

TNFSF14-Derived Molecules as a Novel Treatment for Obesity and Type 2 Diabetes

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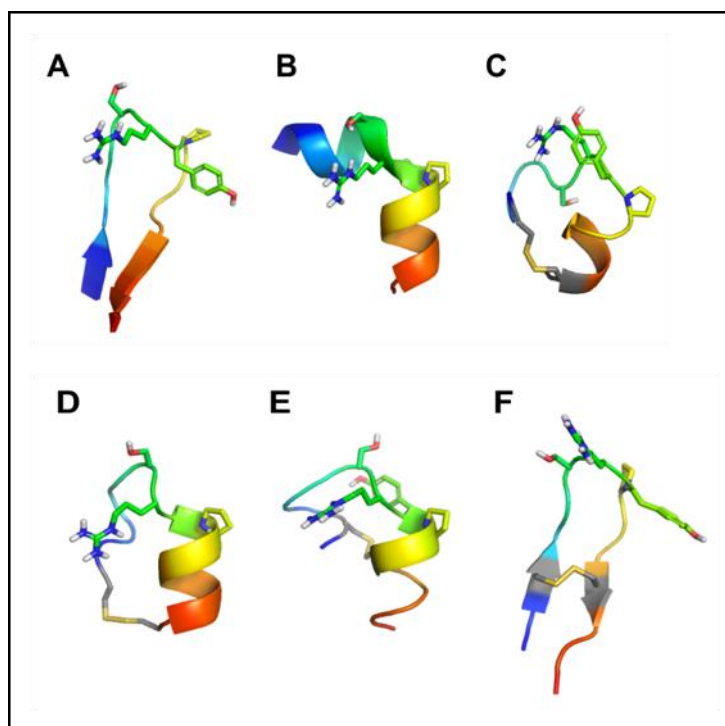


Figure S1. Optimisation of peptide 2 via introduction of disulfide crosslinks to maintain β -hairpin geometry. A. Peptide 2 conformation as in homology-modelled structure of mouse TNFSF14. B. Top-ranked conformation of peptide 2 obtained from PEP-FOLD. C. Top-ranked conformation of peptide 2.1 obtained from PEP-FOLD. D. Top-ranked conformation of peptide 2.2 obtained from PEP-FOLD. E. Top-ranked conformation of peptide 2.3 obtained from PEP-FOLD. F. Top-ranked conformation of peptide 2.4 obtained from PEP-FOLD. Conformations taken from PEP-FOLD were energy minimised in Prime. All panels coloured in red-to-blue rainbow from N- to C-terminus; disulfide crosslinks shown in grey.

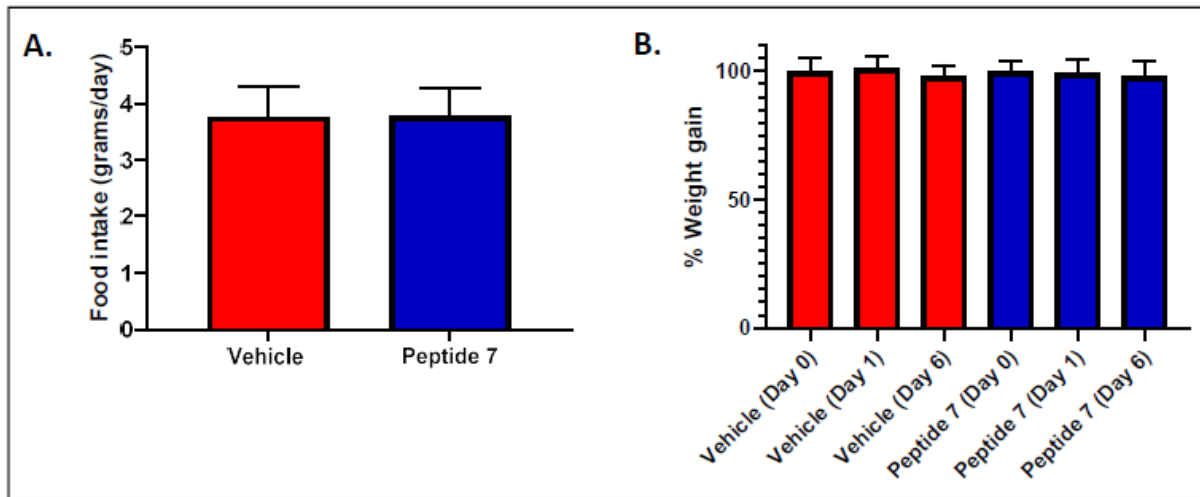


Figure S2. Peptide 7 does not affect food intake or weight loss in high fat diet fed mice. **A.** Daily food intake and **B.** Weight gain after 24hr and 6 days of treatment with vehicle or Peptide 7. Mean + SD.

Supplementary Table 1. Sequence alignments used for homology modelling.

Protein and template	Sequence alignment
mTNFSF14	EVNPA AHLTG ANSSLTGSGGPLLWETQLGLAFLRGLSYHDGALVVTK
hTNFSF14 (PDB 4RSU)	QANPAAHLTGANASLIGIGGPLLWETRLGLAFLRGLTYHDGALVTME : . ***** : ** . * ***** . ***** : ***** : AGYYYIYSKVQLGGVGCPLGLAS . . TITHGLYKRTPRYPEELELLVS PGYYYVYSKVQLSGVGCPLGLANGLPITHGLYKRTSRYPKLELLVS . **** : ***** ***** * * . ***** * * ***** QQSPCGRATSSSRVWWDSSFLGGVVHLEAGEEVVVRVLDRLV RRSPCGRANSS . RVWWDSSFLGGVVHLEAGEEVVVRVPGNRLV . . ***** . ** ***** : ***
mTNFRSF14	RSLPSCKEDEYFVGSECCPKCSPGYRVKEACGELTGTVCPEPCPPGT
hTNFRSF14 (PDB 4RSU)	SAQPSQRQEFLVGDECCPMCPNGYHVKQVCSEHTGTVCAPCPPQTY . **** : : : * : * * * * * * . * * * * : . * * * * * * * * * IAHLNGLSKCLQCQMCDPAMGLRASRNCSTENAVCGCSPGHFCIVQ TAHANGLSKCLPCGVCDPDMGLLTWQECSSWKDTCRCIPGYFCENQ . * * . ***** * . * * * * * * . : * * : . * * * * : * * * DGDHCAACRAYATSSPGQRVQKGGTESQDTLCT DGSHCSTCLQHTTCPPGQRVKRGTHDQDTVCA * * * * : . * : . * : * * * * : * * * * : * .
mLTBR	CRDQEKEYYEPQHRICCSRCPPGTYSKCSRIKRDTCATCAENSYN
hLTBR (PDB 4MXW)	CWDQDKEYYEPMDVCCSRCPPGEFVFAVCSRSQDTVCKTCPHNSYN * * * : ***** * : ***** : * * * * : ***** * * . * * * EHWNYLTICQLCRPCDPV EIAPCTSKRKTQCRCC EHWNHLSTCQLCRPCDIVLGFEVAPCTSDRKAECRCQPGMSCVYLD * * * * : * : . ***** * * : * * * * * * : * * * . . CT NECV * :