

Nucleotide sequence of chicken transforming growth factor-beta 1 (TGF-β 1)

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Two 1800 base pair long clones representing full-length cDNA copies of chicken TGF-β 1 were obtained and sequenced using methods described previously (1). Chicken TGF-β 1 cDNA codes for a primary gene product of 391 amino acids (Fig. 1) with one additional alanine residue at position 238 of the precursor compared to the 390 amino acid human TGF-β 1 precursor (2). Like mammalian TGF-β 1, the predicted chicken TGF-β 1 precursor protein contains a potential signal peptide (residues 1-21), three potential N-linked glycosylation sites, an arg-gly-asp fibronectin cellular recognition signal (residues 245-247) and a tetrabasic arg-his-arg-arg cleavage site (residues 276-279). Chicken TGF-β 1 shows 100%, 71%, 78% and 80% identity with the amino acid sequences of processed human TGF-βs 1 and 2 and chicken TGF-βs 3 and 4, respectively.

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CCCCCCCCCCCCCCCCCCTACCCCTGCCCCATTCCGGGCTGCGGTCTGGAGCCCCAACCCGACTCCCGGAGACTTGACCCCAAAGCTCGGGCGCACCCCCCTG
110 CACACTTCCCCACTCTCAGCTCTCTGCTGAGCCCTGCGCATCCAAGACCCCTCTCGGATCCGGGAGCGGAATCTGTCTCAGACCTGCCTCAGCTTTCATATCAAGACCACCCAC
229 CTCGTGACCGATCTCGCCCATCTCGGTTTTTCGCTAGGATACCGAGAACCACCATCAGAGCTCCCTCCACTCTGCTCTCCGTTCTCCCTGAGAGCTCAACTTCCCTCCC
348 ACCCCAGATCCTCTACTCTTTCTGGGGAGACCCCTCAGCCCTGTAGGGGGGGGGCCCTCCCTCTCTACCCAGCCGGCTCGCACTCTCGGCTGCCGGGGGGCCGGCTCCCCC
1
Met Pro Pro Ser Gly Pro Gly Leu Leu Pro Leu Leu Leu Pro Leu Leu Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu
467 ATG CCG CCT TCG GGG CCT GGG CTC TTG CCG CTG CTG CTG CCG CTG CTG TGG CTG CTA GTG CTG ACG CCT GGC CGG CCG GCC CCG GGA CTG
Ser Thr Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala
557 TCC ACC TGC AAG ACC ATC GAC ATG GAG CTG GTG AAG CCG AAG CCG ATC GAG GCC ATT CCG GGC CAG ATT CTG TCC AAG CTT CCG CTC GCC
75
Ser Pro Pro Ser Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu Tyr Asn Ser Thr Arg Glu Ala Val Ala Gly
647 AGC CCC CCG AGC CAG GGG GAC GTG CCG CCC GGC CCG CTG CCT GAG GCC GTA CTG GCT CTT TAC AAC AGT ACC CCG GAC CCG GTA GCC GGG
100
Glu Ser Val Glu Pro Glu Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu Met Val Glu Ser Gly Asn Gln Ile
737 GAA AGT GTC GAA CCG GAG CCC GAG CCA GAG CCG GAC TAC TAC GCC AAG GAG GTC ALC CCG CTG CTA ATG GTG GAA AGC GGC AAC CAA ATC
125
Tyr Asp Lys Phe Lys Gly Thr Pro His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val Pro Glu Pro Val Leu Leu
827 TAT GAT AAA TTC AAG GGC ACC CCC CAC AGC TTA TAT ATG CTG TTC AAC ACG TCG GAG CTC CCG GAA GCG GTG CCG GAA CCT GTA TTG CTC
175
Ser Arg Ala Glu Leu Arg Leu Arg Leu Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn Asp Ser Trp Gly
917 TCT CGG GCA GAG CTG CCG CTG CTG AGG CTC AAG TTA AAA GTG GAG CAG CAC GTG GAG CTA TAC CAG AAA TAC AGC AAT GAT TCC TGG GGC
200
Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Glu Arg Trp Leu Thr Arg
1007 TAC CTC AGC AAC CCG CTG CTG GCC CCC AGT GAC TCA CCG GAG TGG CTG TCC TTT GAT GTC ACC GGA GTT GTG CCG GAG TGG CTG ACC CCG
225
Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Cys Ser Cys Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Ala Gly Phe
1197 AGA GAG GCT ATA GAG GGT TTT CCG CTC AGT GCC CAC TGT TCC TGT GAC AGC AAA GAT AAC ACA CTC CAC GTG GAA ATT AAC GCA GGG TTC
250
Asn Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln
1287 AAT TCT GGC CGC CCG GGT GAC CTG GCC ACC ATT CAC GGC ATG AAC CCG CCC TTC CTG CTC CTC ATG GCC ACC CCG CTG GAG AGG GCC CAG
275
His Leu His Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr
1377 CAC CTG CAC AGC TCC CCG CAC CCG CGA GCC CTG GAT ACC AAC TAC TGC TTC AGC TCC ACG GAG AAG AAC TGC TGC GTG CCG GAG CTC TAC
325
Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile
1467 ATT GAC TTC CCG AAG GAC CTC GGC TGG AAG TGG ATT CAT GAA CCC AAG GGC TAC CAT GCC AAT TTC TGC CTG GGC CCC TGT CCC TAC ATC
350
Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln
1557 TGG AGC CTA GAC ACT CAG TAC AGC AAG CTC CTG GCT CTG TAC AAC CAG CAC AAC CCG GCG TCG GGC CCG TGC TGC GTG CCG CAG
375
Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys
1647 GCG CTG GAG CCA CTG CCC ATC GTG TAC TAC GTG GGC CCG AAG CCC AAG GTG GAG CAG CTG TCC AAC ATG ATC GTG CTT TCC TGC AAG TGC
391
Ser
1737 AGC TGA GCGCCCGCCCGCCACAGCCCGCCACCCCGGAGCCCGCCCGCCACCCCGCCCGCTCAGCCGGGCTGATTTAAGGACATCGTGCCECAAGCCACTTGGGATCGAT
1854 TAAAGGTGGAGAGAG poly (A)30 GGGGGGGGGGGGGGGGGGG
    
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REFERENCES 1. Jakowlew, S.B. *et al.* (1988) *Mol. Endocrinol.* 2,747-755. 2. Derynck, R. *et al.* (1985) *Nature* 316,701-705.