

Experimental design proforma.

Construction and use of expression vector pFXN-AcGFP1-N1 encoding Frataxin with C-terminal GFP fusion

**Part 1. Design gene specific part of the forward and reverse primers to amplify the coding region of human frataxin, isoform 1 preproprotein for use to create C-terminal fusion with GFP (10 marks)**

Figure 1. Part of the DNA sequence of human frataxin, isoform 1 preproprotein cDNA insert in pOTB7 (IMAGE:4842134) translated using EMBL EBI EMBOSS Sixpack programme to show the three forward open reading frames from nucleotide 1 to 720. The frataxin preproprotein amino acid sequence is highlighted yellow, the DNA sequence of the gene specific part of the forward primer is highlighted in red, the DNA sequence of the gene specific part of the reverse primer is highlighted in pink.

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1  gcggagcggggcggcagacccggagcagc atgtggactctcggggcggcgccac tagccgg 60
   ----:----|----:----|----:----|----:----|----:----|----:----|
1  cgctcgcggcgccgtctgtggcctcgctcgtagacacctgagagcccgcgcgcgctcatcggcc 60
   A E R A A D P E Q H V D S R A P R S S R F1
   R S G R Q T R S S M W T L G R R A V A G F2
   G A G G R P G A A C G L S G A A Q * P A F3

61  cctcctggcggtcacccagcccgccaggcccgagccctcacccgggtcccgcgccggc 120
   ----:----|----:----|----:----|----:----|----:----|----:----|
61  ggaggaccgcagtggtcgggcgggtccgggtctgggagtgggcccgccggcgccggc 120
   P P G V T Q P G P G P D P H P G P A A G F1
   L L A S P S P A Q A Q T L T R V P R P A F2
   S W R H P A R P R P R P S P G S R G R Q F3

121 agagttggccccactctgcggcccgcggtggcctgcgcaccgacatcgatgcgacctgcac 180
   ----:----|----:----|----:----|----:----|----:----|----:----|
121 tctcaaccggggtgagacgcggcgccgacccggacgcgtggctgtagctacgctggacgtg 180
   R V G P T L R P P W P A H R H R C D L H F1
   E L A P L C G R R G L R T D I D A T C T F2
   S W P H S A A A V A C A P T S M R P A R F3

181 gccccgcccgcgaagttcgaaccaacgtggcctcaaccagatttggaatgtcaaaaagca 240
   ----:----|----:----|----:----|----:----|----:----|----:----|
181 cggggcgggcgcggttcaagcttggtgcaccggagttggtctaaaccttacagtttttcgt 240
   A P P R K F E P T W P Q P D L E C Q K A F1
   P R R A S S N Q R G L N Q I W N V K K Q F2
   P A A Q V R T N V A S T R F G M S K S R F3

241 gagtgtctatttgatgaatttgaggaaatctggaactttgggccaccaggctctctaga 300
   ----:----|----:----|----:----|----:----|----:----|----:----|
241 ctcacagataaactacttaaaactccttagaccttgaaacccggtgggtccgagagatct 300
   E C L F D E F E E I W N F G P P R L S R F1
   S V Y L M N L R K S G T L G H P G S L D F2
   V S I * * I * G N L E L W A T Q A L * M F3
  
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301 tgagaccacctatgaaagactagcagaggaaacgctggactccttagcagagtttttga 360  
 ----:----|----:----|----:----|----:----|----:----|----:----|  
 301 actctgggtgatacttttctgatcgtctcctttgacgtgagaaatcgtctcaaaaaact 360  
 \* D H L \* K T S R G N A G L F S R V F \* F1  
 E T T Y E R L A E E T L D S L A E F F E F2  
 R P P M K D \* Q R K R W T L \* Q S F L K F3

361 agaccttgacagacaagccatacacgctttgaggactatgatgtctcctttgggagtgggtg 420  
 ----:----|----:----|----:----|----:----|----:----|----:----|  
 361 tctggaacgtctgttcggtatgtgcaaactcctgatactacagaggaaaccctcaccaca 420  
 R P C R Q A I H V \* G L \* C L L W E W C F1  
 D L A D K P Y T F E D Y D V S F G S G V F2  
 T L Q T S H T R L R T M M S P L G V V S F3

421 cttaactgtcaaactgggtggagatctaggaacctatgtgatcaacaagcagacgcaaaa 480  
 ----:----|----:----|----:----|----:----|----:----|----:----|  
 421 gaattgacagtttgacccacctctagatccttggatacactagtgttcgtctgcggttt 480  
 L N C Q T G W R S R N L C D Q Q A D A K F1  
 L T V K L G G D L G T Y V I N K Q T P N F2  
 \* L S N W V E I \* E P M \* S T S R R Q T F3

481 caagcaaactctggctatcttctccatccagtggacctaagcgttatgactggactgggaa 540  
 ----:----|----:----|----:----|----:----|----:----|----:----|  
 481 gttcgttttagaccgatagaagaggttaggtcacctggattcgcaatactgacctgaccctt 540  
 Q A N L A I F S I Q W T \* A L \* L D W E F1  
 K Q I W L S S P S S G P K R Y D W T G K F2  
 S K S G Y L L H P V D L S V M T G L G K F3

541 aaactgggtgtactcccacgacggcgtgtccctccatgagctgctggccgcagagctcac 600  
 ----:----|----:----|----:----|----:----|----:----|----:----|  
 541 tttagccacatgaggggtgctgccgcacagggaggtactcgacgaccggcgtctcgagt 600  
 K L G V L P R R R V P P \* A A G R R A H F1  
 N W V Y S H D G V S L H E L L A A E L T F2  
 T G C T P T T A C P S M S C W P Q S S L F3

601 taaagccttaaaaaaccaaactggacttgtcttctccttggcctattccgaaaagatgcttg 660  
 ----:----|----:----|----:----|----:----|----:----|----:----|  
 601 atttcggaatttttggtttgacctgaaacagaaggaaccggataaggcctttttctacga 660  
 \* S L K N Q T G L V F L G L F R K R C L F1  
 K A L K T K L D L S S L A Y S G K D A \* F2  
 K P \* K P N W T C L P W P I P E K M L D F3

661 atgccagccccgttttaaggacattaaaagctatcaggccaagaccccagcttcattat 720  
 ----:----|----:----|----:----|----:----|----:----|----:----|  
 661 tacgggtcggggcaaaaattcctgtaattttcgtatgctcgggttctggggtcgaagtaata 720  
 M P S P V L R T L K A I R P R P Q L H Y F1  
 C P A P F \* G H \* K L S G Q D P S F I M F2  
 A Q P R F K D I K S Y Q A K T P A S L C F3

**Table 1. Frataxin gene specific DNA sequences of forward and reverse primers and Tm values**

	DNA sequence	Tm
<b>Forward Primer</b>	atgtggactctcgggcgcgcgcag	67.5°C
<b>Reverse Primer</b>	agcatctttccggaataggccaaggaagac	63°C

**Table 2. Predicted size of PCR product using gene specific forward and reverse primers from Table 1**

Predicted size of DNA fragment	630 bp
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**Table 3. PCR cycling parameters**

Segment	Number of cycles	Temperature	Duration
1	1	95°C	2 minutes
2	30	95°C	20 seconds
		58°C	20 seconds
		72°C	15 seconds
3	1	72°C	3 minutes

**Part 2. Sub-cloning the human frataxin preproprotein gene in-frame with N-terminus of the green fluorescent protein in pAcGFP1-N1 to create a plasmid called pFXN-AcGFP1-N1 (30 marks)**

**Table 4. Choosing restriction enzymes to directionally sub-clone human frataxin preproprotein gene into pAcGFP1-N1**

Promega Restriction Enzyme	Recognition sequence	Recognition sequence in pAcGFP1-N1 MCS (yes/no)	Recognition sequence in frataxin preproprotein coding sequence (yes/no)	Promega buffers (100% activity)
<i>AgeI</i>	A↓CCGGT	Yes	No	K, Multicore
<i>Apal</i>	GGGCC↓C	Yes	No	A
<i>BamHI</i>	G↓GATCC	Yes	No	E
<i>BglII</i>	A↓GATCT	Yes	Yes	D
<i>EcoRI</i>	G↓AATTC	Yes	No	H
<i>HindIII</i>	A↓AGCTT	Yes	No	B, E
<i>KpnI</i>	GGTAC↓C	Yes	No	J
<i>NheI</i>	G↓CTAGC	Yes	No	B, Multicore
<i>PstI</i>	CTGCA↓G	Yes	No	H
<i>SacI</i>	GAGCT↓C	Yes	Yes	E, Multicore, J
<i>SacII</i>	CCGC↓GG	Yes	Yes	A, H, C
<i>SmaI</i>	CCC↓GGG	Yes	Yes	Multicore, J
<i>XhoI</i>	C↓TCGAG	Yes	No	H, D

**Table 5. Possible pairs of restriction enzymes that can added to the forward and reverse PCR primers to sub-clone clone human frataxin preproprotein gene into pAcGFP1-N1**

	Restriction enzyme forward primer	Restriction enzyme reverse primer	Optimum buffer for 100% activity
<b>1</b>	<i>XhoI</i>	<i>PstI</i>	H
<b>2</b>	<i>NheI</i>	<i>AgeI</i>	Multicore
<b>3</b>	<i>HindIII</i>	<i>BamHI</i>	E
<b>4</b>	<i>NheI</i>	<i>HindIII</i>	B
<b>5</b>	<i>XhoI</i>	<i>EcoRI</i>	H

Table 6. Full DNA sequences of final forward and reverse primers (frataxin specific sequence highlighted yellow, *Xho*I recognition sequence highlighted red, *Pst*I recognition sequence highlighted pink, other additional nucleotides highlighted blue).

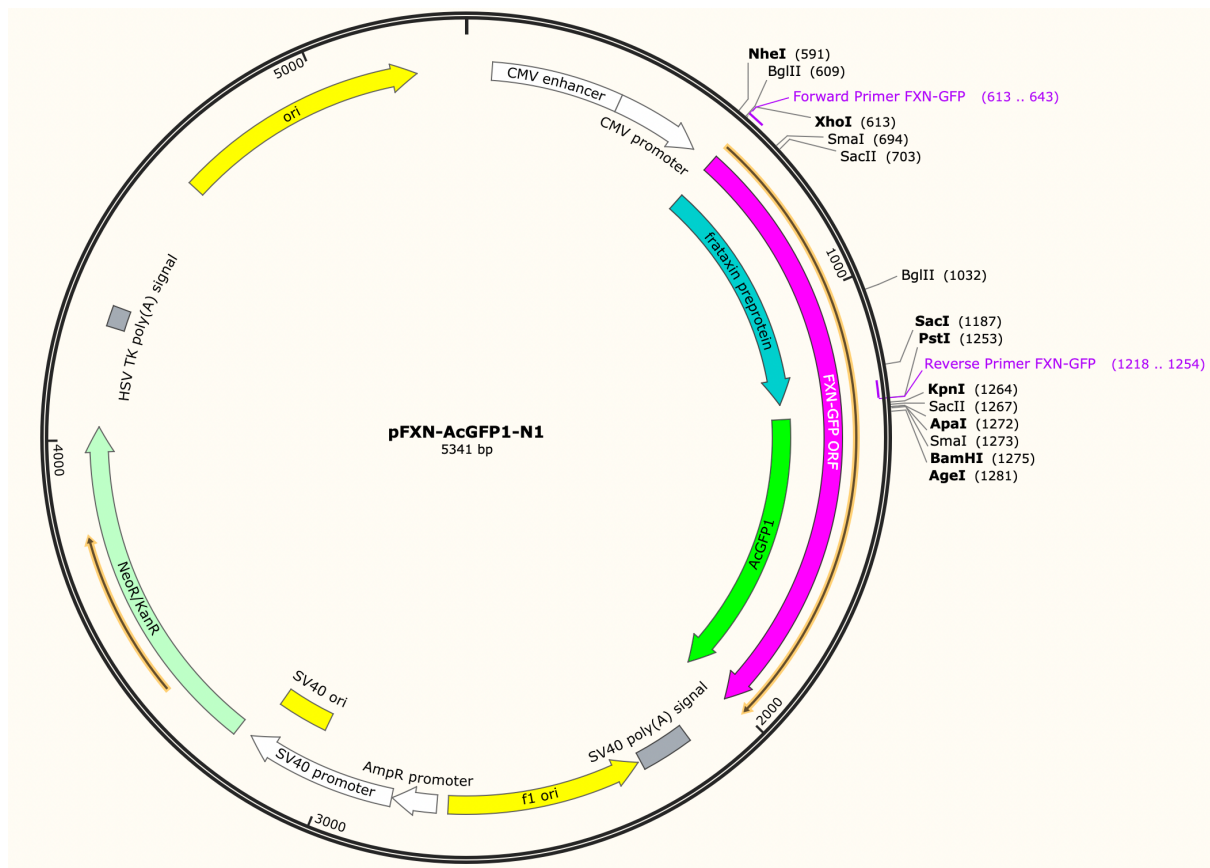
	DNA sequence
Forward Primer	gggctcgagatgtggactctcgggcgccgcgcag
Reverse Primer	gggctgcagagcatctttccggaataggccaaggaagac

**Figure 2. DNA sequence of pFXN-AcGFP1-N1 (frataxin specific sequence highlighted yellow, AcGFP1-N1 sequence highlighted green, XhoI recognition sequence highlighted red, PstI recognition sequence highlighted pink).**

TAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACAT  
 AACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCGCCATTGACGTCAATAATGAC  
 GTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTACGGTAA  
 ACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACG  
 GTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCTACTTGGCAGTACATC  
 TACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGC  
 GGTTTGACTCACGGGGATTCCAAGTCTCACCCCATTTGACGTCAATGGGAGTTTGTGGTGGACCA  
 AAATCAACGGGACTTTCCAAAATGTCGTAACAACCTCCGCCCATTTGACGCAAATGGGCGGTAGGCGT  
 GTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCGCTACCGG  
 ACTCAGATCTCGAGatgtggactctcgggcccgcgcgtagccggcctcctggcgtcaccagcccggcccaggcccagac  
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 cccgcgcgcaagttcgaaccaacgtggcctcaaccagatttggaatgtcaaaaagcagagtgtctatttgatgaatttgaggaaat  
 ctggaactttgggccaccaggctctctagatgagaccacctatgaaagactagcagaggaaacgtggactcttagcagagtttt  
 ttgaagaccttgagacaagccatacacgtttgaggactatgatgtctccttgggagtggtgtcttaactgtcaaactgggtggaga  
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 TGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCTGTGCCCTGGCCACCTGGTGACCACCT  
 GAGCTACGGCGTGAGTGCTTCTCACGCTACCCCGATCACATGAAGCAGCAGACTTCTTCAAGAGC  
 GCCATGCCTGAGGGCTACATCCAGGAGCGCACCATCTTCTCGAGGATGACGGCAACTACAAGTCG  
 CGCGCCGAGGTGAAGTTCGAGGGCGATACCCTGGTGAATCGCATCGAGCTGACCGGCACCGATTTC  
 AAGGAGGATGGCAACATCCTGGGCAATAAGATGGAGTACAACGCCCACAATGTGTACATC  
 ATGACCGACAAGGCCAAGAATGGCATCAAGGTGAACTTCAAGATCCGCCACAACATCGAGGATGGC  
 AGCGTGAGCTGGCCGACCACTACCAGCAGAATACCCCATCGGCGATGGCCCTGTGCTGCTGCC  
 GATAACCACTACCTGTCCACCCAGAGCGCCCTGTCCAAGGACCCCAACGAGAAGCGCGATCACATG  
 ATCTACTTCGGCTTCGTGACCGCCGCCCATCACCCACGGCATGGATGAGCTGTACAAGTGAGCGG  
 CCGCGACTCTAGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCC  
 ACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTT  
 ATAATGGTTACAAATAAAGCAATAGCATCACAAATTCACAAATAAAGCATTTTTTCACTGCATTCT  
 AGTTGTGGTTTGTCCAACTCATCAATGTATCTTAAGGCGTAAATTGTAAGCGTTAATATTTTGTTAA  
 AATTCGCGTTAAATTTTTGTAAATCAGCTATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTT  
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 AAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGA  
 ACCATCACCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCTAAAGGG  
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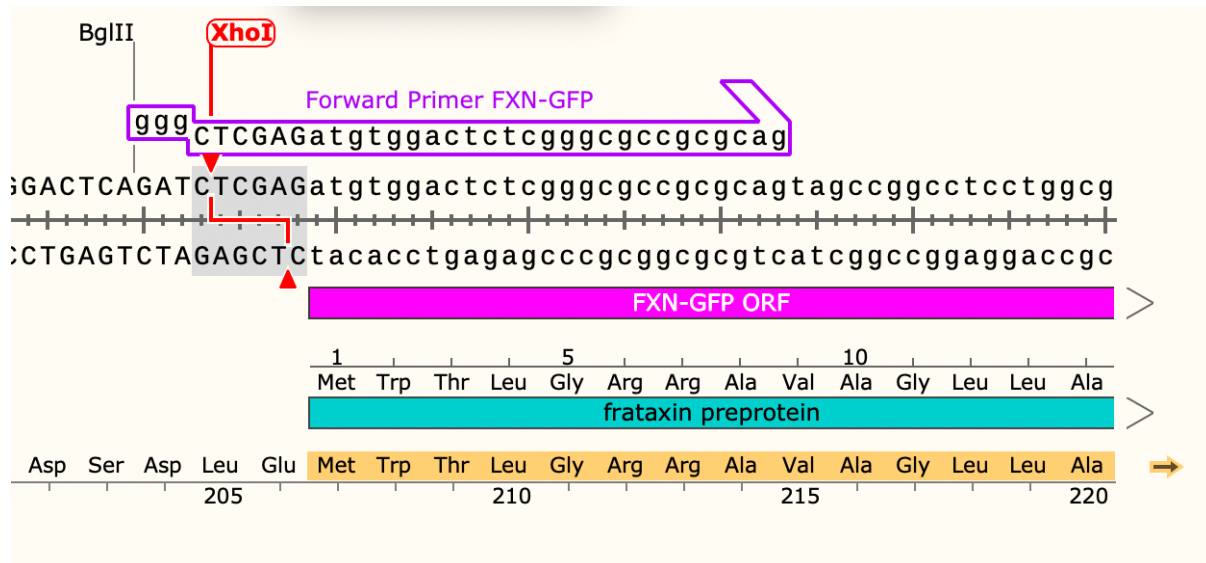
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CCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATG  
CTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGT  
TAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAAGTATGCAAAGCATGCATCTCAATTAGT  
CAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAAGTATGCAAAGCATGCATCTCA  
ATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCC  
CATTCTCCGCCCCATGGCTGACTAATTTTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGA  
GCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAGA  
CAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGG  
TGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCC  
GGCTGTCAGCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACT  
GCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGA  
CGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTC  
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GTTCCGCCAGGCTCAAGGCGAGCATGCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTG  
CTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTG  
GCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGG  
GCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGCAGCGCATCGCCTTCTATCGCT  
TCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCAACCTGC  
CATCACGAGATTCGATTCCACCGCCGCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGA  
CGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCACCCTAGGGGGAG  
GCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGAC  
AGAATAAAACGCACGGTGTTGGGTGCTTTGTTTCATAAACGCGGGGTTTCGGTCCAGGGCTGGCACT  
CTGTCGATACCCACCGAGACCCATTGGGGCCAATACGCCGCGTTTCTTCTTTTCCCCACCCAC  
CCCCAAGTTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGC  
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CTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAAGTGGCTGCTGCCA  
GTGGCGATAAGTCGTGCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGT  
CGGGCTGAACGGGGGGTTCGTGCACACAGCCAGCTTGAGCGAACGACCTACACCGAACTGAGA  
TACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCC  
GGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTAT  
CTTTATAGTCCTGTGCGGTTTTGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGG  
GCGGAGCCTATGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTT  
GCTCACATGTTCTTCTCGCTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT

**Figure 3. Plasmid map of pFXN-AcGFP1-N1 taken from SnapGene.**





**Figure 4. Nucleotide and amino acid sequence showing the start of the FXN-GFP open reading frame and the junction between frataxin preproprotein and pFXN-AcGFP1-N1 taken from SnapGene.**



**Figure 5. Nucleotide and amino acid sequence showing the junction between C terminal amino acids of frataxin preproprotein and the N-terminal amino acids of green fluorescent protein in pFXN-AcGFP1-N1 taken from SnapGene.**

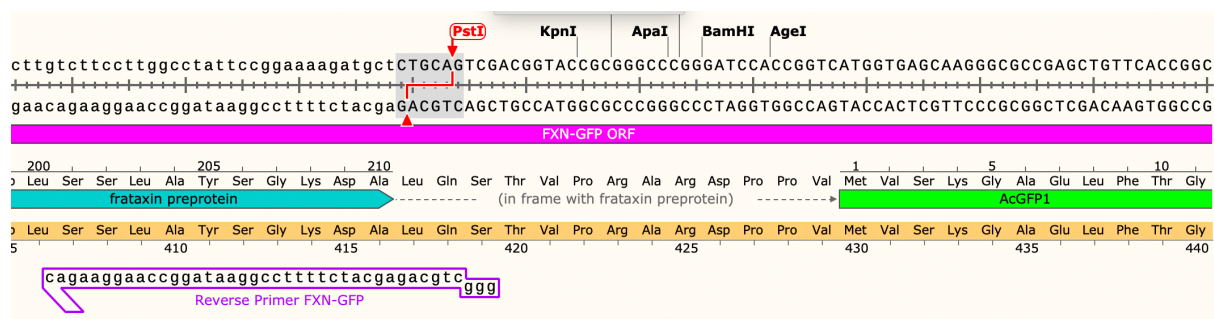
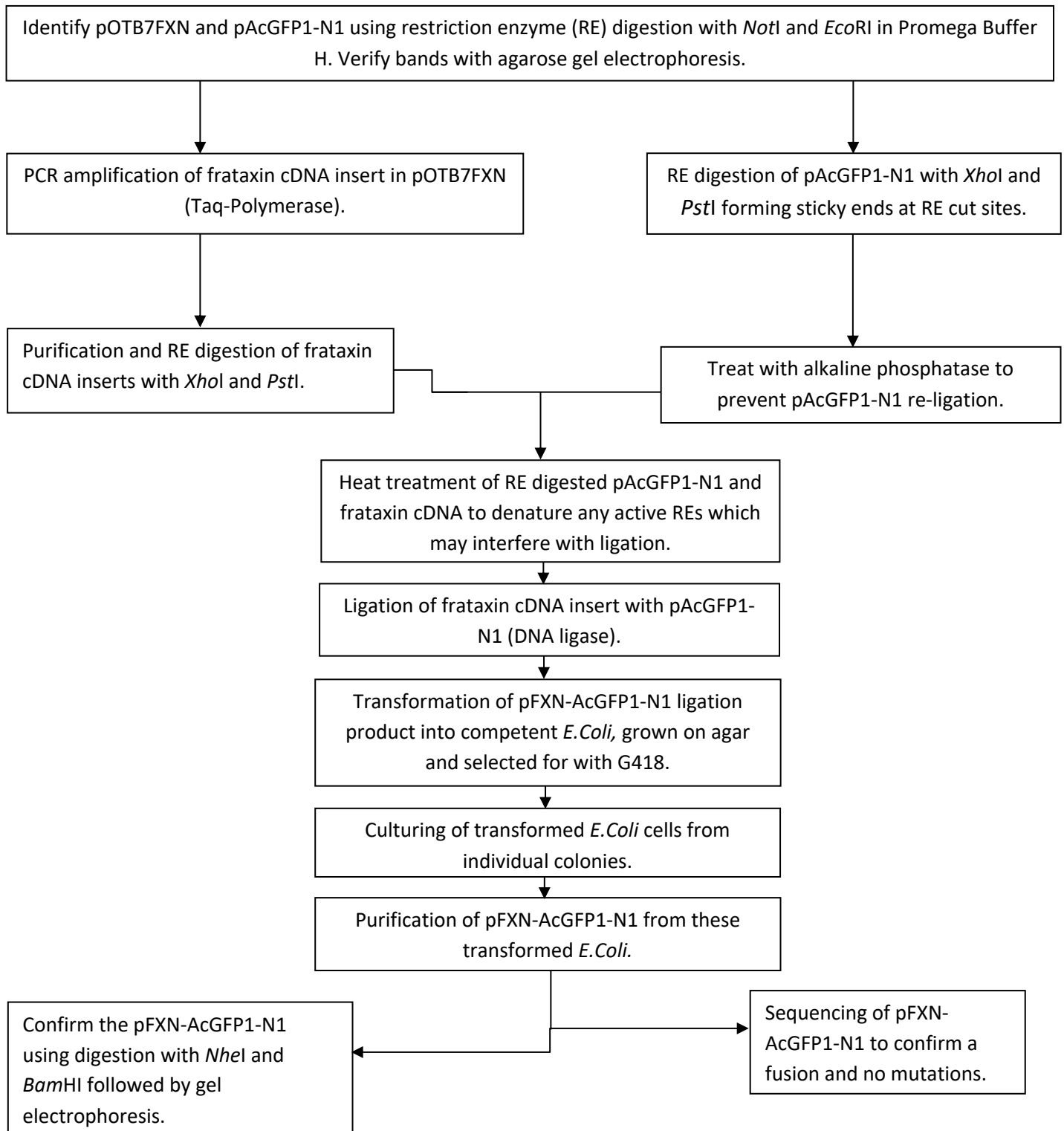


Figure 6. The full amino acid sequence of the FXN-GFP open reading frame from SnapGene pFXN-AcGFP1-N1 with frataxin preproprotein amino acids highlighted yellow, GFP amino acids highlighted green, and any other additional amino acids highlighted blue).

MWTLGRRVAGLLASPSAQAQTLTRVPRPAELAPLCGRRGLRTDIDATCTPRRASSNQRGLNQIW  
 NVKKQSVYLMNLRKSGTLGHPGSLDETTYERLAEETLDSLAEFFEDLADKPYTFEDYDVSFGSGVLTVKL  
 GDLGTYVINKQTPNKQIWLSSPSSGPKRYDWTGKNWVYSHDGVSLHELLAAELTKALKTKLDLSSLA  
 YSGKDALQSTVPRARDPPV MVSKGAELFTGIVPILIELNGDVNGHKFSVSGEGEGDATYGKLTCLKFICTT  
 GKLPVPWPTLVTTLSYGVQCFSRYPDHMKQHDFKFSAMPEGYIQERTIFFEDDGNYKSRAEVKFEGDT  
 LVNRIELTGDFKEDGNILGNKMEYNNAHNVYIMTDKAKNGIKVNFKIRHNIEDGSVQLADHYQQN  
 TPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMIYFGFVTAATHGMDELYK\*

**Part 3. Experimental steps required to construct pFXN-AcGFP1-N1 using standard molecular biology techniques (20 marks)**

**Figure 6. Flow diagram showing experimental steps required to construct pFXN-AcGFP1-N1**



Words: 149

**Part 4. In vivo experimental design. Transfection of pFXN-AcGFP1-N1 into HeLa tissue culture cells. (40 marks)**

In this experiment we will be transfecting a pFXN-AcGFP-N1 plasmid into human HeLa tissue cells (grown in tissue culture medium and maintained in EMEM buffer) to study the intracellular location of frataxin [ATCC, 2021]. Transfection can be non-viral: chemical techniques are lipid-mediated or calcium phosphate co-precipitation, but physical techniques involve electroporation neon transfection systems which we will use in-vivo to introduce 1-5ug of pFXN-AcGFP-N1 DNA into our  $10^6$  HeLa cell sample [ThermoFisher, 2021].

We first trypsinise and harvest our HeLa cells by centrifugation, ready to be measured out in 0.5ml aliquots, suspended in conductive electroporation buffer and mixed with pFXN-AcGFP-N1 in cuvettes on ice. After 5 minutes incubation, electrical pulses (pulse width is determined by capacitance and must maintain 40-80% survival of cells) produce voltage which develop temporary pores in the HeLa cell's phospholipid bilayer: passages to insert our DNA using an electronic pipette tip. The transfected cells are selected for in a medium with G418 as the pFXN-AcGFP-N1 CMV promotor regulates the neomycin resistance gene; successful colonies are then re-cultured at 37°C incubation for 50-60 hours for transient expression [ThermoFisher, 2016][Damdindorj *et al.*, 2014][Potter and Heller, 2003].

Since pAcGFP-N1 is an N-terminal specification, the GFP coding sequence is outside the MCF and the Frataxin-GFP fusion protein produced by pFXN-AcGFP-N1 has GFP at its C-terminal. Fluorescence microscopy under UV at 475nm can be used to observe GFP emission at 505nm and localise Frataxin-GFP produced constitutively (via the CMV promotor) by transfected HeLa cells [Damdindorj *et al.*, 2014][Takarabio, 2022]. The intracellular location of FXN-GFP will be regulated by the frataxin as it is the N-terminal component where signal peptides are located [Palmer and Freeman, 2004]. Based on frataxin studies, the location of fluorescence is expected to be in the mitochondrial protein and iron-sulphur clusters due to its proposed function as an iron chaperone [Adinolfi *et al.*, 2009].

We could further study the relationship between reduced frataxin expression and Friedrich's Ataxia, the effect of various drugs on frataxin concentration in-vivo or changes in extra-mitochondrial frataxin localisation during differentiation: e.g., in enterocyte-like Caco-2 cells [Acquaviva *et al.*, 2005]. For long term studies we can create a stable HeLa cell line by passaging the cells over weeks or months of selection for a colony with the plasmid DNA construct integrated into a chromosome. Transfection can also be used for RNAi studies controlling gene expression with siRNA to treat genetic diseases [Kim and Eberwine, 2010].

Words: 400

## References

Acquaviva, F., De Biase, I., Nezi, L., Ruggiero, G., Tatangelo, F., Pisano, C., Monticelli, A., Garbi, C., Acquaviva, A. M., & Coccozza, S. (2005). Extra-mitochondrial localisation of frataxin and its association with IscU1 during enterocyte-like differentiation of the human colon adenocarcinoma cell line Caco-2. *Journal of cell science*, 118(Pt 17), 3917–3924.

<https://doi.org/10.1242/jcs.02516>

Adinolfi, S., Iannuzzi, C., Prischi, F., Pastore, C., Iametti, S., Martin, S. R., Bonomi, F., & Pastore, A. (2009). Bacterial frataxin CyaY is the gatekeeper of iron-sulfur cluster formation catalyzed by IscS. *Nature structural & molecular biology*, 16(4), 390–396.

<https://doi.org/10.1038/nsmb.1579>

ATCC. (2022). *Product References*. Retrieved from atcc.org:

<https://www.atcc.org/products/ccl-2#product-references>

Damdindorj, L., Karnan, S., Ota, A., Hossain, E., Konishi, Y., Hosokawa, Y., & Konishi, H. (2014). A comparative analysis of constitutive promoters located in adeno-associated viral vectors. *PloS one*, 9(8), e106472. <https://doi.org/10.1371/journal.pone.0106472>

Kim, T. K., & Eberwine, J. H. (2010). Mammalian cell transfection: the present and the future. *Analytical and bioanalytical chemistry*, 397(8), 3173–3178.

<https://doi.org/10.1007/s00216-010-3821-6>

Palmer, E., & Freeman, T. (2004). Investigation into the use of C- and N-terminal GFP fusion proteins for subcellular localization studies using reverse transfection microarrays. *Comparative and functional genomics*, 5(4), 342–353.

<https://doi.org/10.1002/cfg.405>

Potter H. and Heller R. (2003). Transfection by electroporation. *Current protocols in molecular biology*, Chapter 9, Unit–9.3. <https://doi.org/10.1002/0471142727.mb0903s62>

Takarabio. (2022). Protein plasmid products and green fluorescent proteins. Retrieved from Takarabio.com: <https://www.takarabio.com/products/gene-function/fluorescent-proteins/fluorescent-protein-plasmids/cyan-and-green-fluorescent-proteins/acgfp1-fluorescent-protein?catalog=632469>

ThermoFisher. (2016). *Cell culture basics handbook*. Retrieved from thermoFisher.com: <https://www.thermoFisher.com/content/dam/LifeTech/Documents/PDFs/PG1563-PJT1267-COL31122-Gibco-Cell-Culture-Basics-Handbook-Global-FLR.pdf>

ThermoFisher. (2021). *Guidelines for plasmid DNA transfection*. Retrieved from thermoFisher.com: <https://www.thermoFisher.com/uk/en/home/references/gibco-cell-culture-basics/transfection-basics/guidelines-for-plasmid-dna-transfection/optimizing-plasmid-dna-transfection.html>