SUPPORTING INFORMATION

<u>Design and characterization of mutant and wild-type huntingtin proteins produced from a toolkit of scalable eukaryotic expression systems</u>

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Running title: A toolkit of HTT protein resources

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Table S1. Database search results for HTT¹⁻³¹⁴⁴ **Q23 expressed in EXPI293F cells.** Proteins with five or more total no. spectra are listed. Of the peptides which do not correspond to HTT protein, most either have very high scores in the CRAPome (1), suggesting that these are non-specific contaminants of the co-immunoprecipitation step, not true HTT interactors, or they are very low abundance.

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100220[IID] 10	P08238 HS90B	20	7	Q96PX9 PKH4B	12	2	Q13683/ITA7	6	1
Q2DQGI(RRD1AL20 Q2DD1GELR 2 Q2DD3GERD1AL20 Q2DG3GERD1AL20 Q2DG3GERD1AL20 Q2DG3GERD1AL20 Q2DG3GERD1AL20 Q2DG3GERD1AL20 Q2GD3GERD1AL20 Q2GD3GERD1AL20 Q2GD3GERD1AL20 Q2GD3GERD1AL20 Q2GD3GERD1AL20 Q2GD3GERD1AL20 Q2GD3GERD1AL20 Q2GD3GERD1A20 Q2GD3GERD1A20 Q2GD3GERD1A	09BOG0 MBB1A	20	, 5		12	3	Q15005/1111/ Q21 D37/K1109	6	1
1102101 10 10 10 11 <t< td=""><td>P11021/GRP78</td><td>19</td><td>6</td><td>Q50D10 02EH2</td><td>12</td><td>3</td><td>O5IV73 FRPD3</td><td>6</td><td>3</td></t<>	P11021/GRP78	19	6	Q50D10 02EH2	12	3	O5IV73 FRPD3	6	3
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	058FG1/HS904	19	4	O02224 CENPE	11	3	OSIWR5/DOP1	6	1
Qalitation Description Description <thdescription< th=""> <thdescription< th=""></thdescription<></thdescription<>	O8NET8 TRPV3	19	3	Q6222 CERTE	11	2	Q6N069INAA16	6	2
Observe Operation	060814H2B1K	19	3	077333 SETX	11	4	O86XA9HTR5A	6	1
100007[H2D13 10 p Q00007[H2D13 11 q Q01007[H2D13 6 1 P23527[H2B10 18 3 Q924F4[TGRM1 11 3 Q8TD57[DYH3 6 2 P33778[H2B1B 18 3 P21817[RYR1 10 2 Q92997[DVL3 6 1 P57053[H2BFS 18 3 Q12955[ANK3 10 5 Q96004[H2B1A 6 1 P58876[H2B1D 18 3 Q12955[ANK3 10 2 Q960[AKAP9 6 1 P62807[H2B1C 18 3 Q15T1B0[AXDN1 10 2 Q9990[AKAP9 6 3 Q16778[H2B2E 18 3 Q86U86[PB1 10 3 Q9HCK8[CHD8 6 3 Q5QNW6[H2B2F 18 3 Q86V3[QGA3 10 3 Q9P2D1[CHD7 6 3 Q93079[H2B1H 18 3 Q1375[LIPA1 9 4 P09131[P3 5 1 Q9987[H2B1N 18 3 Q1575[HERC1 9 3 Q1576[QGA2 5 2 <td>P06899 H2B11</td> <td>18</td> <td>3</td> <td>Q72555551521X</td> <td>11</td> <td>4</td> <td></td> <td>6</td> <td>1</td>	P06899 H2B11	18	3	Q72555551521X	11	4		6	1
125521 11210 16 5 Q71414 10 11 5 Q81537 D71414 10 2 Q92997 DVL3 6 1 P33778 H2B1B 18 3 Q12955 ANK3 10 5 Q96A08 H2B1A 6 1 P57053 H2B1D 18 3 Q12955 ANK3 10 5 Q96A08 H2B1A 6 1 P58876 H2B1D 18 3 Q1XH10 SKDA1 10 2 Q96QT4 TRPM7 6 1 P62807 H2B1C 18 3 Q5T1B0 AXDN1 10 2 Q99996 AKAP9 6 3 Q16778 H2B2E 18 3 Q86U86 PB1 10 3 Q9HCK8 CHD8 6 3 Q5QNW6 H2B2F 18 3 Q86V13 IQGA3 10 3 Q9PYC9 DYH9 6 1 Q8N257 H2B3B 18 3 Q13136 LIPA1 9 4 P09131 P3 <td>P23527H2B10</td> <td>18</td> <td>3</td> <td>Q000Q4TBCTD</td> <td>11</td> <td>3</td> <td></td> <td>6</td> <td>2</td>	P23527H2B10	18	3	Q000Q4TBCTD	11	3		6	2
1357/6[112B1B] 16 p 121617][KTR1 16 2 Q22777][PVLD p 1 P57053]H2BFS 18 3 Q12955]ANK3 10 5 Q96A08]H2B1A 6 1 P58876]H2B1D 18 3 Q1XH10]SKDA1 10 2 Q96QT4]TRPM7 6 1 P62807]H2B1C 18 3 Q5T1B0]AXDN1 10 2 Q99996]AKAP9 6 3 Q16778]H2B2E 18 3 Q86U86[PB1 10 3 Q9HCK8[CHD8 6 3 Q5QNW6[H2B2F 18 3 Q86V13]IQGA3 10 3 Q9NYC9[DYH9 6 1 Q8N257]H2B3B 18 3 Q8IZD9[DOCK3 10 3 Q9P2D1[CHD7 6 3 Q99877]H2B1H 18 3 Q15751[HERC1 9 3 Q13576[IQGA2 5 2 Q99877]H2B1N 18 3 Q6FI48[SYDM 9 3 Q15746[MYLK 5 1 Q99880[H2B1L 18 3 Q9HBJ7[UBP29 9 3 Q86VV8[RTTN 5	P33778 H2B1B	18	3	P21817 RVR1	10	2	092997/DVI 3	6	1
13/303/I12B13 16 p Q12/33/I14B2 10 p Q20/0400/112D114 p 1 P58876 H2B1D 18 3 Q1XH10 SKDA1 10 2 Q96QT4 TRPM7 6 1 P62807 H2B1C 18 3 Q5T1B0 AXDN1 10 2 Q99996 AKAP9 6 3 Q16778 H2B2E 18 3 Q86U86 PB1 10 3 Q9HCK8 CHD8 6 3 Q5QNW6 H2B2F 18 3 Q86U86 PB1 10 3 Q9NYC9 DYH9 6 1 Q8N257 H2B3B 18 3 Q8IZD9 DOCK3 10 3 Q9P2D1 CHD7 6 3 Q93079 H2B1H 18 3 Q15751 HERC1 9 3 Q13576 IQGA2 5 2 Q99877 H2B1N 18 3 Q15751 HERC1 9 3 Q15746 MYLK 5 1 Q99880 H2B1L 18 3 Q6P148 SYDM 9 3 Q15746 MYLK 5 1 Q99880 H2B1L 18 3 Q9HBJ7 UBP29 9 3 Q86VV8 RTTN 5	P57053 H2BFS	18	3	012955 ANK3	10	5	Q92997107123	6	1
13500[112B1D 10 p Q1A110[ADA11 10 2 Q20Q14[1R1M17 p 1 P62807[H2B1C 18 3 Q5T1B0[AXDN1 10 2 Q99996[AKAP9 6 3 Q16778[H2B2E 18 3 Q86U86[PB1 10 3 Q9HCK8[CHD8 6 3 Q5QNW6[H2B2F 18 3 Q86V13[IQGA3 10 3 Q9NYC9[DYH9 6 1 Q8N257[H2B3B 18 3 Q8IZD9[DOCK3 10 3 Q9P2D1[CHD7 6 3 Q93079[H2B1H 18 3 Q15751[HERC1 9 3 Q13576[IQGA2 5 2 Q99879[H2B1N 18 3 Q6P148[SYDM 9 3 Q15746[MYLK 5 1 Q99880[H2B1L 18 3 Q6P148[SYDM 9 3 Q15746[MYLK 5 1 Q99880[H2B1L 18 3 Q9HBJ7[UBP29 9 3 Q86VV8[RTTN 5 3 Q12931[TRAP1 16 5 Q9P0L2[MARK1 9 1 Q8NBX0[SCPDL 5	P58876 H2B1D	18	3		10	2	Q960T4 TRPM7	6	1
102007[H2B1C 10 p Q31130[H3D111 10 2 Q3775[H1117 p p Q16778[H2B2E 18 3 Q86U86[PB1 10 3 Q9HCK8[CHD8 6 3 Q5QNW6[H2B2F 18 3 Q86V13[IQGA3 10 3 Q9NYC9[DYH9 6 1 Q8N257[H2B3B 18 3 Q8IZD9[DOCK3 10 3 Q9P2D1[CHD7 6 3 Q93079[H2B1H 18 3 Q13136[LIPA1 9 4 P09131[P3 5 1 Q99877[H2B1N 18 3 Q15751[HERC1 9 3 Q13576[IQGA2 5 2 Q99879[H2B1N 18 3 Q6P148[SYDM 9 3 Q15746[MYLK 5 1 Q99880[H2B1L 18 3 Q6P148[SYDM 9 3 Q15746[MYLK 5 1 Q99880[H2B1L 18 3 Q9HBJ7[UBP29 9 3 Q86VV8[RTTN 5 3 Q12931[TRAP1 16 5 Q9P0L2[MARK1 9 1 Q8NBX0[SCPDL 5	P62807 H2B1C	18	3	O5T1B0 AXDN1	10	2	099996 AKAP9	6	3
Q307/16/12/22 10 p Q30006/12/1 10 p Q210006/12/1 p Q210006/12/1 p Q210000/12/1 p Q210000/12/1 p Q210000/12/1 p Q30079/12/1 Q310000/12/1 Q310000/12/1 Q310000/12/1 Q3100000/12/1 Q3100000/12/1 Q3100000/12/1 Q3100000/12/1 Q3100000/12/1 Q3100000/12/1 Q31000000/12/1 Q31000000/12/1 Q310000000/12/1 Q3100000000/12/1 Q310000000000000000/12/1 Q31000000000000000000000000000000000000	016778H2B2E	18	3	086U86 PB1	10	3		6	3
Q8N257 H2B3B 18 3 Q8IZD9 DOCK3 10 3 Q9P2D1 CHD7 6 3 Q93079 H2B1H 18 3 Q13136 LIPA1 9 4 P09131 P3 5 1 Q99877 H2B1N 18 3 Q15751 HERC1 9 3 Q13576 IQGA2 5 2 Q99879 H2B1M 18 3 Q6P148 SYDM 9 3 Q15746 MYLK 5 1 Q99880 H2B1L 18 3 Q6P148 SYDM 9 3 Q15746 MYLK 5 1 Q99880 H2B1L 18 3 Q9HBJ7 UBP29 9 3 Q86VV8 RTTN 5 3 Q12931 TRAP1 16 5 Q9P0L2 MARK1 9 1 Q8NBX0 SCPDL 5 2 Q8IVF2 AHNK2 16 1 Q9P217 ZSWM5 9 3 Q8TD26 CHD6 5 2 Q14647 CHD2 15 2 tr Q5TEC6 Q5TEC6 9 3 Q9ULT8 HECD1 5 3 P04908 H2A1B<	050NW6H2B2F	18	3	O86VI3IIOGA3	10	3	O9NYC9DYH9	6	1
Q91425/[H2B5b] 10 p Q0125/[D00405] 10 p Q1257[[D1057] p Q93079[H2B1H 18 3 Q13136[LIPA1 9 4 P09131[P3 5 1 Q99877[H2B1N 18 3 Q15751[HERC1 9 3 Q13576[IQGA2 5 2 Q99879[H2B1M 18 3 Q6P148[SYDM 9 3 Q15746[MYLK 5 1 Q99880[H2B1L 18 3 Q9HBJ7[UBP29 9 3 Q86VV8[RTTN 5 3 Q12931[TRAP1 16 5 Q9P0L2[MARK1 9 1 Q8NBX0[SCPDL 5 2 Q8IVF2[AHNK2 16 1 Q9P217[ZSWM5 9 3 Q8TD26[CHD6 5 2 Q14647[CHD2 15 2 tr[Q5TEC6[Q5TEC6 9 3 Q9ULT8[HECD1 5 3 P04908[H2A1B 14 4 Q15078[CE290 8 3 1 1	08N257H2B3B	18	3	O8IZD9IDOCK3	10	3	O9P2D1/CHD7	6	3
Q99877 H2B1N 18 3 Q15751 HERC1 9 3 Q13576 IQGA2 5 2 Q99879 H2B1N 18 3 Q6PI48 SYDM 9 3 Q15746 MYLK 5 1 Q99879 H2B1N 18 3 Q6PI48 SYDM 9 3 Q15746 MYLK 5 1 Q99880 H2B1L 18 3 Q9HBJ7 UBP29 9 3 Q86VV8 RTTN 5 3 Q12931 TRAP1 16 5 Q9P0L2 MARK1 9 1 Q8NBX0 SCPDL 5 2 Q8IVF2 AHNK2 16 1 Q9P217 ZSWM5 9 3 Q8TD26 CHD6 5 2 O14647 CHD2 15 2 tr Q5TEC6 Q5TEC6 9 3 Q9ULT8 HECD1 5 3 P04908 H2A1B 14 4 O15078 CE290 8 3 0 0 0	093079H2B1H	18	3	Q012D9 D00105	9	4	P09131/P3	5	1
Q99879 H2B1N 18 3 Q6PI48 SYDM 9 3 Q15746 MYLK 5 1 Q99879 H2B1N 18 3 Q6PI48 SYDM 9 3 Q15746 MYLK 5 1 Q99880 H2B1L 18 3 Q9HBJ7 UBP29 9 3 Q86VV8 RTTN 5 3 Q12931 TRAP1 16 5 Q9P0L2 MARK1 9 1 Q8NBX0 SCPDL 5 2 Q8IVF2 AHNK2 16 1 Q9P217 ZSWM5 9 3 Q8TD26 CHD6 5 2 O14647 CHD2 15 2 tr Q5TEC6 Q5TEC6 9 3 Q9ULT8 HECD1 5 3 P04908 H2A1B 14 4 O15078 CE290 8 3 1 1	099877H2B1N	18	3	Q15751/HFRC1	9	3	013576II0GA2	5	2
Q99880 H2B1L 18 3 Q9HBJ7 UBP29 9 3 Q86VV8 RTTN 5 3 Q12931 TRAP1 16 5 Q9P0L2 MARK1 9 1 Q8NBX0 SCPDL 5 2 Q8IVF2 AHNK2 16 1 Q9P217 ZSWM5 9 3 Q8TD26 CHD6 5 2 O14647 CHD2 15 2 tr Q5TEC6 Q5TEC6 9 3 Q9ULT8 HECD1 5 3 P04908 H2A1B 14 4 O15078 CE290 8 3 1	099879H2B1M	18	3	O6PI48 SVDM	9	3	015746IMVI K	5	1
Q12931 TRAP1 16 5 Q9P0L2 MARK1 9 1 Q8NBX0 SCPDL 5 2 Q8IVF2 AHNK2 16 1 Q9P217 ZSWM5 9 3 Q8TD26 CHD6 5 2 O14647 CHD2 15 2 tr Q5TEC6 Q5TEC6 9 3 Q9ULT8 HECD1 5 3 P04908 H2A1B 14 4 O15078 CE290 8 3 1 1	099880 H2B1L	18	3	O9HBI7IIIBP29	9	3	O86VV8RTTN	5	3
Q8IVF2 AHNK2 16 1 Q9P217 ZSWM5 9 3 Q8TD26 CHD6 5 2 014647 CHD2 15 2 tr Q5TEC6 Q5TEC6 9 3 Q9ULT8 HECD1 5 3 P04908 H2A1B 14 4 015078 CE290 8 3 0 0 0	012931 TR ΔP1	16	5	$O9P0L2 M\Delta RK1$	9			5	2
Constraine Constra	O8IVF2 AHNK2	16	1	O9P217/ZSWM5	9	3	O8TD26CHD6	5	2
P04908 H2A1B 14 4 015078 CE290 8 3	014647 CHD2	15	2	trIO5TEC6IO5TEC6	9	3	O9UILT8 HECD1	5	3
	P04908 H2A1B	14	4	O15078 CE290	8	3		-	-



Figure S1. Western blot analysis of HTT samples from different expression systems. C-terminally FLAG-tagged HTT derived from EXPI293F expression, either by transient transfection or baculoviral transduction in EXPI293F cells or baculoviral transduction in Sf9 cells, were subject to Western Blot analysis with ab109115 which binds an epitope at amino acids 1-100.

A)

1	MATLEKLMKA	FESLKSFQQQ	00000 000000	QQQQQQQQPP	PPPPPPPPQ	L PQPPPQAQP	LLPQPQPPPP	PPPPPPGPAV	AEEPLHRPKK	ELSATKKDRV
101	NHCLTICENI	VAQSVRNSPE	FOKLLGIAME	LFLLCSDDAE	SDVRMVADEC	LNKVIKALMD	SNLPRLQLEL	YKEIKKNGAP	RSLRAALWRF	AELAHLVRPQ
201	KCRPYLVNLL	PCLTRTSKRP	EESVQETLAA	AVPKIMASFG	NFANDNEIKV	LLKAFIANLK	SSSPTIRRTA	AGSAVSICQH	SRRTQYFYSW	LLNVLLGLLV
301	PVEDEHSTLL	ILGVL LTL RY	LVPLLQQQVK	DTSLKGSFGV	TRKEMEVSPS	AEQLVQVYEL	TLHHTQHQDH	NVVTGALELL	QQLFRTPPPE	LLQTLTAVGG
401	IGQLTAAKEE	SGGRSRSGSI	VELIAGGGSS	CSPVLSRKQK	GKVLLGEEEA	LEDDSESRSD	VSSSALTASV	KDEISGELAA	SSGVSTPGSA	GHDIITEQPR
501	SQHTLQADSV	DLASCDLTSS	ATDGDEEDIL	SHSSSQVSAV	PSDPA MDL ND	GTQASSPISD	SS QTTTEGPD	SAVTPS DSSE	IVLDGTDNQY	LGLQIGQPQD
601	EDEEATGILP	DEASEAFRNS	SMALQQAHLL	KNMSHCRQPS	DSSVDKFVLR	DEATEPGDQE	NKPCRIKGDI	GQSTDDDSAP	LVHCVRLLSA	SFLLTGGKNV
701	LVPDRDVRVS	VK ALALSCVG	AAVALHPESF	FSKLYKVPLD	TTEYPEEQYV	SDILNYIDHG	DPQVRGATAI	LCGTLICSIL	SRSRFHVGDW	MGTIRTLTGN
801	TFSLADCIPL	LRKTLKDESS	VTCKLACTAV	RNCVMSLCSS	SYSELGLQLI	IDVLTLRNSS	YWLVRTELLE	TLAEIDFRLV	SFLEAKAENL	HRGAHHYTGL
901	LKLQERVLNN	VVIHLLGDED	PRVRHVAAAS	LIRLVPKLFY	KCDQGQADPV	VAVARDQSSV	YLKLLMHETQ	PPSHFSVSTI	TRIYRGYNLL	PSITDVTMEN
1001	NLSRVIAAVS	HELITSTTRA	LTFGCCEALC	LLSTAFPVCI	WSLGWHCGVP	PLSASDESRK	SCTVGMA TMI	LTLLSSAWFP	LDLSAHQDAL	ILAGNLLAAS
1101	APKSLRSSWA	SEEEANPAAT	KQEEVWPALG	DRALVPMVEQ	LFSHLLKVIN	ICAHVLDDVA	PGPAIKAALP	SLTNPPSLSP	IRRKGKEKEP	GEQASVPLSP
1201	KKGSEASAAS	RQSDTSGPVT	TSKSSSLGSF	YHLPSYLKLH	DVLKATHANY	KVTLDLQNST	EKFGGFLRSA	LDVLSQILEL	ATLQDIGKCV	EEILGYLKSC
1301	FSREPMMATV	CVQQLLKTLF	GTNLASQFDG	LSSNPSKSQG	RAQRLGSSSV	RPGLYHYCFM	APYTHFTQAL	ADASLRNMVQ	AEQENDTSGW	FDVLQKVSTQ
1401	LKTNLTSVTK	NRADKNAIHN	HIRLFEPLVI	KALKQYTTTT	CAÖTŐKŐATD	LLAQLVQLRV	NYCLLDSDQV	FIGFVLKQFE	YIEVGQFRES	EAIIPNIFFF
1501	LVLLSYERYH	SKQIIGIPKI	IQLCDGIMAS	GRKAVTHAIP	ALQPIVHDLF	VLRGTNKADA	GKELETQKEV	VVSMLLRLIQ	YHQVLEMFIL	VLQQCHKENE
1601	DKWKRLSRQI	ADIILPMLAK	QQMHIDSHEA	LGVLNTLFEI	LAPSSLRPVD	MLLRSMFVTP	NTMASVSTVQ	LWISGILAIL	RVLISQSTED	IVLSRIQELS
1701	FSPYLISCTV	INRLRDGDST	STLEEHSEGK	QIKNLPEETF	SRFLLQLVGI	LLEDIVTKQL	KVEM SEQQHT	FYCQELGTLL	MCLIHIFKSG	MFRRITAAAT
1801	RLFRSDGCGG	SFYTLDSLNL	RARSMITTHP	ALVLLWCQIL	LLVNHTDYRW	WAEVQQTPKR	HSLSST KLLS	POMSGEEEDS	DLAAKLGMCN	REIVRRGALI
1901	LFCDYVCQNL	HDSEHLTWLI	VNHIQDLISL	SHEPPVQDFI	SAVHRNSAAS	GLFIQAIQSR	CENLSTPTML	KKTLQCLEGI	HLSQSGAVLT	LYVDRLLCTP
2001	FRVLARMVDI	LACRRVEMLL	AANLQSSMAQ	LPMEELNRIQ	EYLQSSGLAQ	RHQRLYSLLD	RFRLSTMODS	LSPSPPVSSH	PLDGDGHVSL	ETVSPDKDWY
2101	VHLVKSQCWT	RSDSALLEGA	ELVNRIPAED	MNAFMMNSEF	NLSLLAPCLS	LG MSEISGGQ	KSALFEAARE	VTLARVSGTV	QQLPAVHHVF	QPELPAEPAA
2201	YWSKLNDLFG	DAALYQSLPT	LARALAQYLV	VVSKLPSHLH	LPPEKEKDIV	KFVVATLEAL	SWHLIHEQIP	LSLDLQAGLD	CCCLALQLPG	LWSVVSSTEF
2301	VTHACSLIYC	VHFILEAVAV	QPGEQLLSPE	RRTNTPKAIS	EEEEEVDPNT	QNPKYIT AAC	EMVAEMVESL	QSVLALGHKR	NSGVPAFLTP	LLRNIIISLA
2401	RLPLVNSYTR	VPPLVWKLGW	SPKPGGDFGT	AFPEIPVEFL	QEKEVFKEFI	YRINTLGWTS	RTQFEETWAT	LLGVLVTQPL	VMEQEESPPE	EDTERTQINV
2501	LAVQAITSLV	LSAMTVPVAG	NPAVSCLEQQ	PRNKPLKALD	TRFGRKLSII	RGIVEQEIQA	MVSKRENIAT	HHLYQAWDPV	PSLSPATTGA	LISHEKLLLQ
2601	INPERELGSM	SYKLGQVSIH	SVWLGNSITP	LREEEWDEEE	EEEADAPAPS	SPP TSPVNSR	KH RAGVDIHS	CSQFLLELYS	RWILPSSSAR	RTPAILISEV
2701	VRSLLVVSDL	FTERNQFELM	YVTLTELRRV	HPSEDEILAQ	YLVPATCKAA	AVLGMDKAVA	EPVSRLLEST	LRSSHLPSRV	GALHGVLYVL	ECDLLDDTAK
2801	QLIPVISDYL	LSNLKGIAHC	VNIHSQQHVL	VMCATAFYLI	ENTPLOVGPE	FSASIIQMCG	VMLSGSEEST	PSILYHCALR	GLERLLLSEQ	LSRLDAESLV
2901	KLSVDRVNVH	SPHRAMAALG	LMLTCMYTGK	EKVSPGRTSD	PNPAAPDSES	VIVAMERVSV	LFDRIRKGFP	CEARVVARIL	PQFLDDFFPP	QDIMNKVIGE
3001	FLSNQQPYPQ	FMATVVYKVF	QTLHSTGQSS	MVRDWVMLSL	SNFTQRAPVA	MATWSLSCFF	VSASTSPWVA	ALLPHVISRM	GKLEQVDVNL	FCLVATDFYR
3101	HQIEEELDRR	AFQSVLEVVA	APGSPYHRLL	TCLRNVHKVT	TC					

B)

1	MATLEKLMKA	FESLKSFQQQ	00000000000	QQQQQQQQPP	PPPPPPPPQ	LPQPPPQAQP	LLPQPQPPPP	PPPPPGPAV	AEEPLHRPK K	ELSATKKDRV
101	NHCLTICENI	VAQSVRNSPE	FQKLLGIAME	LFLLCSDDAE	SDVRMVADEC	LNKVIKALMD	SNLPRLQLEL	YKEIKKNGAP	RSL RAALWRF	AELAHLVRPQ
201	KCRPYLVNLL	PCLTRTSKRP	EESVQETLAA	AVPKIMASFG	NFANDNEIKV	LLKAFIANLK	SSSPTIRRTA	AGSAVSICQH	SRRTQYFYSW	LLNVLLGLLV
301	PVEDEHSTLL	ILGVLLTLRY	LVPLLQQQVK	DTSLKGSFGV	TRKEMEVSPS	AEQLVQVYEL	TLHHTQHQDH	NVVTGALELL	QQLF RTPPPE	LLQTLTAVGG
401	IGQLTAAKEE	SGGRSRSGSI	VELIAGGGSS	CSPVLSRK QK	GKVLLGEEEA	LEDDSESRSD	VSSSALTASV	KDEISGELAA	SSGVSTPGSA	GHDIITEQPR
501	SQHTLQADSV	DLASCDLTSS	ATDGDEEDIL	SHSSSQVSAV	PSDPAMDLND	GTQASSPISD	SSQTTTEGPD	SAVTPSDSSE	IVLDGTDNQY	LGLQIGQPQD
601	EDEEATGILP	DEASEAF RNS	SMALQQAHLL	KNMSHCROPS	DSSVDKFVLR	DEATEPGDQE	NKPCRIKGDI	GQSTDDDSAP	LVHCVRLLSA	SFLLTGGKNV
701	LVPDRDVRVS	VK ALALSCVG	AAVALHPESF	FSKLYKVPLD	TTEYPEEQYV	SDILNYIDHG	DPQVRGATAI	LCGTLICSIL	SRSRFHVGDW	MGTIRTLTGN
801	TFSLADCIPL	LRKTLKDESS	VTCKLACTAV	RNCVMSLCSS	SYSELGLQLI	I DVLTLR NSS	YWLVRTELLE	TLAEIDFRLV	SFLEAKAENL	HRGAHHYTGL
901	LK LQE RVLNN	VVIHLLGDED	PRVRHVAAAS	LIRLVPKLFY	KCDQGQADPV	VAVARDQSSV	YLKLLMHETQ	PPSHFSVSTI	TRIYRGYNLL	PSITDVTMEN
1001	NLSRVIAAVS	HELITSTTRA	LTFGCCEALC	LLSTAFPVCI	WSLGWHCGVP	PLSASDESRK	SCTVGMATMI	LTLLSSAWFP	LDLSAHQDAL	ILAGNLLAAS
1101	APKSLRSSWA	SEEEANPAAT	KQEEVWPALG	DRALVPMVEQ	LFSHLLKVIN	ICAHVLDDVA	PGPAIKAALP	SLTNPPSLSP	IRRKGKEKEP	GEQASVPLSP
1201	KKGSEASAAS	RQSDTSGPVT	TSKSSSLGSF	YHLPSYLKLH	DVLK ATHANY	KVTLDLQNST	EKFGGFLRSA	LDVLSQILEL	ATLQDIGK CV	EEILGYLKSC
1301	FSREPMMATV	CVQQLLKTLF	GTNLASQFDG	LSSNPSK SQG	RAQ RLGSSSV	RPGLYHYCFM	APYTHFTQAL	ADASLRNMVQ	AEQENDISGW	FDVLQKVSTQ
1401	LKTNLTSVTK	NRADKNAIHN	HIRLFEPLVI	KALKQYTTTT	CNÖTÖKÖNTD	LLAQLVQLRV	NYCLLDSDQV	FIGFVLK QFE	YIEVGQFRES	EAIIPNIFFE
1501	LVLLSYERYH	SKQIIGIPKI	IQLCDGIMAS	GRKAVTHAIP	ALQPIVHDLF	VLRGTNKADA	GK ELETQKEV	VVSMLLRLIQ	YHQVLEMFI L	VLQQCHKENE
1601	dkwk rlsr qı	ADIILPMLAK	QQMHIDSHEA	LGVLNTLF EI	LAPSSLRPVD	MLLRSMFVTP	NTMASVSTVQ	LWISGILAIL	RVLISQSTED	IVLSRIQELS
1701	FSPYLISCTV	INRLRDGDST	STLEEHSEGK	QIKNLPEETF	SRFLLQLVGI	LLEDIVTK QL	KVEMSEQQHT	FYCQELGTLL	MCLIHIFKSG	MFRR ITAAAT
1801	RLFR SDGCGG	SFYTLDSLNL	RARSMITTHP	ALVLLWCQIL	LLVNHTDYRW	WAEVQQTPKR	HSLSSTK lls	PQMSGEEEDS	DLAAKLGMCN	REIVRRGALI
1901	LFCDYVCQNL	HDSEHLTWLI	VNHIQDLISL	SHEPPVQDFI	SAVHR NSAAS	GLFIQAIQSR	CENLSTPTML	KK TLQCLEGI	HLSQSGAVLT	LYVDRLLCTP
2001	FRVLAR MVD1	LACRRVEMLL	AANLQSSMAQ	LPMEELNRIQ	EYLQSSGLAQ	RHORLYSLLD	RFRLSTMODS	LSPSPPVSSH	PLDGDGHVSL	ETVSPDKDWY
2101	VHLVK SQCWT	RSDSALLEGA	ELVNRIPAED	MNAFMMNSEF	NLSLLAPCLS	LGMSEISGGQ	KSALFEAARE	VTLARVSGTV	QQLPAVHHVF	QPELPAEPAA
2201	YWSKLNDLFG	DAALYQSLPT	LARALAQYLV	VVSKLPSHLH	LPPEK EKDIV	KFVVATLEAL	SWHLIHEQIP	LSLDLQAGLD	CCCLALQLPG	LWSVVSSTEF
2301	VTHACSLIYC	VHFILEAVAV	QPGEQLLSPE	RRTNTPK AIS	EEEEEVDPNT	QNPK YITAAC	EMVAEMVESL	QSVLALGHK R	NSGVPAFLTP	LLRNIIISLA
2401	RLPLVNSYTR	VPPLVWKLGW	SPKPGGDFGT	AFPEIPVEFL	QEKEVFKEFI	YRINTLGWTS	RTQFEETWAT	LLGVLVTQPL	VMEQEESPPE	EDTERTQINV
2501	LAVQAITSLV	LSAMTVPVAG	NPAVS CLEQQ	PRNKPLKALD	TRFGRKLSII	RGIVEQEIQA	MVSKRENIAT	HHLYQAWDPV	PSLSPATTGA	LISHEKLLLQ
2601	INPERELGSM	SYKLGQVSIH	SVWLGNSITP	LREEEWDEEE	EEEADAPAPS	SPPTSPVNSR	KHR AGVDIHS	CSQFLLELYS	RWILPSSSAR	RTPAILISEV
2701	VRSLLVVSDL	FTERNQFELM	YVTLTELRRV	HPSEDEILAQ	YLVPATCKAA	AVLGMDKAVA	EPVSRLLEST	LRSSHLPSRV	GALHGVLY VL	ECDLLDDTAK
2801	QLIPVISDYL	LSNLK GIAHC	VNIHSQQHVL	VMCATAFYLI	ENYPLDVGPE	FSASIIQMCG	VMLSGSEEST	PSIIYHCALR	GLER LLLSEQ	LSRLDAESLV
2901	KLSVDRVNVH	SPHRAMAALG	LMLTCMYTGK	EK VSPGR TSD	PNPAAPDSES	VIVAMERVSV	LFDRIRKGFP	CEARVVARIL	PQFLDDFFPP	QDIMNKVIGE
3001	FLSNQQPYPQ	FMATVVYKVF	QTLHSTGQSS	MVRDWVMLSL	SNFTQRAPVA	MATWSLSCFF	VSASTSPW VA	AILPHVISRM	GKLEQVDVNL	FCLVATDFYR
31.01	HOIEEELDRR	AFOSVLEVVA	APGSPYHRLL	TCLRNVHKVT	TC					

Figure S2. Primary sequence coverage maps of Sf9 HTT¹⁻³¹⁴⁴ **Q23.** A) 97% coverage obtained by combining the database search results obtained from 5 enzymes (pepsin, WaLP, MaLP, lysargiNase, and trypsin), and B) 66% coverage obtained from 2 enzymes (lysargiNase and trypsin). NB: table displays HTT Q21 sequence as UniProt database used in sequence search.

A)

1	MATLEKLMKA	FESLKSFQQQ	00000000000	QQQQQQQQPP	PPPPPPPPQ	LPQPPPQAQP	LLPQPQPPPP	PPPPPGPAV	AEEPLHRPK K	ELSATKKDRV
101	NHCLTICENI	VAQSVRNSPE	FQKLLGIAME	LFLLCSDDAE	SDVRMVADEC	LNKVIKALMD	SNLPRLQLEL	YK EIKKNGAP	RSLR AALWRF	AELAHLVRPQ
201	KCRPYLVNLL	PCLTRTSKRP	EESVQETLAA	AVPKIMASFG	NFANDNEIKV	LLK AFIANLK	SSSPTIRRTA	AGSAVSICQH	SRRTQYFYSW	LLNVLLGLLV
301	PVEDEHSTLL	ILGVLLTLRY	LVPLLQQQVK	DTSLK GSFGV	TRKEMEVSPS	AEQLVQVYEL	TLHHTQHQDH	NVVTGALELL	QQLFRTPPPE	LLQTLTAVGG
401	IGQLTAAKEE	SGGRSRSGSI	VELIAGGGSS	CSPVLSR KQK	GK VLLGEEEA	LEDDSESRSD	VSSSALTASV	KDEISGELAA	SSGVSTPGSA	GHDIITEQPR
501	SQHTLQADSV	DLASCDLTSS	ATDGDEEDIL	SHSSSQVSAV	PSDPAMDLND	GTQASSPISD	SSQTTTEGPD	SAVTPSDSSE	IVLDGTDNQY	LGLQIGQPQD
601	EDEEATGILP	DEASEAFRNS	SMALQQAHLL	K NMSHCR QPS	DSSVDKF VLR	DEATEPGDQE	NKPCRIKGDI	GQSTDDDSAP	LVHCVRLLSA	SFLLTGGKNV
701	LVPDR DVRVS	VK ALALSCVG	AAVALHPESF	FSKLYKVPLD	TTEYPEEQYV	SDILNYIDHG	DPQVRGATAI	LCGTLICSIL	SRSRFHVGDW	MGTIRTLTGN
801	TFSLADCIPL	LRKTLKDESS	VTCKLACTAV	RNCVMSLCSS	SYSELGLQLI	IDVLTLRNSS	YWLVR TELLE	TLAEIDFRLV	SFLEAKAENL	HRGAHHYTGL
901	LK LQER VLNN	VVIHLLGDED	PRVRHVAAAS	LIRLVPKLFY	KCDQGQADPV	VAVARDQSSV	YLKLLMHETQ	PPSHFSVSTI	TRIYRGYNLL	PSITDVTMEN
1001	NLSRVIAAVS	HELITSTTRA	LTFGCCEALC	LLSTAFPVCI	SLGWHCGVP	PLSASDESRK	SCTVGMATMI	LTLLSSAWFP	LDLSAHQDAL	ILAGNLLAAS
1101	APKSLRSSWA	SEEEANPAAT	KQEEVWPALG	DRALVPMVEQ	LFSHLLKVIN	ICAHVLDDVA	PGPAIKAALP	SLTNPPSLSP	IRR KGK EKEP	GEQASVPLSP
1201	KKGSEASAAS	RQSDTSGPVT	TSKSSSLGSF	YHLPSYLKLH	DVLKATHANY	KVTLDLQNST	EKFGGFLRSA	LDVLSQILEL	ATLQDIGKCV	EEILGYLKSC
1301	FSREPMMATV	CVQQLLKTLF	GTNLASQFDG	LSSNPSK SQG	RAQR LGSSSV	RPGLYHY CFM	APY THFTQAL	ADASLRNMVQ	AEQENDTSGW	FDVLQKVSTQ
1401	LKTNLTSVTK	NRADK NAIHN	HIRLFEPLVI	K ALK QYTTTT	CAÖTŐKŐATD	LLAQLVQLRV	NYCLLDSDQV	FIGFVLK QFE	YIEVGQFRES	EAIIPNIFFF
1501	LVLLSYERYH	SKQIIGIPKI	IQLCDGIMAS	GRKAVTHAIP	ALQPIVHDLF	VLR GTNKADA	GK eletokev	VVSMLLRLIQ	YHQVLEMFIL	VLQQCHKENE
1601	dk wkrlsr qi	ADIILPMLAK	QQMHIDSHEA	LGVLNTLFEI	LAPSSLRPVD	MLLRSMFVTP	NTMASVSTVQ	LWISGILAIL	RVLISQSTED	IVLSRIQELS
1701	FSPYLISCTV	INRLRDGDST	STLEEHSEGK	QIK NLPEETF	SRFLLQLVGI	LLEDIVTKQL	KVEMSEQQHT	FYCQELGTLL	MCLIHIFKSG	MFR RITAAAT
1801	RLFR SDGCGG	SFYTLDSLNL	RAR SMITTHP	ALVLLWCQIL	LLVNHTDYRW	WAEVQQTPKR	HSLSSTKLLS	POMSGEEEDS	DLAAKLGMCN	REIVRRGALI
1901	LFCDYVCQNL	HDSEHLTW LI	VNHIQDLISL	SHEPPVQDFI	SAVHRNSAAS	GLFIQAIQSR	CENLSTPTML	KKTLQCLEGI	HLSQSGAVLT	LYVDRLLCTP
2001	FRVLAR MVDI	LACRRVEMLL	AANLQSSMAQ	LPMEELNRIQ	EYLQSSGLAQ	RHQRLYSLLD	RFRLSTMQDS	LSPSPPVSSH	PLDGDGHVSL	ETVSPDKDWY
2101	VHLVKSQCWT	RSDSALLEGA	ELVNRIPAED	MNAFMMNSEF	NLSLLAPCLS	LGMSEISGGQ	KSALFEAARE	VTLARVSGTV	QQLPAVHHVF	QPELPAEPAA
2201	YWSKLNDLFG	DAALYQSLPT	LARALAQYLV	VVSKLPSHLH	LPPEKEKDIV	KFVVATLEAL	SWHLIHEQIP	LSLDLQAGLD	CCCLALQLPG	LWSVVSSTEF
2301	VTHACSLIYC	VHFILEAVAV	QPGEQLLSPE	RRTNTPK AIS	EEEEEVDPNT	QNPKYITAAC	EMVAEMVESL	QSVLALGHKR	NSGVPAFLTP	LLRNIIISLA
2401	RLPLVNSYTR	VPPLVWKLGW	SPKPGGDFGT	AFPEIPVEFL	QEK EVFK EFI	YRINTLGWTS	RTOFEETWAT	LLGVLVTQPL	VMEQEESPPE	EDTERTQINV
2501	LAVQAITSLV	LSAM TVPVAG	NPAVSCLEQQ	PRNKPLKALD	TRFGRKLSII	RGIVEQEIQA	MVSKRENIAT	HHLYQAWDPV	PSLSPATTGA	LISHEKLLLQ
2601	INPERELGSM	SYKLGQVSIH	SVWLGNSITP	LREEEWDEEE	EEEADAPAPS	SPPTSPVNSR	KHR AGVDIHS	CSQFLLELYS	RWILPSSSAR	RTPAILISEV
2701	VRSLLVVSDL	FTERNQFELM	YVTLTELRRV	HPSEDEILAQ	YLVPATCKAA	AVLGMDKAVA	EPVSRLLEST	LRSSHLPSRV	GALHGVLYVL	ECDLLDDTAK
2801	QLIPVISDYL	LSNLK GIAHC	VNIHSQQHVL	VMCATAFYLI	ENYPLDVGPE	FSASIIQMCG	VMLSGSEEST	PSIIY HCALR	GLER LLLSEQ	LSRLDAESLV
2901	K LSVDR VNVH	SPHRAMAALG	LMLTC MYTGK	EKVSPGR TSD	PNPAAPDSES	VIVAMERVSV	LFDRIRKGFP	CEARVVARIL	PQFLDDFFPP	QDIMNKVIGE
3001	FLSNQQPYPQ	FMATVVYKVF	QTLHSTGQSS	MVR DWVMLSL	SNFTQR APVA	MATWSLSCF F	VSASTSPWVA	AILPHVISRM	GK leqvdvnl	FCLVATDFYR
3101	HQIEEELDRR	AFQSVLEVVA	APGSPYHRLL	TCLRNVHKVT	TC					

B)

1	MATLEKLMK A	FESLKSFQQQ	00000000000	QQQQQQQQPP	PPPPPPPPQ	LPQPPPQAQP	LLPQPQPPPP	PPPPPPGPAV	AEEPLHRPKK	elsatk kdr v
101	NHCLTICENI	VAQSVRNSPE	FQKLLGIAME	LFLLCSDDAE	SDVRMVADEC	LNK VIK ALMD	SNLPRLQLEL	YK EIKKNGAP	RSLR AALWRF	AELAHLVRPQ
201	K CRPY LVNLL	PCLTRTSKRP	EESVQETLAA	AVPKIMASFG	NFANDNEIKV	LLK AFIANLK	SSSPTIRRTA	AGSAVSICQH	SRRTQYFYSW	LLNVLLGLLV
301	PVEDEHSTLL	$\texttt{ILGVLLTLR} \underline{\textbf{Y}}$	LVPLLQQQVK	DTSLK GSFGV	TRKEMEVSPS	AEQLVQVY EL	TLHHTQHQDH	NVVTGALELL	QQLFRTPPPE	LLQTLTAVGG
401	IGQLTAAKEE	SGGRSRSGSI	VELIAGGGSS	CSPVLSRKQK	GK VLLGEEEA	LEDDSESRSD	VSSSALTASV	KDEISGELAA	SSGVSTPGSA	GHDIITEQPR
501	SQHTLQADSV	DLASCDLTSS	ATDGDEEDIL	SHSSSQVSAV	PSDPAMDLND	GTQASSPISD	SSQTTTEGPD	SAVTPSDSSE	IVLDGTDNQY	LGLQIGQPQD
601	EDEEATGILP	DEASEAFR NS	SMALQQAHLL	KNMSHCRQPS	DSSVDK FVLR	DEATEPGDQE	NKPCRIKGDI	GQSTDDDSAP	LVHCVRLLSA	SFLLTGGK NV
701	LVPDR DVRVS	VK ALALSCVG	AAVALHPESF	FSKLYKVPLD	TTEYPEEQYV	SDILNYIDHG	DPQVR GATAI	LCGTLICSIL	SRSR FHVGDW	MGTIRTLTGN
801	TFSLADCIPL	LRKTLKDESS	VTCKLACTAV	RNCVMSLCSS	SYSELGLQLI	IDVLTLRNSS	YWLVR TELLE	TLAEIDFRLV	SFLEAK AENL	HR GAHHYTGL
901	lk lqer vlnn	VVIHLLGDED	PRVRHVAAAS	LIRLVPKLFY	KCDQGQADPV	VAVARDQSSV	YLK limhetq	PPSHFSVSTI	TRIYRGYNLL	PSITDVTMEN
1001	NLSRVIAAVS	HELITSTTRA	LTFGCCEALC	LLSTAFPVCI	WSLGWHCGVP	PLSASDESRK	SCTVGMATMI	LTLLSSAWFP	LDLSAHQDAL	ILAGNLLAAS
1101	APKSLRSSWA	SEEEANPAAT	KQEEVWPALG	DRALVPMVEQ	LF SHLLK VIN	ICAHVLDDVA	PGPAIKAALP	SLTNPPSLSP	IR RKGK EKEP	GEQASVPLSP
1201	K KGSEASAAS	RQSDTSGPVT	TSKSSSLGSF	YHLPSYLKLH	DVLK ATHANY	KVTLDLQNST	EKFGGFLRSA	LDVLSQILEL	ATLQDIGKCV	EEILGYLKSC
1301	FSREPMMATV	CVQQLLKTLF	GTNLASQFDG	LSSNPSK SQG	RAQR LGSSSV	RPGLYHYCFM	APY THFTQAL	ADASLRNMVQ	AEQENDISGW	FDVLQK VSTQ
1401	LKTNLTSVTK	NRADK NAIHN	HIRLFEPLVI	K ALK QYTTTT	CVQLQKQVLD	LLAQLVQLRV	NYCLLDSDQV	FIGFVLK QFE	YIEVGQFRES	EAIIPNIFFF
1501	LVLLSYERYH	SK qiigipki	IQLCDGIMAS	GRKAVTHAIP	ALQPIVHDLF	VLRGTNKADA	GK ELETQKEV	VVSMLLRLIQ	YHQVLEMFIL	VLQQCHKENE
1601	DKWKRLSR QI	ADIILPMLAK	QQMHIDSHEA	LGVLNTLFEI	LAPSSLRPVD	MLLRSMFVTP	NTMASVSTVQ	LWISGILAIL	RVLISQSTED	IVLSRIQELS
1701	FSPYLISCTV	INR LR DGDST	STLEEHSEGK	QIKNLPEETF	SRFLLQLVGI	LLEDIVTK QL	KVEMSEQQHT	FYCQELGTLL	MCLIHIFKSG	MFRRITAAAT
1801	R LFRSDGCGG	SFY TLDSLNL	RARSMITTHP	ALVLLWCQIL	LLVNHTDYRW	WAEVQQTPKR	HSLSSTK LLS	POMSGEEEDS	DLAAK LGMCN	REIVRRGALI
1901	LFCDYVCQNL	HDSEHLTW LI	VNHIQDLISL	SHEPPVQDFI	SAVHR NSAAS	GLF IQAIQSR	CENLSTPTML	KKTLQCLEGI	HLSQSGAVLT	LYVDRLLCTP
2001	FRVLARMVD1	LACRRVEMLL	AANLQSSMAQ	LPMEELNRIQ	EYLQSSGLAQ	RHQRLYSLLD	RFRLSTMQDS	LSPSPPVSSH	PLDGDGHVSL	ETVSPDKDWY
2101	VHLVKSQCWT	RSDSALLEGA	ELVNRIPAED	MNAFMMNSEF	NLSLLAPC LS	LGMSEISGGQ	KSALFEAARE	VTLARVSGTV	QQLPAVHHVF	QPELPAEPAA
2201	YWSKLNDLFG	DAALYQSLPT	LAR ALAQY LV	VVSKLPSHLH	LPPEKEKDIV	KFVVATLEAL	SWHLIHEQIP	LSLDLQAGLD	CCCLALQLPG	LWSVVSSTEF
2301	VTHACSLIYC	VHF ILEAVAV	QPGEQLLSPE	RRTNTPKAIS	EEEEEVDPNT	QNPKYITAAC	EMVAEMVESL	QSVLALGHKR	NSGVPAFLTP	LLRNIIISLA
2401	RLPLVNSY TR	VPPLVWKLGW	SPKPGGDFGT	AFPEIPVEFL	QEK EVFK EFI	YRINTLGWTS	RTQFEETWAT	LLGVLVTQPL	VMEQEESPPE	EDTERTQINV
2501	LAVQAITSLV	LSAMTVPVAG	NPAVSCLEQQ	PRNKPLK ALD	TRFGRK LSII	RGIVEQEIQA	MVSKRENIAT	HHLYQAWDPV	PSLSPATTGA	LISHEKLLLQ
2601	INPERELGSM	SYKLGQVSIH	SVWLGNSITP	LREEEWDEEE	EEEADAPAPS	SPPTSPVNSR	KHR AGVDIHS	CSQFLLELYS	RWILPSSSAR	RTPAILISEV
2701	VRSLLVVSDL	FTERNQFELM	YVTLTELRRV	HPSEDEILAQ	YLVPATCKAA	AVLGMDKAVA	EPVSRLLEST	LRSSHLPSRV	GALHGVLYVL	ECDLLDDTAK
2801	QLIPVISDYL	LSNLK GIAHC	VNIHSQQHVL	VMCATAFYLI	ENYPLDVGPE	FSASIIQMCG	VMLSGSEEST	PSIIYHCALR	GLER LLLSEQ	LSRLDAESLV
2901	K LSVDR VNVH	SPHRAMAALG	LMLTCMYTGK	EKVSPGRTSD	PNPAAPDSES	VIVAMERVSV	LFDR IRKGFP	CEARVVAR IL	PQFLDDFFPP	QDIMNK VIGE
3001	FLSNQQPYPQ	FMATVVYKVF	QTLHSTGQSS	MVRDWVMLSL	SNFTQRAPVA	MATWSLSCFF	VSASTSPW VA	AILPHVISRM	GK leqvdvnl	FCLVATDFYR
3101	HQIEEELDRR	AFQSVLEVVA	APGSPYHRLL	TCLRNVHKVT	TC					

Figure S3. Primary sequence coverage maps of EXPI293F HTT¹⁻³¹⁴⁴ Q23 digested with trypsin. A) 77% coverage obtained from solution, and B) 62% coverage from a gel band. NB: table displays HTT Q21 sequence as UniProt database used in sequence search.



Figure S4. Exemplary spectra of pepsin digested HTT¹⁻³¹⁴⁴ Q23 from Sf9. Full data can be found through PRIDE (2) with accession PXD010865.



Figure S4 continued.



Figure S5. Exemplary spectra of trypsin or lysargiNase digested HTT¹⁻³¹⁴⁴ Q23 from Sf9. Full data can be found through PRIDE (2) with accession PXD010865.





Figure S5 continued.









Figure S5 continued.



Figure S6. Exemplary spectra of trypsin digested HTT¹⁻³¹⁴⁴ Q23 from EXPI293F.

Full data can be found through PRIDE (2) with accession PXD010865.



Figure S6 continued.



Figure S6 continued.



Figure S6 continued.









Figure S7. Mapping HTT posttranslational modifications identified from HTT¹⁻³¹⁴⁴ samples from Sf9 and EXPI293F cells onto the HTT structure.

HTT is viewed top-down looking through the void in the N-terminal HEAT domain on the right hand side. Phosphorylation sites are shown in pink and all other modification sites are shown in green. As these samples were expressed in the absence of the stabilising HAP40 protein, it is likely that the more conformationally flexible apo HTT protein molecule would have greater exposure of different domain surfaces that would permit more sites to be modified than might be estimated from assessing the HTT-HAP40 molecule.

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