

Erratum

Recombinant human J-chain: Fix the protein aggregations and yield maximize

El-Rashdy M. Redwan, Saleh M. Matar and Ihab A. Serour

[*Human Antibodies 15(3) (2006), 95–102*]

When this article was originally published, the last three sentences of the abstract appeared incorrect. The correct abstract is presented below.

Polymeric immunoglobulin (dimeric IgA and pentameric IgM) molecules can assembly by using the immunoglobulin J (joining) chain and across the epithelial cell layers. Based on its amino acid and gene sequences data, disulfide bond (2 bonds) assignment secondary structure predictions, and chemical properties, a model for J-chain folding has been proposed. However, the crystal structure of the J-chain protein is still far from obtained, because the J-chain expression and its protein downstream has a permanent aggregation

problems, due to its two free thiol groups. Our work focused on the chemical blocking of free cysteines-SH or to mutate these cysteines into serine residues. The chemical blocking yielded partially soluble proteins with new structures (carboxyamidomethyl cysteine and carboxyamidomethyl methionine) at cysteine and methionine residues. While mutate the cysteines^{15,69} into serine has been yielded a complete soluble (11.5 mg/l) J-chain protein which migrate (SDS-PAGE) at 27 KDa. We were used pET22b expression vector and *E. coli* BL21 (DE3) to produce the J-chain protein. For maximization the production yield of j-chain foreign protein, the batch culture was developed. We described the scaling-up production in term of kinetic behavior to the recombinant *E.coli* and optimization of cultivation parameters in 3-L bench-top bioreactor. The process was automated through a computer aided data bioprocessing system *AFS-BioCommand* multi-process management program to regulate the cell growth rate, temperature, pH and agitation speed based on dissolved oxygen. The results showed an obvious increasing in biomass by 5.98 g/L after about 27 h.