

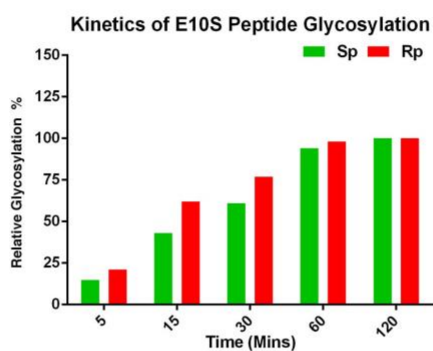
SUPPORTING INFORMATION

The conserved threonine-rich region of the HCF-1_{PRO} repeat activates promiscuous OGT:UDP-GlcNAc glycosylation and proteolysis activities

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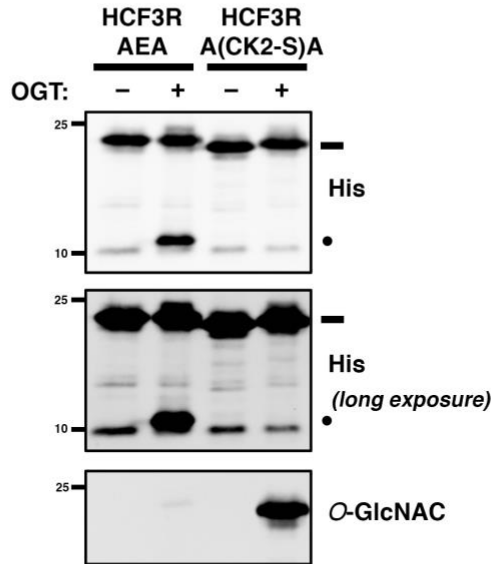
Supplementary Figure 1



Supplementary Figure 1. Kinetics of E10S peptide glycosylation by S_p- and R_p-αS-UDP-GlcNAc.

In vitro peptide glycosylation assay was performed using HCF-1_{PRO}-repeat 2 E10S peptide, by incubating with WT OGT and either S_p-αS-UDP-GlcNAc (green bar) or R_p-αS-UDP-GlcNAc (red bar) as indicated. Samples were withdrawn at indicated time intervals and peptide glycosylation was detected using LC-MS as described in materials and methods. O-GlcNAcylation of the E10S peptide at different time points was normalized to the O-GlcNAcylation levels at 120 minute time point.

Supplementary Figure 2



Supplementary Figure 2. OGT mediated cleavage and glycosylation of HCF3R substrates.

HCF3R-AEA or chimeric HCF3R-A(CK2-S)A protein were incubated with or without OGT for 6 hr. HCF3R protein cleavage and glycosylation was assayed by SDS-PAGE and immunoblotting using an anti-His antibody (for cleavage) and RL2 anti-O-GlcNAc antibody (glycosylation). Anti-OGT was used to detect levels of OGT protein. Chimeric HCF3R-A(CK2-S)A protein did not undergo any cleavage (lack of cleavage band in long exposure) but was heavily glycosylated as compared to native HCF3R-AEA substrate.

(■, un-cleaved HCF3R substrate; ●, cleaved product.)

Supplementary Table 1

Glycosylation assay peptides

Peptide Name	Peptide Sequence	Purity
CK2 (17-mer)	KKKYPPGGSTPV S SANMM	97%
E10S (26-mer)	VRVCSNPPC S THETGTTNTATTATSN	96%
Ch10 (28-mer)	KKKYPPGGSTPV S THETGTTNTATTATSN	98%
Ch13 (28-mer)	KKKYPPGGSTPV S SANTGTTNTATTATSN	96%
Ch13 T14A (28-mer)	KKKYPPGGSTPV S SAN <u>A</u> GTTNTATTATSN	99%
Ch13 T14Y (28-mer)	KKKYPPGGSTPV S SAN <u>Y</u> GTTNTATTATSN	95%
Ch13 T(17-22)A (28-mer)	KKKYPPGGSTPV S SANTGT <u>A</u> <u>N</u> <u>A</u> <u>A</u> <u>A</u> <u>A</u> ATSN	99%

Cleavage assay peptides

Peptide Name	Peptide Sequence	Purity
HCF-SHORT (32-mer)	YVRVCSNPPC E THQTGTTNTATTATSNMAGQH -NH ₂	98%
CK2(S10) – Thr-rich* (32-mer)	KKKPPGGSTPV S SANTGTTNTATTATSNMAGQH -NH ₂	98%
CK2(E10) – Thr-rich* (32-mer)	KKKPPGGSTPV E SANTGTTNTATTATSNMAGQH -NH ₂	99%
CK2(E10) – Thr-rich* (32-mer)	KKKPPGGSTPV E SANTGT <u>A</u> <u>N</u> <u>A</u> <u>A</u> <u>A</u> <u>A</u> ATSNMAGQH -NH ₂	99%
CK2(E9S10)– Thr-rich* (33-mer)	KKKPPGGSTP V E SANTGTTNTATTATSNMAGQH -NH ₂	98%

Supplementary Table 2

HCF3R-AEA

PGTVTLVCSNPPCATHETGTTNTATTTVVANLGGHPQPTQVQFVCDRQEAAAASLVTST
VGQQNGSVVRVCSNPPCE^UTHETGTTNTATTATSNMAGQHGC SNPPCATHETGTTNTA
TTAMSSVGAN

HCF3R-ASA

PGTVTLVCSNPPCATHETGTTNTATTTVVANLGGHPQPTQVQFVCDRQEAAAASLVTST
VGQQNGSVVRVCSNPPCS^UTHETGTTNTATTATSNMAGQHGC SNPPCATHETGTTNTA
TTAMSSVGAN

HCF3R-A(CK2-S)A

PGTVTLVCSNPPCATHETGTTNTATTTVVANLGGHPQPTQVQFVCDRQEAAAASLVTST
VGQQNGSVVRPGGSTPV^SSANTGTTNTATTATSNMAGQHGC SNPPCATHETGTTNTA
TTAMSSVGAN

HCF3R-A(CK2-E)A

PGTVTLVCSNPPCATHETGTTNTATTTVVANLGGHPQPTQVQFVCDRQEAAAASLVTST
VGQQNGSVVRPGGSTPV^ESANTGTTNTATTATSNMAGQHGC SNPPCATHETGTTNTA
TTAMSSVGAN