# APPLICATIONS



### Method Optimization for Purity Analysis of IgG Isotypes and F-Fusion Proteins by Intact Reversed Phase

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#### **Overview**

A primary analytical technique for purity for recombinant proteins is reversed phase LC (RPLC). This simple, robust methodology has a relatively short analysis time, as well being high resolution, capable of separation of hydrophobic variants such as oxidation, glycoforms, and clipping. As such, it is a common analytical approach for monoclonal antibodies (mAbs), especially considering it can be implemented at both intact and subunit levels without extensive method optimization.

However, different recombinant proteins present other challenges, requiring deviation from a platform method that was developed on a humanized, IgG1 mAb. For example, different isotypes of IgG, including IgG2 and IgG4s, have disulfide variants and Fab arm exchange variants, which must be characterized. Fc-fusion proteins are another, well established recombinant protein modality. These present many analytical challenges, as their glycosylation can vary considerably, Consequently, this makes the analysis of Fc-Fusions at the intact level somewhat challenging.

Methods for intact reversed phase often employ shallow gradient slopes (less than <1% B per column volume) over short periods of time (<15 minutes). For example, a gradient program used might be 30-40% B in 5 minutes, with gradient slope being 0.4% B per column volume. This shallow gradient within a tight window of organic might work reasonably well for mAbs of the same isotype, e.g. humanized IgG1. However, deviation in isotype or working with Fc-fusions may not work under these conditions.

Figure 1 shows Etanercept, a recombinant protein composed of a humanized Fc conjugated to the Tumor Necrosis Factor (TNF) receptor. Using an intact reversed phase LC method developed for mAbs, the analyte elutes very early in the gradient, with a k' of <2. Reducing the sample causes the protein to almost elute in the void. Figure 2 shows Panitumumab, an IgG2, that is too hydrophobic for the 40% B gradient, thus elutes in gradient program wash.

Consequently, if one is working with proteins of different physicochemical properties, it might be more prudent to then increase the gradient slope slightly and extend the organic window to facilitate separation of analytes of varying hydrophobicities. Figure 3 implements method where the gradient program starts earlier and elutes later than the aforementioned IgG1 method; 20-45% B. To ensure that gradient slope is relatively shallow, the gradient time is extended to 10 minutes.

The resulting method uses a 0.6% B per column volume gradient slope. Although this is steeper than the previously run method, when working with multiple protein formats, one can use this method as a platform for screening, then optimize further depending on the method needs. As shown in Figure 3, a range of analytes, from bispecifics, to different isotypes and fusion proteins, all elute within an acceptable portion of the gradient program. Purity can be assessed accordingly and again, as method requirements become more stringent, a shallower gradient might be implemented.

In summary, purity analysis by reversed phase LC is a primary method for the analysis of recombinant proteins. Fc-fusions and other monoclonal antibody isotypes may behave quite differently chromatographically. However, by simply adjusting gradient programs to optimize capacity factor or retention time, one can develop a streamlined, "platform" method for purity analysis that may be optimized depending on method requirements.

#### **HPLC Conditions**

Column:	hiaZan 2 6 um Wide Dara C4
	bioZen 2.6 μm WidePore C4
Dimension:	100 x 2.1 mm
Part No.:	00D-4786-AN
Mobile Phase A:	0.1 % TFA in Water
Mobile Phase B:	0.1 % TFA in Acetonitrile
Gradient Program:	30-40% B in 5 minutes (Figure 1,2), 0.4 % B/CV
	20-45% B in 10 minutes (Figure 3), 0.6 % B/CV
Flow-rate:	0.8 mL/min
Temperature:	80° C
Detection:	UV-Vis @ 280 nm
Injection:	
Samples:	As indicated (0.5 mg/mL)



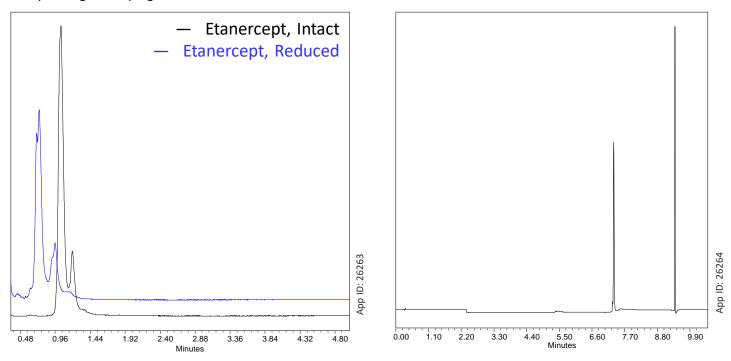


#### Figure 1. Etanercept Using Standard IgG1 Gradient

Overlay of etanercept, intact and non-reduced. Because it is heavily glycosylated and thus more hydrophilic, it elutes early in the gradient program.

#### Figure 2. IgG2 Using Standard IgG1 Gradient

Chromatogram of panitumumab, a hydrophobic IgG2 which elutes at the end of the gradient program, thus eluting almost completely in the wash.



#### Figure 3. Gradient Program Optimization for Different mAb Formats and Fc Fusions

Chromatogram stack for various recombinant proteins. From top to bottom: Panitumumab (IgG2), Etanercept (FcFusion), Denosumab (IgG2), Nivolumab (IgG4), and Emicizumab (Bispecific). By modifying the gradient slope-widening the elution program and extending the gradient length, acceptable impurity profiles are obtained for all molecules.

0.140 0.105 ⊋ 0.070 0.035 0.000	Panitumumab (IgG2)	
0.16 0.12 ₹ 0.08 0.04	Etanercept (Fc-Fusion)	
0.48 0.36 2 0.24 0.12 0.00	Denosumab (IgG2)	
0.24 0.18 ₹ 0.12 0.06 0.00	Nivolumab (IgG4)	55
0.60 0.45 ⊋ 0.30 0.15 0.00 5.00	Emicizumab (Bispecific)	App ID: 26265



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