

Supplementary Data 1 - Protein accession numbers, oligonucleotide primers, DNA and amino-acid sequences of ^NFc-CXCL^C fusion proteins

CXCL protein (residues / accession No.)	Construct for expression	Fusion protein
hCXCL1/GRO α (38-107 / P09341)	gWiz-LS-Fc(mIgG2)-His ₆ -linker-TEV-hCXCL1 ³⁸⁻¹⁰⁷ -G ₂ -AviTag	^N Fc-hCXCL1 ^C
hCXCL5/ ENA-78 (43-114 / P42830)	gWiz-LS-Fc(mIgG2)-His ₆ -linker-TEV-hCXCL5 ⁴³⁻¹¹⁴ -G ₂ -AviTag	^N Fc-hCXCL5 ^C
hCXCL8/IL-8 (29-99 / P10145)	gWiz-LS-Fc(mIgG2)-His ₆ -linker-TEV-hCXCL8 ²⁹⁻⁹⁹ -G ₂ -AviTag	^N Fc-hCXCL8 ^C
mCXCL1/KC (28-96 / P12850)	gWiz-LS-Fc(mIgG2)-His ₆ -linker-TEV-mCXCL1 ²⁸⁻⁹⁶ -G ₂ -AviTag	^N Fc-mCXCL1 ^C
mCXCL2/MIP-2 (31-100 / P10889)	gWiz-LS-Fc(mIgG2)-His ₆ -linker-TEV-mCXCL2 ³¹⁻¹⁰⁰ -G ₂ -AviTag	^N Fc-mCXCL2 ^C
mCXCL5/LIX (48–118 / P50228)	gWiz-LS-Fc(mIgG2)-His ₆ -linker-TEV-mCXCL5 ⁴⁸⁻¹¹⁸ -G ₂ -AviTag	^N Fc-mCXCL5 ^C

Primer name	Primer sequence (5' to 3')
Forward-hCXCL1-Fc	5' -CTGGGTACCGAGAACCTGTACTTCCAAGCCACCGAGCTGAGATGCCAGTGCCTGC-3'
Forward-hCXCL5-Fc	5' -CTGGGTACCGAGAACCTGTACTTCCAAGTGCTGCGCGAGCTGAGATGCGTGTGC-3'
Forward-hCXCL8-Fc	5' -CTGGGTACCGAGAACCTGTACTTCCAAGCCAAAGAACTGCGGTGCCAGTGCATCAAG-3'
Forward-mCXCL1-Fc	5' -CTGGGTACCGAGAACCTGTACTTCCAAGCCAACGAGCTGCGGTGCCAGTGCCTGC-3'
Forward-mCXCL2-Fc	5' -CTGGGTACCGAGAACCTGTACTTCCAAGCCAGCGAGCTGCGGTGCCAGTGCCTG-3'
Forward-mCXCL5-Fc	5' -CTGGGTACCGAGAACCTGTACTTCCAAGCCACCGAGCTGAGATGCGTGTGCCTGACC-3'
Reverse-CXCL-Fc-AviTag	5' -GATCTTTTATTAGCCAGAAGTGATCTTTATCATCACTCGTGCCACTCGATTTTCTGG-3'

Sequences of genes coding for ELR⁺ CXCL chemokines fused to the C-terminus of Fc domain: ^NFc-CXCL^C

DNA sequences of genes are provided. Start and stop codons are shown in black bold. The sequences include the secretory leader peptide (LS, in grey underlined), the Fc domain derived from a mouse IgG2 (mIgG2) heavy-chain C_H2 and C_H3 constant regions (in grey), the hexa-histidine tag (His₆, in red bold), a flexible linker (in black underlined), a TEV protease recognition site (in blue bold), a active CXCL (in black), a Gly-Gly dipeptide spacer (G₂, in black italic and underlined), and a BirA peptide substrate for site-specific biotinylation (AviTag, in green bold).

gWiz-LS-Fc(mIgG2)-His₆-linker-TEV-hCXCL1³⁸⁻¹⁰⁷-G₂-AviTag

ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCACGATGTGAGCCCAGAGTGCCCATAACACAGAACCCCTGTCTCCACTCAAAGAGTGTCCCCCATGCGCAGCTCCAGACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCATGGTCCATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGACGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAAACACAGAGCCCTCCCATCCCCATCGAGAAAACCATCTCAAACCCAGAGGGCCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACCAGCAGAAGAGATGACTAAGAAAGAGTTTCAGTCTGACCTGCATGATCACAGGCTTCTTACCTGCCGAAATTGCTGTGGACTGGACCAGCAATGGGCGTACAGAGCAAAACTACAAGAACACCGCAACAGTCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTCAGAGTACAAAAGAGCACTTGGGAAAGAGGAAGTCTTTTCGCCTGCTCAGTGGTCCACGAGGGTCTGCACAATCACCTTACGACTAAGACCATCTCCCGGTCTCTGGGTAAA**CACCATCACCATCATCAC**TCTTCTGGCGTGGATCTGGGTACC**GAGAACCTGTACTTCCAA**GCCACCGAGCTGAGATGCCAGTGCCTGCAGACCCTGCAGGGCATCCACCCCAAGAACATCCAGAGCGTGAACGTGAAGTCCCCTGGCCCCCACTGCGCCAGACCGAAGTGATCGCCACCCTGAAGAACGGCCGGAAGGCCTGCCTGAACCCCGCCAGCCCCATCGTGAAGAAAATCATCGAGAAGATGCTGAACAGCGACAAGAGCAAC**GGCGGAGGCCTGAACGACATCTTCGAGGCCAGAAAATCGAGTGGCACGAGTGATGATAA**

gWiz-LS-Fc(mIgG2)-His₆-linker-TEV-hCXCL5⁴³⁻¹¹⁴-G₂-AviTag

ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCACGATGTGAGCCCAGAGTGCCCATAACACAGAACCCCTGTCTCCACTCAAAGAGTGTCCCCCATGCGCAGCTCCAGACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCATGGTCCATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGACGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAAACACAGAGCCCTCCCATCCCCATCGAGAAAACCATCTCAAACCCAGAGGGCCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACCAGCAGAAGAGATGACTAAGAAAGAGTTTCAGTCTGACCTGCATGATCACAGGCTTCTTACCTGCCGAAATTGCTGTGGACTGGACCAGCAATGGGCGTACAGAGCAAAACTACAAGAACACCGCAACAGTCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTCAGAGTACAAAAGAGCACTTGGGAAAGAGGAAGTCTTTTCGCCTG

CTCAGTGGTCCACGAGGGTCTGCACAATCACCTTACGACTAAGACCATCTCCCGGTCTCTGGGTAAACACCATCACCATCATCACTCTTCTGGCGTGGATC
TGGGTACCGAGAACCTGTACTTCCAAGTGCTGCGCGAGCTGAGATGCGTGTGCCTGCAGACCACCCAGGGCGTGCACCCCAAGATGATCAGCAACCTCCAG
GTGTTTCGCCATCGGCCCCCAGTGCAGCAAGGTGGAAGTGGTGGCCAGCCTGAAGAACGGCAAAGAGATCTGCCTGGACCCCGAGGCCCCATTCTGAAGAA
AGTGATCCAGAAGATCCTGGACGGCGGCAACAAAGAGAACGGCGGAGGCCTGAACGACATCTTCGAGGCCAGAAAATCGAGTGGCAGAGTGATGATAA

gWiz-LS-Fc(mIgG2)-His₆-linker-TEV-hCXCL8²⁹⁻⁹⁹-G₂-AviTag

ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCACGATGTGAGCCCAGAGTGCCCATAACACAGAACCCCTGTCTCCACT
CAAAGAGTGTCCCCCATGCGCAGCTCCAGACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTCCCTGAGCC
CCATGGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGACGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAA
ACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAA
CAACAGAGCCCTCCCATCCCCCATCGAGAAAACCATCTCAAAACCCAGAGGGCCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACCAGCAGAAGAGA
TGACTAAGAAAGAGTTTCACTCTGACCTGCATGATCACAGGCTTCTTACCTGCCGAAATTGCTGTGGACTGGACCAGCAATGGGCGTACAGAGCAAAACTAC
AAGAACACCGCAACAGTCCTGGACTCTGATGGTTCTTACTTTCATGTACAGCAAGCTCAGAGTACAAAAGAGCACTTGGGAAAGAGGAAGTCTTTTCGCCTG
CTCAGTGGTCCACGAGGGTCTGCACAATCACCTTACGACTAAGACCATCTCCCGGTCTCTGGGTAAACACCATCACCATCATCACTCTTCTGGCGTGGATC
TGGGTACCGAGAACCTGTACTTCCAAGCCAAAGAACTGCGGTGCCAGTGCATCAAGACCTACAGCAAGCCCTTCCACCCCAAGTTCATCAAAGAACTGAGA
GTGATCGAGAGCGGCCCTCACTGCGCCAACACCGAGATCATCGTGAAGCTGAGCGACGGCAGAGAGCTGTGCCTGGACCCCAAAGAAAATGGGTGCAGCG
GGTGGTGGAAAAGTTCTGAAGCGGGCCGAGAACAGCGGCGGAGGCCTGAACGACATCTTCGAGGCCAGAAAATCGAGTGGCAGAGTGATGATAA

gWiz-LS-Fc(mIgG2)-His₆-linker-TEV-mCXCL1²⁸⁻⁹⁶-G₂-AviTag

ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCACGATGTGAGCCCAGAGTGCCCATAACACAGAACCCCTGTCTCCACT
CAAAGAGTGTCCCCCATGCGCAGCTCCAGACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTCCCTGAGCC
CCATGGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGACGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAA
ACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAA
CAACAGAGCCCTCCCATCCCCCATCGAGAAAACCATCTCAAAACCCAGAGGGCCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACCAGCAGAAGAGA
TGACTAAGAAAGAGTTTCACTCTGACCTGCATGATCACAGGCTTCTTACCTGCCGAAATTGCTGTGGACTGGACCAGCAATGGGCGTACAGAGCAAAACTAC
AAGAACACCGCAACAGTCCTGGACTCTGATGGTTCTTACTTTCATGTACAGCAAGCTCAGAGTACAAAAGAGCACTTGGGAAAGAGGAAGTCTTTTCGCCTG
CTCAGTGGTCCACGAGGGTCTGCACAATCACCTTACGACTAAGACCATCTCCCGGTCTCTGGGTAAACACCATCACCATCATCACTCTTCTGGCGTGGATC
TGGGTACCGAGAACCTGTACTTCCAAGCCAAAGAGCTGCGGTGCCAGTGCCTGCAGACCATGGCCGGCATCCACCTGAAGAACATCCAGAGCCTGAAGGTG
CTGCCCAGCGGCCCTCACTGCACCCAGACCGAAGTGATGCCACCCTGAAGAACGGCAGAGAGGCCTGCCTGGATCCCGAGGCCCCCTGGTGCAGAAAAT
CGTGCAGAAAATGCTGAAGGGCGTGCCCAAGGGCGGAGGCCTGAACGACATCTTCGAGGCCAGAAAATCGAGTGGCAGAGTGATGATAA

gWiz-LS-Fc(mIgG2)-His₆-linker-TEV-mCXCL2³¹⁻¹⁰⁰-G₂-AviTag

ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCACGATGTGAGCCCAGAGTGCCCATAACACAGAACCCCTGTCTCCACT
CAAAGAGTGTCCCCCATGCGCAGCTCCAGACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTCCCTGAGCC
CCATGGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGACGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAA
ACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAA
CAACAGAGCCCTCCCATCCCCCATCGAGAAAACCATCTCAAAACCCAGAGGGCCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACCAGCAGAAGAGA
TGACTAAGAAAGAGTTTCAGTCTGACCTGCATGATCACAGGCTTCTTACCTGCCGAAATTGCTGTGGACTGGACCAGCAATGGGCGTACAGAGCAAAACTAC
AAGAACACCGCAACAGTCCTGGACTCTGATGGTTCTTACTTTCATGTACAGCAAGCTCAGAGTACAAAAGAGCACTTGGGAAAGAGGAAGTCTTTTCGCCTG
CTCAGTGGTCCACGAGGGTCTGCACAATCACCTTACGACTAAGACCATCTCCCGGTCTCTGGGTAAA**CACCATCACCATCATCAC**TCTTCTGGCGTGGATC
TGGGTACC**GAGAACCTGTACTTCCA**AGCCAGCGAGCTGCGGTGCCAGTGCCTGAAAACCTGCCCGGGTGGACTTCAAGAACATCCAGAGCCTGAGCGTG
ACCCCCCTGGCCCTCACTGTGCCAGACCGAAGTGATCGCCACCCTGAAGGGCGGCCAGAAAGTGTGCCTGGACCCCGAGGCCCCCTGGTGCAGAAGAT
CATCCAGAAGATCCTGAACAAGGGCAAGGCCAACGGCGGA**GGCCTGAACGACATCTTCGAGGCCAGAAAATCGAGTGGCACGAGTGATGATAA**

gWiz-LS-Fc(mIgG2)-His₆-linker-TEV-mCXCL5⁴⁸⁻¹¹⁸-G₂-AviTag

ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCACGATGTGAGCCCAGAGTGCCCATAACACAGAACCCCTGTCTCCACT
CAAAGAGTGTCCCCCATGCGCAGCTCCAGACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTCCCTGAGCC
CCATGGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGACGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAA
ACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAA
CAACAGAGCCCTCCCATCCCCCATCGAGAAAACCATCTCAAAACCCAGAGGGCCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACCAGCAGAAGAGA
TGACTAAGAAAGAGTTTCAGTCTGACCTGCATGATCACAGGCTTCTTACCTGCCGAAATTGCTGTGGACTGGACCAGCAATGGGCGTACAGAGCAAAACTAC
AAGAACACCGCAACAGTCCTGGACTCTGATGGTTCTTACTTTCATGTACAGCAAGCTCAGAGTACAAAAGAGCACTTGGGAAAGAGGAAGTCTTTTCGCCTG
CTCAGTGGTCCACGAGGGTCTGCACAATCACCTTACGACTAAGACCATCTCCCGGTCTCTGGGTAAA**CACCATCACCATCATCAC**TCTTCTGGCGTGGATC
TGGGTACC**GAGAACCTGTACTTCCA**AGCCACCGAGCTGAGATGCGTGTGCCTGACCGTGACCCCAAGATCAACCCCAAGCTGATCGCCAACCTGGAAGTG
ATCCCTGCCGGCCCTCAGTGCCCCACCGTGGAAGTGATTGCCAAGCTGAAGAACCAGAAAGAAGTGTGCCTGGACCCCGAGGCCCCCTGATCAAGAAGAT
CATCCAGAAGATCCTGGGCAGCGACAAGAAGAAAGCCGGCGGA**GGCCTGAACGACATCTTCGAGGCCAGAAAATCGAGTGGCACGAGTGATGATAA**

Amino-acid sequences of ELR⁺ CXCL chemokines fused to the C-terminus of Fc domain: ^NFc-CXCL^C

Amino acid sequences of translated polypeptides are shown. The sequences include the secretory leader peptide (LS, in grey underlined), the Fc domain derived from a mouse IgG2 (mIgG2) heavy-chain C_H2 and C_H3 constant regions (in grey), the hexa-histidine tag (His₆^{tag}, in red bold), a flexible linker (in black underlined), a TEV protease recognition site (in blue bold), a active CXCL (in black), a Gly-Gly dipeptide spacer (G₂, in black italic and underlined), and a BirA peptide substrate for site-specific biotinylation (AviTag, in green bold).

LS-Fc-His₆-linker-TEV-hCXCL1³⁸⁻¹⁰⁷-G₂-AviTag

MRVPAQLLGLLLLLWLPGARCEPRVPITQNPCPPLKECPPCAAPDLLGGPSVFIFPPKIKDVLMISLSPMVTCTVVVDVSEDDPDVQISWVNNVEVHTAQ**TQ**
THREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNRALPSPIEKTISKPRGPVRAPQVYVLP**PPAE**EMTKKEFSLTCMITGFLPAEIAVDWTSNGRTEQNY
KNTATVLDSGSYFMYSKLRVQKSTWERGSLFACSVVHEGLHNHLTTKTISRSLGK**HHHHHH**SSGVDLGT**ENLYFQ**ATELRCQCCLQTLQGIHPKNIQSVNV
KSPGPHCAQTEVIATLKNGRKACLNPA**SP**IVKKIIEKMLNSDKSN**GGGLNDIFEAQKIEWHE**--

LS-Fc-His₆-linker-TEV-hCXCL5⁴³⁻¹¹⁴-G₂-AviTag

MRVPAQLLGLLLLLWLPGARCEPRVPITQNPCPPLKECPPCAAPDLLGGPSVFIFPPKIKDVLMISLSPMVTCTVVVDVSEDDPDVQISWVNNVEVHTAQ**TQ**
THREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNRALPSPIEKTISKPRGPVRAPQVYVLP**PPAE**EMTKKEFSLTCMITGFLPAEIAVDWTSNGRTEQNY
KNTATVLDSGSYFMYSKLRVQKSTWERGSLFACSVVHEGLHNHLTTKTISRSLGK**HHHHHH**SSGVDLGT**ENLYFQ**VLRELRCVCLQTTQGVHPKMISNLQ
VFAIGPQCSKVEVVASLKNGKEICLDPEAPFLKKVIQKILDGGNKEN**GGGLNDIFEAQKIEWHE**--

LS-Fc-His₆-linker-TEV-hCXCL8²⁹⁻⁹⁹-G₂-AviTag

MRVPAQLLGLLLLLWLPGARCEPRVPITQNPCPPLKECPPCAAPDLLGGPSVFIFPPKIKDVLMISLSPMVTCTVVVDVSEDDPDVQISWVNNVEVHTAQ**TQ**
THREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNRALPSPIEKTISKPRGPVRAPQVYVLP**PPAE**EMTKKEFSLTCMITGFLPAEIAVDWTSNGRTEQNY
KNTATVLDSGSYFMYSKLRVQKSTWERGSLFACSVVHEGLHNHLTTKTISRSLGK**HHHHHH**SSGVDLGT**ENLYFQ**AKELRCQCIKTYSKPFHPKFIKELR
VIESGPHCANTEIIIVKLSDGRELCLDPKENWVQRVVEKFLKRAENS**GGGLNDIFEAQKIEWHE**--

LS-Fc-His₆-linker-TEV-mCXCL1²⁸⁻⁹⁶-G₂-AviTag

MRVPAQLLGLLLLLWLPGARCEPRVPITQNPCPLKECPPCAAPDLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWVNNVEVHTAQTQ
THREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNRALPSPIEKTISKPRGPVRAPQVYVLP
PPAEEMTKKEFSLTCMITGFLPAEIAVDWTSNGRTEQNY
KNTATVLDSGSYFMYSKLRVQKSTWERGSLFACSVVHEGLHNHLTTKTISRSLGKHHHHHHSSGVDLGTENLYFQANELRCQCLQTMAGIHLKNIQSLKV
LPSGPHCTQTEVIATLKNGREACLDPEAPLVQKIVQKMLKGVPKGGGLNDIFEAQKIEWHE--

LS-Fc-His₆-linker-TEV-mCXCL2³¹⁻¹⁰⁰-G₂-AviTag

MRVPAQLLGLLLLLWLPGARCEPRVPITQNPCPLKECPPCAAPDLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWVNNVEVHTAQTQ
THREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNRALPSPIEKTISKPRGPVRAPQVYVLP
PPAEEMTKKEFSLTCMITGFLPAEIAVDWTSNGRTEQNY
KNTATVLDSGSYFMYSKLRVQKSTWERGSLFACSVVHEGLHNHLTTKTISRSLGKHHHHHHSSGVDLGTENLYFQASELRCQCLKTLPRVDFKNIQSLSV
TPPGPHCAQTEVIATLKGQKVCLDPEAPLVQKIIQKILNKGKANGGGLNDIFEAQKIEWHE--

LS-Fc-His₆-linker-TEV-mCXCL5⁴⁸⁻¹¹⁸-G₂-AviTag

MRVPAQLLGLLLLLWLPGARCEPRVPITQNPCPLKECPPCAAPDLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWVNNVEVHTAQTQ
THREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNRALPSPIEKTISKPRGPVRAPQVYVLP
PPAEEMTKKEFSLTCMITGFLPAEIAVDWTSNGRTEQNY
KNTATVLDSGSYFMYSKLRVQKSTWERGSLFACSVVHEGLHNHLTTKTISRSLGKHHHHHHSSGVDLGTENLYFQATELRCVCLTVTPKINPKLIANLEV
IPAGPQCPTVEVIAKLKNQKEVCLDPEAPVIKKIIQKILGSDKKKAGGGLNDIFEAQKIEWHE--