

prot_acc	pep_rank	pep_exp_mz	pep_exp_mr	pep_exp_z	pep_score	pep_expect	pep_seq	pep_var_mod	pep_var_mod_pos
GPSGXVSAQLXR 6 8 5 0 1371_1370	1	675.8392	1349.6638	2	87.72	2.50E-09	GPSGSVSAQLLR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 8 8 0 0 1761_1760	1	660.8371	1319.6596	2	84.3	3.70E-09	GPSGVVSAQLAR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 0 4 0 0 81_80	1	625.798	1249.5815	2	81.61	6.90E-09	GPSGAVSQAQLAR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 5 5 5 0 1111_1110	1	464.2531	1389.7375	3	79.96	1.00E-08	GPSGLVSLAQLLR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 5 8 3 0 1167_1166	1	705.8599	1409.7053	2	78.83	1.30E-08	GPSGLVSAQLFR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 3 9 0 0 781_780	1	716.8343	1431.654	2	76.03	2.50E-08	GPSGFVSAQLAR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 2 1 8 0 437_436	1	697.8198	1393.6251	2	74.94	3.20E-08	GPSGEVSDAQLVR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 0 5 8 0 117_116	1	667.8453	1333.676	2	74.71	3.40E-08	GPSGAVSLAQLVR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 0 4 5 0 91_90	1	646.8214	1291.6283	2	74.69	3.40E-08	GPSGAVSQAQLLR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 3 0 5 0 611_610	1	691.8446	1381.6747	2	73.66	4.30E-08	GPSGFVSAQLLR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 1 9 7 0 395_394	1	715.8185	1429.6224	2	73.66	4.50E-08	GPSGDVSAQLTR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 5 5 3 0 1107_1106	1	712.8685	1423.7225	2	72.32	5.90E-08	GPSGLVSLAQLFR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 5 0 0 0 1001_1000	1	653.8292	1305.6439	2	71.86	6.50E-08	GPSGLVSAQAQLAR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 5 5 0 0 1011_1010	1	674.8526	1347.6906	2	71.71	6.70E-08	GPSGLVSAQAQLLR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 5 5 5 0 1111_1110	1	518.9528	1553.8366	3	71.65	6.80E-08	SLPFKLSPLLFGR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 4 5 0 1 902_901	1	476.9143	1427.7212	3	69.91	1.00E-07	SGPFKLSPLAFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 8 8 3 0 1767_1766	1	698.8525	1395.6905	2	69.22	1.20E-07	GPSGVVSAQLFR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 2 1 1 1 424_423	1	691.7951	1381.5757	2	68.8	1.30E-07	GPSGEVSDAQLDK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 0 2 8 0 57_56	1	675.8243	1349.634	2	67.88	1.60E-07	GPSGAVSEAQLVR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 5 5 1 0 1103_1102	1	696.8475	1391.6805	2	67.85	1.60E-07	GPSGLVSLAQLDR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 5 3 8 0 1077_1076	1	705.8612	1409.7079	2	67.1	1.90E-07	GPSGLVSAQLVR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 5 8 8 0 1177_1176	1	681.8611	1361.7077	2	66.86	2.10E-07	GPSGLVSAQLVR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 8 1 0 0 1621_1620	1	668.8165	1335.6185	2	66.39	2.30E-07	GPSGVVSDAQLTR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 2 2 9 0 459_458	1	736.8241	1471.6336	2	64.98	3.20E-07	GPSGEVSEAQLYR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 0 9 9 0 199_198	1	538.2564	1611.7474	3	64.78	3.30E-07	SAPFKYSPLYFGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 5 8 6 0 1173_1172	1	675.8428	1349.6711	2	64.76	3.30E-07	GPSGLVSAQLSR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 4 5 5 1 912_911	1	490.9302	1469.7688	3	64.72	3.50E-07	SGPFKLSPLLFGR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 0 3 5 0 71_70	1	516.2653	1545.7741	3	64.53	3.50E-07	SAPFKFSPLLFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 9 4 4 0 1889_1888	1	664.8036	1327.5927	2	63.58	4.40E-07	GPSGVVSAQAQLGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 5 3 5 0 1071_1070	1	712.8687	1423.7229	2	63.46	4.50E-07	GPSGLVSAQAQLR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 5 4 5 0 1091_1090	1	667.8449	1333.6753	2	63.41	4.60E-07	GPSGLVSAQAQLLR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 4 5 4 0 909_908	1	639.8138	1277.6131	2	63.34	4.60E-07	GPSGGVSLAQLGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 3 3 6 0 673_672	1	716.8315	1431.6484	2	63.11	4.90E-07	GPSGFVSAQAQLSR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 3 3 1 1 664_663	1	716.8315	1431.6484	2	63.11	4.90E-07	GPSGFVSAQAQLDK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 2 7 8 0 557_556	1	690.8287	1379.6429	2	63.08	4.90E-07	GPSGEVSTAQLVR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 9 5 5 0 1911_1910	1	720.8658	1439.7171	2	63.03	5.00E-07	GPSGVVSAQAQLLR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 6 8 8 1 1378_1377	1	654.8318	1307.649	2	63.03	5.00E-07	GPSGSVSAQLVK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 5 5 6 0 1131_1130	1	682.8473	1363.68	2	62.99	5.00E-07	GPSGLVSSAQLLR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 5 5 2 0 1105_1104	1	524.2725	1569.7956	3	62.97	5.00E-07	SLPFKLSPLFGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 2 0 2 0 405_404	1	690.8113	1379.6081	2	62.96	5.10E-07	GPSGEVSAQAQLER	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 2 6 0 0 521_520	1	669.8049	1337.5953	2	62.82	5.20E-07	GPSGEVSSAQLAR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 0 5 5 0 111_110	1	674.8527	1347.6908	2	62.62	5.50E-07	GPSGAVSLAQLLR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 3 3 8 0 677_676	1	722.8527	1443.6908	2	62.59	5.50E-07	GPSGFVSAQAQLVR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 0 5 5 0 111_110	1	504.9374	1511.7905	3	62.47	5.70E-07	SAPFKLSPLFGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 2 8 2 0 565_564	1	704.8264	1407.6382	2	62.43	5.70E-07	GPSGEVSAQAQLER	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 8 1 5 0 1631_1630	1	689.8387	1377.6629	2	62.3	5.90E-07	GPSGVVSDAQLLR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 0 4 9 0 99_98	1	671.8113	1341.6081	2	61.87	6.50E-07	GPSGAVSQAQLYR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 1 1 2 0 225_224	1	705.7982	1409.5818	2	61.75	6.70E-07	GPSGDVSDAQLER	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 0 0 0 0 1_0	1	632.806	1263.5975	2	61.75	6.70E-07	GPSGAVSQAQLAR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 1 1 9 0 239_238	1	722.8089	1443.6032	2	61.53	7.00E-07	GPSGDVSDAQLYR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 0 1 5 0 31_30	1	675.8217	1349.6289	2	61.49	7.10E-07	GPSGAVSQAQLTR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 5 5 7 0 1115_1114	1	689.8577	1377.7008	2	60.89	8.10E-07	GPSGLVSLAQLTR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 9 6 3 1 1928_1927	1	710.8292	1419.6438	2	60.83	8.30E-07	GPSGVVSSAQLFK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 6 5 5 0 1312_1311	1	500.9336	1499.7789	3	60.7	8.50E-07	SSPFKLSPLFGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 5 0 8 1 1018_1017	1	653.8419	1305.6693	2	60.66	9.00E-07	GPSGLVSAQAQLVK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 6 3 5 0 1271_1270	1	521.5966	1561.768	3	60.42	9.10E-07	SSPFKLSPLFGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 5 3 2 0 1065_1064	1	720.8473	1439.68	2	60.23	9.50E-07	GPSGLVSAQAQLR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 9 6 9 1 1940_1939	1	718.8262	1435.6378	2	60	1.00E-06	GPSGVVSSAQLYK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 5 3 5 1 1072_1071	1	520.9457	1559.8154	3	59.9	1.00E-06	SLPFKLSPLFGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 2 1 2 0 425_424	1	712.8058	1423.597	2	59.1	1.20E-06	GPSGEVSDAQLER	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 5 0 9 0 1019_1018	1	699.8427	1397.6709	2	59.08	1.20E-06	GPSGLVSAQAQLYR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 5 5 8 0 1117_1116	1	688.8684	1375.7223	2	59.04	1.20E-06	GPSGLVSLAQLVR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 0 0 0 1 2_1	1	467.5717	1399.6931	3	59.02	1.30E-06	SAPFKASPLAFGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 4 5 5 0 911_910	1	749.8951	1497.7756	2	58.93	1.30E-06	SGPFKLSPLFGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 2 2 8 0 457_456	1	704.8271	1407.6396	2	58.79	1.30E-06	GPSGEVSEAQLVR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 4 9 4 1 990_989	1	488.9022	1463.6847	3	58.65	1.40E-06	SGPFKYSPLFGR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 5 8 8 1 1178_1177	1	500.2738	1497.7997	3	58.65	1.40E-06	SLPFKYSPLFGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 2 2 2 0 445_444	1	719.814	1437.6135	2	58.63	1.40E-06	GPSGEVSEAQLER	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 3 9 3 0 787_786	1	754.8499	1507.6852	2	58.31	1.50E-06	GPSGFVSAQAQLFR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 2 3 5 0 471_470	1	720.8478	1439.6811	2	58.26	1.50E-06	GPSGEVSAQAQLLR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 6 3 9 1 1280_1279	1	528.9213	1583.742	3	58.17	1.50E-06	SSPFKLSPLFGR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 6 5 0 1 1302_1301	1	486.9181	1457.7324	3	58.12	1.50E-06	SSPFKLSPLAFGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 5 9 5 0 1191_1190	1	535.6132	1603.8176	3	57.83	1.60E-06	SLPFKYSPLFGR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 0 6 0 1 122_121	1	472.9023	1415.6852	3	57.67	1.70E-06	SAPFKSPLAFGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 4 5 3 0 907_906	1	511.5936	1531.759	3	57.66	1.70E-06	SGPFKLSPLFGR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 5 5 5 1 1112_1111	1	509.6177	1525.8312	3	57.61	1.70E-06	SLPFKLSPLFGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 3 3 5 0 671_670	1	729.8602	1457.7058	2	57.26	1.90E-06	GPSGFVSAQAQLLR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 5 6 1 0 1123_1122	1	683.8207	1365.6269	2	57.15	1.90E-06	GPSGLVSSAQLDR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 3 5 5 0 711_710	1	475.5812	1423.7219	3	57.08	2.00E-06	GPSGFVSLAQLLR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 0 2 9 0 59_58	1	707.8217	1413.6289	2	56.94	2.00E-06	GPSGAVSEAQLYR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 8 4 5 1 1692_1691	1	646.8347	1291.6549	2	56.54	2.70E-06	GPSGVVSAQAQLLR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 3 3 3 0 667_666	1	746.8522	1491.6898	2	56.42	2.30E-06	GPSGFVSAQAQLFR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 4 8 9 1 980_979	1	502.9187	1505.7342	3	56.42	2.30E-06	SGPFKYSPLFGR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 3 3 3 0 667_666	1	552.9372	1655.7898	3	56.4	2.30E-06	SFPFKSPLFGR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 4 5 0 0 901_900	1	728.8707	1455.7269	2	56.2	2.40E-06	SGPFKLSPLAFGR	Phospho (ST)	0.0000001000000.0

GPSGXVSAQXLXR 2 5 5 0 511_510	1	703.8558	1405.6971	2	55.83	2.60E-06	GPSGEVSLAQLLR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 4 5 2 1 906_905	1	496.2497	1485.7272	3	55.78	2.60E-06	SGPFKLSPLFEGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 0 5 0 1 102_101	1	481.5865	1441.7376	3	55.68	2.70E-06	SAPFKLSPLAFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 5 6 2 1 1126_1125	1	676.8275	1351.6404	2	55.61	2.70E-06	GPSGLVSSAQLEK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 2 5 0 1 502_501	1	500.9215	1499.7427	3	55.13	3.10E-06	SEPFKLSPLAFGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 4 2 5 0 851_850	1	505.5849	1513.733	3	54.9	3.20E-06	SGPFKESPLLFGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 2 1 9 0 439_438	1	729.8164	1457.6183	2	54.78	3.30E-06	GPSGEVSDAQLYR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 9 3 4 0 1869_1868	1	709.827	1417.6395	2	54.77	3.30E-06	GPSGVVSAQQLGR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 8 5 9 0 1719_1718	1	530.9414	1589.8024	3	54.57	3.50E-06	SVPFKLSPLYFGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 5 0 4 1 1010_1009	1	632.8184	1263.6223	2	54.45	3.60E-06	GPSGLVSAQQLGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 9 4 1 0 1883_1882	1	693.8062	1385.5979	2	54.43	3.60E-06	GPSGVVSGAQLDR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 0 5 3 1 108_107	1	506.9303	1517.7691	3	54.32	3.70E-06	SAPFKLSPLFFGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 1 3 5 0 271_270	1	530.9287	1589.7641	3	54.24	3.80E-06	SDPFKFSPLLFGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 5 1 7 0 1035_1034	1	690.8281	1379.6417	2	54.11	3.90E-06	GPSGLVSDAQLTR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 1 8 7 0 375_374	1	683.8218	1365.629	2	54.03	4.00E-06	GPSGDVSAQQLTR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 0 2 4 0 49_48	1	654.8008	1307.5871	2	54	4.00E-06	GPSGAVSEAQLGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 5 0 5 1 1012_1011	1	660.8499	1319.6852	2	53.82	4.10E-06	GPSGLVSAQQLK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 5 3 5 0 1071_1070	1	530.2785	1587.8137	3	53.71	4.30E-06	SLPFKFSPLFGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 6 6 6 1 1334_1333	1	642.7951	1283.5757	2	53.57	4.40E-06	GPSGSVSSAQLSK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 8 5 5 1 1712_1711	1	674.866	1347.7174	2	53.45	4.50E-06	GPSGVVSLAQLLK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 8 5 1 0 1703_1702	1	514.929	1541.765	3	53.25	4.70E-06	SVPFKLSPLDFGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 0 1 4 0 29_28	1	647.7932	1293.5718	2	53.17	4.80E-06	GPSGAVSDAQLGR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 3 5 8 1 718_717	1	516.2745	1545.8018	3	53.17	4.80E-06	SFPFKLSPLVFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 0 9 0 1 182_181	1	664.8157	1327.6169	2	53.14	4.90E-06	GPSGAVSQAQLAK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 6 5 3 1 1308_1307	1	685.8395	1369.6644	2	53.1	4.90E-06	GPSGSVSLAQLFK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 4 0 9 0 819_818	1	502.9094	1505.7064	3	52.99	5.00E-06	SGPFKASPLYFGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 9 5 8 0 1917_1916	1	713.8577	1425.7008	2	52.67	5.40E-06	GPSGVVSLAQLVR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 5 0 1 1 1004_1003	1	661.8212	1321.6279	2	52.58	5.50E-06	GPSGLVSAQQLDK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 2 0 9 0 419_418	1	526.9165	1577.7277	3	52.56	5.50E-06	SEPFKASPLYFGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 6 1 6 1 1234_1233	1	656.7925	1311.5704	2	52.54	5.60E-06	GPSGSVSDAQLSK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 6 4 4 1 1290_1289	1	612.7846	1223.5547	2	52.13	6.10E-06	GPSGSVSGAQLGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 4 5 4 1 910_909	1	472.2426	1413.7061	3	51.96	6.40E-06	SGPFKLSPLGFGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 0 6 4 1 130_129	1	468.2303	1401.669	3	51.95	6.40E-06	SAPFKSSPLGFGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 5 8 8 0 1177_1176	1	509.6092	1525.8057	3	51.85	6.50E-06	SLPFKVSPLVFGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 2 5 0 0 501_500	1	510.2566	1527.7479	3	51.8	6.60E-06	SEPFKLSPLAFGR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 5 5 6 0 1113_1112	1	510.2687	1527.7843	3	51.76	6.70E-06	SLPFKLSPLSFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 5 8 4 1 1170_1169	1	646.8342	1291.6538	2	51.5	8.50E-06	GPSGLVSAQQLGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 5 8 6 1 1174_1173	1	661.8394	1321.6643	2	51.48	7.10E-06	GPSGLVSAQQLSK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 9 8 3 1 1968_1967	1	716.8476	1431.6806	2	51.47	7.10E-06	GPSGVVSAQQLFK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 4 5 5 1 912_911	1	653.8419	1305.6693	2	51.42	7.60E-06	GPSGGVSLAQLLK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 8 5 8 1 1718_1717	1	667.8574	1333.7002	2	51.4	7.20E-06	GPSGVVSLAQLVK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 4 0 0 0 801_800	1	472.2338	1413.6795	3	51.31	7.40E-06	SGPFKASPLAFGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 2 8 3 1 568_567	1	699.838	1397.6614	2	51.29	7.40E-06	GPSGEVSAQQLFK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 3 2 0 1 642_641	1	685.8217	1369.6288	2	51.24	7.50E-06	GPSGVVSEAQLAK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 4 3 3 1 868_867	1	687.8262	1373.6379	2	51.2	7.60E-06	GPSGGVSAQQLFK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 5 1 5 1 1032_1031	1	682.8445	1363.6744	2	51.09	7.80E-06	GPSGLVSDAQLLK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 5 0 0 1 1002_1001	1	639.8261	1277.6377	2	50.96	8.00E-06	GPSGLVSAQQLAK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 4 5 8 1 918_917	1	646.8343	1291.654	2	50.89	9.80E-06	GPSGGVSLAQLVK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 0 5 5 1 112_111	1	660.8495	1319.6844	2	50.87	8.20E-06	GPSGAVSLAQLLK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 3 0 2 0 605_604	1	699.8238	1397.633	2	50.86	8.20E-06	GPSGVVSAQQLER	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 2 3 8 1 478_477	1	699.8375	1397.6605	2	50.68	8.60E-06	GPSGEVSAQQLVK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 5 5 1 0 1103_1102	1	519.6005	1555.7797	3	50.5	8.90E-06	SLPFKLSPLDFGR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 9 5 3 1 1908_1907	1	537.6061	1609.7966	3	50.35	9.20E-06	SVPFKLSPLFFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 3 0 0 0 601_600	1	670.8209	1339.6273	2	50.27	9.40E-06	GPSGVVSAQQLAR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 0 4 0 1 82_81	1	611.7953	1221.5761	2	50.24	9.50E-06	GPSGAVSQAQLAK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 0 0 8 0 17_16	1	486.2496	1455.727	3	50.12	9.70E-06	SAPFKASPLVFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 5 5 5 1 1112_1111	1	681.8735	1361.7325	2	50.12	9.70E-06	GPSGLVSLAQLLK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 6 5 2 0 1305_1304	1	515.5885	1543.7437	3	50.06	9.90E-06	SSPFKLSPLFEGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 3 4 6 0 693_692	1	671.8094	1341.6042	2	49.56	1.10E-05	GPSGVVSGAQLSR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 5 2 8 1 1058_1057	1	682.8471	1363.6797	2	49.5	1.30E-05	GPSGLVSAQQLVK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 9 0 0 0 1801_1800	1	678.8187	1355.6228	2	49.42	1.10E-05	GPSGVVSAQQLAR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 3 4 5 0 691_690	1	684.8373	1367.6601	2	49.25	1.20E-05	GPSGVVSGAQLLR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 0 3 8 1 78_77	1	502.2584	1503.7533	3	49.24	1.20E-05	SAPFKFSPLVFGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 7 8 0 1 1562_1561	1	486.9181	1457.7324	3	49.21	1.20E-05	STPFKVSPLAFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 0 5 8 1 118_117	1	653.8422	1305.6699	2	49.17	1.30E-05	GPSGAVSQAQLVK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 6 4 1 0 1283_1282	1	655.7889	1309.5632	2	49.08	1.20E-05	GPSGSVSGAQLDR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 0 5 2 1 106_105	1	668.8307	1335.6469	2	49.02	1.30E-05	GPSGAVSQAQLFK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 9 4 6 1 1894_1893	1	665.8062	1329.5978	2	48.93	1.30E-05	GPSGVVSGAQLSK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 2 7 5 0 551_550	1	697.8377	1393.6609	2	48.81	1.30E-05	GPSGEVSTAQLLR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 0 7 8 1 158_157	1	647.8242	1293.6339	2	48.8	1.30E-05	GPSGAVSTAQLVK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 4 7 8 0 957_956	1	654.8182	1307.6219	2	48.79	1.30E-05	GPSGGVSTAQLVR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 8 8 9 0 1779_1778	1	706.8516	1411.6887	2	48.69	1.40E-05	GPSGVVSAQQLYR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 5 3 9 0 1079_1078	1	737.8573	1473.7	2	48.65	1.40E-05	GPSGLVSAQQLYR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 9 6 4 0 1929_1928	1	679.8065	1357.5985	2	48.55	1.40E-05	GPSGVVSSAQLGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 6 8 5 1 1372_1371	1	661.839	1321.6635	2	48.54	1.40E-05	GPSGSVSAQQLK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 0 4 4 0 89_88	1	618.7905	1235.5665	2	48.47	1.40E-05	GPSGAVSQAQLGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 5 8 9 0 1179_1178	1	713.8579	1425.7013	2	48.45	1.40E-05	GPSGLVSAQQLYR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 6 4 1 1 1284_1283	1	641.7877	1281.5609	2	48.42	1.40E-05	GPSGSVSGAQLDK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 6 0 6 1 1214_1213	1	634.7977	1267.5809	2	48.2	1.50E-05	GPSGSVSAQQLSK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 1 5 3 1 308_307	1	699.8368	1397.659	2	48.18	1.50E-05	GPSGDVSLAQLFK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 8 0 0 1 1602_1601	1	632.8196	1263.6246	2	48.05	1.60E-05	GPSGVVSAQQLAK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 4 5 3 1 908_907	1	670.8344	1339.6543	2	47.76	1.70E-05	GPSGGVSLAQLFK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 5 3 5 1 1072_1071	1	698.8654	1395.7162	2	47.67	1.70E-05	GPSGLVSAQQLLK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 2 4 7 0 495_494	1	501.5713	1501.6919	3	47.63	2.30E-05	SEPFKGSPLTFGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQXLXR 3 8 9 0 779_778	1	730.8503	1459.6861	2	47.5	1.80E-05	GPSGVVSAQQLYR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 9 0 4 1 1810_1809	1	493.574	1477.7001	3	47.46	1.80E-05	SVPFKASPLGFGK	Phospho (ST)	0.0000001000000.0

SXPFKXSPLXFRG 5 6 2 1 1126_1125	1	506.2537	1515.7392	3	47.46	1.80E-05	SLPFKSSPLEFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 8 3 3 1 1668_1667	1	708.8492	1415.6838	2	47.44	1.80E-05	GPSGVVSAQLFK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 9 4 4 1 1890_1889	1	650.8005	1299.5864	2	47.4	1.80E-05	GPSGVVSAQQLGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 4 6 5 0 931_930	1	654.8175	1307.6205	2	47.39	1.80E-05	GPSGVVSAQQLGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 3 8 3 1 768_767	1	527.6044	1579.7913	3	47.31	1.90E-05	SFPFKVSPPLFFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 8 8 8 1 1778_1777	1	660.8498	1319.685	2	47.15	1.90E-05	GPSGVVSAQQLVK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 4 3 8 1 878_877	1	497.5865	1489.7375	3	46.9	2.00E-05	SGPFKFSPLVFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 5 6 5 1 1132_1131	1	668.847	1335.6794	2	46.82	2.10E-05	GPSGLVSAQQLK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 2 4 1 0 483_482	1	676.7955	1351.5764	2	46.72	2.10E-05	GPSGEVSAQQLDR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 3 0 5 1 612_611	1	677.8419	1353.6692	2	46.4	2.30E-05	GPSGFVSAQQLK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 0 9 5 1 192_191	1	685.8394	1369.6643	2	46.39	2.30E-05	GPSGAVSAQQLK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 5 5 0 1 1102_1101	1	495.6021	1483.7843	3	46.14	2.40E-05	SLPFKLSPLAFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 3 3 5 1 672_671	1	715.8577	1429.7008	2	46.12	2.40E-05	GPSGFVSAQQLK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 6 4 2 1 1286_1285	1	487.5656	1459.675	3	46.07	2.50E-05	SSPFKGSPLFFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 1 5 3 0 307_306	1	713.839	1425.6634	2	45.92	2.60E-05	GPSGDVSLAQLFR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 1 5 5 0 311_310	1	696.8476	1391.6806	2	45.72	2.70E-05	GPSGDVSLAQLLR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 6 8 6 1 1374_1373	1	648.8134	1295.6123	2	45.71	2.70E-05	GPSGSVSAQQLSK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 3 4 9 1 700_699	1	695.8237	1389.6328	2	45.64	2.70E-05	GPSGFVSAQQLYK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 5 4 9 0 1099_1098	1	692.8359	1383.6572	2	45.62	2.70E-05	GPSGLVSAQQLYR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 3 0 8 0 617_616	1	511.5933	1531.758	3	45.6	2.80E-05	SFPFKASPLVFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 4 6 5 1 932_931	1	640.8158	1279.617	2	45.58	2.80E-05	GPSGVVSAQQLK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 9 9 3 0 1907_1906	1	546.9414	1637.8024	3	45.51	2.80E-05	SYPFKLSPLFFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 2 6 6 1 534_533	1	663.8002	1325.5858	2	45.48	2.80E-05	GPSGEVSAQQLSK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 1 6 1 1 324_323	1	670.79	1339.5654	2	45.46	2.80E-05	GPSGDVSAQQLDK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 6 3 9 0 1279_1278	1	538.2552	1611.7437	3	45.28	3.00E-05	SSPFKFSPLVFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 5 1 9 0 1039_1038	1	721.8398	1441.6651	2	45.27	3.00E-05	GPSGLVDAQQLYR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 8 6 4 1 1730_1729	1	633.8083	1265.6021	2	45.26	3.00E-05	GPSGVVSAQQLGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 0 4 6 1 94_93	1	619.7925	1237.5705	2	45.24	3.00E-05	GPSGAVSAQQLSK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 3 3 5 0 671_670	1	541.6088	1621.8045	3	45.1	3.10E-05	SFPFKFSPLFFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 3 0 6 1 614_613	1	664.8156	1327.6167	2	44.99	3.20E-05	GPSGFVSAQQLSK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 0 4 4 1 90_89	1	604.787	1207.5595	2	44.75	3.30E-05	GPSGAVSAQQLGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 9 9 3 0 1987_1986	1	844.8965	1687.7785	2	44.63	3.40E-05	SYPFKLSPLFFGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 4 2 4 1 850_849	1	477.5626	1429.6659	3	44.55	3.50E-05	SGPFKESPLGFGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 1 3 3 0 267_266	1	542.2563	1623.7472	3	44.51	3.50E-05	SDPFKFSPLFFGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 0 9 0 0 181_180	1	760.8682	1519.7218	2	44.43	3.60E-05	SAPFKYSPLAFGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 3 1 2 1 626_625	1	707.8174	1413.6202	2	44.43	3.60E-05	GPSGFVDAQQLGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 2 3 5 1 472_471	1	706.8448	1411.675	2	44.42	3.60E-05	GPSGEVSAQQLK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 8 9 0 0 1781_1780	1	692.8333	1383.6521	2	44.36	3.70E-05	GPSGVVSAQQLAR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 4 3 5 1 872_871	1	502.2585	1503.7535	3	44.23	3.80E-05	SGPFKFSPLFFGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 0 9 3 1 188_187	1	523.5898	1567.7475	3	44.18	3.80E-05	SAPFKYSPLFFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 1 1 1 1 224_223	1	684.7863	1367.558	2	44.08	3.90E-05	GPSGDVDAQQLDK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 5 3 4 0 1069_1068	1	684.8365	1367.6584	2	44.01	4.00E-05	GPSGLVSAQQLGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 9 1 1 1 1824_1823	1	708.8074	1415.6002	2	43.99	4.00E-05	GPSGVVDAQQLDK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 8 2 6 1 1654_1653	1	669.8192	1337.6238	2	43.94	4.00E-05	GPSGVVSEAQQLSK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 0 1 9 0 39_38	1	700.8138	1399.613	2	43.86	4.10E-05	GPSGAVDAQQLYR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 7 9 5 1 1592_1591	1	467.5669	1399.6788	3	43.74	4.20E-05	GPSGTVSAQQLK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 5 3 3 1 1068_1067	1	532.2739	1593.7999	3	43.68	4.30E-05	SLPFKFSPLFFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 5 5 6 1 1114_1113	1	668.8472	1335.6799	2	43.66	4.30E-05	GPSGLVSAQQLSK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 9 0 8 1 1818_1817	1	678.8317	1355.6488	2	43.57	4.40E-05	GPSGVVSAQQLYK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 8 8 3 1 1768_1767	1	684.8498	1367.685	2	43.53	4.40E-05	GPSGVVSAQQLFK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 5 1 0 0 1021_1020	1	675.8212	1349.6279	2	43.4	4.60E-05	GPSGLVDAQQLAR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 0 3 5 1 72_71	1	677.8417	1353.6688	2	43.33	4.60E-05	GPSGAVSAQQLK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 5 9 3 0 1187_1186	1	546.9413	1637.8022	3	43.29	4.70E-05	SLPFKYSPLFFGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 3 3 4 0 669_668	1	783.8785	1565.7425	2	43.22	4.80E-05	SFPFKFSPLGFGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 7 8 2 1 1566_1565	1	758.8766	1515.7386	2	43.02	5.00E-05	STPFKVSPLFFGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 4 8 5 0 971_970	1	495.593	1483.7573	3	42.86	5.20E-05	SGPFKVSPLFFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 0 6 8 1 138_137	1	640.8161	1279.6177	2	42.74	5.30E-05	GPSGAVSAQQLVK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 9 4 2 1 1886_1885	1	686.8109	1371.6072	2	42.73	5.30E-05	GPSGVVSAQQLGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 0 4 1 1 84_83	1	633.7901	1265.5656	2	42.7	5.40E-05	GPSGAVSAQQLDK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 3 0 8 1 618_617	1	670.8358	1339.6571	2	42.69	5.40E-05	GPSGFVSAQQLYK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 5 1 7 0 1035_1034	1	515.5886	1543.7439	3	42.61	5.50E-05	SLPFKDSPLTFFGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 5 0 0 0 1001_1000	1	735.8785	1469.7424	2	42.56	5.50E-05	SLPFKASPLAFGR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 2 5 3 0 507_506	1	535.6002	1603.7786	3	42.46	5.70E-05	SEPFKLSPLFFGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 4 5 1 1 904_903	1	736.8631	1471.7116	2	42.44	5.70E-05	SGPFKLSPLDFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 0 9 9 0 199_198	1	724.832	1447.6494	2	42.42	5.70E-05	GPSGAVSAQQLYR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 2 5 2 0 505_504	1	711.8345	1421.6544	2	42.37	5.80E-05	GPSGEVSAQQLER	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 3 3 9 1 680_679	1	740.8472	1479.6798	2	42.35	5.80E-05	GPSGFVSAQQLYK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 6 2 0 1 1242_1241	1	492.2376	1473.691	3	42.32	5.90E-05	SSPFKESPLAFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 3 3 2 1 666_665	1	732.8361	1445.6576	2	42.28	5.90E-05	GPSGFVSAQQLGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 3 3 3 1 668_667	1	732.8495	1463.6845	2	42.25	6.00E-05	GPSGFVSAQQLFK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 8 3 5 1 1672_1671	1	691.8578	1381.701	2	42.2	6.00E-05	GPSGVVSAQQLK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 6 4 6 1 1294_1293	1	627.7902	1253.5658	2	42.12	6.10E-05	GPSGSVSAQQLSK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 0 4 3 0 87_86	1	663.8119	1325.6093	2	42.08	6.20E-05	GPSGAVSAQQLFR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 1 9 0 1 382_381	1	686.8129	1371.6113	2	42.06	6.20E-05	GPSGDVSAQQLAK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 3 9 0 0 799_798	1	563.6002	1687.7788	3	42	6.30E-05	SFPFKYSPLVFGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 7 3 3 1 1468_1467	1	528.2619	1581.7639	3	42	6.30E-05	STPFKFSPLFFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 3 4 4 1 690_689	1	642.8027	1283.5909	2	41.93	6.40E-05	GPSGFVSAQQLGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 5 8 3 0 1167_1166	1	525.6092	1573.8057	3	41.91	6.40E-05	SLPFKVSPLFFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 9 4 0 1 1882_1881	1	657.8082	1313.6018	2	41.9	6.50E-05	GPSGVVSAQQLAK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 5 5 7 1 1116_1115	1	675.8545	1349.6944	2	41.82	6.60E-05	GPSGLVSLAQLTK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 9 9 5 0 1991_1990	1	552.2726	1653.7959	3	41.61	6.90E-05	SYPFKYSPLFFGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 9 3 4 1 1870_1869	1	518.9182	1553.7326	3	41.56	7.00E-05	SYPFKFSPLGFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 6 4 2 1 1286_1285	1	648.7952	1295.5759	2	41.4	7.20E-05	GPSGSVSAQQLGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQQLXR 0 1 1 1 24_23	1	662.7944	1323.5742	2	41.36	7.30E-05	GPSGAVDAQQLDK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 4 0 8 1 818_817	1	707.8596	1413.7046	2	41.32	7.40E-05	SGPFKASPLVFGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFRG 6 0 6 0 1213_1212	1	730.8487	1459.6828	2	41.19	7.60E-05	SSPFKASPLSFGK	Phospho (ST)	0.0000001000000.0

GPSGXVSAQLXR 2 0 8 1 418_417	1	661.8235	1321.6325	2	41.19	0.00014	GPSGEVSAALQV	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 5 8 6 0 1173_1172	1	505.5963	1513.7671	3	41.18	7.60E-05	SLPFKVSPLSFR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 5 5 3 1 1108_1107	1	698.8657	1395.7169	2	41.13	7.70E-05	GPSGLVSLAQLFK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 4 8 4 1 970_969	1	618.8029	1235.5912	2	41.1	7.80E-05	GPSGGVSAVQLGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 5 8 4 0 1169_1168	1	742.886	1483.7575	2	40.94	8.10E-05	SLPFKVSPLGFR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 2 3 0 1 462_461	1	685.8209	1369.6273	2	40.92	8.10E-05	GPSGEVSAFQALAK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 2 0 0 0 401_400	1	661.8084	1321.6023	2	40.87	8.20E-05	GPSGEVSAALQAR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 5 0 6 1 1014_1013	1	647.8239	1293.6333	2	40.85	8.20E-05	GPSGLVSAALQSK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 9 5 5 1 1912_1911	1	706.8631	1411.7116	2	40.84	8.20E-05	GPSGVVSLAQLLK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 8 0 4 1 1610_1609	1	625.8107	1249.6069	2	40.71	8.50E-05	GPSGVVSAALQGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 7 4 5 0 1491_1490	1	496.253	1485.7372	3	40.54	8.80E-05	STPFKGSPLLFGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 0 4 3 1 88_87	1	649.8104	1297.6062	2	40.53	8.90E-05	GPSGAVSAAQLSK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 3 3 0 1 662_661	1	694.8336	1387.6526	2	40.46	9.00E-05	GPSGFVSAFQALAK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 3 4 6 1 694_693	1	657.809	1313.6035	2	40.37	9.20E-05	GPSGFVSGAQLSK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 0 3 0 1 62_61	1	656.8194	1311.6242	2	40.36	9.20E-05	GPSGAVSAAQLAK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 9 0 1 0 1803_1802	1	522.2447	1563.7122	3	40.12	9.70E-05	SYPFKASPLDFGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 6 1 5 1 1232_1231	1	669.8209	1337.6273	2	39.92	0.0001	GPSGSVSDAQLLK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 3 3 8 1 678_677	1	708.85	1415.6855	2	39.77	0.00011	GPSGFVSAALQVYK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 9 0 9 1 1820_1819	1	710.8288	1419.643	2	39.71	0.00011	GPSGVVSAALQYK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 3 8 4 1 770_769	1	663.8262	1325.6379	2	39.66	0.00011	GPSGFVSAALQGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 4 9 5 0 991_990	1	516.925	1547.7531	3	39.48	0.00011	SGPFKYSPLLFGR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 9 8 8 0 1977_1976	1	788.9	1575.7855	2	39.39	0.00012	SYPFKVSPLVFR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 1 6 8 0 337_336	1	676.813	1351.6114	2	39.31	0.00012	GPSGDVSSAQLVR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 4 4 1 1 884_883	1	626.7823	1251.55	2	39.3	0.00012	GPSGGVSGAQLDK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 9 5 0 0 1901_1900	1	521.5966	1561.7678	3	39.16	0.00012	SYPFKLSPLAFGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 5 9 3 0 1187_1186	1	737.8557	1473.6968	2	39.11	0.0002	GPSGLVSYAQLFR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 9 0 9 0 1819_1818	1	806.8809	1611.7473	2	39.05	0.00012	SYPFKASPLVFR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 9 8 3 0 1967_1966	1	542.27	1623.788	3	39.02	0.00013	SYPFKVSPLFFGR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 9 9 5 1 1992_1991	1	542.9385	1625.7936	3	38.99	0.00013	SYPFKVSPLFFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 9 3 3 1 1868_1867	1	740.8478	1479.681	2	38.98	0.00013	GPSGVVSAALQFK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 4 5 6 0 913_912	1	491.5808	1471.7204	3	38.92	0.00013	SGPFKLSPLSFR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 4 7 4 0 949_948	1	715.843	1429.6715	2	38.88	0.00013	SGPFKTSPLGFR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 9 6 2 1 1926_1925	1	701.8163	1401.618	2	38.78	0.00013	GPSGVVSSAQLK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 9 0 0 1 1802_1801	1	498.2461	1491.7164	3	38.63	0.00014	SYPFKASPLAFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 9 8 9 0 1979_1978	1	738.848	1475.6815	2	38.59	0.00014	GPSGVVSAALQYR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 2 1 9 1 440_439	1	715.8136	1429.6126	2	38.35	0.00015	GPSGEVSDAQLYK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 5 5 1 1 1104_1103	1	682.8447	1363.6749	2	38.28	0.00015	GPSGLVSLAQLDK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 4 1 7 0 835_834	1	496.8999	1487.6779	3	38.1	0.00015	SGPFKDSPLTFGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 4 2 0 1 842_841	1	640.7991	1279.5837	2	38.04	0.00016	GPSGGVSEAQLAK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 5 9 3 1 1188_1187	1	537.6072	1609.7997	3	37.77	0.00017	SLPFKYSPLFFGK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 9 4 7 1 1896_1895	1	672.8139	1343.6133	2	37.72	0.00017	GPSGVVSGAQLTK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 1 8 6 1 374_373	1	662.8109	1323.6073	2	37.71	0.00017	GPSGDVSAALQSK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 5 7 0 0 1141_1140	1	668.8352	1335.6559	2	37.29	0.00019	GPSGLVSTAQLAR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 9 2 5 0 1851_1850	1	810.8949	1619.7752	2	37	0.0002	SYPFKESPLLFGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 9 7 5 0 1951_1950	1	476.9019	1427.684	3	36.94	0.0002	GPSGVVSTAQLLR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 0 3 5 0 71_70	1	691.8445	1381.6745	2	36.93	0.0002	GPSGAVSFAQLLR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 6 3 3 1 1268_1267	1	702.8319	1403.6493	2	36.78	0.00021	GPSGSVSAALQFK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 8 2 8 0 1657_1656	1	771.8893	1541.764	2	36.77	0.00021	SVPFKESPLVFR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 8 0 0 1 1602_1601	1	476.9146	1427.7218	3	36.77	0.00021	SVPFKASPLAFGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 4 0 3 1 808_807	1	731.8603	1461.706	2	36.65	0.00022	SGPFKASPLFFGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 9 4 2 0 1885_1884	1	782.863	1563.7114	2	36.57	0.00022	SYPFKGSPLFFGR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 0 5 1 0 103_102	1	757.8737	1513.7328	2	36.33	0.00023	SAPFKLSPLDFGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 9 3 4 1 1870_1869	1	695.8237	1389.6328	2	36.17	0.00024	GPSGVVSAALQGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 9 1 9 1 1840_1839	1	543.5837	1627.7294	3	36.15	0.00024	SYPFKDSPLYFR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 2 1 6 1 434_433	1	677.7972	1353.5799	2	36.11	0.00024	GPSGEVSDAQLSK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 8 0 3 1 1608_1607	1	670.8343	1339.6541	2	36.08	0.00025	GPSGVVSAALQFK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 2 1 2 1 426_425	1	698.8032	1395.5918	2	35.94	0.00025	GPSGEVSDAQLK	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 4 4 4 1 890_889	1	597.7795	1193.5444	2	35.92	0.00026	GPSGGVSGAQLGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 0 0 8 1 18_17	1	714.8673	1427.7201	2	35.89	0.00026	SAPFKASPLVFR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 5 6 5 0 1131_1130	1	764.8998	1527.7851	2	35.77	0.00026	SLPFKKSPLFFGR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 3 9 8 0 797_796	1	812.9023	1623.7901	2	35.62	0.00027	SVPFKYSPLVFR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 9 5 0 1 1902_1901	1	512.2638	1533.7696	3	35.58	0.00028	SYPFKLSPLAFGK	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 4 8 4 1 970_969	1	700.8499	1399.6852	2	35.49	0.00028	SGPFKVSPLGFR	Phospho (ST)	0.0000001000000.0
SXPFKXSPLXFR 9 0 3 0 1807_1806	1	798.8837	1595.7528	2	35.25	0.0003	SYPFKASPLFFGR	Phospho (ST)	0.0000001000000.0
GPSGXVSAQLXR 6 7 9 1 1360_1359	1	687.8201	1373.6256	2	35.16	0.0003	GPSGSVSTAQLYK	Phospho (ST)	0.0000001000000.0