2. STRUCTURE [OMS721, CATALENT PHARMA SOLUTIONS]

OMS721 is comprised of variable regions of human origin, fused to a hybrid IgG4 constant region of human origin containing a single additional S/P mutation in the hinge region to enhance stability of the antibody. OMS721 is secreted as a disulfide-linked glycosylated tetramer consisting of two identical 445 amino acid heavy chains and two identical 212 amino acid lambda light chains (the total number of amino acids is 1314). The amino acid sequences of these chains are shown in Figure 1 and Figure 2. The theoretical isoelectric point is 8.36, and the average mass of the amino acid chains combined is 143,087 Da. The asparagine residue (N) at position 295 of the heavy chain is glycosylated and is indicated in underlined bold text.

Figure 1: Amino Acid Sequence of OMS721 Light Chain

```
10          20          30          40          50          60
QPVLTQPPSL SVSPGQTASI TCSGEKLGDK YAYWYQQKPG QSPVLVMYQD KQRPSGIPER

         70          80          90         100         110         120
FSGSNSGNTA TLTISGTQAM DEADYYCQAW DSSTAVFGGG TKLTVLGQPK AAPSVTLFPP

        130         140         150         160         170         180
SSEELQANKA TLVCLISDFY PGAVTVAWKA DSSPVKAGVE TTTPSKQSNN KYAASSYLSL

        190         200         210
TPEQWKSHRS YSCQVTHEGS TVEKTVAPTE CS
```

Figure 2: Amino Acid Sequence of OMS721 Heavy Chain

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10         20         30         40         50         60
QVTLKESGPV LVKPTETLTL TCTVSGFSLS RGKMGVSWIR QPPGKALEWL AHIFSSDEKS

        70         80         90        100        110        120
YRTSLKSRLT ISKDTSKNQV VLTMTNMDPV DTATYYCARI RRGGIDYWGQ GTLVTVSSAS

       130        140        150        160        170        180
TKGPSVFPLA PCSRSTSEST AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL

       190        200        210        220        230        240
YSLSSVVTVP SSSLGTKTYT CNVDHKPSNT KVDKRVESKY GPPCPPCPAP EFLGGPSVFL

       250        260        270        280        290        300
FPPKPKDTLM ISRTPEVTCV VVDVSQEDPE VQFNWYVDGV EVHNAKTKPR EEQFNSTYRV

       310        320        330        340        350        360
VSVLTVLHQD WLNGKEYKCK VSNKGLPSSI EKTISKAKGQ PREPQVYTLP PSQEEMTKNQ

       370        380        390        400        410        420
VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG SFFLYSRLTV DKSRWQEGNV

       430        440
FSCSVMHEAL HNHYTQKSLS LSLGK
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Glycosylation Pattern

OMS721 has an N-linked glycosylation site at asparagine (N) residue 295 of the heavy chain as highlighted in Figure 2.

Other Post-Translational Modifications

Post-translational modifications of OMS721 included oxidation, deamidation, N-terminal pyroglutamic acid formation, and processing of C-terminal lysine of the heavy chain. The heavy chain N-terminus is predominantly pyroglutamic acid. The light chain N-terminal glutamine remains unmodified as determined by intact mass analysis.

Molecular Formula

$C_{6340}H_{9902}N_{1680}O_{1993}S_{48}$ (based on amino acid content)

Relative Molecular Mass

Molecular weight: 143,087 Da (theoretical, based on amino acid content)