Supplementary table 1. Identification and posttranslational modification characterization of mouse hippocampal proteins differentially expressed between NaCl group and SGS742 administration group with nano-LC-CID-MS/MS and nano-LC-ETD-MS/MS respectively

Group	Acc No.	Protein Name	CID score	CID coverage	CID peptides (ion score / mass error (Da))	ETD score	ETD coverage	ETD peptides (ion score / mass error (Da))
NaCl	P63101	14-3-3 protein zeta/delta	829	60%	[1] M*DKNELVQK [9] M1 acetylation (57 / 0.02) [12] LAEQAER [18] (44 / 0.20) [12] LAEQ*AER [18] Q15 deamidation (45 / 0.24) [19] YDDMAACMK [27] (41 / 0.14) [19] YDDMAACM*K [27] M26 oxidation (46 / 0.09) [19] YDDM*AACMK [27] M22 oxidation (57 / 0.14) [19] YDDMAAC*MK [27] C25->S (52 / 0.13) [28] SVTEQGAELSNEER [41] (108 / 0.02) [28] S*VTEQGAELSNEER [41] S28->A (109 / 0.05) [28] SVTEQ*GAELSNEER [41] Q32 deamidation (62 / 0.02) [28] SVTEQGAELSNEE*R [41] E40 methylation (102 / 0.08) [28] SVTEQGAE*LSNEER [41] E35 methylation (74 / 0.09) [42] NLLSVAYK [49] (51 / 0.03) [61] VVSSIEQK [68] (69 / 0.05) [61] VV*SSIEQK [68] V62->L/I (70 / 0.01) [84] EKIETELR [91] (53 / 0.12) [86] IETELR [91] (39 / 0.11) [92] DICNDVLSLLEK [103] (74 / 0.13) [104] FLIPNASQPESK [115] (51 / 0.06) [128] YLAEVAAGDD [137] (49 / -0.10) [128] YLAEVAAGDDK [138] (51 / 0.02) [128] YLAEVAAGDDKK [139] (70 / 0.16) [139] K*GIVDQSQQAYQEAFEISK [157] K139->T (83 / -0.12) [140] GIVDQSQQAYQEAFEISK [157] (141 / -0.04) [158] KEMQPTHPIR [167] (47 / 0.21) [158] KEM*QPTHPIR [167] M160 oxidation (59 / 0.21) [159] EMQPTHPIR [167] (48 / 0.12) [159] EM*QPTHPIR [167] M160 oxidation (37 / 0.19) [168] LGLALNF*SVF [177] F174 oxidation (47 / 0.19) [175] SVFYYEILNSPEK [187] (67 / 0.11) [175] SVFYYEILNS*PEK [187] S184 phosphorylation (44 / 0.09) [178] YYEILNSPEK [187] (72 / 0.15) [178] YYEILNS*PEK [187] S184 phosphorylation (41 / 0.15) [178] YYEILN*SPEKAC [189] N183->I/L (46 / -0.04) [194] TAFDEAIAELDTLS*EESYK [212] S207->N (86 / -0.01) [229] TSDTQGDEAEAGEGGEN [245] (86 / 0.10)	575	74%	[1] M*DKNELVQK [9] M1 acetylation (42 / 0.02) [12] LAEQAER [18] (31 / 0.17) [19] YDDMAACMK [27] (31 / 0.21) [28] SVTEQGAELSNEER [41] (108 / 0.01) [28] S*VTEQGAELSNEER [41] S28->A (85 / 0.05) [28] SVTEQGAELSNEER* [41] R41 deamidation (72 / 0.02) [28] SVTEQGAE*LSNEER* [41] E35 metylation (66 / 0.09) [42] NLLSVAYK [49] (45 / 0.12) [42] NLLSVAYKNVVGAR [55] (35 / 0.45) [61] VVSSIEQK [68] (50 / 0.21) [61] V*VSSIEQK [68] V61->L/I (58 / 0.01) [84] EKIETELR [91] (37 / 0.12) [86] IETELR [91] (49 / 0.12) [92] DICNDVLSLLEK [103] (57 / 0.13) [104] FLIPNASQPESK [115] (51 / 0.08) [128] YLAEVAAGDDK [138] (32 / 0.06) [128] YLAEVAAGDDKK [139] (78 / 0.16) [130] AEVAA*G [135] A134->E (36 / 0.14) [139] K*GIVDQSQQAYQEAFEISK [157] K139->T (45 / 0.18) [140] GIVDQSQQAYQEAF [153] (46 / 0.14) [140] GIVDQSQQAYQEAFEISK [157] (82 / -0.04) [151] EAFEISK [157] (41 / 0.08) [158] KEM*QPTHPIR [167] M160 oxidation (33 / 0.16) [168] LGLALNF*SVF [177] F174 oxidation (46 / 0.19) [175] SVFYYEILNSPEK [187] (64 / 0.11) [178] YYEILNSPEK [187] (50 / 0.15) [194] TAFDEAIAELDTLS*EESYK [212] S207->N (49 / -0.01) [213] DSTLIMQLLR [222] (62 / 0.04) [213] DSTLIM*QLLR [222] M218 oxidation (62 / 0.01) [229] TSDTQGDEAEAGEGGEN [245] (41 / 0.10)

					[213] DSTLIMQLLR [222] (44 / 0.04) [213] DSTLIM*QLLR [222] M218 oxidation (43 / 0.15)			
NaCl	P80314	T-complex protein 1 subunit beta	978	59%	[2] A*SLSLAPVNIFK [13] A2 acetylation (76 / 0.09) [26] LSSFIGAIAIGDLVK [40] (107 / 0.13) [46] KGMDKIL*L [53] L52->S (36 / 0.15) [58] DAALM*VTNDGATILK [72] M62 oxidation (94 / 0.20) [90] VQDDEVGDGTTSVTVLAAELLR [111] (98 / -0.10) [139] EALLSSAVDHGSDEAR [154] (81 / -0.02) [182] LAVEAVLR [189] (53 / 0.20) [192] GSGNLEAIHVIK [203] (42 / 0.08) [237] ILIANTGM*DTDK [248] M244 oxidation (49 / 0.18) [323] LALVTGGEIASTFDHPELVK [342] (64 / -0.05) [348] LIEEVM*IGEDK [358] M353 oxidation (93 / 0.17) [377] LALVTGGEIASTFDHPELVK [388] (87 / 0.13) [389] SLHDALCVLAQTVK [402] (61 / 0.30) [445] MLPTIIADNAGYDSADLVAQLR [466] (70 / 0.19) [502] QVLLSAAEAAEVILR [516] (105 / 0.02)	598	53%	[1] M*A*SLSLAPVNIFK [13] N-term: Met-loss, A2 acetylation (41 / 0.12) [26] LSSFIGAIAIGDLVK [40] (75 / 0.13) [58] DAALM*VTNDGATILK [72] M62 oxidation (67 / 0.20) [90] VQDDEVGDGTTSVTVLAAELLR [111] (47 / 0.13) [139] EALLSSAVDHGSDEAR [154] (74 / 0.11) [192] GSGNLEAIHVIK [203] (40 / 0.08) [237] ILIANTGM*DTDK [248] M244 oxidation (49 / 0.18) [348] LIEEVM*IGEDK [358] M353 oxidation (41 / 0.17) [377] LALVTGGEIASTFDHPELVK [388] (69 / 0.23) [432] EAVAM*ESFAK [441] M436 oxidation (44 / 0.22) [445] MLPTIIADNAGYDSADLVAQLR [466] (86 / 0.19) [445] M*LPTIIADNAGYDSADLVAQLR [466] M445 oxidation (80 / -0.03)
NaCl	Q8BMF4	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase	278	27%	[282] DVPLGAPLCIIVEK [295] (40 / 0.23) [383] DIDSFVPSK [391] (40 / 0.20) [392] AAPAAAAAM*APPGPR [406] M400 oxidation (43 / 0.14) [407] VAPAPAGVFTDIPISNIR [424] (64 / 0.13) [469] ISVNDFIIK [477] (56 / 0.19) [486] VPEANSSWMD*TVIR [499] D495->Y (60 / 0.18) [528] GLETIASDVVSLASK [542] (93 / 0.14) [548] LQPHEFQGGTF [558] (43 / 0.17) [548] LQPHEFQGGTFTISNLGM*FGIK [569] M565 oxidation (49 / -0.07) [570] NFSAIINPPQAC [581] (50 / 0.11) [582] ILAIGASEDK [591] (54 / 0.17) [600] GFDVASVM*SVTLSCDHR [616] M607 oxidation (35 / 0.16) [633] YLEKPITM*LL [642] M640 oxidation (42 / 0.09)	254	25%	[93] VPLPSLSPTM*QAGTIAR [109] M102 oxidation (50 / 0.24) [282] DVPLGAPLCIIVEK [295] (36 / 0.23) [407] VAPAPAGVFTDIPISNIR [424] (107 / 0.14) [469] ISVNDFIIK [477] (56 / 0.19) [528] GLETIASDVVSLASK [542] (89 / 0.14) [548] LQPHEFQGGTFTISNLGM*FGIK [569] M565 oxidation (38 / -0.04) [633] YLEKPITM*LL [642] M640 oxidation (35 / 0.09)
NaCl	Q8JZK9	Hydroxymethylglutaryl-CoA synthase, cytoplasmic	302	26%	[47] YTIGLGQAR [55] (49 / 0.11) [90] LEVGTETIIDK [100] (61 / 0.10) [278]MFLNDFLNDQNR[289] (48 / 0.11) [292]NSIYSGLEAFGDVK[305] (111 / 0.11) [306]LEDTYFDR[313] (46 / 0.15) [322]ASSELFNQK[330] (40 / 0.13) [370]VGVFSYGSGLAATLY[384] (93 / 0.06) [388]VTQDATPGSALDK[400] (66 / 0.12) [401]ITASLCDLK[409] (49 / 0.17) [416]TCVAPDVFAENMK[428] (47 / 0.07) [416]TCVAPDVFAENM*K[428] M427 oxidation (47 / 0.10)	112	18%	[47]YTIGLGQAR[55] (36 / 0.11) [90]LEVGTETIIDK[100] (39 / 0.10) [278]MFLNDFLNDQNR[289] (40 / 0.11) [292]NSIYSGLEAFGDVK[305] (40 / 0.11) [306]LEDTYFDR[313] (51 / 0.15) [388]VTQDATPGSALDK[400] (64 / 0.12) [416]TCVAPDVFAENM*K[428] M427 oxidation (39 / 0.13) [503]LPATSAESESAVISN*GEH[520] N517 deamidation (83 / -0.11)

NaCl	**P63038**	**60 kDa heat shock protein, mitochondrial precursor**	**827**	**48%**	**[61]TVIIEQSWGSPK[72] (85 / 0.07) [61]TVIIEQSW*GSPK[72] W68 dioxidation (65 / 0.10) [97]LVQDVANNTN*EEAGDGTTTATVLAR[121] N106 deamidation (79 / 0.23) [134]GANPVEIR[141] (58 / 0.18) [143]GVMLAVDAVIAELKK[157] (60 / 0.14) [169]AQVATIS*AN[177] S175->A (46 / 0.15) [196]KGVITVK[202] (38 / 0.23) [237]C*EFQDAYVLLSEK[249] C237 Ammonia-loss (75 / 0.17) [293]VGLQVVAVK[301] (52 / 0.09) [302]APGFGDNR[309] (42 / 0.22) [345]VGEVIVTK[352] (53 / 0.17) [371]IQEITEQLDITTSEYEK[387] (135 / 0.05) [397]LSDGVAVLK[405] (61 / 0.06) [406]VGGTSDVEVNEK[417] (103 / 0.15) [421]VTDALNATR[429] (75 / 0.10) [430]AAVEEGIVLGGGCALLR[446] (62 / 0.19) [463]IGIEIIK[469] (45 / 0.09) [482]NAGVEGSLIVEK[493] (64 / 0.22) [527]TALLDAAGVASLLTTAEAVVTEIPK[551] (71 / 0.21)**	**1043**	**52%**	**[61]TVIIEQSWGSPK[72] (55 / 0.07) [158]QSKPVTTPEEIAQVATISAN*GDK[180] N177 deamidation (85 / 0.24) [206]TLNDELEIIEGM*K[218] M217 oxidation (61 / 0.21) [293]VGLQVVAVK[301] (35 / 0.13) [302]APGFGDNR[309] (36 / 0.22) [345]VGEVIVTK[352] (41 / 0.11) [397]LSDGVAVLK[405] (52 / 0.13) [406]VGGTSDVEVNEK[417] (48 / 0.15) [421]VTDALNATR[429] (49 / 0.10) [430]AAVEEGIVLGGGCALLR[446] (67 / 0.19) [482]NAGVEGSLIVEK[493] (63 / 0.22) [527]TALLDAAGVASLLTTAEAVVTEIPK[551] (74 / 0.21) [552]EEK*DPGM*GAMGGMGGGMGGG[571] K554->M, M558 oxidation (42 / 0.19)**
NaCl	**P06151**	**L-lactate dehydrogenase A chain**	**926**	**59%**	**[6]DQLIVNLLK[14] (70 / 0.22) [36] AISILMK[42] (38 / 0.23) [43]DLADELALVDVMEDK[57] (100 / 0.17) [60]GEMMDLQHGSLFLK[73] (41 / 0.24) [60]GEM*MDLQHGSLFLK[73] M62 oxidation (63 / 0.15) [91]LVIITAGAR[99] (62 / 0.12) [107] LNLVQR[112] (49 / 0.19) [113] NVNIFK[118] (38 / 0.10) [133] LLIVSNPVDILTY[145] (94 / 0.20) [133] LLIVSNPVDILTYVAWK[149] (97 / 0.03) [158] VIGSGCNLDSAR[169] (96 / 0.15) [158] VIGSGCN*LDSAR[169] N64 deamidation (68 / 0.18) [172] YLMGER[177] (35 / 0.19) [213] SLNPELGTDADK[224] (73 / 0.23) [213] SLNPELGTDADKEQWK[228] (90 / 0.08) [233] QVVDSAYEVIK[243] (71 / 0.16) [251] AIGLSVADLAESIMK[265] (110 / 0.24) [279] GLYGINEDVFLSVPC[293] (56 / 0.15) [294] ILGQNGISDVVK[305] (93 / 0.24) [294] ILGQ*NGISDVVK[305] Q297 deamidation (73 / 0.18) [294] ILGQN*GISDVVK[305] N298 deamidation (70 / 0.23) [306] VTLTPEEEAR[315] (50 / 0.19) [319] SADTLWGIQK[328] (61 / 0.23)**	**1054**	**57%**	**[6]DQLIVNLLK[14] (43 / 0.18) [22]KI*TVVGVGA[30] I23->V (34 / 0.13) [38] SI*LMKDLAD[46] I39->N (37 / 0.25) [43]DLADELALVDVMEDK[57] (74 / 0.21) [43]DLADELALVDVM*EDK[57] M54 oxidation (104 / 0.23) [58]LKGEM*M*DLQHGSLFLK[73] M62, M63 oxidation (112 / 0.21) [60]GEMMDLQHGSLFLK[73] (61 / 0.24) [60]GEM*MDLQHGSLFLK[73] M62 oxidation (118 / 0.21) [91]LVIITAGAR[99] (56 / 0.12) [107] LNLVQR[112] (31 / 0.19) [133] LLIVSNPVDILTYVAWK[149] (49 / 0.03) [158] VIGSGCNLDSAR[169] (60 / 0.15) [172] YLMGER[177] (31 / 0.19) [213] SLNPELGTDADK[224] (61 / 0.23) [213] SLNPELGTDADKEQWK[228] (40 / 0.04) [233] QVVDSAYEVIK[243] (44 / 0.16) [251] AIGLSVADLAESIMK[265] (76 / 0.24) [251] AIGLSVADLAESIM*K[265] M264 oxidation (54 / 0.17) [269] RVHPISTMIK[278] (37 / 0.16) [294] ILGQNGISDVVK[305] (45 / 0.24) [306] VTLTPEEEAR[315] (47 / 0.19) [319] SADTLWGIQK[328] (40 / 0.23) [319] SADTLW*GIQK[328] W324 dioxidation(44 / 0.18)**

					[319] SADTLW*GIQK [328] W324 dioxidation(49 / 0.18)			
NaCl	P46638	Ras-related protein Rab-11B	88	16%	[14]VVLIGDSGVGK [24] (36 / 0.14) [42]STIGVEFATR [51] (83 / 0.19)			
NaCl	P17182	Alpha-enolase	823	58%	[16]GNPTVEVDLYTAK [28] (72 / 0.10) [61]GVSQAVEHINK [71] (64 / 0.26) [61]GVSQ*AVEHINK [71] Q64 deamidation (57 / 0.07) [72]TIAPALVSK [80] (42 / 0.12) [81]KVNVVEQEK [89] (45 / 0.24) [82]VNVVEQEK [89] (42 / 0.14) [93]LMIEMDGTENK [103] (63 / 0.18) [93]LM*IEM*DGTENK [103] M94, M97 oxidation (46 / 0.16) [163]LAMQEFMILPVGASSFR [179] (41 / 0.13) [163]LAM*QEFM*ILPVGASSFR [179] M165, M169 oxidation (64 / 0.17) [169] M*ILPVGASSFR [179] M169 oxidation (39 / 0.05) [203] DATNVGDEGGFAPNILENK [221] (104 / 0.10) [222] EALELLK [228] (33 / 0.23) [234] AGYTDQVVIGM*DVAASEFYR [253] M244 oxidation (44 / 0.24) [270] YITPDQLADLYK [281] (51 / 0.25) [307] FTASAGIQVVGDDLTVTNPK [326] (127 / -0.03) [336] SCNCLLLK [343] (33 / 0.06) [344] VNQIGSVTESLQACK [358] (104 / 0.07) [359] LAQSNGWGV*M*VSHR [372] M368 oxidation, V367->M (52 / 0.20)	730	53%	[16]GNPTVEVDLYTAK [28] (52 / 0.10) [72]TIAPALVSK [80] (50 / 0.12) [81]KVNVVEQEK [89] (33 / 0.24) [93]LMIEMDGTENK [103] (48 / 0.18) [93]LM*IEMDGTENK [103] M94 oxidation (49 / 0.21) [93]LM*IEM*DGTENK [103] M94, M97 oxidation (49 / 0.12) [163]LAMQEFMILPVGASSFR [179] (70 / 0.13) [222] EALELLK [228] (39 / 0.23) [307] FTASAGIQVVGDDLTVTNPK [326] (124 / -0.03) [344] VNQIGSVTESLQACK [358] (105 / 0.08) [413] IEEELGSK [420] (45 / 0.17)
NaCl	Q99KI0	Aconitate hydratase, mitochondrial precursor	2239	53%	[32] VAMSHFEPSEYIR [44] (58 / 0.10) [32] VAM*SHFEPSEYIR [44] M34 oxidation (64 / 0.10) [51] NINIVR [56] (37 / 0.20) [69] IVYGHLDDPANQEIER [84] (77 / 0.03) [69] IVYGHL*DDPANQEIER [84] L74->M (62 / 0.16) [76] DPANQEIER [84] (44 / 0.23) [77] PANQEIER [84] (68 / 0.11) [96] VAMQDATAQMAMLQF [110] (71 / 0.05) [96] VAM*QDATAQM*AMLQFISSGLPK [117] M98, M105 oxidation (36 / 0.16) [118] VAVPSTIHCDHLIEAQVGGEK [138] (49 / -0.09) [145] DINQEVYNFLATAGAK [160] (76 / 0.22) [161] YGVGFWR [167] (43 / 0.25) [168] PGSGIIHQIILENY [181] (58 / 0.23) [168] PGSGIIHQIILENYAYPGVLLIGTDSHTPN [197] (55 / -0.12) [234] LTGSLSGWTSPK [245] (63 / 0.14) [234] LTGSLSGW*TSPK [245] W241 oxidation (53 / 0.18) [234] LTGSLSGW*TSPK [245] W241 dioxidation (75 / 0.12)	2208	51%	[32] VAMSHFEPSEYIR [44] (74 / 0.17) [32] VAM*SHFEPSEYIR [44] M34 oxidation (84 / 0.14) [51] NINIVR [56] (35 / 0.20) [59] LNRPLTLSEK [68] (38 / 0.22) [62] PLTLSEK [68] (36 / 0.15) [69] IVYGHLDDPANQEIER [84] (61 / -0.002) [96] VAMQDATAQMAMLQF [110] (70 / 0.05) [118] VAVPSTIHCDHLIEAQVGGEK [138] (103 / 0.10) [118] VAVPSTIHCDHLIEAQ*VGGEK [138] Q133 deamidation (103 / 0.14) [145] DINQEVYNFLATAGAK [160] (111 / 0.22) [161] YGVGFWR [167] (41 / 0.25) [234] LTGSLSGWTSPK [245] (61 / 0.14) [234] LTGSLSGW*TSPK [245] W241 oxidation (45 / 0.01) [234] LTGSLSGW*TSPK [245] W241 dioxidation (51 / 0.12) [251] VAGILTVK [258] (52 / 0.08) [259] GGTGAIVEYHGPGVDSISC [277] (58 / 0.19) [313] TDIANLAEEFK [323] (37 / 0.14) [351] G*PFTPDLAHPVADVGTVAEK [370] G351

					251 VAGILTVK 258 (57 / 0.08) **313 TDIANLAEEFK 323 (79 / 0.14)** **371 EGWPLDIR 378 (46 / 0.34)** **379 VGLIGSCTNSSYEDMGR 395 (105 / 0.10)** **379 VGLIGSCTNSSYEDM*GR 395 M393 oxidation (90 / 0.07)** **379 VGLIGSCTN*SSYEDMGR 395 N387 deamidation (58 / 0.16)** **379 VGLIGSCTN*SSYEDM*GR 395 N387 deamidation, M393 oxidation (77 / 0.22)** **402 QALAHGLK 409 (65 / 0.16)** **412 SQFTITPGSEQIR 424 (67 / 0.10)** **430 DGYAQILR 437 (47 / 0.16)** **430 DGYAQ*ILR 437 Q434 deamidation (47 / 0.12)** **438 DVGGIVLAN 446 (47 / 0.35)** **438 DVGGIVLANACGPCIGQWDR 457 (73 / 0.24)** **438 DVGGIVLANACGPCIGQW*DR 457 W455 dioxidation (64 / 0.20)** **447 ACGPCIGQWDR 457 (51 / 0.20)** **452 IGQWDR 457 (42 / -0.03)** **466 NTIVTSYNR 474 (44 / 0.18)** **480 NDANPETHAF 489 (38 / 0.25)** **480 NDANPETHAFVTSPEI*VTALAIAGTLK 506 I495->N (69 / 0.21)** **507 FNPETDFLTGK 517 (63 / 0.19)** **522 FKLEAPDADELPR 534 (94 / 0.11)** **524 LEAPDADELPR 534 (80 / 0.20)** **535 SDFDPGQDTYQHPPK 549 (40 / 0.09)** **556 VDVSPTSQR 564 (46 / 0.14)** **565 LQLLEPFDK 573 (41 / 0.22)** **565 LQLLEPFDKWDGK 577 (43 / 0.22)** **574 WDGKDLEDLQILIK 587 (54 / 0.11)** **578 DLEDLQILIK 587 (78 / 0.18)** **592 CTTDHISAAGPWLK 605 (58 / 0.18)** **592 C*TTDHISAAGPWLK 605 C592 Ammonia-loss (53 / 0.13)** **592 CTTDHISAAGPWLK* 605 K605 dioxidation (45 / 0.14)** **592 CTTDHISAAGPW*LK 605 W603 dioxidation (41 / 0.17)** **608 GHLDNISNNLLIGAINIENGK 628 (92 / -0.08)** **634 NAVTQEFGPVPDTAR 648 (106 / 0.05)** **634 N*AVTQEFGPVPDTAR 648 N634->I (79 / -0.05)** **634 N*AVTQEFGPVPDTAR 648 N634 deamidation (83 / 0.22)** **634 NAVTQE*FGPVPDTAR 648 E639 methylation (64 / 0.14)** **657 WVVIGDENYGEGSSR 671 (104 / 0.23)** **657 W*VVIGDENYGEGSSR 671 W657 dioxidation**		**Myristoyl (N-term G) (50 / 0.14)** **357 LAHPVADVGTVAEK 370 (48 / 0.23)** **379 VGLIGSCTNSSYEDMGR 395 (105 / 0.17)** **379 VGLIGSCTNSSYEDM*GR 395 M393 oxidation (96 / 0.09)** **379 VGLIGSCTN*SSYEDMGR 395 N387 deamidation (72 / 0.16)** **379 VGLIGSCTNSSYEDMGR* 395 R395 oxidation (85 / 0.07)** **379 VGLIGSCTN*SSYEDM*GR 395 N387 deamidation, M393 oxidation (110 / 0.17)** **399 VAKQALAHGLKCKSQFTITPGSEQIR 424 (54)** **402 QALAHGLK 409 (35 / 0.16)** **412 SQFTITPGSEQIR 424 (63 / 0.10)** **430 DGYAQILR 437 (77 / 0.16)** **438 DVGGIVLANACGPCIGQWDR 457 (88 / 0.24)** **466 NTIVTSYNR 474 (65 / 0.06)** **466 N*TIVTSYNR 474 N466 deamidation (37 / 0.15)** **480 NDANPETHAFVTSPEIVTALAIAGTLK* 506 K506->E (149 / 0.22)** **507 FNPETDFLTGK 517 (55 / 0.18)** **522 FKLEAPDADELPR 534 (62 / 0.11)** **524 LEAPDADELPR 534 (41 / 0.20)** **535 SDFDPGQDTYQHPPK 549 (51 / 0.09)** **556 VDVSPTSQR 564 (54 / 0.14)** **574 WDGKDLEDLQILIK 587 (69 / 0.24)** **592 CTTDHISAAGPWLK 605 (79 / 0.17)** **592 C*TTDHISAAGPWLK 605 C592 Ammonia-loss (90 / 0.13)** **608 GHLDNISNNLLIGAINIENGK 628 (143 / 0.23)** **615 NNLLIGAIN*IE 625 N623->T (41 / 0.23)** **634 NAVTQEFGPVPDTAR 648 (93 / 0.14)** **634 N*AVTQEFGPVPDTAR 648 N634->I (50 / -0.05)** **657 WVVIGDENYGEGSSR 671 (81 / 0.23)** **657 WVVIGDENY*GEGSSR 671 Y665 oxidation (47 / 0.13)** **701 KQGLLPLTFADPSDYNK 717 (49 / 0.02)** **701 KQGLLPLTFADPSDYN*K 717 N716 deamidation (68 / -0.07)** **753 LLNHTF* 758 F758->L/I (40 / 0.21)**

					(52 / 0.07) ^{672} EHAALEPR ^{679} (54 / 0.12) ^{694} IHETNLK ^{700} (32 / 0.21) ^{701} KQGLLPLTFADPSDYNK ^{717} (37 / 0.02) ^{724} LTIQGLK ^{730} (36 / 0.10) ^{731} DFAPGKPLK ^{739} (32 / 0.08)			
NaCl	Q922D8	C-1-tetrahydrofolate synthase, cytoplasmic	833	38%	^{2} APAGILNGK ^{10} (46 / 0.16) ^{2} APAGILN*GK ^{10} N8 deamidtaion (55 / 0.24) ^{11} LVSAQIR ^{17} (40 / 0.16) ^{47} DDSNLYINVK ^{56} (81 / 0.22) ^{59} AAEEIGIK ^{66} (72 / 0.14) ^{75} TSTESEVLK ^{83} (33 / 0.16) ^{98} IVQLPLDSENSINTEAVINAIAPEK ^{122} (46 / 0.17) ^{123} DVDGLTSVSAGK ^{134} (67 / 0.03) ^{158} EAGVQIAGR ^{166} (37 / 0.21) ^{209} GDILVVATGQPEM*VK ^{223} M221 oxidation (59 / 0.09) ^{251} KVVGDVAYDEAK ^{262} (63 / 0.21) ^{252} VVGDVAYDEAK ^{262} (74 / 0.20) ^{283} LM*QSTVESAQR ^{293} M284 oxidation (43 / 0.17) ^{330} LIGNLAR ^{336} (34 / 0.24) ^{355} VLLSALDR ^{362} (65 / 0.21) ^{371} YVVVTGITPTPLGEGK ^{386} (84 / 0.06) ^{411} Q*PSQGPTFGIK ^{421} Q411 Gln->pyro-Glu (51 / 0.24) ^{464} IFHELTQTDK ^{473} (54 / 0.21) ^{488} KFSDIQIR ^{495} (51 / 0.02) ^{505} TDPTTLTDDEINR ^{517} (99 / 0.16) ^{543} KITIGQSPTEK ^{553} (54 / 0.18) ^{642} IAHGNSSIIADR ^{653} (61 / 0.22) ^{694} IAHGNSSIIADR ^{702} (72 / 0.19) ^{698} VATVRALK* ^{705} K705->I (41 / -0.04) ^{706} MHGGGPTVTAGLPLPK ^{721} (75 / 0.19) ^{722} AYTEEDLDLVEK ^{733} (70 / 0.21) ^{761} TDTDAELDLVSR ^{772} (109 / 0.14) ^{776} EHGAFDAVK ^{784} (38 / 0.21) ^{833} IYGADDIELLPEAQNK ^{848} (51 / 0.21) ^{855} QGFGNLPICMAK ^{866} (38 / 0.19) ^{867} THLSLSHNPEQK ^{878} (45 / 0.21)	394	38%	^{11} LVSAQIR ^{17} (44 / 0.16) ^{47} DDSNLYINVK ^{56} (44 / 0.22) ^{75} TSTESEVLK ^{83} (41 / 0.16) ^{123} DVDGLTSVSAGK ^{134} (39 / 0.03) ^{158} EAGVQIAGR ^{166} (57 / 0.21) ^{167} HAVVVGR ^{173} (35 / 0.19) ^{209} GDILVVATGQPEM*VK ^{223} M221 oxidation (57 / 0.09) ^{251} KVVGDVAYDEAK ^{262} (53 / 0.21) ^{252} VVGDVAYDEAK ^{262} (51 / 0.20) ^{330} LIGNLAR ^{336} (53 / 0.24) ^{355} VLLSALDR ^{362} (42 / 0.21) ^{371} YVVVTGITPTPLGEGK ^{386} (35 / 0.06) ^{447} H*AITAANN ^{454} H447->Q (36 / 0.12) ^{464} IFHELTQTDK ^{473} (36 / 0.21) ^{505} TDPTTLTDDEINR ^{517} (54 / 0.16) ^{505} TD*PTTLTDDEINR ^{517} D506->N (51 / 0.12) ^{543} KITIGQSPTEK ^{553} (57 / 0.17) ^{590} VVASSK*K ^{596} K595->N (34 / 0.20) ^{642} IAHGNSSIIADR ^{653} (53 / 0.22) ^{694} IAHGNSSIIADR ^{702} (53 / 0.19) ^{698} VATVRALK* ^{705} K705->I (42 / -0.04) ^{706} M*HGGGPTVTAGLPLPK ^{721} M706 oxidation (55 / 0.19) ^{761} TDTDAELDLVSR ^{772} (51 / 0.14) ^{776} EHGAFDAVK ^{784} (36 / 0.21) ^{903} LVGTM*STMPG ^{912} M907->V (37 / 0.16)
NaCl	P14211	Calreticulin precursor	619	43%	^{18} DPAIYFK ^{24} (49 / 0.13) ^{25} EQFLDGDAWTNR ^{36} (75 / 0.13) ^{25} EQFLDGDAW*TNR ^{36} W33 dioxidation (59 / 0.10) ^{74} FYALSAK ^{80} (38 / 0.13) ^{88} GQTLVVQFTVK ^{98} (83 / 0.19) ^{99} HEQNIDCGGGYVK ^{111} (41 / 0.10) ^{112} LFPSGLDQK ^{120} (40 / 0.14)	592	35%	^{25} EQFLDGDAWTNR ^{36} (62 / 0.13) ^{88} GQTLVVQFTVK ^{98} (54 / 0.19) ^{99} HEQNIDCGGGYVK ^{111} (58 / 0.10) ^{112} LFPSGLDQK ^{120} (45 / 0.14) ^{121} DMHGDSEYNIMFGPDICGPGTK ^{142} (94 / 0.22) ^{121} DM*HGDSEYNIMFGPDICGPGTK ^{142} M122 oxidation (77 / 0.13) ^{121} DM*HGDSEYNIM*FGPDICGPGTK ^{142} M122,

					[121] DMHGDSEYNIMFGPDICGPGTK [142] (88 / 0.22) [121] DM*HGDSEYNIMFGPDICGPGTK [142] M122 oxidation (68 / 0.13) [121] DM*HGDSEYNIM*FGPDICGPGTK [142] M122, M131 oxidation (59 / 0.06) [144] VHVIFNYK [151] (44 / 0.11) [163] CKDDEFTHLY [172] (49 / 0.16) [173] TLIVRPDNTYEVK [185] (54 / 0.16) [249] KPEDWDEEMDGEWEPPVIQNPEYK [272] (35 / -0.05) [309] DSFAVLGLDLWQVK [322] (37 / 0.06) [323] SGTIFDNFLITNDEAYAEEFGNETWGVTK [351] (41 / -0.25)			M131 oxidation (53 / 0.06) [143] KVHVIFNYK [151] (39 / 0.19) [144] VHVIFNYK [151] (35 / 0.11) [173] TLIVRPDNTYEVK [185] (55 / 0.16) [208] IKDPDAAKPEDWDER [222] (40 / 0.13) [309] DSFAVLGLDLWQVK [322] (37 / 0.06)
SGS742	P63101	14-3-3 protein zeta/delta	1054	71%	[1] M*DKNELVQK [9] M1 acetylation (Protein N-term) (63 / 0.04) [19] YDDMAACMK [27] (50 / 0.06) [19] YDDMAACM*K [27] M26 oxidation (50 / 0.11) [19] YDDMAA*CM*K [27] A24->T, M26 oxidation (37 / 0.09) [28] SVTEQGAELSNEER [41] (117 / 0.07) [28] S*VTEQGAELSNEER [41] S28->A (109 / 0.12) [28] SVTEQ*GAELSNEER [41] Q32 deamidation (84 / -0.02) [28] SVTEQGAE*LSNEER [41] E35 methylation (94 / 0.07) [42] NLLSVAYK [49] (53 / 0.02) [61] VVSSIEQK [68] (70 / 0.16) [61] VV*SSIEQK [68] V62->L/I (83 / 0.05) [84] EKIETELR [91] (47 / 0.19) [86] IETELR [91] (40 / 0.09) [92] DICNDVLSLLEK [103] (84 / 0.10) [104] FLIPNASQPESK [115] (62 / 0.02) [128] YLAEVAAGDDKK [139] (64 / 0.16) [128] YLAEVAAG*DDKK [139] G135->V (35 / -0.02) [139] K*GIVDQSQQAYQEAFEISK [157] K139->T (45 / 0.21) [140] GIVDQSQQAYQEAF [153] (62 / 0.11) [140] GIVDQSQQAYQEAFEISK [157] (137 / -0.004) [158] KEM*QPTHPIR [167] M160 oxidation (34 / 0.08) [159] EMQPTHPIR [167] (46 / 0.22) [168] LGLALNFSVF* [177] F177 oxidation (49 / 0.17) [174] FSVFYYEILNSPEK [187] (76 / 0.11) [178] YYEILNSPEK [187] (63 / 0.21) [178] YYEILNS*PEK [187] S184 phosphorylation (47 / 0.15) [194] TAFDEAIAELDTLS*EESYK [212] S207->N (130 / -0.10)	922	71%	[1] M*DKNELVQK [9] M1 acetylation (Protein N-term) (42 / 0.04) [1] M**DKNELVQK [9] M1 acetylation (Protein N-term) and oxidation (42 / 0.15) [28] SVTEQGAELSNEER [41] (102 / 0.02) [28] S*VTEQGAELSNEER [41] S28->A (80 / 0.09) [28] SVTEQGAE*LSNEER [41] E35 methylation (52 / 0.07) [34] AELSN*E [39] N38->Y (36 / 0.06) [42] NLLSVAYK [49] (64 / 0.18) [61] VVSSIEQK [68] (52 / 0.38) [61] V*VSSIEQK [68] V61->L/I (59 / 0.05) [61] VV*SSIEQK [68] V62->L/I (49 / 0.16) [69] TE*GAEKKQ [76] E70 methylation (35 / 0.16) [84] EKIETELR [91] (40 / 0.10) [86] IETELR [91] (55 / 0.09) [92] DICNDVLSLLEK [103] (58 / 0.10) [104] FLIPNASQPESK [115] (54 / 0.05) [126] YR*YLAEVAAGDDKK [139] R127->K/Q (37 / 0.25) [128] YLAEVAAGDDKK [139] (94 / 0.15) [130] AEVAAGD*D*K [138] D136, D137 methylation (41 / 0.24) [139] K*GIVDQSQQAYQEAFEISK [157] K139->T (87 / 0.21) [140] GIVDQSQQAYQEAFEISK [157] (94 / -0.004) [151] EAFEISK [157] (44 / 0.01) [152] A*FEISK [157] A152->G (35 / -0.10) [168] LGLALNF*SVF [177] F174 oxidation (43 / 0.17) [174] FSVFYYEILNSPEK [187] (55 / 0.11) [178] YYEILNSPEK [187] (50 / 0.21) [194] TAFDEAIAELDTLS*EESYK [212] S207 formylation (124 / 0.06) [213] DSTLIM*QLLR [222] M218 oxidation (62 / 0.14) [213] DSTLIM*QLLR [222] M218 dioxidation (35 / 0.15)

					^{213} DSTLIMQL ^{220} (32 / 0.16) ^{213} DSTLIM*QLLR ^{222} M218 oxidation (56 / 0.11) ^{223} DNLTLWTSDTQGDEAEAGEGGEN ^{245} (63 / 0.15) ^{223} DNLTLWTSDTQGDEAEAGEGGEN* ^{245} N245 deamidation (84 / -0.21)			
SGS742	P80314	T-complex protein 1 subunit beta	1128	56%	^{2} A*SLSLAPVNIFK ^{13} A2 acetylation(Protein N-term) (105 / 0.10) ^{26} LSSFIGAIAIGDLVK^{40} (100 / 0.12) ^{58} DAALMVTNDGATILK^{72} (69 / 0.19) ^{58} DAALM*VTNDGATILK^{72} M62 oxidation (83 / 0.20) ^{90} VQDDEVGDGTTSVTVLAAELLR^{111} (70 / 0.20) ^{139} EALLSSAVDHGSDEAR^{154} (113 / 0.15) ^{182} LAVEAVLR^{189} (55 / 0.14) ^{192} GSGNLEAIHVIK^{203} (54 / 0.13) ^{205} LGGSLADSYLDEGFLLDK^{222} (117 / 0.08) ^{237} ILIANTGMDTDK^{248} (77 / 0.16) ^{237} ILIANTGM*DTDK^{248} M244 oxidation (61 / 0.12) ^{264} VAEIEHAEK^{272} (54 / 0.16) ^{285} HGINCFINR^{293} (41 / 0.16) ^{348} LIEEVMIGEDK^{358} (82 / 0.14) ^{348} LIEEVM*IGEDK^{358} M353 oxidation (76 / 0.21) ^{377} GATQQILDEAER^{388} (90 / 0.20) ^{377} GATQ*QILDEAER^{388} Q380 deamidation (90 / 0.22) ^{382} I*LDEAER ^{388} I382 acetylation (N-term) (43 / -0.02) ^{389} SLHDALCVLAQTVK^{402} (54 / 0.22) ^{420} AVTQLANR ^{427} (42 / 0.22) ^{432} EAVAMESFAK^{441} (58 / 0.19) ^{432} EAVAM*ESFAK ^{441} M436 oxidation (79 / 0.20) ^{445} M*LPTIIADNAGYDSADLVAQLR ^{466} M445 oxidation (49 / 0.24) ^{482} EGTIGDMAVLGITESFQVK ^{500} (56 / 0.13) ^{502} QVLLSAAEAAEVILR ^{516} (125 / 0.19)	756	59%	^{1} M*A*SLSLAPVNIFK ^{13} N-term: Met-loss, A2 acetylation (58 / 0.14) ^{14} AGADEER*AE^{22} R20->M (33 / 0.19) ^{26} LSSFIGAIAIGDLVK^{40} (77 / 0.12) ^{58} DAALMVTNDGATILK^{72} (50 / 0.19) ^{58} DAALM*VTNDGATILK^{72} M62 oxidation (68 / 0.20) ^{90} VQDDEVGDGTTSVTVLAAELLR^{111} (91 / 0.20) ^{139} EALLSSAVDHGSDEAR^{154} (84 / 0.11) ^{182} LAVEAVLR^{189} (44 / 0.14) ^{192} GSGNLEAIHVIK^{203} (59 / 0.18) ^{205} LGGSLADSYLDEGFLLDK^{222} (54 / 0.08) ^{237} ILIANTGMDTDK^{248} (59 / 0.16) ^{237} ILIANTGM*DTDK^{248} M244 oxidation (53 / 0.12) ^{237} ILIANTGM*DTDKIK ^{250} M244 oxidation (54 / 0.23) ^{264} VAEIEHAEK^{272} (33 / 0.16) ^{348} LIEEVM*IGEDK^{358} M353 oxidation (44 / 0.21) ^{377} GATQQILDEAER^{388} (54 / 0.20) ^{432} EAVAMESFAK^{441} (46 / 0.19) ^{432} EAVAM*ESFAK ^{441} M436 oxidation (64 / 0.20) ^{502} QVLLSAAEAAEVILR ^{516} (74 / 0.19)
SGS742	Q8BMF4	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase	63	6%	^{392} AAPAAAAAM*APPGPR ^{406} M400 oxidation (63 / 0.16)	46	6%	^{147} ILVPEGTR ^{154} (46 / 0.21)
SGS742	Q8JZK9	Hydroxymethylglutaryl-CoA synthase, cytoplasmic	306	22%	^{47} YTIGLGQAR ^{55} (66 / 0.23) ^{292} NSIYSGLEAFGDVK ^{305} (122 / 0.17) ^{306} LEDTYFDR ^{313} (50 / 0.15) ^{322} ASSELFNQK ^{330} (38 / 0.26) ^{370} VGVFSYGSGLAATLY ^{384} (43 / 0.03) ^{388} VTQDATPGSALDK ^{400} (71 / 0.17)	150	22%	^{47} YTIGLGQAR ^{55} (39 / 0.23) ^{187} LIFDRGL*RG ^{195} L193->S (35 / 0.20) ^{292} NSIYSGLEAFGDVK ^{305} (71 / 0.21) ^{306} LEDTYFDR ^{313} (51 / 0.15) ^{322} ASSELFNQK ^{330} (35 / 0.23) ^{388} VTQDATPGSALDK ^{400} (64 / 0.16)

					[401] ITASLCDLK [409] (53 / 0.22) [416] TCVAPDVFAENM*K [428] M427 oxidation (58 / 0.15)			[416] TCVAPDVFAENM*K [428] M427 oxidation (37 / 0.17)
SGS742	P63038	60 kDa heat shock protein, mitochondrial precursor	426	29%	[61] TVIIEQSWGSPK [72] (66 / 0.05) [97] LVQDVANN*TNEEAGDGTTTATVLAR [121] N104 deamidation (75 / -0.004) [134] GANPVEIR [141] (61 / 0.28) [143] GVMLAVDAVIAELK [156] (75 / 0.21) [169] AQVATIS*AN [177] S175->A (46 / 0.18) [293] VGLQVVAVK [301] (73 / 0.12) [345] VGEVIVTK [352] (60 / 0.13) [353] DDAM*LLK [359] M356 oxidation (42 / 0.20) [397] LSDGVAVLK [405] (64 / 0.02) [406] VGGTSDVEVNEK [417] (78 / 0.15)	543	25%	[97] LVQDVANNTNEEAGDGTTTATVLAR* [121] R121 deamidation (103 / -0.004) [169] AQVATIS*AN [177] S175->A (38 / 0.18) [293] VGLQVVAVK [301] (36 / 0.12) [302] APGFGDNR [309] (34 / 0.19) [330] LNLNL*EDVQ [338] L334->Q (39 / 0.16) [345] VGEVIVTK [352] (38 / 0.13) [397] LSDGVAVLK [405] (63 / 0.02) [406] VGGTSDVEVNEK [417] (50 / 0.15) [447] CIPALDSLKPANEDQK [462] (35 / 0.25) [474] IPAM*TIAK [481] M477 oxidation (35 / 0.20) [524] VVRTA*LLDA [532] A528->D (39 / -0.14)
SGS742	P06151	L-lactate dehydrogenase A chain	584	43%	[6] DQLIVNLLK[14] (47 / 0.25) [43] DLADELALVDVMEDK[57] (101 / 0.07) [43] DLADELALVDVM*EDK[57] M54 oxidaiton (85 / 0.16) [91] LVIITAGAR[99] (60 / 0.17) [107] LNLVQR[112] (50 / 0.21) [158] VIGSGCNLDSAR[169] (101 / 0.20) [233] QVVDSAYEVIK[243] (68 / 0.21) [233] Q*VVDSAYEVIK[243] Q233 deamidation (44 / 0.21) [294] ILGQNGISDVVK[305] (39 / 0.11) [306] VTLTPEEEAR[315] (37 / 0.25)	493	36%	[43]DLADELALVDVM*EDK [57] M54 oxidation (72 / 0.16) [82]DYCVTANSK [90] (33 / 0.07) [91]LVIITAGAR [99] (41 / 0.17) [158] VIGSGCNLDSAR [169] (44 / 0.20) [233] QVVDSAYEVIK [243] (46 / 0.09) [270] VHPISTM*IK [278] M276 oxidation (40 / 0.14) [306] VTLTPEEEAR [315] (46 / 0.25)
SGS742	P46638	Ras-related protein Rab-11B	45	4%	[42]STIGVEFATR [51] (45 / 0.11)			
SGS742	P17182	Alpha-enolase	547	46%	[16] GNPTVEVDLYTAK[28] (88 / 0.25) [33] AAVPSGASTGIYEALELR[50] (71 / 0.13) [61] GVSQAVEHINK[71] (66 / 0.17) [81] KVNVVEQEK[89] (37 / 0.13) [93] LM*IEM*DGTENK[103] M94, M97 oxidation (40 / 0.14) [133]HIADLAGNPEVILPVPAFNVINGGSHAGNK*[162] K162->E (51 / 0.05) [184] IGAEVYHNLK[193] (67 / 0.25) [203] DATNVGDEGGFAPN[216] (71 / 0.19) [203] DATNVGDEGGFAPNILENK[221] (94 / 0.19) [222] EALELLK[228] (36 / 0.24) [234] AGYTDQ*VVIGM*DVAASEFYR[253] Q239 deamidation, M244 oxidation (44 / 0.001) [270] YITPDQLADLYK[281] (44 / 0.15) [336] SCNCLLLK[343] (32 / 0.09) [344] VNQIGSVTESLQACK[358] (106 / 0.20)	863	44%	[10] EIFDSR[15] (35 / 0.11) [16] GNPTVEVDLYTAK[28] (52 / 0.22) [61] GVSQAVEHINK[71] (57 / 0.21) [72] TIAPALVSK[80] (59 / 0.07) [93] LM*IEM*DGTENK[103] M94, M97 oxidation (37 / 0.14) [203] DATNVGDEGGFAPN[216] (55 / 0.19) [307] FTASAGIQVVGDDLTVTNPK[326] (72 / 0.07) [344] VNQIGSVTESLQACK[358] (69 / 0.20) [344] VNQIGSVTESLQ*ACK[358] Q355 deamidation (52 / -0.05)

SGS742	Q99KI0	Aconitate hydratase, mitochondrial precursor	1627	51%	[32] VAMSHFEPSEYIR [44] (65 / 0.19) [32] VAM*SHFEPSEYIR [44] M34 oxidation (63 / 0.11) [51] NINIVR [56] (37 / 0.11) [59] LNRPLTLSEK [68] (46 / 0.15) [69] IVYGHLDDPANQEIER [84] (67 / -0.02) [77]PANQEIER [84] (54 / 0.13) [118] VAVPSTIHCDHLIEAQVGGEK [138] (99 / -0.23) [118] VAVPSTI*HCDHLIEAQVGGEK [138] I124->M (53 / 0.03) [145] DINQEVYNFLATAGAK [160] (111 / -0.001) [150]V*YNFLATAGAK [160] V150 methylation (50 / -0.03) [234] LTGSLSGWTSPK [245] (63 / 0.17) [234]LTGSLSGW*TSPK [245] W241 oxidation (41 / 0.13) [234]LTGSLSGW*TSPK [245] W241 dioxidation (70 / 0.13) [251] VAGILTVK [258] (54 / 0.07) [313] TDIANLAEEFK [323] (79 / 0.16) [379] VGLIGSCTNSSYEDMGR [395] (112 / 0.04) [379] VGLIGSCTNSSYEDM*GR [395] M393 oxidation (98 / 0.06) [379]VGLIGSCTN*SSYEDMGR[395] N387 deamidation (101 / 0.11) [402] QALAHGLK [409] (48 / 0.21) [412] SQFTITPGSEQIR [424] (76 / 0.08) [430] DGYAQILR [437] (45 / 0.14) [447]ACGPCIGQWDR[457] (50 / 0.03) [466] NTIVTSYNR [474] (42 / 0.14) [466] N*TIVTSYNR [474] N466 deamidation (39 / 0.13) [480] NDANPETHAF[489] (38 / 0.22) [507] FNPETDFLTGK [517] (61 / 0.11) [522] FKLEAPDADELPR [534] (82 / 0.12) [524] LEAPDADELPR [534] (73 / 0.15) [556] VDVSPTSQR [564] (55 / 0.14) [556] VDVSPTSQR* [564] R564 deamidation (40 / 0.16) [565] LQLLEPFDK [573] (43 / 0.21) [565] LQLLEPFDKWDGK [577] (34 / -0.12) [578] DLEDLQILIK [587] (84 / 0.12) [592] CTTDHISAAGPWLK [605] (66 / 0.14) [634] NAVTQEFGPVPDTAR [648] (62 / 0.07) [634] N*AVTQEFGPVPDTAR [648] N634 deamidation (102 / 0.11) [657] WVVIGDENYGEGSSR [671] (109 / 0.07) [672] EHAALEPR [679] (52 / 0.14) [701] KQGLLPLTFADPSDYNK [717] (42 / 0.06) [702] QGLLPLTFADPSDYNK [717] (84 / 0.06) [724] LTIQGLK [730] (42 / 0.11)	2061	49%	[32] VAMSHFEPSEYIR [44] (54 / 0.19) [32] VAM*SHFEPSEYIR [44] M34 oxidation (77 / 0.19) [51] NINIVR [56] (35 / 0.11) [58] RLNRPLTLSEK [68] (45 / 0.14) [59] LNRPLTLSEK [68] (38 / 0.14) [69] IVYGHLDDPANQEIER [84] (71 / -0.02) [69] IVYGHLDDPANQ*EIER [84] Q80 deamidation (53 / 0.24) [118] VAVPSTIHCDHLIEAQVGGEK [138] (105 / 0.17) [145] DINQEVYNFLATAGAK [160] (74 / -0.001) [234] LTGSLSGWTSPK [245] (74 / 0.17) [234] LTGSLSGW*TSPK [245] W241 dioxidation (38 / 0.13) [251] VAGILTVK [258] (34 / 0.07) [351] G*PFTPDLAHPVADVGTVAEK [370] G351 Myristoyl (N-term G) (71 / 0.11) [357] LAHPVADVGTVAEK [370] (49 / 0.17) [379] VGLIGSCTNSSYEDMGR [395] (118 / 0.25) [379] VGLIGSCTNSSYEDM*GR [395] M393 oxidation (108 / 0.14) [379] VGLIGSCTNSSYEDMGR* [395] R395 deamidation (58 / 0.11) [402] QALAHGLK [409] (36 / 0.21) [412] SQFTITPGSEQIR [424] (49 / 0.08) [430] DGYAQILR [437] (57 / 0.13) [466] NTIVTSYNR [474] (65 / 0.15) [495] IVTALAI*AG[503] I501->S (40 / 0.12) [507] FNPETDFLTGK [517] (51 / 0.11) [522] FKLEAPDADELPR [534] (70 / 0.12) [524] LEAPDADELPR [534] (48 / 0.18) [556] VDVSPTSQR [564] (54 / 0.15) [578] DLEDLQILIK [587] (47 / 0.12) [592] CTTDHISAAGPWLK [605] (77 / 0.17) [592] C*TTDHISAAGPWLK [605] C592 Ammonia-loss (N-term C) (51 / 0.002) [592] CTTDHISAAGPWLK* [605] K605 dioxidation (40 / 0.17) [615] NNLLIGAIN*IE [625] N623->T (41 / 0.15) [634] NAVTQEFGPVPDTAR [648] (84 / 0.07) [657] WVVIGDENYGEGSSR [671] (95 / 0.07) [681] LGGRAIIT*KS [690] T688->M (38 / 0.19) [701] KQGLLPLTFADPSDYNK [717] (46 / 0.06) [702] QGLLPLTFADPSDYNK [717] (65 / 0.06)
SGS742	Q922D8	C-1-tetrahydrofolate synthase, cytoplasmic	856	43%	[11] LVSAQIR [17] (45 / 0.21) [47] DDSNLYINVK [56] (82 / 0.25)	512	38%	[47] DDSNLYINVK [56] (44 / 0.25) [75] TSTESEVLK [83] (50 / 0.13)

					[59] AAEEIGIK [66] (54 /0.12) [123] DVDGLTSVSAGK [134] (68 / -0.005) [151] GCLELIK [157] (38 / 0.25) [158] EAGVQIAGR [166] (50 / 0.14) [209] GDILVVATGQPEM*VK [223] M221 oxidation (60 / 0.06) [251] KVVGDVAYDEAK [262] (71 / 0.11) [252] VVGDVAYDEAK [262] (62 / 0.21) [314] TPVPSDIAISR [324] (64 / 0.15) [355] VLLSALDR [362] (65 / 0.11) [371] YVVVTGITPTPLGEGK [386] (64 / 0.05) [411] Q*PSQGPTFGIK [421] Gln411->pyro-Glu (N-term Q) (43 / 0.21) [464] IFHELTQTDK [473] (52 / 0.21) [505] TDPTTLTDDEINR [517] (82 / 0.09) [543] KITIGQSPTEK [553] (40 / 0.02) [544] ITIGQSPTEK [553] (52 / 0.09) [642] IAHGNSSIIADR [653] (69 / 0.06) [658] LVGPEGFVVTEAGFGADIGM*EK [679] M677 oxidation (63 / 0.25) [687] YSGLQ*PHVVVLVATVR [702] Q691 deamidation (41 / -0.03) [694] VVVLVATVR [702] (76 / 0.23) [698] VATVRALK* [705] K705->I (41 / -0.02) [706] M*HGGGPTVTAGLPLPK [721] M706 oxidation (42 / 0.21) [722] AYTEEDLDLVEK [733] (70 / 0.14) [747] MFGVPVVVAVNVFK [760] (50 / 0.10) [761] TDTDAELDLVSR [772] (111 / 0.14) [776] EHGAFDAVK [784] (51 / 0.13) [785] C*THWAEGGQGALALAQAVQR [804] C785 Pyridylethyl (42 / 0.17) [833] IYGADDIELLPEAQNK [848] (57 / 0.16) [867] THLSLSHNPEQK [878] (61 / 0.16)			[123] DVDGLTSVSAGK [134] (39 / -0.01) [158] EAGVQIAGR [166] (57 / 0.17) [209] GDILVVATGQPEM*VK [223] M221 oxidation (46 / 0.06) [251] KVVGDVAYDEAK [262] (38 / 0.11) [252] VVGDVAYDEAK [262] (45 / 0.21) [355] VLLSALDR [362] (59 / 0.11) [371] YVVVTGITPTPLGEGK [386] (43 / 0.05) [371] YVVVTGITPTPLGEGK* [386] K386->E (77 / 0.25) [464] IFHELTQTDK [473] (48 / 0.19) [499] RLGIEK [504] (35 / 0.20) [505] TDPTTLTDDEINR [517] (47 / 0.09) [543] KITIGQSPTEK [553] (38 / 0.02) [590] VVASSK*K [596] K595->N (34 / 0.12) [658] LVGPEGFVVTEAGFGADIGM*EK [679] M677 oxidation (41 / 0.25) [694] VVVLVATVR [702] (36 / 0.23) [706] M*HGGGPTVTAGLPLPK [721] M706 oxidation (60 / 0.25) [722] AYTEEDLDLVEK [733] (36 / 0.14) [747] MFGVPVVVAVNVFK [760] (58 / 0.14) [761] TDTDAELDLVSR [772] (54 / 0.14) [776] EHGAFDAVK [784] (33 / 0.13) [833] IYGADDIELLPEAQNK [848] (78 / 0.25) [838] D*IELLPEAQ [846] D838->G (43 / 0.23) [867] THLSLSHNPEQK [878] (53 / 0.15)
SGS742	**P14211**	**Calreticulin precursor**	**417**	**48%**	[18] DPAIYFK [24] (43 / 0.18) [25] EQFLDGDAWTNR [36] (65 / 0.16) [25] EQFLDGDAW*TNR [36] W33 dioxidation (59 / 0.14) [74] FYALSAK [80] (35 / 0.09) [99] HEQNIDCGGGYVK [111] (57 / 0.17) [112] LFPSGLDQK [120] (38 / 0.17) [121] DM*HGDSEYNIM*FGPDICGPGTK [142] M122, M131 oxidation (62 / 0.21) [121] DMHGD*SEYNIMFGPDICGPGTK [142] D125 oxidation (54 / 0.21) [143] KVHVIFNYK [151] (38 / 0.24) [144] VHVIFNYK [151] (34 / 0.24) [163] CKDDEFTHLY [172] (49 / 0.21)	**634**	**36%**	[25] EQFLDGDAWTNR [36] (63 / 0.19) [56] FYGDLEKDK [64] (42 / 0.28) [99] HEQNIDCGGGYVK [111] (59 / 0.17) [112] LFPSGLDQK [120] (43 / 0.18) [121] DM*HGDSEYNIM*FGPDICGPGTK [142] M122, M131 oxidation (59 / 0.21) [143] KVHVIFNYK [151] (43 / 0.24) [144] VHVIFNYK [151] (34 / 0.24) [154] NVLINK [159] (41 / 0.10) [163] CKDDEFTHLY [172] (41 / 0.20) [173] TLIVRPDNTYEVK [185] (39 / 0.21) [186] IDNSQVESGSLEDDW*DFLPPK [206] W200 dioxidation (70 / 0.12)

					^{163} CKDDEFTHLYTLIVRPDNTYEVK ^{185} (38 / 0.09) **^{173} TLIVRPDNTYEVK ^{185} (52 / 0.21)** **^{279} QIDNPDYK ^{286} (30 / 0.16)** **^{287} GTWIHPEIDNPEYSPDANIYAYDSF ^{311} (51 / -0.01)** **^{392} DEDEDEEDEKEEDEEESPGQAK ^{413} (60 / 0.12)**			

Sequence conflicts are provided as e.g. D495->Y indicating that tyrosine was replacing aspartate as given in the UniProtKB database. It must be stated that in the current study hippocampal proteins were detected and that sequences in the database are from other organs probably explaining “conflicts”. Therefore the wording “sequence conflicts may not be in the strict sense” and may probably reflect sequence differences to database.