRWSRIVFPF.T
452	458	433.2992	864.5839	864.4857	24	2	W.SRIVFPF.T
452	460	557.3855	1112.7564	1112.6018	26	2	W.SRIVFPF.T.F.S
452	463	731.0498	1460.0850	1459.7863	15	2	W.SRIVFPF.T.F.S.L.F.N
464	473	673.9727	1345.9309	1345.6706	15	2	F.NLVYWL.YV.N.-

GABA_A receptor β3
Condition 8: sequence coverage 36%

Sequence		Observed	Mr(expt)	Mr(calc)	Ions score	Charge state	Sequence (MS/MS)
Start	End						
30	41	662.4449	1322.8753	1322.6176	33	2	N.DPGNMSFVKETV.D
31	41	612.8992	1223.7838	1223.5856	23	2	D.PGNMSFVKETV.D
42	48	418.7956	835.5767	835.4803	28	2	V.DKLLKGY.D
49	61	480.3119	1437.9140	1437.7728	15	3	Y.DIRLRPDFGGPPV.C
49	67	710.4871	2128.4394	2128.0557	20	3	Y.DIRLRPDFGGPPVCGMNI.D
49	72	877.1000	2628.2782	2627.3199	41	3	DIRLRPDFGGPPVCGMNI.D
55	67	681.9394	1361.8642	1361.6107	7	2	P.DFGGPPVCGMNI.D
73	80	478.7343	955.4540	955.3626	39	2	I.DMVSEVM.D
81	93	916.0259	1830.0372	1829.8083	24	2	M.DYTLTMYFQQYWR.D
114	125	756.0061	1509.9977	1509.7140	25	2	A.DQLWVPDITYFLN.D
120	125	386.7517	771.4889	771.3439	24	2	P.DITYFLN.D
187	196	629.3899	1256.7653	1256.5461	18	2	T.DDIEFYWRGG.D
295	306	457.9340	1370.7801	1370.8173	40	3	R.ETLPKIPYKAI.D
352	361	602.4202	1202.8259	1202.6367	21	2	N.DRSKSEINRV.D
362	372	576.3861	1150.7576	1150.5804	50	2	V.DAHGNILLAPM.D
362	372	584.3500	1166.6855	1166.5753	46	2	V.DAHGNILLAPM.D
363	372	526.8489	1051.6832	1051.5484	31	2	D.AHGNILLAPM.D
373	386	737.4801	1472.9456	1472.6201	27	2	M.DVHNEMNEVAGSVG.D
387	395	505.8165	1009.6184	1009.4828	22	2	G.DTRNSAISF.D
396	404	540.8645	1079.7145	1079.5359	22	2	F.DNSGIQYRK.Q
396	417	857.8483	2570.5230	2570.1753	20	3	F.DNSGIQYRKQSMPEKGHGRYMG.D
407	417	639.6646	1277.3146	1277.5645	15	2	S.MPKEGHGRYMG.D
452	460	557.4048	1112.7950	1112.6018	10	2	W.SRIVFPFTF.S

GABA_A receptor β3

Condition 9: sequence coverage 35%

Sequence		Observed	Mr(expt)	Mr(calc)	Ions score	Charge state	Sequence (MS/MS)
Start	End						
30	41	662.4313	1322.8480	1322.6176	35	2	N.DPGNMSFVKETV.D
30	41	670.4334	1338.8523	1338.6125	27	2	N.DPGNMSFVKETV.D
42	48	418.8092	835.6039	835.4803	17	2	V.DKLLKGY.D
42	48	418.8186	835.6227	835.4803	28	2	V.DKLLKGY.D
49	67	705.1411	2112.4014	2112.0608	17	3	Y.DIQLRPDFGGPPVCVGMNI.D
55	67	681.9617	1361.9088	1361.6107	14	2	P.DFGGPPVCVGMNI.D
73	80	478.7485	955.4825	955.3626	34	2	I.DMVSEVNM.D
81	93	916.1046	1830.1946	1829.8083	21	2	M.DYTLTMYFQQYWR.D
86	93	611.0845	1220.1544	1220.5437	25	2	T.MYFQQYWR.D
88	93	464.2835	926.5524	926.4398	22	2	Y.FQQYWR.D
114	119	379.2806	756.5467	756.3806	51	2	A.DQLWVP.D
120	125	386.7659	771.5173	771.3439	16	2	P.DTYFLN.D
164	170	466.7428	931.4711	931.5239	12	2	M.DLRRYPL.D
187	196	629.3930	1256.7713	1256.5461	18	2	T.DDIEFYWRGG.D
295	306	457.9991	1370.9754	1370.8173	25	3	R.ETLPKIPYVKAI.D
352	361	602.4188	1202.8230	1202.6367	15	2	N.DRSKSEINRV.D
362	372	584.4108	1166.8071	1166.5753	49	2	V.DAHGNILLAPM.D
373	386	737.4388	1472.8631	1472.6201	15	2	M.DVHNEMNEVAGSVG.D
387	395	505.8362	1009.6578	1009.4828	22	2	G.DTRNSAIF.D
396	404	540.8533	1079.6921	1079.5359	28	2	F.DNSGIQYRK.Q
396	417	847.2087	2538.6042	2538.1855	17	3	F.DNSGIQYRKQSMPEKGHGRYMG.D

GABA_A receptor β3

Condition 10: sequence coverage 33%

Sequence		Observed	Mr(expt)	Mr(calc)	Ions score	Charge state	Sequence (MS/MS)
Start	End						
30	41	662.4313	1322.8480	1322.6177	35	2	N.DPGNMSFVKETV.D
42	48	418.8186	835.6227	835.4803	28	2	V.DKLLKGY.D
49	67	705.1411	2112.4014	2112.0609	17	3	Y.DIRLRPDFGGPPVCGMNI.D
55	67	681.9617	1361.9088	1361.6108	14	2	P.DFGGPPVCGMNI.D
73	80	478.7485	955.4825	955.3627	34	2	I.DMVSEVNM.D
81	93	916.1046	1830.1946	1829.8083	21	2	M.DYTLTMYFQQYWR.D
86	93	611.0845	1220.1544	1220.5437	25	2	T.MYFQQYWR.D
88	93	464.2835	926.5524	926.4399	22	2	Y.FQQYWR.D
114	119	379.2806	756.5467	756.3806	51	2	A.DQLWVP.D
120	125	386.7659	771.5173	771.3439	16	2	P.DTYFLN.D
187	196	629.3930	1256.7713	1256.5462	18	2	T.DDIEFYWRGG.D
295	306	457.9991	1370.9754	1370.8173	25	3	R.ETLKPYPVKAL.D
352	361	602.4188	1202.8230	1202.6367	15	2	N.DRSKSEINRV.D
362	372	576.3930	1150.7714	1150.5805	46	2	V.DAHGNILLAPM.D
373	386	737.4388	1472.8631	1472.6202	15	2	M.DVHNEMNEVAGSVG.D
387	395	505.8362	1009.6578	1009.4829	22	2	G.DTRNSAIF.D
396	404	540.8533	1079.6921	1079.5360	28	2	F.DNSGIQYRK.Q
396	417	847.2087	2538.6042	2538.1856	17	3	F.DNSGIQYRKQSMPEKGGHGRYMG.D