**S1: Examples for fits rated by annotators as “Bad” (A), “Reasonable” (B) and “Good” (C).**

The neighboring categories clearly show an overlap (e.g. supplement S1 Ai with Biii or Bii with Ci) while the categories “bad” and “good” are clearly distinct from each other. Individually, while some curves rating may fit into a neighboring category, overall the ratings appear to reflect the actual quality of the data. Thus, the rating provides an indication of the data’s quality. Overall the majority of publications do not directly include raw data or fits to their data, and when they do, their quality is more often bad rather than good. Similar conclusions have been made by Rich & Myszka in their yearly surveys of biosensor literature(1–9).

**A** **i)** Interaction of mAB A20G2 and vaccinia virus protein A33.(10) Method: BLI. **ii)** Binding of the lectin HOL-18 to Porcine Stomach Mucin (PSM).(11) Method: SPR. **iii)** Binding of VEGF165-ATTO 647N to CD44s.(12) Method: Fluorescence Correlation Microscopy (FCS).
**B** **i)** Interaction of Grx5 with Ssq1.(13) Method: MST. **ii)** Binding of RNA-aptamer CLN64 to c-Met.(14) Method: BLI. **iii)** Binding of SecB to MBP.(15) Method: BLI.
**C** **i)** Binding of gp42 C114S to EBV gHgL.(16) Method: BLI. **ii)** Binding of vWC2-3 to Tsg.(17) Method: SPR. **iii)** Binding of the chemical compound 991 to AMPK complex α1β1γ1.(18) Method: BLI.
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**S2: Important aspects of kinetic data submission**

As previously stated, information on binding interactions is shared varyingly throughout publications. Guidelines for publishing data from different methods in biosciences do exist (such as the Minimal Information About a Microarray Experiment (MIAME) guideline), but to date none cover information on publishing data from binding interaction experiments. Below is a brief overview of current issues and their possible solutions:

Key points for kinetics data submission:

1. **Interaction Partners with unique identifiers**:
While many publications present the interacting entities, not all do so in a comprehensible manner.
**Proposal:** Each entity should be displayed in a separate column and clearly labeled as interaction partner, i.e. interaction partner 1/2.
**Proposal:** Columns should not be subdivided. Additional classifications such as Igg vs. Fab must be derivable from the identifying column or get an entry in an additional column.
2. **Binding parameters**:

Currently, several formats are used to display rate constants, such as different SI-prefixes (e.g. mM), units within the table row or sub-multiples (e.g. 104) displayed as a separate factor in the header.
**Proposal:** Only use non-prefixed units (e.g. [M]) in the header and display sub-multiples in the corresponding cells in scientific notation (e.g. 1.9e-9)
**Proposal:** Display standard deviation in separate columns next to their corresponding value.

1. **Method and Device used**
Currently methods and devices are only mentioned in the method-section of the corresponding article. But both influence the result in varying manner and should be directly visible alongside the data, especially in publications where multiple methods have been used.
**Proposal:** Display both in separate columns.

**S3: Form fields shown in the annotation view.**

Shown are fieldnames (black), additional descriptions/units (green) and examples for each field (blue). The rightmost column shows the rating section, comprised of four questions regarding the quality of raw data and corresponding fits.

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