

# ACCURATE CONSTANT, $K_d$ , VIA TRANSIENT INCOMPLETE SEPARATION (ACTIS)

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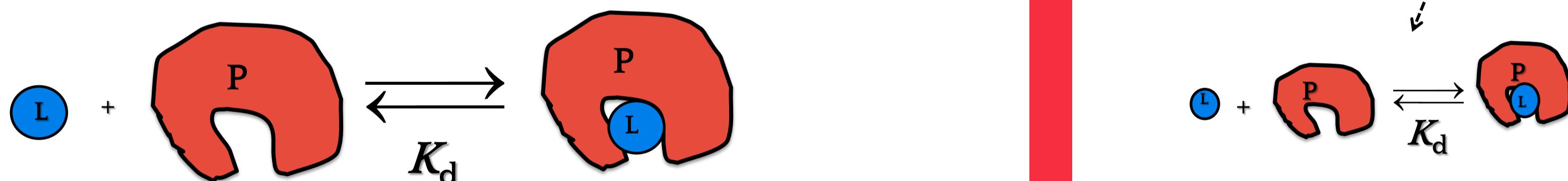


## 1. MOTIVATION

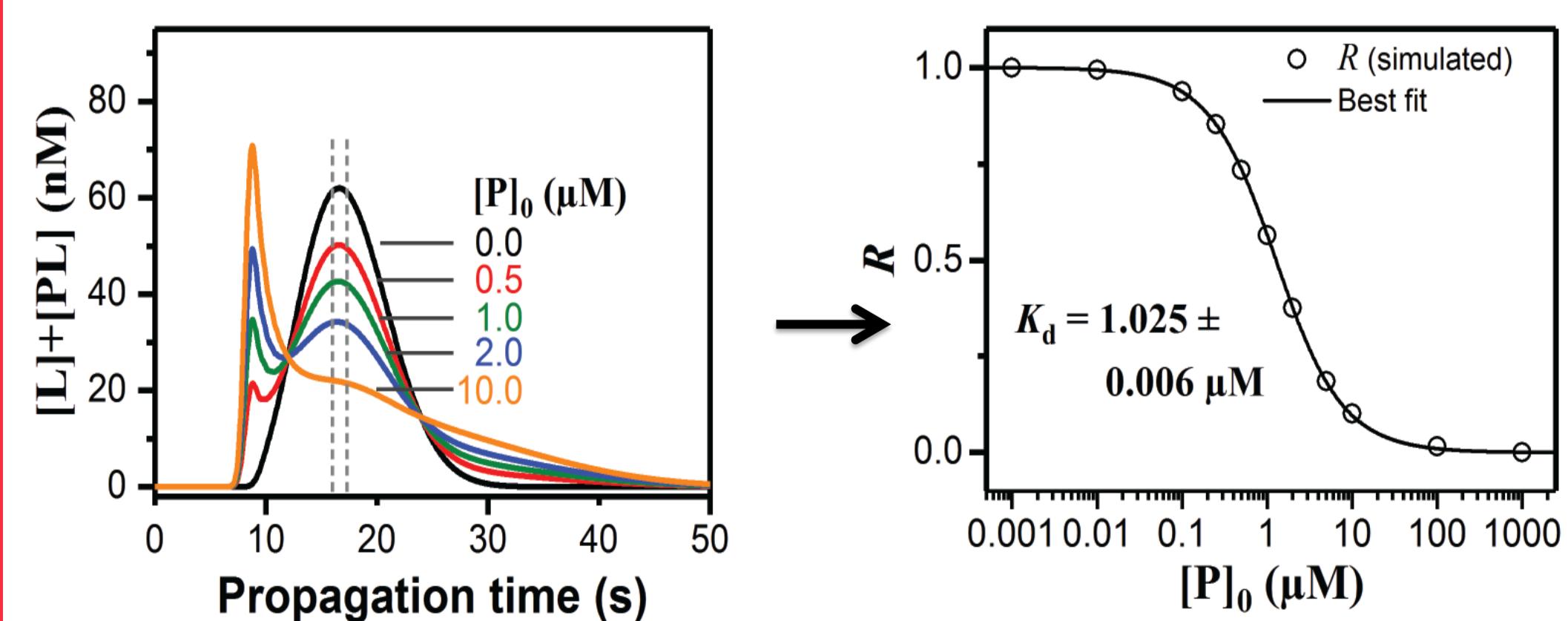
- Hit ranking for later stages of drug development is based on values of  $K_d$  of complexes between a small drug molecule and a target (protein).
- Currently mainly calorimetric and biosensoric approaches are used to find  $K_d$  of such complexes, but they suffer from inaccuracies as large as multiple orders of magnitude.
- We recently introduced "Accurate Constant via Transient Incomplete Separation" (ACTIS), a non-biosensoric and non-calorimetric approach for finding  $K_d$ , which appears to be free of inherent sources of inaccuracy

## 2. MODEL

Reversible binding of proteins (P) to small-molecule ligands (L) to form a complex (PL) was taken as our model

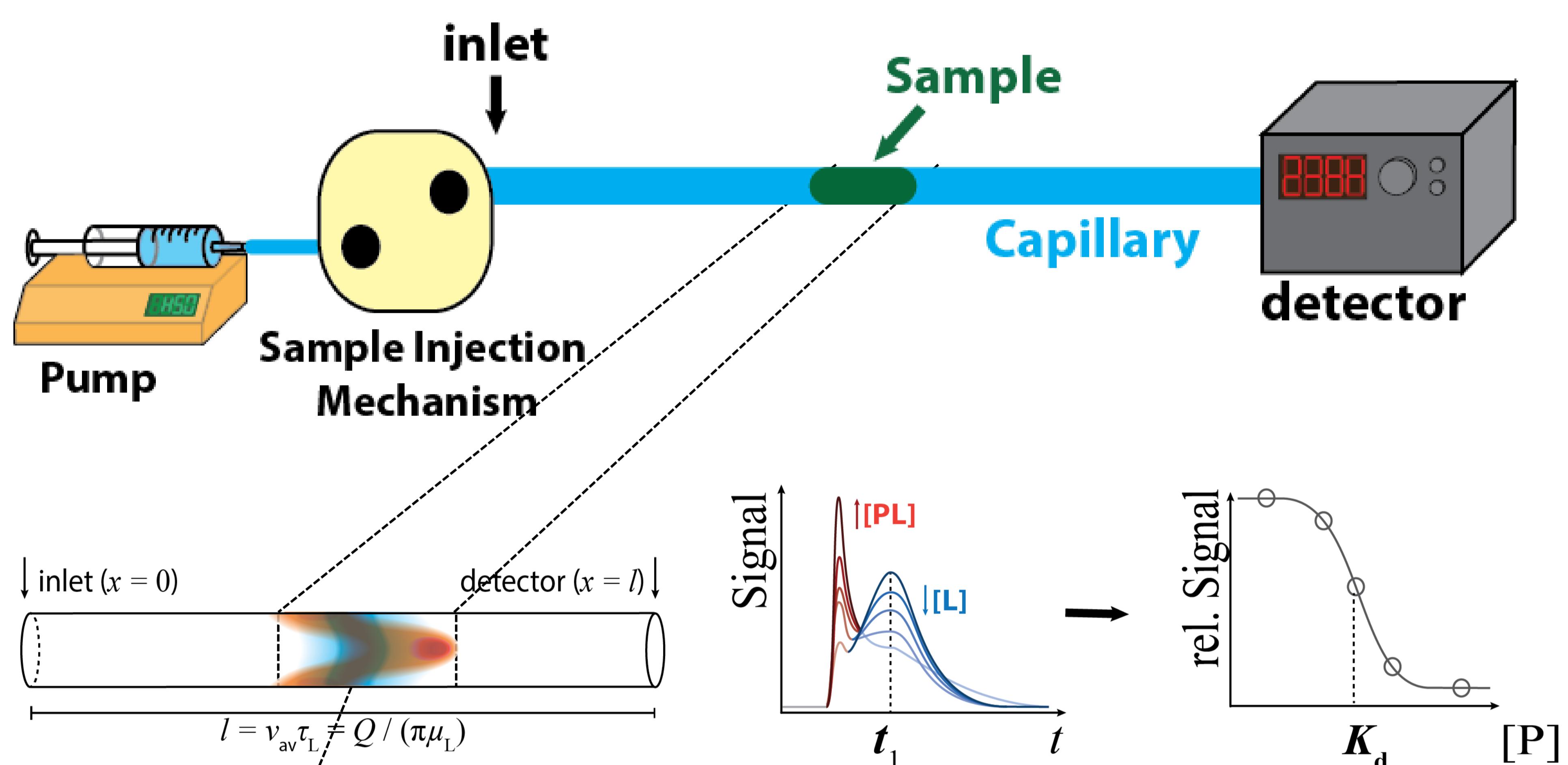


## 4. SIMULATIONS



Accuracy of less than 3 % with numerical simulations including non idealities of a real experiment

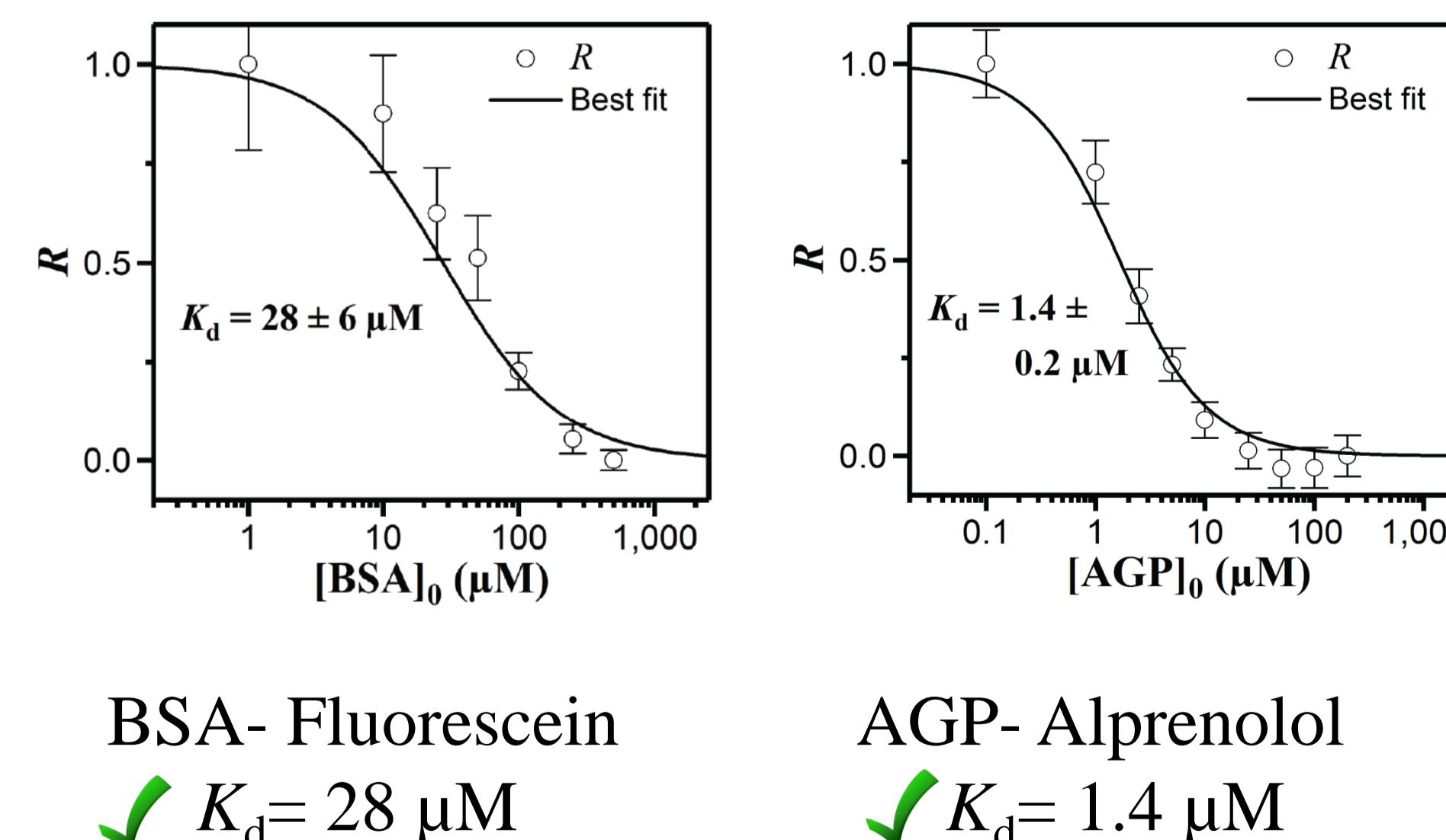
# AS SIMPLE AS TIS



## ALL YOU NEED FOR $K_d$ DETERMINATION:

- Capillary, valve, pump and a detector
- Equilibrium mixture of your system
- 60 to 90 seconds for a run

## 5. EXPERIMENTS

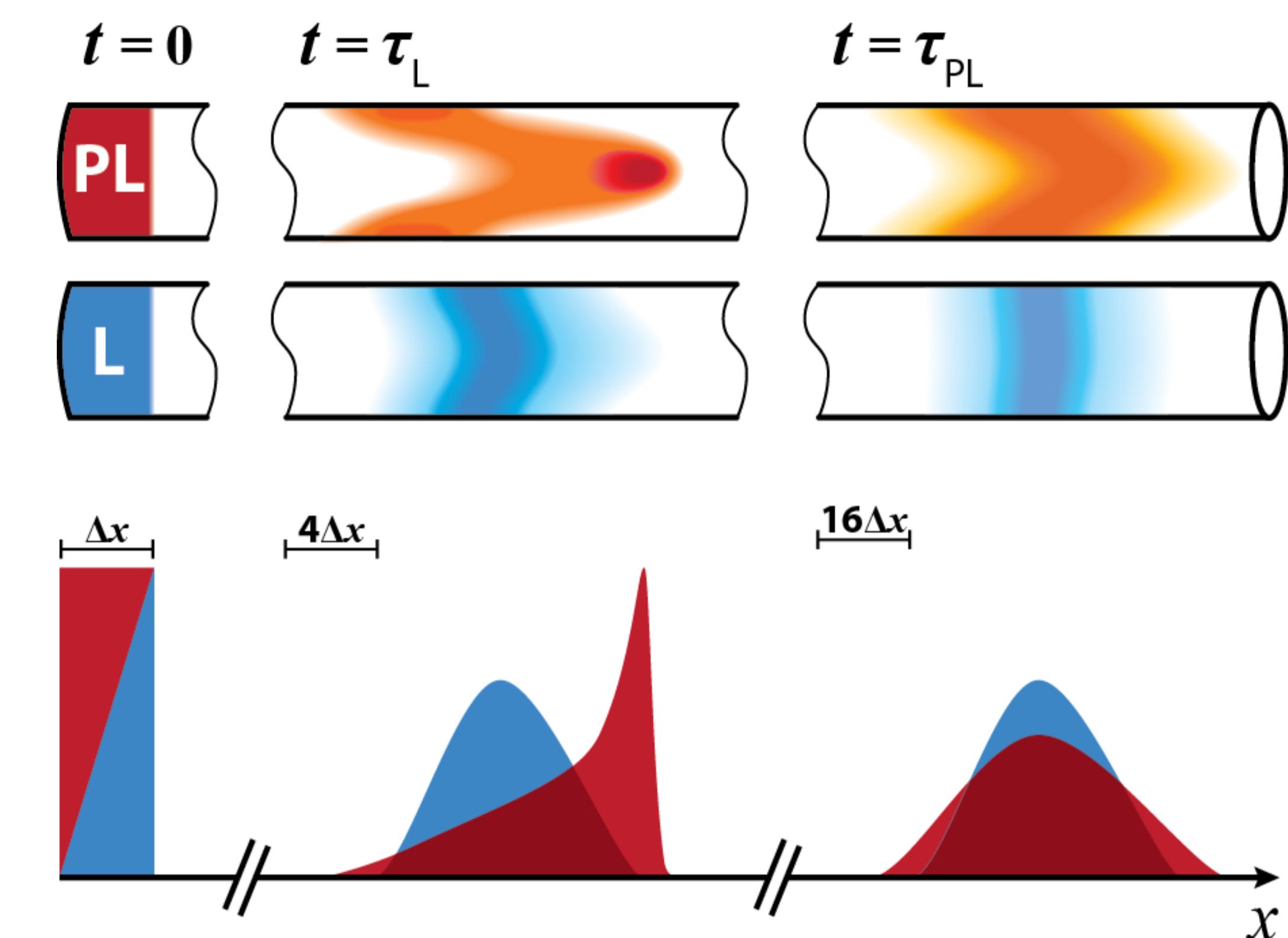


Experimental results are in agreement with literature values

## 6. ADVANTAGES AND LIMITATIONS

- Fast enough: Not prone to protein absorption
- Label-free and immobilization-free
- Compatible with most detectors
- Simple instrumentation
- Interacting species should have at least 2 times difference in diffusion coefficient
- Upper  $K_d$  value limited by protein solubility
- Lower  $K_d$  value limited by limit of detection of the ligand

## 3. TRANSIENT INCOMPLETE SEPARATION (TIS)



- $\tau_x$  is  $a^2 / \mu_x$  where  $a$  is the capillary radius and  $\mu_x$  the diffusion coefficient of specie  $x$
- At  $t = \tau_L$  L is fully diffused and PL is not fully diffused
- The separation is incomplete i.e. there is an overlap in distributions and transient i.e. no separation at  $t = \tau_{PL}$

## 7. CONCLUSION AND FURTHER STUDIES

ACTIS been successfully used to measure the  $K_d$  of Protein – Small molecule. The next steps are measuring  $K_d$  for :

- Protein – Aptamer interactions
- Protein – Protein interactions

### Reference

[1] Sisavath, N.; Rukundo, J. L.; Le Blanc, J. C. Y.; Galievsky, V. A.; Bao, J.; Kochmann, S.; Stasheuski, A. S.; Krylov, S. N. *Angewandte Chemie* 2019, 131 (20), 6707-6711.

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