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**EFFECT OF LEUCINE-PROTEIN HIGH-CARBOHYDRATE
POST-EXERCISE NUTRITION ON SUBSEQUENT
PERFORMANCE AND THE PROTEIN REGULATED GENOMIC
AND SIGNALLING EVENTS GOVERNING ADAPTIVE
REMODELLING**

A Thesis

Presented in partial fulfilment of the requirements

For the degree of Doctor of Philosophy

In

Nutritional Science

Massey University,
Albany,
New Zealand.

Jasmine Sarah Thomson

2010

DOCTOR OF PHILOSOPHY

Massey University

(Nutritional Science)

Auckland, New Zealand

TITLE: Effect of leucine-protein high-carbohydrate post-exercise nutrition on subsequent performance and the protein regulated genomic and signalling events governing adaptive remodelling

AUTHOR: Jasmine S. Thomson, BSc, MSc

SUPERVISOR: Dr. David S. Rowlands

CO-SUPERVISORS: Assoc. Prof. Welma Stonehouse, Dr. Ajmol Ali

NUMBER OF PAGES: xxiii; 354

ABSTRACT

Recovery from prolonged endurance exercise requires fuel replenishment and ultrastructure repair to restore cellular homeostasis; and improvement requires adaptive remodelling. Timing nutrient intake to closely follow exercise may be advantageous to recovery and subsequent performance by facilitating the adaptive processes stimulated by exercise. The objective of this research was to firstly determine if leucine-enriched protein feeding after hard training improved subsequent performance, and secondly to explore the candidate means by which protein-rich post-exercise nutrition mediates recovery, primarily transcriptomic and signalling mechanisms.

Study 1 Ten male cyclists ingested leucine-enriched protein-carbohydrate (0.1/0.4/1.2/0.2 g·kg⁻¹·h⁻¹ leucine/protein/carbohydrate/fat) or isocaloric high-carbohydrate control (0.06/1.6/0.2 g·kg⁻¹·h⁻¹) meals following 2-2.5 h high-intensity interval training on 3 consecutive days. Cyclists performed a repeat-sprint performance test 39 h after training, and markers of physiological recovery and mood state were examined. *Study 2* Eight male cyclists ingested protein (0.4/1.2/0.2 g·kg⁻¹·h⁻¹ protein/carbohydrate/fat) or isocaloric high-carbohydrate control (0.03/1.6/0.2 g·kg⁻¹·h⁻¹) beverages following a single 1.75 h high-intensity interval cycling bout. Muscle tissue samples were collected from the vastus lateralis before exercise, 3-h and 48-h post-exercise. The transcriptome response was assessed by Illumina microarray, candidate gene expression by real time RT-PCR; and phospho-protein signalling by Western blot.

Leucine-enriched feeding increased mean sprint power by 2.5% (99% confidence limits, ±3.1%; $P = 0.013$) and reduced overall tiredness during sprints by 13% (90% confidence limits, ±9.2%). Serum creatine kinase was 19% (90% confidence limits, ±18%) lower than control, but difference in lactate dehydrogenase and muscle pain were trivial and unclear. In the second study, protein-carbohydrate feeding led to moderate and very large increases in cell signalling to translation; mTOR, 4E-BP1 and RPS6 phosphorylation by 3-h. Bioinformatics analysis indicates protein ingestion

effects the transcriptome response involved in immune/inflammatory processes, tissue development (extracellular matrix, cytoskeletal, and sarcomere remodelling), and metabolism consistent with increased fatty acid oxidation, compared to control.

Post-exercise protein and carbohydrate coingestion during a period of hard training enhances subsequent high-intensity endurance performance and may reduce membrane disruption in comparison to high-carbohydrate feeding. Furthermore, the mechanism responsible for protein-nutrition mediated adaptation may be through enhancing protein translation and fine-tuning the gene expression profile induced by exercise.

ACKNOWLEDGEMENTS

First I would like to thank Dr David Rowlands, for guidance, support, motivation, and the huge amount of energy you contribute to anything you are involved in.

To my secondary supervisors, Assoc. Prof. Welma Stonehouse and Dr Ajmol Ali, I appreciate your help and guidance with my writing. To Welma, thanks also for being so approachable and for providing emotional support when needed.

To my collaborators, Brian Timmons, Frederic Raymond, Andreas Fuerholz, Robert Mansourian, Marie-Camille Zawhlen, Sylviane Metairon, Elisa Glover, Trent Stellingwerff, Martin Krussman, and Mark Tarnopolsky thank you for your help

Thanks to the various lab staff of whom I spent a large portion of my time with, and especially the following technicians and students; Holly, Amy, Dave, Simon, Carlos, Helen, Andy, Andre, and Dave G for your help and friendship.

Thanks also to Dr Andrew Foskett for phlebotomy assistance, Dr Beatrix Jones for statistical assistance.

Thanks once again to my subjects, who volunteered so much time and effort, and still came out smiling at the end of it all.

Finally, to my husband Paul, thank you my love for giving me so much emotional and financial support, and for never doubting me.

STATEMENT OF CONTRIBUTION

CHAPTER 3: Leucine-protein supplemented recovery feeding enhances subsequent cycling performance in well-trained men

The principal investigator of this study was Jasmine Thomson. Study conception and design were provided by Jasmine Thomson, Dr. David Rowlands, with contributions from Dr. Ajmol Ali. The ethics proposal was written by Jasmine Thomson. Subjects were recruited and the study was coordinated by Jasmine Thomson. The supplements were formulated and prepared by Jasmine Thomson in the Institute of Food, Nutrition and Human Health Food Technology Laboratories, Massey University, Auckland. The data was collected largely by Jasmine Thomson with help from Dr. Ajmol Ali, Dr. Andrew Foskett, with assistance from Simon Bennett. Blood preparation was done by Jasmine Thomson assisted by Simon Bennett, and analyzed for Creatine Kinase and Lactate Dehydrogenase through LabPlus. Urine and sweat samples were collected and prepared by Jasmine Thomson, Kjeldahl digests and nitrogen determination by distillation and titration performed by Jasmine Thomson. Serum amino acids were analysed by HPLC at research laboratory at McMaster University by Tracey Rerecich. Statistical analyses were performed by Jasmine Thomson with guidance from Dr David Rowlands and Dr Beatrix Jones. The manuscript was written and prepared by Jasmine Thomson with guidance from Dr. David Rowlands, Dr. Ajmol Ali, and Assoc. Prof. Welma Stonehouse.

CHAPTER 4: Increased specificity of immune response, myocyte remodelling, and metabolic gene expression and signalling to translation with protein feeding after prolonged exercise

Study conception and design were provided by Dr. David Rowlands, Dr. Mark Tarnopolsky and Jasmine Thomson. The study was performed within the Departments of Medical Science and Pediatrics and Medicine, McMaster University research laboratories under supervision of Dr. Mark Tarnopolsky. Subjects were recruited by Jasmine Thomson. The supplements were prepared by Stuart Lowther of Life Science Nutritionals Inc. Biological

samples were collected by Dr. Mark Tarnopolsky, Dr. David Rowlands, Dr. Brian Timmons and Jasmine Thomson. Samples were prepared by Holly Robertshaw, Ming-Hua Fu, Changhua Ye, Michaela Devries, David Rowlands and Jasmine Thomson. Insulin assay performed by Suzanne Southward, and glucose by Tracy Rerecich. RNA extraction was done by Holly Robertshaw assisted by Jasmine Thomson. Western blotting was performed by Elisa Glover, and real-time RT-PCR by Holly Robertshaw, and Changhua Ye. Micro array analysis was done at the Nestle Research Centre, Vers-chez-les-Blanc, Lausanne, Switzerland. Data Analyses were performed by Dr. David Rowlands, Jasmine Thomson and Brian Timmons, apart from the Array data which was performed Frederic Raymond, Robert Mansourian, Sylviane Metairon, Andreas Fuerholz, and Elisa Glover. Bioinformatics was by Andreas Fuerholz, David Rowlands, and Frederic Raymond. The manuscript was written and prepared by Jasmine Thomson with guidance from Dr. David Rowlands, and contributions from Frederic Raymond (Illumina array methods) and Andreas Fuerholz (bioinformatics).

The studies were funded by Massey University Research Fund, Sport and Recreation New Zealand, Life Science Nutritional (Canada), and Nestec (Switzerland).

RESEARCH ETHICS

Ethical approval was obtained from the applicable research ethics bodies for each study (Massey University Palmerston North Ethics Committee; and Hamilton Health Sciences/McMaster University, Hamilton, Ontario). The potential risks and management of risks involved is detailed below;

All participants were screened via a health questionnaire for pre-existing conditions to ensure they were physically healthy and able to take part in the studies. Participants were limited to athletes in regular training, and individuals who were neither disabled nor elderly and at increased risk of injury or discomfort during the exercise and performance portions of the research. Some fatigue during exercise and performance trials was to be expected, however this expected to be of a similar level to that normally experienced in participant's own endurance training and competition. Maximal effort was requested of participants in both the VO_{2max} and performance testing and associated discomfort was thought to be normal for this level of athlete, and in fact adaptive and beneficial to health. There may have been some discomfort and minor risk of infection associated with blood catheter insertion and muscle biopsy procedures. Discomfort in each instance was minimised by having subjects lie prone on a hospital bed, and blood and biopsy procedures were performed by trained phlebotomists and medics with experience in the procedures. It was considered that the amount of blood and muscle tissue samples taken to pose no risk of adverse health effects. Risk of infection was minimised by following sterile procedural guidelines.

Social and psychological risks were minimised by ensuring privacy and confidentiality of participants throughout data collection and data storage periods. Initially we obtained informed consent and communicated to participants their rights to discontinue or withdraw from the studies at any time. We also ensured there were adequate change and shower facilities, and we minimised the number of observers in the laboratory at any one time while subjects were being examined and tests conducted. Following data

collection and identifying information has been stored securely in locked filing cabinet in locked office with access to only those principally involved in the studies.

We aimed to reduce economic risk to participants by reimbursing them for travel and time where necessary.

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ABBREVIATIONS AND ACRONYMS

4EBP1	Eukaryotic initiation factor 4E binding protein 1
AA	Amino acid
AADA2	Aralkylamine N-acetyltransferase
AANAT	Aralkylamine N-acetyltransferase
ACOX1	Acyl-CoA oxidase 1, palmitoyl
ACSL1	Acyl-CoA synthetase long-chain family member 1
ACTA2	Actin, alpha 2, smooth muscle, aorta
ACTC1	Actin, alpha, cardiac muscle 1
ADCYAP1	Adenylate cyclase activating polypeptide 1 (pituitary)
ADD	Adducin
ADORA2A	Adenosine A2a receptor
ADP	Adenosine diphosphate
AEBSF	Aprotinin, Leupeptin, Bestatin, Pepstatin
AKT	Protein kinase B
AKT1	AKT substrate 1 (proline-rich)
AMP	Adenosine monophosphate
AMPK	Adenosine monophosphate kinase
ANGPT2	Angiopoietin 2
ANOVA	Analysis of variance
AS3MT	Arsenic (+3 oxidation state) methyltransferase
ATP	Adenosine triphosphate
B2M	Beta 2 microglobulin
BCL2	B-cell CLL/lymphoma 2
BCL2L14	BCL2-like 14 (apoptosis facilitator)
BCOADK	Branched-chain 2- oxo-acid dehydrogenase kinase
BDNF	Brain-derived neurotrophic factor
C1QA	Complement component 1, q subcomponent, A chain
C1QB	Complement component 1, q subcomponent, B chain
C1QC	Complement component 1, q subcomponent, C chain
C1S	Complement component 1, s subcomponent
C21orf127	Chromosome 21 open reading frame 127
CABP5	Calcium binding protein 5
CALML5	Calmodulin-like 5
CaMK	Calcium/calmodulin-dependent protein kinase II

CAMKID	Calcium/calmodulin-dependent protein kinase ID
CAMKII	Calcium/calmodulin-dependent protein kinase II
CASP1	Caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)
CASP10	Caspase 10, apoptosis-related cysteine peptidase
CASP3	Caspase 3, apoptosis-related cysteine peptidase
CCL22	Chemokine (C-C motif) ligand 22
CCL5	Chemokine (C-C motif) ligand 5
CD36	Cluster of Differentiation 36
CD86	CD86 molecule
cDNA	Complimentary deoxyribonucleic acid
CEBPB	CCAAT/enhancer binding protein (C/EBP), beta
cFOS	FOS proto-oncogene
CHAT	Choline O-acetyltransferase
CHO	Carbohydrate
CI	Confidence interval
CIB2	Calcium and integrin binding family member 2
cJUN	JUN proto-oncogene
CK	Creatine kinase
CL	Confidence limit
CLCN4	Chloride channel protein 4
COL10A1	Collagen, type X, alpha 1
COL11A2	Collagen, type XI, alpha 2
COL18A1	Collagen, type XVIII, alpha 1
COL1A1	Collagen, type I, alpha 1
COL1A2	Collagen, type I, alpha 2
COL22A1	Collagen, type XXII, alpha 1
COL3A1	Collagen, type III, alpha 1
COL5A1	Collagen, type V, alpha 1
COL5A2	Collagen, type V, alpha 2
COL6A1	Collagen, type VI, alpha 1
COL6A3	Collagen, type VI, alpha 3
COLQ	Collagen-like tail subunit (single strand of homotrimer) of asymmetric acetyl cholinesterase
CON	Control condition

CPS1	Carbamoyl-phosphate synthase 1, mitochondrial
CPT1	Carnitine palmitoyltransferase I
CPT2	Carnitine palmitoyltransferase 2
CREB	cAMP response element binding protein
cRNA	Complementary ribonucleic acid
CROT	Carnitine O-octanoyltransferase
CT	Cycle threshold
CTSC	Cathepsin C
CV	Coefficient of variation
CXCL12	Chemokine (C-X-C motif) ligand 12
CXCL2	Chemokine (C-X-C motif) ligand 2
CXCR4	Chemokine (C-X-C motif) receptor 4
CYCS	Cytochrome c, somatic
CYP2U1	Cytochrome P450, family 2, subfamily U, polypeptide 1
CYP46A1	Cytochrome P450, family 46, subfamily A, polypeptide 1
<i>d</i>	¹⁵ N dose
DDIT3	DNA-damage-inducible transcript 3 (C/EBP-homologous protein, CHOP, GADD153)
DEPC	Diethylpyrocarbonate
DLAT	Dihydrolipoamide S-acetyltransferase
DMD	Dystrophin
DNA	Deoxyribonucleic acid
DNAJ	40 kDa heat shock protein (HSP40)
Dnase	Deoxyribonuclease
DNMT3	DNA (cytosine-5-)-methyltransferase 3 alpha
DNMT3B	DNA (cytosine-5-)-methyltransferase 3 beta
DSCR1	Regulator of calcineurin 1 (RCAN1, MCIP1)
DTT	Glucose assay buffer
EAA	Essential amino acids
ECH1	Enoyl CoA hydratase 1, peroxisomal
ECM	Extracellular matrix
EDN1	Endothelin 1
EDTA	Ethylenediaminetetraacetic acid
EE	Estimated energy expenditure
EE1A1	Eukaryotic translation elongation factor 1 alpha 1

EFEMP1	EGF-containing fibulin-like extracellular matrix protein 1
EFNB1	Ephrin-B1
EFNB3	EPH receptor B3
EGF	Epidermal growth factor
EGTA	Ethylene glycol tetra acetic acid
EIF1AX	Eukaryotic translation initiation factor 1A, X-linked
eIF2B	Eukaryotic translation initiation factor 2B
eIF4E	Eukaryotic translation initiation factor 4E
eIF4G	Eukaryotic translation initiation factor 4G
EIF5B	Eukaryotic translation initiation factor 5B
ELISA	Enzyme-Linked Immunosorbent Assay, enzyme immunoassay
eNOS	Endothelial nitric oxide synthase 3 (endothelial cell)
EPHA2	EPH receptor A2
ERK 1/2	Mitogen-activated protein kinase
ES	Effect Size
ESR1	Estrogen receptor 1
Ex _{study}	Estimated energy expenditure for study exercise protocol
FABP3	Fatty acid binding protein 3
FABP5	Fatty acid binding protein 5
FAK	Focal adhesion kinase
FBLN1	Fibulin 1
FBLN2	Fibulin 2
FBXL3	F-box and leucine-rich repeat protein 3
FBXO24	F-box protein 24
FBXO32	F-box protein 32
FGF2	Fibroblast growth factor 2
FOXO1a	Forkhead box O1
FOXO3	Forkhead box O3
G6PDH	Glucose-6-phosphate dehydrogenase
GADD45B	Growth arrest and DNA-damage-inducible, beta
GAPDH	Glyceraldehyde-3-phosphate dehydrogenase
GCN5	General control of amino-acid synthesis 5-like 2
GDF1	Growth differentiation factor 1
GDF8	Myostatin
GEA	Global Error Assessment

GLUT4	Glucose transporter type 4
GRS	Graphic rating scale
GSK3	Glycogen synthase
GβL	G-protein beta-subunit like protein
HAT1	Histone acetyltransferase 1
HCHO	High carbohydrate condition
HDAC8	Histone deacetylase 8
HEPES	4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid buffer
HGF	Hepatocyte growth factor
HMGCS2	3-hydroxy-3-methylglutaryl-CoA synthase 2 (mitochondrial)
HSP70	Heat shock 70 kDa protein 1A (HSPA1A)
HSPA1A	Heat shock 70 kDa protein 1A (HSP70)
hVPS34	Phosphatidylinositol 3-kinase catalytic subunit type 4
ICMT	Isoprenylcysteine carboxyl methyltransferase
IFI6	Interferon, alpha-inducible protein 6
IFITM2	Interferon induced transmembrane protein 2 (1-8D)
IFNA1	Interferon, alpha 1
IGF1	Insulin-like growth factor 1
IKBKB	Inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta
IL	Interleukin
IL17D	Interleukin 17D
IL1F6	Interleukin 1 family, member 6
IL1F8	Interleukin 1 family, member 8
IL22	Interleukin 22
IPA	Ingenuity pathway analysis
IRF8	Interferon regulatory factor 8
IRS1	Insulin receptor substrate 1
ITGAM	Integrin, alpha M (complement component 3 receptor 3 subunit)
ITGB1	Integrin, beta 1
ITGB2	Integrin, beta 2
JNK	c-Jun N-terminal kinases
LAMA4	Laminin, alpha 4
LCHO	Low carbohydrate condition
LDH	Lactate Dehydrogenase

LPIN1	Lipin 1
LPL	Lipoprotein lipase
LRFN5	Leucine rich repeat and fibronectin type III domain containing 5
MAPK	Mitogen-activated protein kinase
MDA	Malonyldialdehyde
MEF2	Myocyte enhancer factor 2
MG	Macro-glycogen
MHC	Myosin heavy chain
MHCII	Major Histocompatibility Complex class II
MLC1SA	Myosin, light chain 6B, alkali, smooth muscle and non-muscle (MYL6B)
MMP13	Matrix metalloproteinase 13 (collagenase 3)
MMP19	Matrix metalloproteinase 19
MMP9	Matrix metalloproteinase 9 (92 kDa gelatinase, type IV collagenase)
MRCL3	Myosin, light chain 12A, regulatory, non-sarcomeric1 (MYL12A)
MRF4	Myogenic factor 6 (also known as Muscle-specific regulatory factor 4)
MRFAP1L1	Morf4 family associated protein 1-like 1
mRNA	Messenger ribonucleic acid
MTMR6	Myotubularin related protein 6
mTOR	Mammalian target of rapamycin
mTORC1	Mammalian target of rapamycin complex 1
MUC4	Mucin 4, cell surface associated
MuRF1	Muscle-specific RING finger protein 1
MYBPH	Myosin binding protein H
MYF5	Myogenic factor 5
MYH1	Myosin, heavy chain 1, skeletal muscle, adult
MYH8	Myosin, heavy chain 8, skeletal muscle, perinatal
MYL1	Myosin, light chain 1, alkali; skeletal, fast
MYL2	Myosin, light chain 2, regulatory, cardiac, slow
MYL3	Myosin, light chain 3, alkali; ventricular, skeletal, slow
MYL4	Myosin, light chain 4, alkali; atrial, embryonic
MYL5	Myosin, light chain 5, regulatory
MYLPP	Myosin light chain, phosphorylatable, fast skeletal muscle

MYOD1	Myogenic differentiation 1
MYOG	Myogenin (myogenic factor 4)
MYST2	MYST histone acetyltransferase 2
<i>n</i>	Sample number
NADP	Nicotinamide adenine dinucleotide phosphate
NCBI GEO	Gene expression omnibus
NDST2	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2
N_E	Nitrogen excretion
NES	Mestin
NFAT	Nuclear factor of activated T-cells
NF-kB	Nuclear factor-kB
NFKB1A	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1
N_I	Nitrogen intake
NKIRAS2	Nuclear factor of kappa light polypeptide inhibitor interacting Ras-like 2
NMR	Nuclear magnetic resonance spectroscopy
NPB	Net protein balance
NTN4	Metrin 4
NTNG2	Metrin G2
<i>p</i>	Test statistic probability considered significant at the α -level 0.05
p70S6K	Ribosomal protein S6 kinase, 70 kDa
p90RSK	Ribosomal protein S6 kinase, 90 kDa
PA	Physical Activity
Panther GO	Panther gene ontology mapping
PB	Protein breakdown
PCR	Polymerase chain reaction
PDE	Phosphodiesterase
PDGFB	Platelet-derived growth factor beta polypeptide
PDHA2	Pyruvate dehydrogenase (lipoamide) alpha 2
PDK	Pyruvate dehydrogenase kinase
PDK1	Phosphoinositide dependent protein kinase 1
PDZRN3	PDZ domain containing ring finger 3
PECI	Peroxisomal D3,D2-enoyl-CoA isomerase
PFKFB1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1

PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3
PFKM	Phosphofructokinase, muscle
PG	Pro-glycogen
PGC-1 α	PPAR gamma coactivator 1 alpha
PH	Plekstrin homology domain containing proteins
PI3K	Phosphoinositide 3-kinase
PIK3CA	Phosphoinositide-3-kinase, catalytic, alpha polypeptide
PKC	Protein kinase C
PLA ₂	Phospholipase A ₂
PLIN2	Perilipin 2
PLTP	Phospholipid transfer protein
POMS	Profile of mood states short-form questionnaire
PPAR	Peroxisome proliferator-activated receptor
PPAR γ	Peroxisome proliferator-activated receptor gamma
PPARGC1 α	Peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
PPM2C	Pyruvate dehydrogenase phosphatase catalytic subunit 1 (PDP1)
PRAS40	40 kDa proline-rich AKT substrate
PS	Protein synthesis
PTN, Ptn	Protein condition
Q	Nitrogen flux
qPCR	Real time reverse transcription polymerase chain reaction
<i>r</i>	Pearson's correlation (one-tailed)
Rab 7	GTPase Rab 7
Rag A/B/C/D	Ras-related GTP-binding proteins
RARA	Retinoic acid receptor, alpha
REDD1/2	Deoxyribonucleic acid-damage-inducible transcript 4
RFFL	Ring finger and FYVE-like domain containing 1
RHEB	Ras homolog enriched in brain
RHOA	Ras homolog gene family, member A
RHOC	Ras homolog gene family, member C
RHOJ	Ras homolog gene family, member J
RMR	Resting metabolic rate
RNA	Ribonucleic acid
RNAase	Ribonuclease

ROS	Reactive oxygen species
RPE	Ratings of perceived exertion
RPL27A	Ribosomal protein L27a
RPL7	Ribosomal protein L7
RPLP0	Ribosomal protein, large, P0
RPLP1	Ribosomal protein, large, P1
RPS6	40S ribosomal protein S6
RPS6KA1	Ribosomal protein S6 kinase, 90 kDa, polypeptide 1
rRNA	Ribosomal ribonucleic acid
RSP24	Ribosomal protein S24
RSP3A	Ribosomal protein S3a
RT	Reverse transcription
RT-PCR	Real time reverse transcription polymerase chain reaction
S100A8	S100 calcium binding protein A8
S100A9	S100 calcium binding protein A9
S6K	Ribosomal protein S6 kinase, 70 kDa (formerly known as p70S6K)
SAS	Statistical Analysis Software
SCD	Stearoyl-CoA desaturase (delta-9-desaturase)
<i>SD</i>	Standard deviation
SDC2	Syndecan 2
SDF1	Chemokine (C-X-C motif) ligand 12 (CXCL12)
SDS PAGE	Sodium dodecyl sulphate polyacrylamide gel electrophoresis
SEMA3C	Sema domain, immunoglobulin domain, short basic domain, secreted, (semaphorin) 3C
SEMA3F	Sema domain, immunoglobulin domain, short basic domain, secreted, (semaphorin) 3F
SEMA6A	Sema domain, transmembrane domain, and cytoplasmic domain, (semaphorin) 6A
Ser	Serine rich binding motif
SERCA	Sarco/endoplasmic reticulum calcium transporting ATPase
SIRT5	Sirtuin 5
SIRT6	Sirtuin 6
SLC1A5	Neutral amino acid transporter solute carrier family 1
SLC25A20	Solute carrier family 25 (carnitine/acylcarnitine translocase),

	member 20
SLC2A4	Solute carrier family 2 (facilitated glucose transporter), member 4 (GLUT4)
SLC7A11	Solute carrier family 7, (cationic amino acid transporter, y+ system) member 11
SLC7A5	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 5
SLC7A5/SLC3A2	Bi-directional antiporter
SLC7A8	Solute carrier family 7 (amino acid transporter, L-type), member 8
SLCO1B1	Solute carrier organic anion transporter family, member 1B1
SLCO2A1	Solute carrier organic anion transporter family, member 2A1
SLIT2	Slit homolog 2
SMAD3	SMAD family member 3
SMARCA3	Helicase-like transcription factor (HLTF)
SNP sites	Single nucleotide polymorphism or single nucleotide (A, T, C, or G) difference
SOCS3	Suppressor of cytokine signalling 3
SOD	Superoxide dismutase
SPSS	Statistical Package for the Social Sciences
SR	Sarcoplasmic reticulum
SREBP	Sterol response element binding protein
SULT1A1	Sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1
SYK	Spleen tyrosine kinase
TBK1	TANK-binding kinase 1
TBS-T	Tris buffered saline solution with the detergent Tween-20
TGFB1	Transforming growth factor, beta 1
Thr	Threonine rich binding motif
TIMP1	TIMP metalloproteinase inhibitor 1
TIMP2	TIMP metalloproteinase inhibitor 2
TLR3	Toll-like receptor 3
TNC	Tenascin C
TNF	Tumour necrosis factor
TNFRSF19	Tumour necrosis factor receptor super family, member 19
TNFSF11	Tumour necrosis factor (ligand) super family, member 11

TNN	Tenascin N
TNNT2	Troponin T type 2 (cardiac)
TNXB	Tenascin XB
tr:T	Tracer to tracee ratio
TRIM46	Tripartite motif-containing 46
TRIM5	Tripartite motif-containing 5
TRIM9	Tripartite motif-containing 9
Tris	Tris(hydroxymethyl)aminomethane buffer
TSC1	Tuberous sclerosis protein 1, (hamartin)
TSC1-TSC2	Hamartin-tuberin complex
TSC2	Tuberous sclerosis protein 2 (tuberin)
TUBA1	Tubulin alpha-1A chain
Tween	Polysorbate detergent
Tyr	Tyrosine rich binding motif
UBE2	Ubiquitin-conjugating enzyme E2
UBE2J2	Ubiquitin-conjugating enzyme E2, J2
UCP3	Uncoupling protein 3 (mitochondrial, proton carrier)
VEGF	Vascular endothelial growth factor
VEGFA	Vascular endothelial growth factor A
VIM	Vimentin
VO _{2max}	Maximal volume of oxygen consumed
Vsp15	Vacuole sorting protein 15
W _{max}	Peak power output
WNT5A	Wingless-type MMTV integration site family, member 5A
YY1	YY1 transcription factor
ZNRF2	Zinc and ring finger 2