Appendix 1. Measures of confidence for identification MS/MS analysis of proteins with significantly altered levels upon DHA or fish oil intervention

Protein	Accession	Mr$_{exp}$ (kDa)	Mr$_{theor}$ (kDa)	Protein score*	No. matched peptides	Peptide sequences	Peptide charges
Lipid/cholesterol metabolism							
ApoA-I	Q8BPD5	24·9	30·5	126	3	TQVQSVIDK	+2
						VQPYLDEFQK	+2
						VAPLGAELQESAR	+2
Peroxisomal CoA diphosphatase NUDT7	Q99P30	33	27·1	233	6	NNLIDDAK	+2
						YSHLSSNK	+2
						LYLMFTVR + Ox (M)	+2
						FSVLVPLLAR	+2
						EPGEVCFPGGK	+2
						DPVDTDDTATALR	+2
Dienoyl-CoA isomerase	O35459	31	36·4	78	3	ELVECFQK	+2
						YCTQDAFFQIK	+2
						APEEVSDHNYESIQVTSAQK	+3
Protein/peptide metabolism							
Acyl-peptide hydrolase	Q8R146	83·8	82·3	88	3	VVFDSVQR	+2
						SFNLSALEK	+2
						SALYYVDLSGGK	+2
Branched-chain ketoacid dehydrogenase E1, beta polypeptide	Q6P3A8	35·7	43·6	146	3	LGVSCEVIDLR	+2
						TIVPWDVDTVCK	+2
						SGDLFNCGSLTIR	+2
Pyridoxal kinase	Q8K183	37·2	35·3	99	2	SQELHELYEGLK	+3
						AEAGEGQKPSPAQLELR	+3
Ornithine aminotransferase	P29758	47·2	48·7	185	5	ESVEIINK	+2
						GLLNAIVIR	+2
						LPSDVVTSVR	+2
						LAPPLVIKEDEIR	+3
						KTEQGPPSSEYIFER	+3
Phenylalanine hydroxylase	Q91WV1	49·9	52·3	189	5	DFLGGLAFR	+2
						NTVPWFPR	+2
						QFADIAYNYR	+2
						VEVLDNTQQLK	+2
						TFAATIPRPFSVR	+3
Selenium-binding protein 2	Q63836	57·5	53·1	219	5	QFYPDLIR	+2
						LILPGLISSR	+2
						VIEASEIQAK	+2
						IYVVDVGSEPR	+2
						IPGGPQMIQLSLDGK + Ox (M)	+2
Aldehyde dehydrogenase 9A1	Q9JLJ2	48·6	56·8	171	5	CQVLLEAAR	+2
						EVNLAVENAK	+2
						VEPVDASGTEK	+2
						ISFTGSVPTGVK	+2
						VTIEYYSQLK	+2
Glutamate dehydrogenase (precursor)	P26443	50·5	61·6	456	14	YNLGLDLR	+2
						TAAYVNAIEK	+2
						VYNEAGVTFT	+2
						NYTDNELEK	+2
						CAVVDVPFGGAK	+2
						YSTDVSVDEVK	+2
						DDGSWEVIEGYR	+2
						DIVHSGLAYTMER + Ox (M)	+3
						IIAEGANGPTTPEADK	+3
						IIAEGANGPTTPEADK	+2
						TFVVQGFGNVGLHSMR + Ox (M)	+3
						GFIGPGIDVPAPDMSTGER + Ox (M)	+3
						KGFIGPGIDVPAPDMSTGER + Ox (M)	+3
						IIAEGANGPTTPEADKIFLER	+3
Carbohydrate metabolism							
Ketohexokinase	P97328	30·2	33·3	196	6	VSVEIEKPR	+2
						KCGLQGFDGIV	+2
						HLGFQSAVEALR	+2
						TIILYDTNLPDVSAK	+3
						TIILYDTNLPDVSAK	+2
						GGNASNSCTVLSLLGAR	+2
GAPDH	P16858	12·9	36·1	104	3	VVDLMAYMASK + 2 Ox (M)	+2
						VVDLMAYMASKE + 2 Ox (M)	+2
						VPTPNVSVVDLTCR	+2
Fructose 1,6 bisphosphatase	Q9QXD6	36·9	37·2	246	8	GNIYSLNEGYAK	+2
						DFDPAINEYLQR	+2
						DFDPAINEYLQR	+3

Appendix 1. *Continued*

Protein	Accession	Mr_{exp} (kDa)	Mr_{theor} (kDa)	Protein score*	No. matched peptides	Peptide sequences	Peptide charges
						TLVYGGIFLYPANK	+2
						STDEPSEKDALQPGR	+3
						KLDILSNDLVINMLK + Ox (M)	+3
						LLYECNPIAYVMEK + Ox (M)	+2
						LLYECNPIAYVMEK + Ox (M)	+3
Alpha enolase	P17182	45·8	47·3	288	9	TIAPALVSK	+2
						IEEELGSK	+2
						VNVVEQEK	+2
						SCNCLLLK	+2
						IGAEVYHNLK	+2
						GVSQAVEHINK	+2
						LMIEMDGTENK + 2 Ox (M)	+2
						GNPTVEVDLYTAK	+2
						IDKLMIEMDGTENK + 2 Ox (M)	+3
Phosphomutase-1	Q9D0F9	63·7	61·6	541	16	LYIDSYEK	+2
						SMPTSGALDR	+2
						SMPTSGALDR + Ox (M)	+2
						LSGTGSAGATIR	+2
						FFGNLMDASK + Ox (M)	+2
						QEATLVVGGDGR	+2
						IALYETPTGWK	+2
						IDAMHGVVGPYVK.K + Ox (M)	+3
						TIEEYAICPDLK	+2
						YDYEEVEAEGANK	+2
						TQAYPDQKPGTSGLR	+3
						FNISNGGPAPEAITDK	+3
						FNISNGGPAPEAITDK	+2
						ADNFEYSDPVDGSISK	+2
						ADNFEYSDPVDGSISK	+3
						LSLCGEESFGTGSDHIR	+3
Oxidative stress/antioxidants							
HSP60	P63038	58·7	61·1	400	9	LSDGVAVLK	+2
						IGIEIIKR	+2
						VTDALNATR	+2
						NAGVEGSLIVEK	+2
						VGGTSDVEVNEK	+2
						TVIIEQSWGSPK	+2
						VGGTSDVEVNEKK	+3
						GYISPYFINTSK	+2
						VGEVIVTKDDAMLLK + Ox (M)	+3
Peroxiredoxin 3	Q8K4K8	26·1	27·9	67	2	ELSLDDFK	+2
						GTAVVNGEFK	+2
3-Hydroxyisobutyrate dehydrogenase	Q99L13	31·3	35·8	155	5	DLGLAQDSATSTK	+2
						EAGEQVASSPAEVAEK	+2
						MGAVFMDAPVSGGVGAAR + 2 Ox (M)	+2
						TPVGFIGLGNMGNPMAK + 2 Ox (M)	+3
						KGSLLIDSSTIDPSVSK	+3
Aldehyde dehydrogenase 7A1	Q9DBF1	57·4	59·3	215	5	QAVSMFVR.A + Ox (M)	+2
						QGLSSSIFTK	+2
						EVALMVQER.F + Ox (M)	+2
						GAPTTSLVSVAVTK	+2
						VNLLSFTGSTQVGK	+2
Peroxiredoxin 6	O08709	25	24·8	299	7	NFDEILR	+2
						VVFIFGPDK	+2
						LPFPIIDDK	+2
						LSILYPATTGR	+2
						DFTPVCTTELGR	+2
						DINAYNGETPTEK	+2
						KGESVMVVPTLSEEEAK + Ox (M)	+3
3-Hydroxyanthranilic acid dioxygenase	Q78JT3	29·9	32·9	364	11	SWVEENR	+2
						ELPFPLNTR	+2
						IMFVGGPNTR.K + Ox (M)	+2
						QGEIFLLPAR	+2
						ASFQPPVCNK	+2
						RLESELDGLR	+2
						TGKPNPDQLLK	+2
						FANTMGLVIER	+2
						AQGSVALSVTQDPAR	+2
						YYVGDTEDVLFEK	+2

Appendix 1. *Continued*

Protein	Accession	Mr_{exp} (kDa)	Mr_{theor} (kDa)	Protein score*	No. matched peptides	Peptide sequences	Peptide charges
Isovaleryl-CoA dehydrogenase	Q9JHI5	40·6	46·6	282	8	QDVDVWLWQQEGSSK	+3
						GMPGFSTSK + Ox (M)	+2
						GITAFIVEK	+2
						QYVYNVAK	+2
						FLQENLAPK	+2
						IGQFQLMQGK + Ox (M)	+2
						VPAANVLSQESK	+2
						LYEIGAGTSEVR	+2
Aldehyde dehydrogenase 2 (precursor)	Q3UJW1	49	57	419	12	AQEIDQTNDFK	+2
						TIEEVVGR	+2
						YYAGWADK	+2
						VVGNPFDSR	+2
						YGLAAAVFTK	+2
						LLCGGGAAADR	+2
						AAFQLGSPWR	+2
						LGPALATGNVVVMK + Ox (M)	+3
						LGPALATGNVVVMK + Ox (M)	+3
						GYFIQPTVFGDVK	+2
						TEQGPQVDETQFK	+2
						TEQGPQVDETQFK	+3
Hydroxypyruvate reductase	Q3T9Z2	34·6	35·7	314	8	ELGEYGLQAYTEVK	+2
						LLDAAGANLR	+2
						LPEAIEEVK	+2
						GEAMPSELKL + Ox (M)	+2
						NTAIFINISR	+2
						RLPEAIEEVK	+2
						VFVTGPLPAEGR	+2
						NCVILPHIGSATYK	+3
						DLEQGVVGAHGLLCR	+3
Methionine cycle							
Methionine adenosyltransferase	Q91X83	50·8	44·1	234	6	ELLEVVNK	+2
						SEFPWEVPK	+2
						FVIGGPQGDAGVTGR	+2
						ICDQISDAVLDAHLK	+3
						YLDEDTVYHLQPSGR	+3
						TQVTVQYMQDNGAVIPVR + Ox (M)	+3
Methionine adenosyltransferase	Q91X83	50·3	44·1	170	4	ELLEVVNK	+2
						FVIGGPQGDAGVTGR	+3
						YLDEDTVYHLQPSGR	+3
						TQVTVQYMQDNGAVIPVR + Ox (M)	+3
Formyltetrahydrofolate dehydrogenase	Q8CIF2	94·6	99·5	309	9	LIAEGTAPR	+2
						FLFPEGIK	+2
						GQALPEVVAK	+2
						TDVAAPFGGFK	+2
						LQAGTVFVNTYNK	+2
						SPLIIFADCDLNK	+2
						ANATEFGLASGVFTR	+2
						GVVNILPGSGSLVGQR	+2
						RPQPEEGATYEGIQK	+3
S-adenosylhomocysteine hydrolase	Q8BPI7	21·8	48·0	144	2	VAVVAGYGDVGK	+2
						VPAINVNDSVTK	+2
Adenosylhomocysteinase	P50247	44·4	48·0	371	11	ATDVMIAGK + Ox (M)	+2
						MMSNGILK.V + 2 Ox (M)	+2
						ESLIDGIKR	+2
						RIILLAEGR	+2
						VNIKPQVDR	+2
						WLNENAVEK	+2
						VAVVAGYGDVGK	+2
						VPAINVNDSVTK	+2
						ALDIAENEMPGLMR + 2 Ox (M)	+2
						GISEETTTGVHNLYK	+3
						KALDIAENEMPGLMR + 2 Ox (M)	+3
Other functions							
Malate dehydrogenase	P14152	33·1	36·6	92	2	LGVTADDVK	+2
						GEFITTVQQR	+2
Ester hydrolase homologue	Q91V76	33·4	35	120	4	EPFTFPVR	+2
						VYDLNEIAK	+2
						NPADGACLLEK	+2
						TGELNFVSCMR + Ox (M)	+2

Appendix 1. *Continued*

Protein	Accession	Mr_{exp} (kDa)	Mr_{theor} (kDa)	Protein score*	No. matched peptides	Peptide sequences	Peptide charges
Regucalcin	Q64375	32·0	33·9	307	9	QPDAGNIFK	+2
						DGLNAEGLLR	+2
						LWVACYNGGR	+2
						QLGGYVATIGTK	+2
						WDTVSNQVQR	+2
						VAVDAPVSSVALR	+2
						DYSEMYVTCAR + Ox (M)	+2
						DEQIPDGMCIDAEGK + Ox (M)	+2
						YFAGTMAEETAPAVLER + Ox (M)	+2
Soluble epoxide hydrolase	P34914	63·6	63·6	169	5	AISQSGVVISK	+2
						LGIFGFLSTGDK	+2
						LQFWTETLPR	+2
						VTQPEVDTPLGR	+2
						FSAPLPPQPWEGVR	+2
Nicotinate nucleotide pyrophosphorylase	Q91X91	35·3	31·8	100	3	CSGIASAAATAVEVAR	+2
						CSGIASAAATAVEVAR	+3
						VEVECSSLEEAFR	+2

Mr_{exp}, experimental molecular weight; Mr_{theor}, theoretical molecular weight; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; HSP, heat shock protein.

* Probability-based Mowse score for MS/MS-based identifications: individual ion scores $>$ 27 indicate identity or extensive homology ($P < 0·05$).