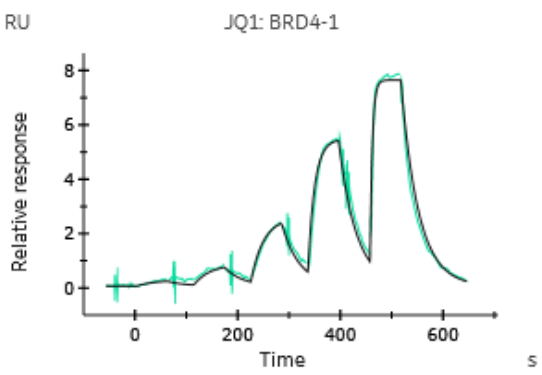
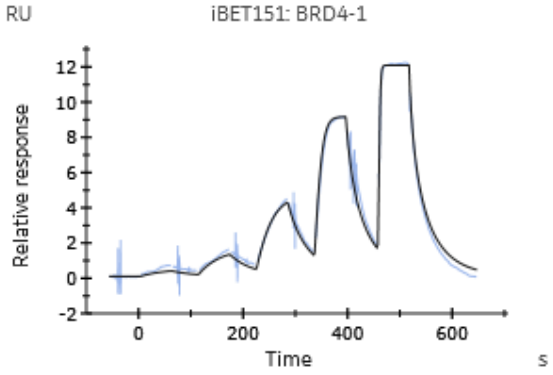
# SPR study of BRD4-1

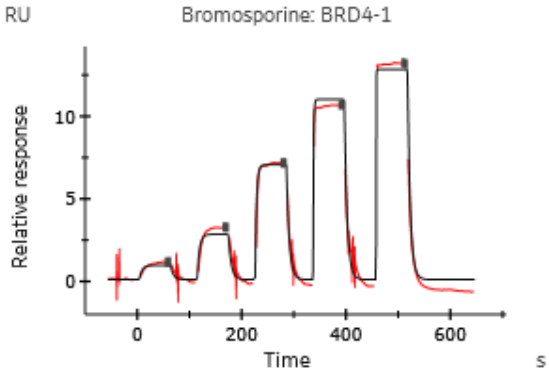
(Bromodomain-containing protein 4 domain 1**,** Protein HUNK1)

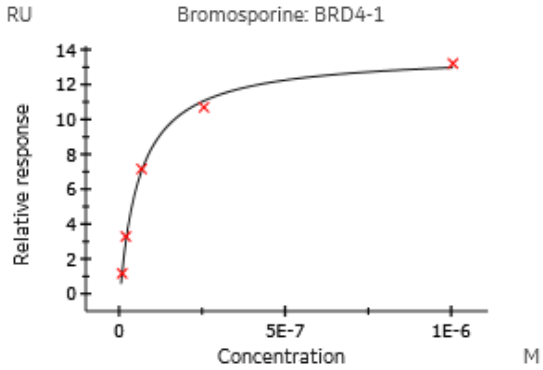
- **CAT#:** BRD4-1
- **Enzyme:** Human BRD4-1
- **Scientific Information:** O60885 (http://www.expasy.org/uniprot/O60885)

- **Close affinity, different kinetics:** JQ1 and Bromsporine both showed sub-nano molar binding affinity to the BRD4-1. Bromosporine dissociates about10 times faster than JQ1, which reflects a short on-target residence time.



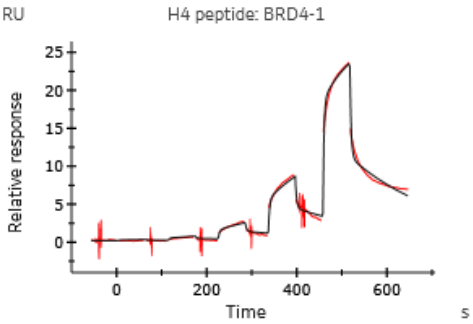




| Compound | ka (1/Ms) | kd (1/s) | KD (M) | KD (M) by steady state affinity fitting | to 50% dissociation ($t_{1/2}$) |
|---|---|---|---|---|---|
| **JQ1** | 1.56E+06 | 2.14E-02 | 1.37E-08 | N/A | 32.4s |
| **Bromosporine** | 3.15E+06 | 1.85E-01 | 5.86E-08 | 6.45E-8 | 3.8s |



*Quality Data. Quality Support.*

- **Reveal Bivalent binder**
  Data from H4 peptide (Histone H4 peptide (1-21) K5/8/12/16Ac) could only be fitted well to a bivalent analyte model. This agrees with previously published structural studies. As KD1 is significantly lower than KD2, it can be seen as the apparent KD for comparing with IC50 data.




| Compound | ka1 (1/Ms) | kd1 (1/s) | ka2 (1/RUs) | kd2 (1/s) | KD1 (M) | KD2 (M) |
|---|---|---|---|---|---|---|
| **H4 peptide** | 3.94E+04 | 3.46E-01 | 1.85E-04 | 2.53E-03 | 8.78E-06 | 1.36E+01 |

- **Data reproducibility**
  Kinetic fitting parameters of three independent run of JQ1 binding to BRD4-1

| Replicate | ka (1/Ms) | kd (1/s) | KD (M) |
|---|---|---|---|
| **Run 1** | 1.56E+06 | 2.14E-02 | 1.37E-08 |
| **Run 2** | 1.89E+06 | 2.91E-02 | 1.54E-08 |
| **Run 3** | 2.08E+06 | 2.72E-02 | 1.33E-08 |