

YMTHE, Volume 27

Supplemental Information

Engineered DNA Vaccination against

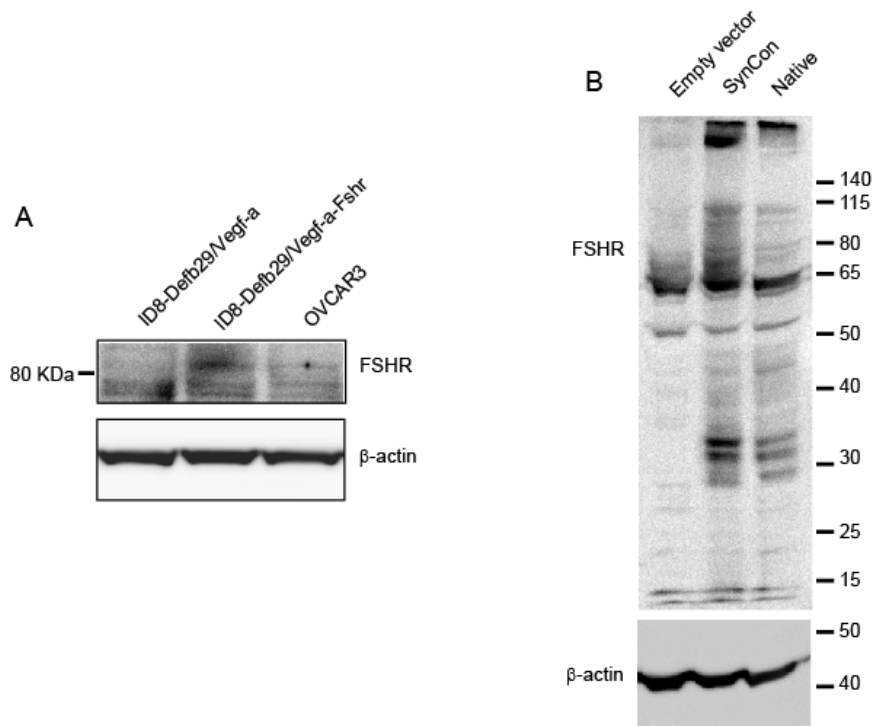
Follicle-Stimulating Hormone Receptor Delays

Ovarian Cancer Progression in Animal Models

Alfredo Perales-Puchalt, Krzysztof Wojtak, Elizabeth K. Duperret, Xue Yang, Anna M. Slager, Jian Yan, Kar Muthumani, Luis J. Montaner, and David B. Weiner

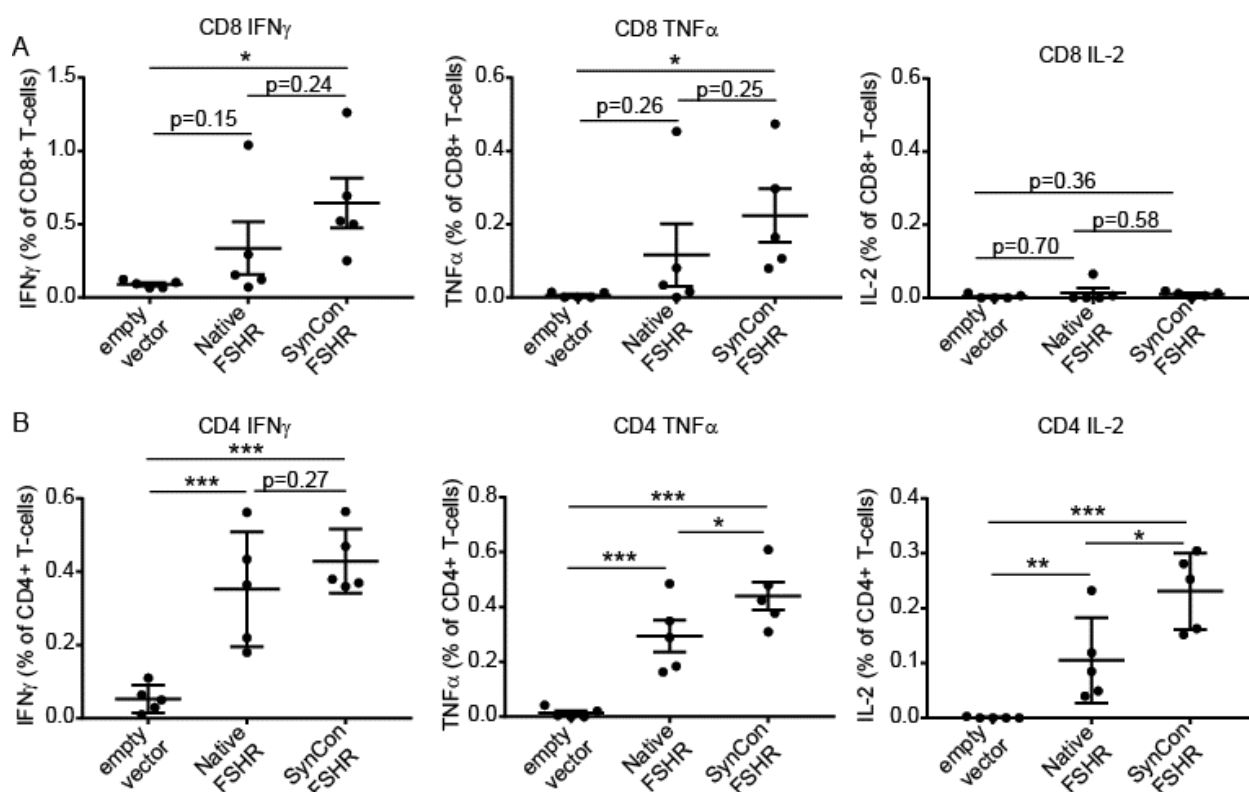
SUPPLEMENTAL FIGURES

SUPPLEMENTAL FIGURE 1



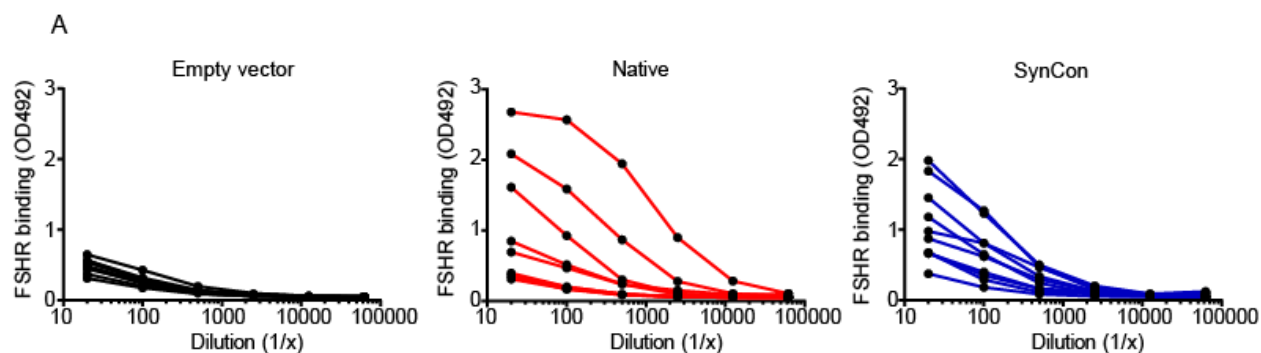
Supplemental Figure 1. Expression of SynCon and native FSHR vaccines. Western blot of protein derived from (A) OVCAR3, ID8-Defb29/Vegf-a-Fshr and ID8-Defb29/Vegf-a and (B) murine FSHR SynCon vaccine, murine native FSHR vaccine or empty vector transfected 293T cells (10% gel MOPS buffer) blotted for FSHR and β -actin (representative of 2 experiments)

SUPPLEMENTAL FIGURE 2



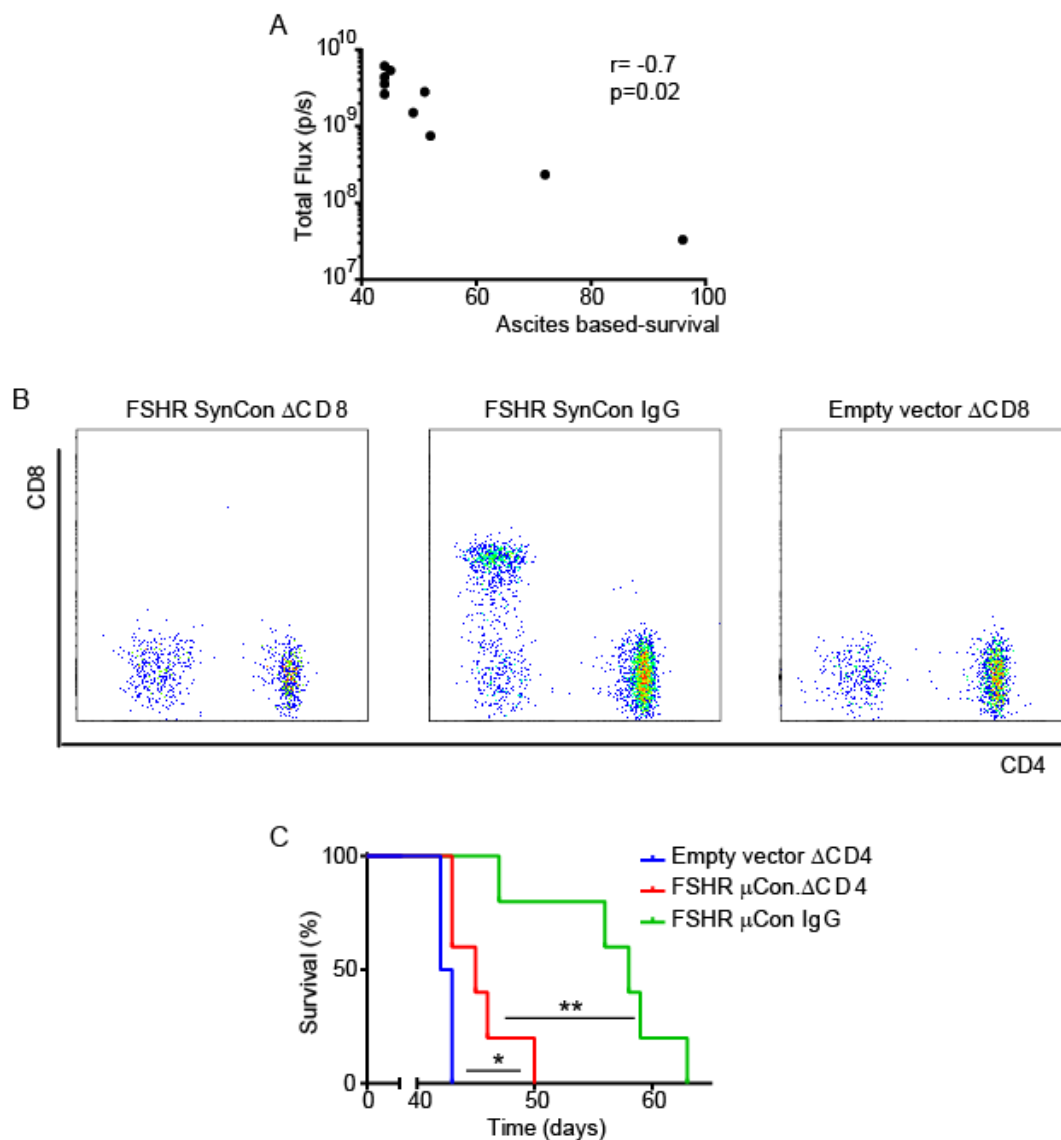
Supplemental Figure 2. Mouse FSHR DNA vaccine generates strong CD8 and CD4 responses when pulsed with vaccine matched peptides. Percentage of IFN γ , TNF α and IL-2 produced by (A) CD8+ or (B) CD4+ T cells from the spleen of mice immunized with FSHR SynCon vaccine, FSHR native vaccine or empty vector stimulated with consensus vaccine matched peptides. ANOVA. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

SUPPLEMENTAL FIGURE 3



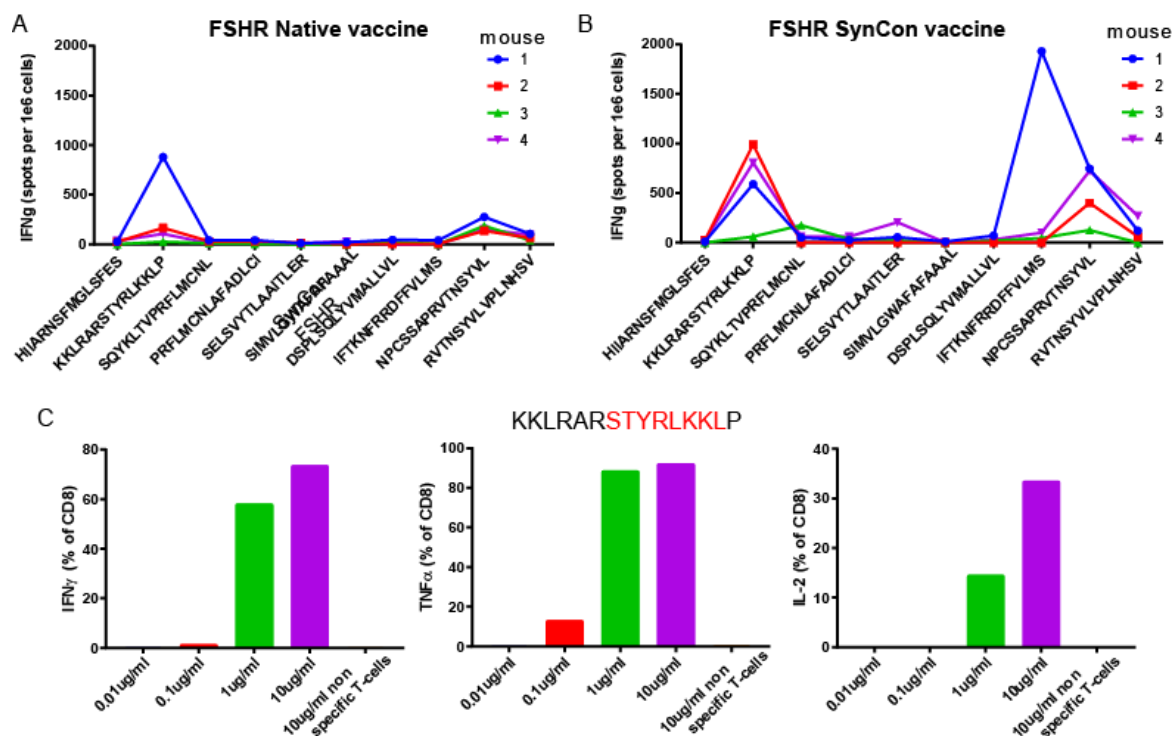
Supplemental Figure 3. Mouse FSHR DNA vaccine generates antibodies against FSHR. (A) Binding of sera from mice vaccinated with FSHR vaccine, native FSHR or pVAX empty vector to the extracellular domain of native murine FSHR in a binding ELISA. Each curve represents one mouse.

SUPPLEMENTAL FIGURE 4



Supplemental Figure 4. CD8 and CD8 depletion experiment. (A) Correlation between luciferase expression and ascites-based survival in luciferase transfected ID8-*Defb29/Vegf-a-Fshr* tumor challenge. **(B)** We vaccinated mice and challenged with ID8-*Defb29/Vegf-a-Fshr* one week after the last immunization. One day prior to the tumor challenge and twice weekly thereafter we administered either anti-mouse CD8 or rat polyclonal IgG. Flow plots showing CD4⁺ and CD8⁺ T cells in the tumor microenvironment of the different groups at day 21 after tumor inoculation. **(C)** Survival plot of the FSHR SynCon vaccine or pVAX empty vector with or without CD8 depletion (n=5 mice per group). Pearson correlation, Log-rank. *p<0.05, **p<0.01

SUPPLEMENTAL FIGURE 5



Supplemental Figure 5. Murine FSHR SynCon vaccine increases the number and intensity of immunogenic sequences of FSHR. (A&B) IFN γ ELISpot of splenocytes from mice immunized with murine FSHR SynCon vaccine, native FSHR vaccine or empty vector pulsed with FSHR derived peptides predicted to bind with high affinity to H2-K(b) or H2-D (b) (n=4 mice per group). (C) Percentage of IFN γ , TNF α and IL-2 produced by CD8⁺ T cells expanded from mice immunized with murine FSHR SynCon vaccine expanded with KKLRRARSTYRLKKLP peptides and stimulated with the same peptides at different doses.

SUPPLEMENTAL FIGURE 6

A IEDB Analysis Resource

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MHC-I Binding Prediction Results

Input Sequences

#	Name	Sequence
1	sp P35378 FSHR_MOUSE Follicle-stimulating hormone receptor DE=Mus musculus CX-10090 GN=Fshr FE-2 SV-2	MALLLVSLAFLGSGSGCHHLLCHSNRVFLCODSKVTEIPDLPRIVAIE LRFVLTSLRVIPKGFSGCTDLEKICISQNDVLCVICADVSNLPNLIICI RIEKANNLLYINPEAFQNLPSLRVLLISATGIRKLPAPFKIQSLQKVLLD IQDRIINIHIIARNSFMGLSFESVILWLNKNGIQEIHCAFNGTQLDELNL SDNNI FFI PNDVFGAGSGPVVITPSTKVVYSPIHKKI RARSTY RLKXKLSLDKFWLIEASLTVPSHCCAFANIRQTSLELHPICIKSIESRD IDDMTPGDQFVSLVDDEPSYKSGDMLYSEGDYDLNCFVDVTCSPK AFNPCCDINGVILRVLIWFSILAITGNTTVLWLTTSQYKLTVPRLM CNLAFADLCIGIYLLIASVDIHTKSCVHVAIDMQTGAGCDAAGFFTVF ASFI SVYTI AATTI FRMHTTTHAQI FCKVQI CHAASTPM GWAFAPAAA LFPZFGISSYKVSICLPHNDISPLSOLYVWLLVNLALAFVVICGCTYH IYLTVRNPNIVSSRDTKIAKRNATLITDGLMAPILFTAISAGLVPL ITVSKKILLVLFYFINSCLMPLVAFITKFRDRDFVLSKFGCYEVQA QIVKTESSITHNFSSKKNPCSSAPRVTSVWLVPLNHSVQN

Prediction method: IEDB recommended | Low percentile_rank = good binders

Download result

Citations

Check to expand the result:

Allele	#	Start	End	Length	Peptide	Method used	Percentile_rank	ANN IC50(nM)	ANN rank	SMM IC50(nM)	SMM rank
H-2-Kb	1	455	462	8	SVYTLAAI	Consensus (ann/smm)	0.3	11.70	0.2	75.24	0.4
H-2-Kb	1	401	408	8	CNLAFADL	Consensus (ann/smm)	0.25	24.33	0.2	48.75	0.3
H-2-Kb	1	679	686	8	NSYVLVPL	Consensus (ann/smm)	0.3	32.62	0.3	53.30	0.3
H-2-Kb	1	248	255	8	STYRLKKL	Consensus (ann/smm)	0.35	35.52	0.3	68.35	0.4
H-2-Kb	1	527	534	8	QIYVPAI I	Consensus (ann/smm)	0.55	72.50	0.3	174.46	0.6

B IEDB Analysis Resource

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MHC-I Processing Prediction Results

Input Sequences

#	Name	Sequence
1	sp P35378 FSHR_MOUSE Follicle-stimulating hormone receptor DE=Mus musculus CX-10090 GN=Fshr FE-2 SV-2	MALLLVSLAFLGSGSGCHHLLCHSNRVFLCODSKVTEIPDLPRIVAIE LRFVLTSLRVIPKGFSGCTDLEKICISQNDVLCVICADVSNLPNLIICI UNLPSLHVLLENIKRLHUA-HKIQSLQKVLLDUNNIIHIIARNSFMGLSFESVILWLNKNGIQEIHCAFNGTQLDELNL SDNNI FFI PNDVFGAGSGPVVITPSTKVVYSPIHKKI RARSTY LPHGLENLKLRARSTYRLKXKLSLDKFWLIEASLTVPSHCCAFANIRQTSLELHP ICIKSIESRDIDDMTPGDQFVSLVDDEPSYKSGDMLYSEGDYDLNCFVDVTCSPK FDFANPCDDINGVILRVLIWFSILAITGNTTVLWLTTSQYKLTVPRLM CNLAFADLCIGIYLLIASVDIHTKSCVHVAIDMQTGAGCDAAGFFTVF LLLGGLYLLLVSLVLIHTKSCVHVAIDMQTGAGCDAAGFFTVFISEL SVYTLVPLITL FRMHTTTHAQI FCKVQI CHAASTPM GWAFAPAAA LFPZFGISSYKVSICLPHNDISPLSOLYVWLLVNLALAFVVICGCTYH SPSOLYVWLLVNLALAFVVICGCTYH IYLTVRNPNIVSSRDTKIAKRNATLITDGLMAPILFTAISAGLVPL FLCNAPLFFAISASLVPLITVSKKILLVLFYFINSCLMPLVAFITKFRDRDFVLSKFGCYEVQA LNSKFGCYEVQAQIVKTESSITHNFSSKKNPCSSAPRVTSVWLVPLNHSVQN

Prediction method: recommended | High Score = high efficiency

Download result

Citations

Allele	#	Start	End	Peptide Length	Peptide	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
H-2-Kb	1	488	501	14	LVNLGMNFAAVIL	1.39	0.54	-1.21	1.93	0.72	18.2
H-2-Kb	1	490	501	12	VLGMVFAVAL	1.39	0.40	-1.21	1.79	0.56	18.2
H-2-Kb	1	493	501	9	WAFAPDAL	1.39	0.46	-1.58	1.85	0.50	22.7
H-2-Kb	1	490	502	13	VLGMVFAAALF	1.20	1.08	-1.81	2.26	0.47	84.6
H-2-Kb	1	489	501	13	MVLGMVFAAAL	1.39	0.51	-1.45	1.90	0.44	26.5
H-2-Kb	1	248	255	8	STYRLKKL	1.52	0.57	-1.06	2.08	0.42	45.7
H-2-Kb	1	100	100	9	TARNFPRGI	1.47	0.47	-1.05	1.94	0.28	44.9

Supplemental Figure 6. STYRLKKL is an FSHR derived octamer predicted to be efficiently processed and bind H2-K(b) with high affinity. (A) Screenshot showing the binding prediction to MCH-I of 8-mers derived from murine FSHR to H2-K(b) and H2-D(b) using the immunopeptide database (<http://tools.iedb.org/mhci/>). (B) Screenshot showing the proteasome and TAP processing prediction of all potential FSHR-derived peptides and binding to H2-K(b) and H2-D(b) using the immunopeptide database (<http://tools.iedb.org/processing/>).

SUPPLEMENTAL METHODS**Mouse SynCon FSHR DNA sequence**

ATGGA CTGGACCTGGATTCTGTTCTTGGTGGCCGCTGCCACAAGGGTGC ACTCCTGC
CACC ACTGGCTGTGCCACTGTTCTAACAGGGTGTTCCTGTGCCAGGACAGCAAGGTG
ACCGAGATCCCTCCCGATCTGCCCCGGAACGCCATCGAGCTGCGCTTCGTGCTGACA
AAGCTGAGAGTGATCCCTAAGGGCTCCTTCTCTGGCTTTGGAGATCTGGAGAAGATC
GAGATCTCCAGAACGACGTGCTGGAAGTGATCGAGGCCGACGTGTT CAGCAACCT
GCCTAAGCTGCACGAGATCCGGATCGAGAAGGCCAACACCTGCTGTACATCAACC
CCGAGGCTTTCCAGAACCTGCCTAGCCTGCGCTACCTGCTGATCTCCAACACCGGCA
TCAAGCACCTGCCAGCCGTGCACAAGATCCAGAGCCTGCAGAAGGTGCTGCTGGAC
ATCCAGGATAACATCAACATCCACATCATCGCTAGAACTCCTTCATGGGACTGTCT
TTTGAGAGCGTGATCCTGTGGCTGAACAAGAACGGCATCCAGGAGATCCACA ACTG
TGCCTTTAACGGAACACAGCTGGACGAGCTGAACCTGTCTGATAACAACAACCTGG
AGGAGCTGCCTAACGACGTGTTCCAGGGCGCCAGCGGACCAGTGATCCTGGATATC
TCCAGGACCAAGGTGCACTCTCTGCCCAACCACGGCCTGGAGAACCTGAAGAAGCT
GAGGGCCAGATCCACATACAGACTGAAGAAGCTGCCTTCTCTGGACAAGTTCGTGA
CCCTGATGGAGGCTTCTCTGACATAACCAAGCCACTGCTGTGCCTTTGCTAACTGGA
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ATCGACGATATGACCCAGATCGGAGATCAGCGCGTGAGCCTGATCGACGATGAGCC
CTCCTACGGCAAGGGATCTGACATGATGTACAGCGAGTTCGACTTTGATCTGTGCAA
CGAGGTGGTGGATGTGACATGTTCCCAAAGCCCGACGCCTTCAACCCCTGCGAGG
ATATCATGGGCTACAACATCCTGCGGGTGCTGATCTGGTTTATCTCCATCCTGGCTAT
CACCGGAAACACCACAGTGCTGGTGGTGGT GACCACATCTCAGTACAAGCTGACAG
TGCCTCGCTTCTGATGTGCAACCTGGCCTTTGCTGACCTGTGCATCGGCATCTACCT
GCTGCTGATCGCCTCTGTGGATATCCACACCAAGAGCCAGTACCACA ACTACGCCAT
CGACTGGCAGACCGGCGCTGGATGTGATGCTGCCGGATTCTTTACAGTGTTGCGCTC
CGAGCTGAGCGTGTAACCCCTGACAGCTATCACCCCTGGCCAGGGCTCACACCATCAC
ACACGCCATGCAGCTGGAGTGCAAGGTGCAGCTGAGACACGCTGCCTCTATCATGG
TGCTGGGCTGGACATTCGCTTTTGCTGCCGCTCTGTTCCCAATCTTTGGAATCAGCTC
CTACATGAAGGTGTCCATCTGTCTGCCTATGGACATCGATAGCCCACTGTCCCAGCT
GTACGTGATGGCCCTGCTGGTGGTGAACGTGCTGGCCTTCGTGGTCATCTGCGGCTG
TTACACCCACATCTACCTGACAGTGCGGAACCCCAACATCGTGTCTAGCTCCTCTGA
CACCAAGATCGCCAAGCGCATGGCTACCCTGATCTTCACAGATTTTCTGTGCATGGC
CCCAATCAGCTTCTTTGCCATCAGCGCCTCCCTGAAGGTGCCCTGATCACCGTGAG
CAAGGCTAAGATCCTGCTGGTGGTGTCTTCTACCCAATCAACTCCTGCGCCAACCCCTT
TCTGTACGCTATCTTCACAAAGAACTTTCGGCGCGACTTCTTTATCCTGATGAGCAA
GTTCCGGATGTTACGAGATGCAGGCCAGATCTACCGGACCGAGACAAGCTCCGCCA
CCCACA ACTTTCACGCTAGGAAGTCCC ACTGCAGCAGCGCCCCAGGGTGACAAAC
TCTTACGTGCTGGTGCCTCTGAACCACAGCGTG CAGA ACTGATAA