

## Supplementary Information - METHODS

### **Library**

The library screened contained 1664 compounds, arrayed in 96-well plates (Thermo Scientific™ Nunc™ 96-Well Polystyrene Conical Bottom) as single compounds at 10 mM in DMSO, sealed and stored at -20 °C (for more details, refer to Hamon *et al.* (1)). The quality of all compounds was assured by the vendors as greater than 90% pure with provided quality control data.

### **HTRF Setup Assays**

Titration curves were optimized, keeping donor and donor-coupled proteins at constant concentration and increasing acceptor/acceptor-coupled proteins concentrations to avoid the 'hook effect' (2). Screening conditions were selected at 80% of the maximum observed signal when assessing the titration curve. This protocol ensures the optimization of a sufficient signal to noise ratio to perform HTS with adequate Z'. This optimization is crucial to achieve optimal sensitivity required for the detection of even weak small-molecule inhibitors of each protein-protein interaction. An estimated minimum of 2 to 3 value for signal to noise is necessary to ensure reliable HTS. Such signal to noise ratio was observed for each PPI complex at 80% of the maximum measured signal. The estimated time to reach equilibrium, the period of stability of the measured signal and the DMSO tolerance were evaluated to ensure stability of the signal during HTS (data not shown).

### **HTRF screen**

HTRF assays were performed in white 384 Well Small Volume™ HiBase Polystyrene Microplates (Greiner) with a total working volume of 20 µL. Compounds were dispensed, with either 400 nL per well (2% final DMSO), from a concentration stock of 1mM in 100% DMSO for the primary screen, or with serial DMSO dilutions for secondary screening, counter screen and IC<sub>50</sub> measurement assays, using a Mosquito Crystal pipetting robot platform (TTP labtech). For bromodomain selectivity assays, 200 nL of compounds were dispensed to obtain a 1% final concentration of DMSO. Primary screening assays have been performed in monoplicate while secondary screenings, counter screens and IC<sub>50</sub> measurements were performed in triplicates.

All HTRF reagents were purchased from CisBio Bioassays and reconstituted according to the supplier protocols. For each assay 14.7 µL of mix1 (Table S3) is added in the assay wells, containing previously dispensed inhibitors, according to the final concentration and buffer described in Table S3, using a Biomek NX MC pipetting robot (Beckman). After 1 h incubation, 4.9 µL of protein B is added. HTRF signals were measured, after a final incubation, using a PHERAstar FS (BMG Labtech) with an excitation filter at 337 nm and

fluorescence wavelength measurement at 620 and 665 nm, an integration delay of 60  $\mu$ s and an integration time of 400  $\mu$ s. Results were analyzed with a two-wavelengths signal ratio: [intensity (665 nm)/intensity (620 nm)]\*10<sup>4</sup>. Percentage of inhibition was calculated using the following equation: % inhibition = [(compound signal) - (min signal)] / [(max signal) - (min signal)] \* 100, where 'max signal' is the signal ratio with the compound vehicle alone (DMSO) and 'min signal' the signal ratio without protein B (Table S3). The Z' factor is calculated using the following equation:  $Z' = 1 - [3(\text{SD of max}) + 3(\text{min SD})] / [(\text{mean max signal}) - (\text{mean min signal})]$ , where SD is the standard deviation. For IC<sub>50</sub> measurements, values were normalized and fitted with Prism (GraphPad software) using the following equation:  $Y = 100 / (1 + ((X / \text{IC}_{50})^{\text{Hill slope}}))$ .

### **Autofluorescence experiment**

Autofluorescence experiments were performed at 20  $\mu$ M final inhibitor concentration with 2% final concentration of DMSO. 400 nL of compounds were dispensed in 384 well plates as previously described, and 19.6  $\mu$ L of buffer (Hepes 50 mM pH 7.5, 150 mM NaCl, 0.1% BSA (Sigma)) were then added. After overnight incubation at 4 °C HTRF signals were measured. Analyses were performed directly comparing the 620 and 665 nm fluorescence values with the fluorescence values at the same wavelength of the buffer + vehicle (DMSO). Thresholds have been set up at 10 times the control value measured at 665 nm and 50 times the control value at 620 nm.

### **SNAP-tag® labeling**

The HTRF assay for the NS3/NS5 complex has been set-up using a SNAP-tag construct. This 20 kDa tag is based on a family of enzymes called « suicide enzymes » as they react covalently with their substrate which blocks the enzyme and prevents any subsequent enzymatic activity (3). SNAP-tag is a mutant version of the DNA repair protein O<sup>6</sup>-alkylguanine-DNA alkyltransferase that reacts specifically and rapidly with benzylguanine (BG) derivatives, leading to an irreversible covalent bond. A large variety of BG derivatives have been engineered to label proteins of interest with fluorophores compatible with *in vivo* imaging, microscopy or even immobilization on a specific support. We used one of these derivatives, 'BG Red', as acceptor for our HTRF assay. This type of labeling presents a main advantage compared to « classic » labeling since it does not require secondary labeled-antibodies to label the protein of interest with a HTRF compatible fluorophore.

SNAP-tag tagged protein were incubated at a final concentration of 20  $\mu$ M in presence of 3 times excess of Tag-lite ® SNAP Red (CisBio Bioassays) in Hepes 50 mM pH 7.5, 150 mM NaCl overnight at 4 °C in the dark in low absorbent tubes. Labeled protein and unreacted dye were then separated using Illustra NAP-5 Columns (GE healthcare). Protein concentration and labeling efficiency was evaluated by measuring protein and dye absorbance,

respectively at 280 and 650 nm using a NanoDrop 2000 (Thermo scientific). Proteins were stored at -80 °C after addition of BSA at a final concentration of 0.1%.

### ***Molecular biology***

#### *Dengue Virus Proteins*

Dengue virus proteins were amplified from a synthetic gene (GeneArt, Life technologies) of dengue serotype 3 of Singapore. Non-structural protein 3 (NS3) fused, through G4-S-G4 linker, on the N-terminal part with hydrophilic core of 18 amino acid (43-60) of NS2B protein (NS3-NS2B) of dengue virus serotype 3 (DV3), amplified from the synthetic gene (forward primer :

GGGGACAAGTTTGTACAAAAAAGCAGGCTTAGAAAACCTGTA CTTCCAGGGTGCAGATC  
TGACCGTTGAAAAAGC, reverse primer:

GGGGACCACTTTGTACAAGAAAGCTGGGTCTATTACCAAATTGCGCCTTCGCTTTC),

have been cloned in a pETG-30A (Arie Geerlof, EMBL, Hamburg, Germany) by Gateway® recombination (Life technologies) for GST fusion. For the cloning of methyltransferase domain of non-structural protein 5 (MTase NS5) we used a modified Gateway® pDEST™ 17 Vector (Life technologies) (insertion of an XhoI restriction site between His tag and attR1 site by site directed mutagenesis). SNAP-tag previously amplified from pSNAP-tag® (T7)-2 Vector (New England Biolabs) (forward primer: GGG GCT CGA GTT ATG GAC AAA GAT TGC GAA ATG AAA C, reverse primer: ATA TAC TCG AGT CCC AGA CCC GGT TTA CCC AG) was inserted by restriction ligation in XhoI site. The coding sequence of MTaseNS5 DV3 amplified (forward primer:

GGGGACAAGTTTGTACAAAAAAGCAGGCTTAGAAAACCTGTA CTTCCAGGGTGGTACAG  
GTAGCCAGGGTG, reverse primer:

GGGGACCACTTTGTACAAGAAAGCTGGGTCTATTAATGACGGGTGCCTGCACCCAG)

from the synthetic gene was then sub cloned in this vector by Gateway® recombination (Life technologies) resulting in a MTase NS5 fused with His and SNAP-tag on the N-terminal part.

#### *GRASP55 PDZ domains*

To generate GRASP55 expression constructs, the full-length mouse GORASP2 cDNA encoding the mGRASP55 protein was amplified by polymerase chain reaction (PCR) using the oligonucleotides CTCGAGATGGGCTCCTCGCAGAGC and GGATCCCCAGAAGGCTCTGAAGCATCTGC.

The amplification product was cloned in the pGEM - T Easy vector (Promega). Then, this mouse GORASP2 cDNA was used as template for PCR amplification of the open reading frame (ORF) for mGRASP55 PDZ12 (aa 2 - 208) and mGRASP55 Full - length (FL) (aa 2 - 451) using forward and reverse oligonucleotides flanked by attb1 and attb2 recombination sites. The following primers pairs were used:

the forward primer was: GGGGACAAGTTTGTACAAAAAAGCAGGCTTCGGCTCCTCGCAGAGCGTCGAGAT and the reverse primers were : GGGGACCACTTTGTACAAGAAAGCTGGGTCTTATTCAAAGGGGCGTGTAGGTATTCCGGT GCA and GGGGACCACTTTGTACAAGAAAGCTGGGTCTTAAGAAGGCTCTGAAGCATCTGCATCAG AC for mGRASP55 PDZ12 and mGrasp55 FL respectively. The amplicons were cloned by the BP reaction into pDONRZeo to produce the corresponding entry vectors. The coding sequences were transferred by LR cloning in pDEST<sup>TM</sup>15 prokaryotic expression vectors intended to produce the corresponding Nterminal GST-tagged fusion protein.

#### *Syntenin PDZ domains*

Human syntenin1 cDNA (4) was cloned in 3' into the pGEX-5X vector (Amersham Pharmacia Biotech AB) for the expression of recombinant GST-syntenin1 full length.

### ***Protein expression and purification***

#### *Dengue Virus Proteins*

The dengue virus proteins were expressed in T7 Express Competent *E. coli* (NEB). Cells were grown in LB medium (Euromedex) at 37 °C until OD<sub>600</sub> = 0.6 was reached and then induced using 0.5 mM isopropylβD-thiogalactopyranoside (IPTG) and cultured overnight at 17 °C for NS2B-NS3-GST and 5 hrs at 25 °C for MTaseNS5 SNAP-tag fusion. Cells were pelleted by centrifugation (10 min at 7,000g), and pellets were re-suspended in 20 mM HEPES (pH 7,5), 500 mM NaCl, 10% glycerol, 5 mM Imidazole, 2 mM 2-Mercaptoethanol, 1 mg/mL lysozyme, 22 µg/mL DNase I and 0.2 mM of benzamidine. After sonication and centrifugation (30 min at 45,000g), the supernatant was purified on HisPur<sup>TM</sup> Cobalt or GST agarose resin (Thermo Scientific). Elution fractions containing protein were then loaded onto a Superdex 75 or 200 gel filtration column (GE Healthcare) and eluted with 50 mM Hepes (pH 7.5), 300 mM NaCl, 1 mM DTT. Purified proteins were further concentrated and stored at -80 °C.

#### *GRASP55 PDZ domains*

The production of N-terminal GST-tagged GRASP fusion proteins were accomplished by induction for 3 h at 37 °C or 18 h at 25 °C with 0.2 mM IPTG in *E. coli* BL21 (DE3) bacteria cells transformed with the purified pDEST<sup>TM</sup>15 GRASP expression plasmids. Fusion proteins were recovered from the cell lysates by conventional affinity chromatography on Glutathione resin.

#### *Syntenin PDZ domain*

*E.coli* ER2566 cells were transformed with the human syntenin1 pGEX-5X expression vector.

Expression of N-terminally GST tagged syntenin 1 full length was induced at 30 °C and by the addition of IPTG (Fisher Scientific). Protein was purified using GSTrap4B columns 28-4017-45 (GE Healthcare) using an Akta Explorer system (GE Healthcare).

#### *Nef protein & SH3 domain from Hck*

For the Hck SH3 domain, the prokaryotic expression vector and the GST affinity chromatography purification protocol have been previously described in (5).

For the HIV-1 Nef WT protein, the prokaryotic expression vector and the His affinity chromatography purification protocol have been kindly provided by Dr. Sebastian Breuer as described in (6). For both Hck-SH3 and HIV-1 Nef WT, protein peak fractions were further purified using a Superdex 75 10/300 GL column (GE Healthcare) in 20 mM TRIS pH 8.0, 150 mM NaCl Buffer.

#### *BRD4*

For isothermal titration Calorimetry (ITC), thermal shift assay (TSA) and crystallogenes, BRD4(1) was produced and purified using a histidine tag affinity chromatography as described by Filipakopoulos *et al.* (7). For these experiments, a pNIC28-BSA4 expression vector containing BRD4(1) and a Tobacco Etch Virus (TEV) protease cleavage site have kindly been provided by Stefan Knapp laboratory from the SGC at the University of Oxford. After size exclusion chromatography, the fractions presenting pure BRD4 after TEV cleavage of the histidine tag were pooled and concentrated to 25 mg/mL for crystallogenes. For ITC assays, the protein was concentrated up to at 6 mg/mL and the DTT was removed using a buffer exchange column (PD10 from GE healthcare) equilibrated with 10 mM HEPES pH 7.5, 150 mM NaCl. For HTRF experiments, a BRD4(1) synthetic gene that includes a TEV cleavage site was purchased from LifeTechnology in a pDONR transport vector before cloning into a pDEST<sup>TM</sup>15 expression vector for GST affinity purification. Protein production and purification was carried out using similar protocols and buffers as used for the His-BRD4(1) system. Purification was carried on GST affinity resin (Thermo Scientific) and reduced glutathione was used for protein release. GST-BRD4(1) was further purified by size exclusion chromatography on a Superdex 16/60 Hiload column (GE Healthcare) using 20 mM TRIS pH 8.0, 150 mM NaCl Buffer.

#### **Bromodomain selectivity Profiles**

Selectivity profiles of bromodomain inhibitors were performed as described in HTRF screen and HTRF Setup Assays sections. Concentration of histone peptide was optimized to ensure sufficient signal to noise ratio, sufficient sensitivity for detection of weak inhibitors and comparable data from one bromodomain to another. HTRF detection reagents

(EPIgeneous™ Binding Domain kits) were purchased from Cisbio Bioassays and used according to supplier's protocol. GST tagged bromodomain proteins were purchased from BPS Bioscience and histone peptide from Anaspec.

### **Fusion protein, counter screen assays**

**GST-biotinylation:** Purified Glutathione S-transferase was biotinylated with Sulfo-NHS-LC-biotin (ThermoFischer) at a 10 : 1 biotin : protein molar ratio in Phosphate Buffer Saline pH 8.3 for 40 min on ice followed by quenching with 100 mM glycine pH 8.3 and removal of free biotin by desalting on PD10 column.

**GST-SNAP:** GST-Snap fusion protein was provided as custom reagent from Cisbio Bioassays and labeled with BG-Red as previously described.

**GST-His:** GST-His fusion protein has been produced via Gateway plasmid pETG30A (Arie Geerlof, EMBL, Hamburg, Germany) in *E. coli* as previously described for dengue virus protein production.

### **Cells and Cell Culture**

The human leukemia cell line Jurkat (ATCC® TIB-152) was maintained in RPMI-1640 medium supplemented with 10% FBS at 37 °C and 5% CO<sub>2</sub>. Human osteosarcoma cell line (U2OS, ATCC® HTB-96™) was maintained in DMEM supplemented with 10% FBS at 37 °C and 5% CO<sub>2</sub>.

### **Western blot**

Non-treated Jurkat cells and Jurkat cells treated during 24 hours with compound #1, compound #2 or DMSO were lysed in RIPA lysis buffer (Tris HCl pH 7.5 50 mM, NaCl 150 mM, Triton 1%, SDS 0.1%, sodium deoxycholate 1%) supplemented with protease inhibitor cocktail (P8340, Sigma-Aldrich) and 1 mM PhenylMethylSulfonyl Fluoride (Sigma-Aldrich). 50 µg of protein were loaded onto 10% acrylamide SDS/PAGE and then transferred to nitrocellulose Hybond C-extra membranes, 45 micron (GE Healthcare). The membranes were saturated with 5% (wt/vol) skim milk in TBST [Tris-buffered saline/0.1% (vol/vol) Tween 20] 1 hour at room temperature and incubated with anti-myc antibody (clone 9E10, sc40 Santa Cruz) at a 1 : 500 dilution in 0.5% (wt/vol) skimmed milk in TBST overnight at 4 °C. Membranes were then washed with TBST, incubated with an HRP-conjugated anti-mouse secondary antibody (polyclonal goat anti mouse P0447, Pierce) at a 1 : 20,000 dilution in TBST 1 hour at room temperature. Immunoreactive bands were revealed using SuperSignal™ West Dura Extended Duration Substrate (Pierce) detection reagents. Quantification was performed using ImageJ software.

### **Fluorescence Recovery After Photobleaching (FRAP)**

FRAP studies were performed essentially as described (8). In brief, U2OS cells were transfected (Fugene HD; Roche) with mammalian over-expression constructs encoding GFP fused to the N-terminus of human full-length BRD4. The FRAP and imaging system consisted of a Zeiss LSM 710 laser-scanning and control system (Zeiss) coupled to an inverted Zeiss Axio Observer.Z1 microscope equipped with a high-numerical-aperture (N. A. 1.3) 40 x oil immersion objective (Zeiss). Samples were placed in an incubator chamber capable of maintaining temperature and humidity. FRAP and GFP fluorescence imaging were both carried out with an argon-ion laser (488 nm) and with a PMT detector set to detect fluorescence between 500-550 nm. Once an initial scan had been taken, a region of interest corresponding to approximately 50% of the entire GFP positive nucleus was empirically selected for bleaching. A time lapse series was then taken to record GFP recovery using 1% of the power used for bleaching. The image datasets and fluorescence recovery data were exported from ZEN 2009, the microscope control software, into Microsoft Excel to determine the average half-time for full recovery for 10-20 cells per treatment point. Where appropriate, inhibitor was added 1 hour before imaging, which was carried out 24 hours after transfection.

### ***Isothermal titration calorimetry***

ITC was used to evaluate the thermodynamics parameters of the binding between BRD4(1) and the selected compounds, using ITC conditions previously described by Filippakopoulos *et al.* (7). Purified BRD4(1) was extensively dialyzed in the ITC buffer containing 10 mM HEPES pH 7.5 and 150 mM NaCl. Compounds were diluted directly in the last protein dialysate prior to experiments. Titrations were carried out on a MicroCal ITC200 microcalorimeter (GE Healthcare, Piscataway, NJ). Each experiment was designed using a titrant concentration (protein in the syringe) set 10 to 15 times the analyte concentration (compound in the cell generally between 10 and 30  $\mu$ M) and generally using 13 to 17 injections at 15 °C. A first small injection (generally 0.2  $\mu$ L) was included in the titration protocol in order to remove air bubbles trapped in the syringe prior titration. Raw data were scaled to zero by subtracting a negative control experiment (buffer injected in the cell containing the same compound concentration) or after setting the zero to the titration saturation heat value when possible. Integrated raw ITC data were fitted to a one site non-linear least squares fit model using the MicroCal Origin plugin as implemented in Origin 9.1 (Origin Lab). Finally,  $\Delta G$  and  $T\Delta S$  values were calculated from the fitted  $\Delta H$  and  $K_A$  values using the equations  $\Delta G = -R.T.\ln K_A$  and  $\Delta G = \Delta H - T\Delta S$ .

### ***Differential scanning fluorimetry***

Differential scanning fluorimetry (DSF) or Thermal Shift Assay (TSA) was performed as

described previously (9). A protein/Sypro® orange mix containing 2  $\mu$ M BRD4(1) and a 1 : 1,000 dilution of dye in DMSO (as supplied by Life Technologies) was prepared just before plate setup in 50 mM HEPES pH 7.5, 200 mM NaCl. 19.5  $\mu$ L of the protein/Sypro orange mix was aliquoted into a 96-well plate and 0.5  $\mu$ L of compounds (2 mM 100% DMSO, final concentration of 50  $\mu$ M 2.5% DMSO) or DMSO for control were dispensed. For experiment performed with DTT and tween, 5mM of DTT or 0.012% (0.3 CMC) were added to previously described buffer. After sealing with optical tape, the plates were centrifuged at 1,000 rpm for 1 min at room temperature. Each experiment was performed in triplicate. Thermal melting experiments were carried out using a CFX96 Real Time PCR machine (Biorad). The plates were first equilibrated at 25 °C for 2 min in the PCR machine before starting the thermal melting experiment. The plates were heated by 1 °C per 60 sec from 25 to 95 °C and the fluorescence intensity was recorded at each temperature step using the built-in FRET filter. Raw fluorescence data were treated using Excel files adapted from (9) and  $T_m$  measured using a Boltzmann fit equation from GraphPad Prism software.

### ***Crystallography***

BRD4(1)-Inhibitor co-crystallization was performed at 19 °C (292K) using the hanging drop vapor diffusion method. For the complex with 1 mM of compound #2, 12 mg/mL of BRD4(1) preparation was mixed at a 1 : 1 ratio with the precipitant solution (0.3 M Sodium Formate, 0.1 M NaCl, 22% (w/v) PEG 3350, 10% (w/v) ethylene glycol) and crystals grew to diffracting quality within 5-7 days. Co-crystallization experiments with 5 mM of compound #1 were carried using the same protocol (Sodium Formate was replaced by 0.3 M NaNO<sub>3</sub>) and crystals grew to diffracting quality within 3 weeks. Crystals were cryo-protected using the precipitant solution supplemented with 10% glycerol and were flash frozen in liquid nitrogen. Data for compound #1 and compound #2 were respectively collected at the ESRF beamlines ID23-2 and ID30A-3. Indexing, integration and scaling were performed using XDS (10). Initial phases were calculated by molecular replacement with Phaser MR (CCP4 suite) (11) using a model of the first domain of BRD4 (extracted from the Protein Data Bank accession code: 2OSS). Initial models for the protein and the ligands were built in COOT (12). The cycles of refinement were carried out with Refmac5 (CCP4 suite (11)). Data collection and refinement statistics can be found in Table S2. The models and structure factors have been deposited with Protein Data Bank accession code for compound #1: 5DLZ and compound #2: 5DLX.

### ***“PAINS” and Aggregators predictions***

Pan-assay interference compounds (“PAINS”) predictions are indicated based on FAFDrugs<sup>3</sup> (<http://fafdrugs3.mti.univ-paris-diderot.fr/index.html>) (13–15). Default parameters and “Filter Pan Assay Interference Compounds (PAINS) Filter A” have been chosen for analysis.

Aggregator predictions are indicated based on Aggregator advisor website (<http://advisor.bkslab.org/>) (16).

### **ACCESSION CODES**

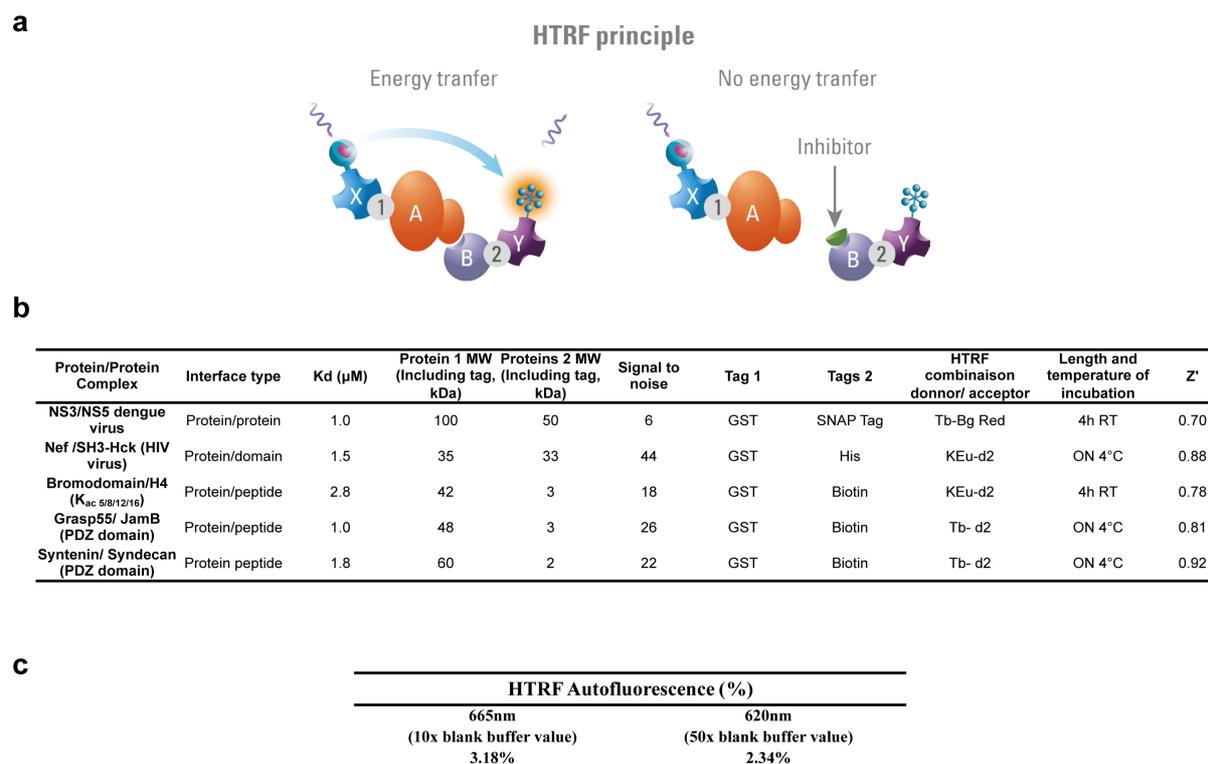
Coordinates and structure factors of refined BRD4(1) complexed with compound 1 and 2 have been deposited in the Protein Data Bank with accession code 5DLZ and 5DLX.

## SI References

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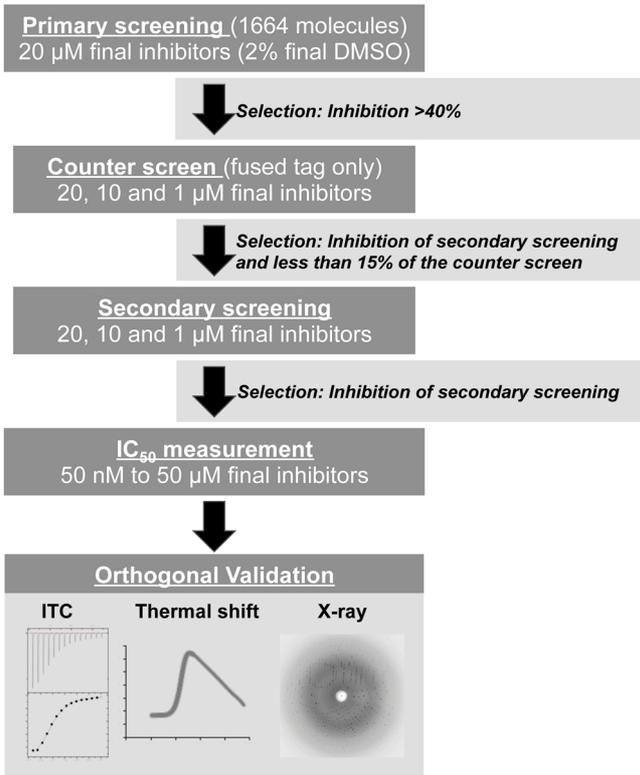
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## Supplementary Information - Figures

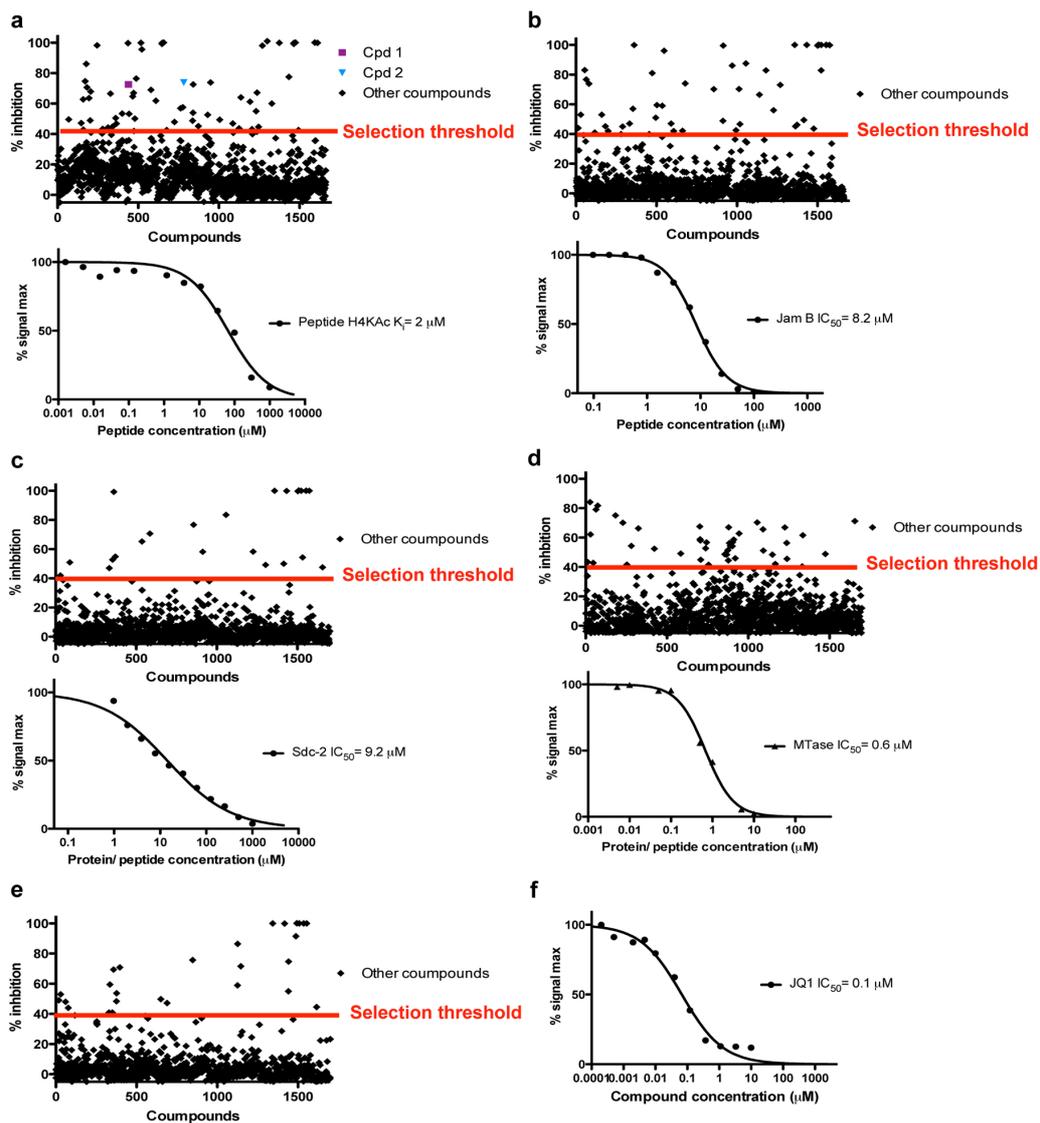


**Figure S1: Principle of the HTRF assays and characterization of the 2P2I<sub>3D</sub> chemical database.** a) HTRF assay principle, b) HTRF assays parameters, c) Summary of the autofluorescence experiments. Compounds have been considered as autofluorescent, when fluorescence values were respectively higher than 10 and 50 times the values of the buffer alone at 665 and 620 nm.

## General Screening Cascade

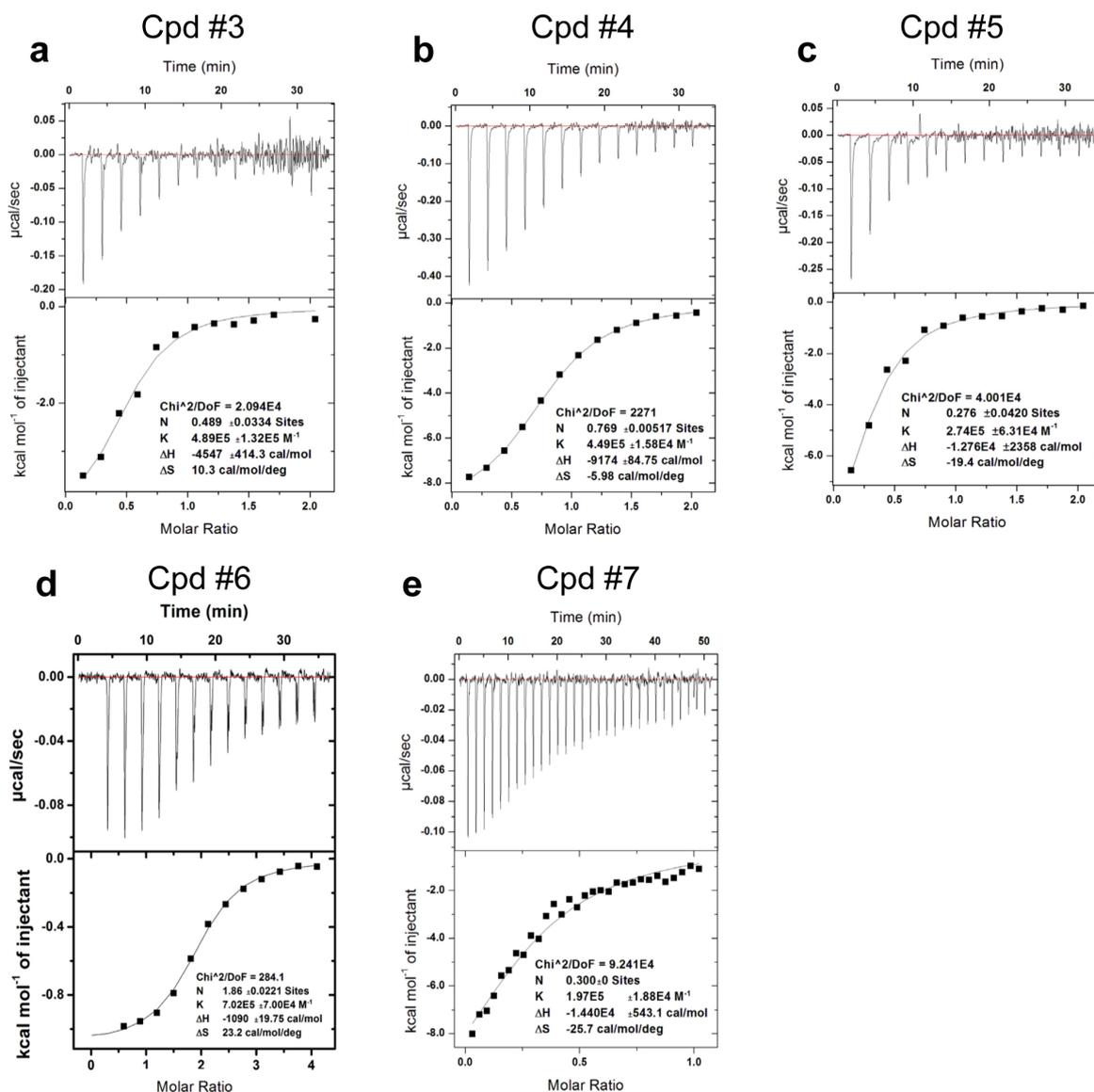


**Figure S2: General screening cascade.** Primary screenings were performed at 20  $\mu\text{M}$  final concentration of each compounds. We selected compounds with a percentage of inhibition higher than 40% for the second step (secondary screenings and counter screens). We selected for the subsequent IC<sub>50</sub> measurements, only compounds inhibiting the secondary screening and less than 15% of the counter screen signal. Compounds with suitable dose response curves were validated by orthogonal experiments (isothermal titration calorimetry, thermal shift assays and X-ray crystallography).

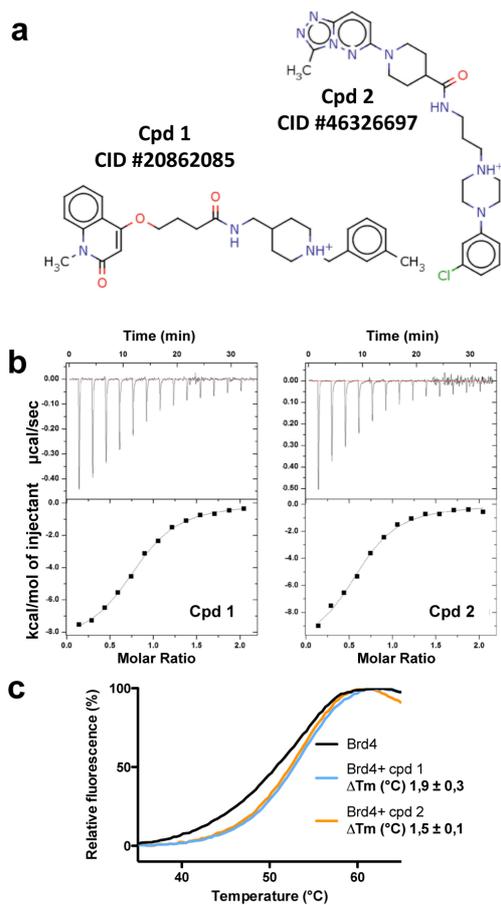


**Figure S3: Overall quality-control (distribution) of the HTRF assay.** Distribution of the percentage of inhibition values obtained during the primary screenings and competition curve obtained with untagged protein of peptide of HTRF assay.

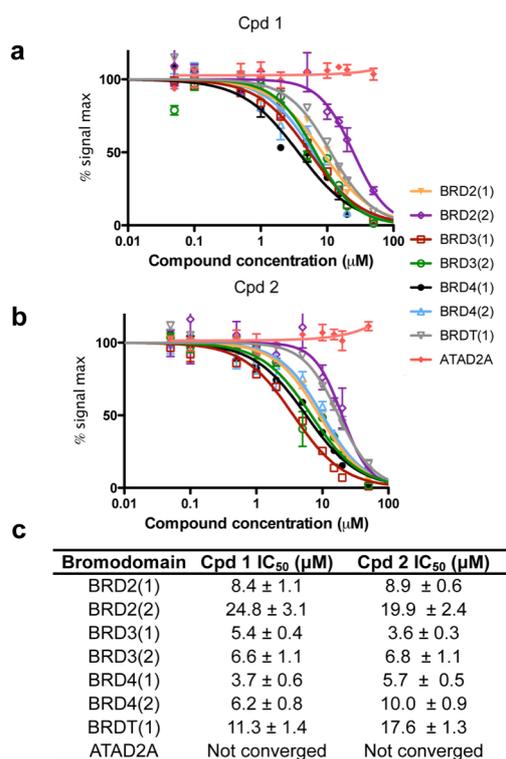
a) Bromodomain screening, Compound #1 is highlighted in purple and compound #2 in blue. b) Grasp screening, c) Syntenin screening, d) Dengue screening and e) Nef screening, competition curves are not available with HCK peptide. f) competition curve of BRD4/H4 peptide assay with (+) JQ1 compound.



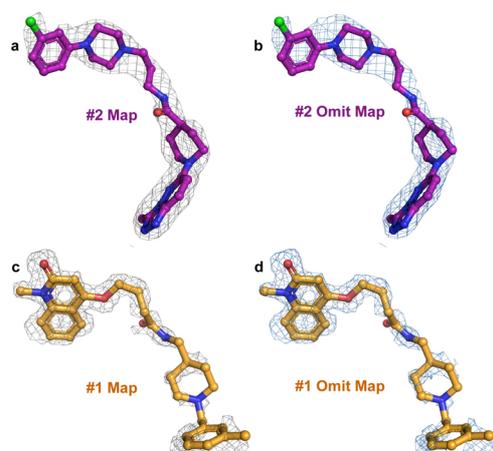
**Figure S4: ITC thermograms for the binding of “thermal shift sensitive” compounds #3 (a) to #7 (e) to BRD4(1) protein**



**Figure S5: Chemical structures and biophysical characterization of compounds #1 and #2.** a) Chemical structures of compounds #1 and #2. b) ITC thermograms for the binding of compounds #1 ( $K_D = 1,8 \mu M$ ) and #2 ( $K_D = 2.0 \mu M$ ) to BRD4(1). c) Thermal shift experiments performed as 3 independent experiments with compounds #1 and #2 on bromodomain BRD4(1). The black curve represents BRD4(1) alone in presence of 2.5% DMSO, the blue curve BRD4(1) with a 25 fold excess of compound 1 ( $50 \mu M$  2.5% DMSO,  $\Delta T_m = 1.9 \text{ }^\circ C$ ) and orange curve with compound 2 ( $\Delta T_m = 1.5 \text{ }^\circ C$ ).

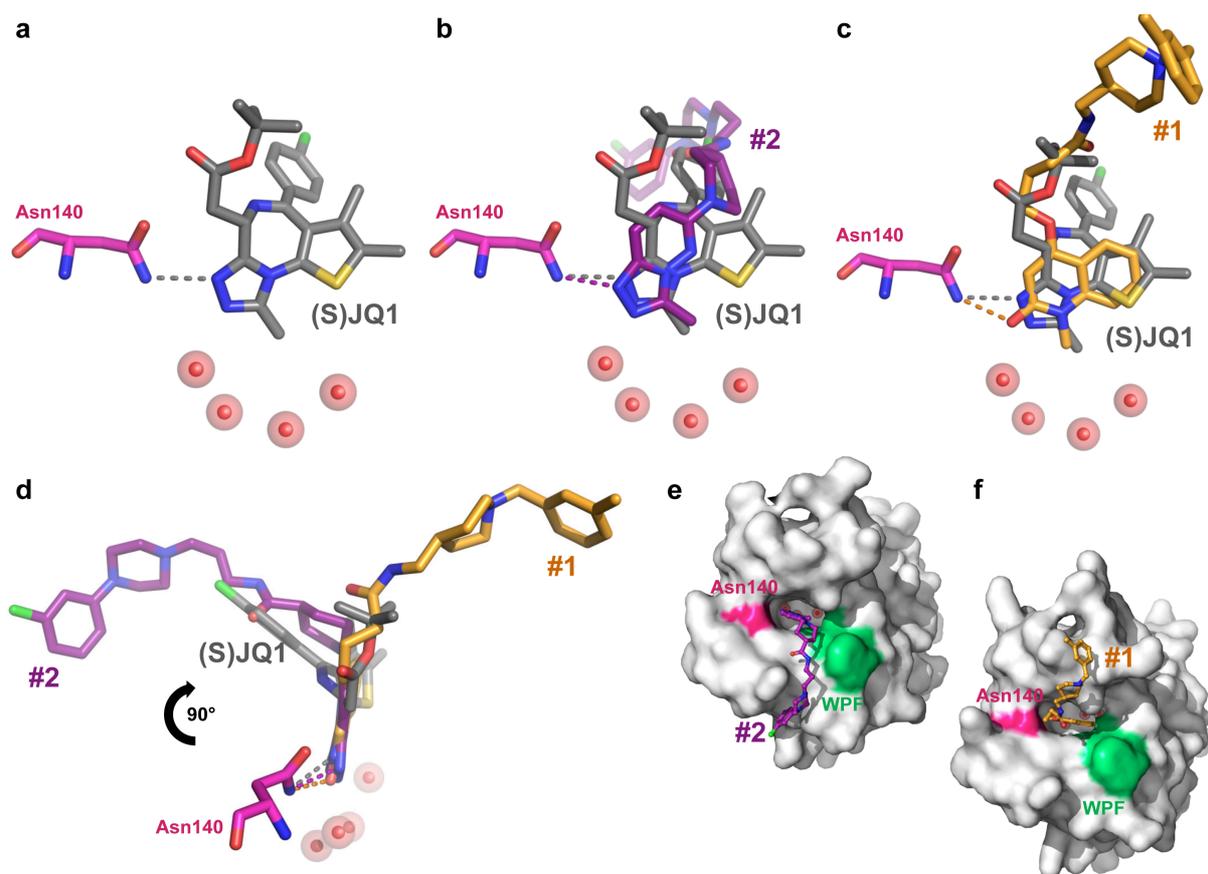


**Figure S6: Selectivity of compounds #1 and #2.** a) Selectivity profiles of compounds #1 and b) #2 on BET bromodomains, BRD2(1) (yellow), BRD2(2) (purple), BRD3(1) (red), BRD3(2) (green), BRD4(1) (black), BRD4(2) (blue), BRDT(1) (grey), ATAD2A (orange), using HTRF assays  
 c) IC<sub>50</sub> values (± SEM, N=3) of bromodomain selectivity experiments with compound #1 and compound #2.



**Figure S7: 2Fo-Fc map and omit map around compounds #1 and #2.**

- a) 2Fo-Fc map contoured at  $1\sigma$  around compound **#2**. This map is very well defined for the entire molecule.
- b) 2Fo-Fc omit map contoured at  $1\sigma$  around the compound **#2**.
- c) 2Fo-Fc map around compound **#1**. This map indicated a lack of electron density for a part of the compound located outside of the N-acetylated binding pocket.
- d) 2Fo-Fc omit map contoured at  $1\sigma$  sigma around compound **#1**.



**Figure S8: Binding mode of (S)JQ1 compared to compounds #1 and #2.**

a) (S)JQ1, a pan-BET inhibitor (grey) in complex with BRD4(1) and detailed view of the the N140 residue (pink) hydrogen bond interaction (dash line). The four highly conserved water molecules (red spheres) are located at the bottom of the cavity.

b) Superimposition of (S)JQ1 with compound #2 (purple). The triazolo moieties of these two compounds are superimposed, with a slight shift.

c) Superimposition of (S)JQ1 (grey) with compound #1 (orange). The oxoquinoline moiety of compound #1 is in the same plane as the thieno-triazolo-diazepine moiety of (S)JQ1.

d) Superimposition of (S)JQ1, compound #1 and compound #2 with a 90° rotation. The chlorophenyl-piperazinyl-piperidinecarboxamide substituents of compound #1 are oriented in the same direction as the (S)JQ1 chlorophenyl moiety, engaging the shelf between the BC loop and the WPF motif. The methylphenyl-piperidinyl-butanamide substituents of compound #2 are oriented in the opposite direction.

e) Surface representations of BRD4(1) in complex with compound #2 and f) with compound #1. The surface of N140 is colored in pink while the surface of the WPF shelf is highlighted in green.

## Supplementary Information – Tables

**Table S1: 2D chemical structure of “thermal shift sensitive” compounds**

Compound #	Structure	PubChem Compound Identifier (CID)	Compound #	Structure	PubChem Compound Identifier (CID)
1		20862085	12		44715900
2		46326697	13		45360407
3		7134939	14		45360408
4		20937233	15		50816819
5		71694343	16		1306476
6		60498769	17		5793057
7		71693175	18		40777317
8		4658136	19		40776845
9		16416191	20		25313771
10		71694343	21		44716462
11		3324458			

**Table S2: X-ray data collection and refinement statistics**

	Cpd 1 (pdb: 5DLZ)	Cpd 2 (pdb: 5DLX)
<b>Crystal parameters</b>		
Space group	P2 <sub>1</sub> 2 <sub>1</sub> 2 <sub>1</sub>	P2 <sub>1</sub> 2 <sub>1</sub> 2 <sub>1</sub>
Unit-cell dimensions		
a, b, c (Å)	37.26, 44.24, 78.44	41.72, 48.51, 58.09
$\alpha$ , $\beta$ , $\gamma$ (°)	90.00, 90.00, 90.00	90.00, 90.00, 90.00
<b>Data collection</b>		
Beamline	ESRF – ID23-2	ESRF – ID30A-3
Wavelength (Å)	0.8726	0.9677
Resolution range (Å)	50 - 1.70	50 - 1.90
Total reflections	64144 (14342)	46717 (6904)
Unique reflections	9741 (2221)	9664 ( 1505)
Completeness (%)	96.3 (95.2)	99.3 (97.8)
Average $I/\sigma$	7.54 (4.15)	20.09 (3.73)
Rfactor obs (%)	14.9 (42.1)	4.2 (37.9)
Redundancy	4.47 (4.38)	4.83 (4.59)
<b>Structure Refinement</b>		
Starting model for Molecular Replacement	2OSS	2OSS
Resolution range (Å)	39.22 - 1.70	37.25 - 1.80
Rfree	0.3339	0.20707
R value		
Working + test set	0.25529	0.12959
Working set	0.25122	0.12547
Solvent (%)	42.92	37.31
R.m.s.d.		
Bond lengths (Å)	0.028	0.028
Angles (°)	2.329	2.316

**Table S3: HTRF assay pipetting procedures**

Protein A		Protein B		HTRF reagent A (CisBio)		HTRF reagent B (CisBio)		Buffer assay	Final incubation	Final DMSO concentration	N between partners
Name	Final Concentration (nM)	Name	Final Concentration (nM)	Name	Final Concentration (nM)	Name	Final Concentration (nM)				
Mix1		Mix 2		Mix1							
Syntenin1FL-GST	2.5	Syndecan 2 peptide-Biot	47.5	MAb Anti GST-Tb	0.8	Streptavidin d2	10	Buffer A	ON 4°C	2%	19
GRASP55-GST	1.6	JamB peptide-Biot	5.9	MAb Anti GST-Tb	0.8	Streptavidin d2	1.25	Buffer A	ON 4°C	2%	3.7
NS3-GST	5	NS5Mtase-SNAP	15	MAb Anti GST-Tb	0.8	SNAP Red	-	Buffer A	4h RT	2%	3
NEF FL-His	2.5	GST-Hck-SH3	2.5	MAB Anti His-K	1	GST-d2	1.25	Buffer B	ON 4°C	2%	1
Mix 1				Mix 2							
Bromodomaln BRD4(1)-GST	5	H4 KAc 5/8/12/16 peptide	100	MAB Anti GST-K	0.5	Streptavidin d2	12.5	Buffer B	3h RT	2%	20
BRD4(1)-GST	5	H4 KAc 5/8/12/16 peptide	25	MAB Anti GST-K	0.5	Streptavidin d2	3.1	Buffer B	3h RT	1%	5
BRD4(2)-GST	5	H4 KAc 5/8/12/16 peptide	40	MAB Anti GST-K	0.5	Streptavidin XL665	5	Buffer B	3h RT	1%	8
BRD2(1)-GST	5	H4 KAc 5/8/12/16 peptide	15	MAB Anti GST-K	0.5	Streptavidin d2	1.9	Buffer B	3h RT	1%	3
BRD2(2)-GST	5	H4 KAc 5/8/12/16 peptide	15	MAB Anti GST-K	0.5	Streptavidin XL665	1.9	Buffer B	3h RT	1%	3
BRD3(1)-GST	5	H4 KAc 5/8/12/16 peptide	10	MAB Anti GST-K	0.5	Streptavidin d2	1.25	Buffer B	3h RT	1%	2
BRD3(2)-GST	5	H4 KAc 5/8/12/16 peptide	200	MAB Anti GST-K	0.5	Streptavidin XL665	25	Buffer B	3h RT	1%	40
BRDT(1)-GST	5	H4 KAc 5/8/12/16 peptide	20	MAB Anti GST-K	0.5	Streptavidin d2	2.5	Buffer B	3h RT	1%	4
ATAD2A-GST	5	H4 KAc 5/8/12/16 peptide	80	MAB Anti GST-Tb	0.5	Streptavidin XL665	10	Buffer B	3h RT	1%	16
GST-Biotin	6.25	-		MAB Anti GST-Tb	0.8	Streptavidin d2	5	Buffer A	ON 4°C	2%	-
GST-SNAP	10	-		MAB Anti GST-Tb	0.8	SNAP Red	-	Buffer A	4h RT	2%	-
GST-His	2.5	-		MAB Anti His-K	1	GST-d2	1.25	Buffer B	ON 4°C	2%	-

Buffer A 50 mM HEPES, pH 7.5, 150 mM NaCl, 0.1% BSA

Buffer B 50mM KPO4, pH7, BSA 0,1%, 0.1 M KF