

## HCR™ IF protocol for sample on slide

This protocol has not been validated for all sample types and should only be used as a template.

### Technical support

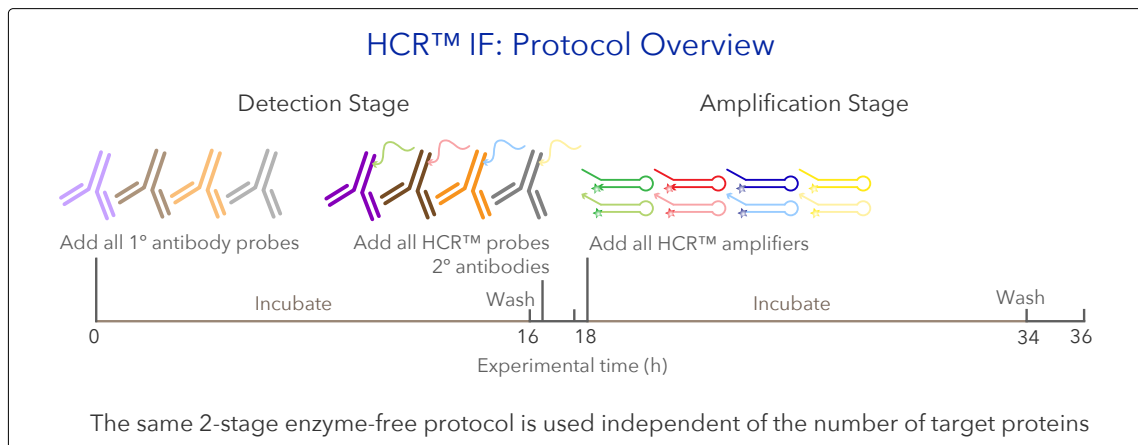
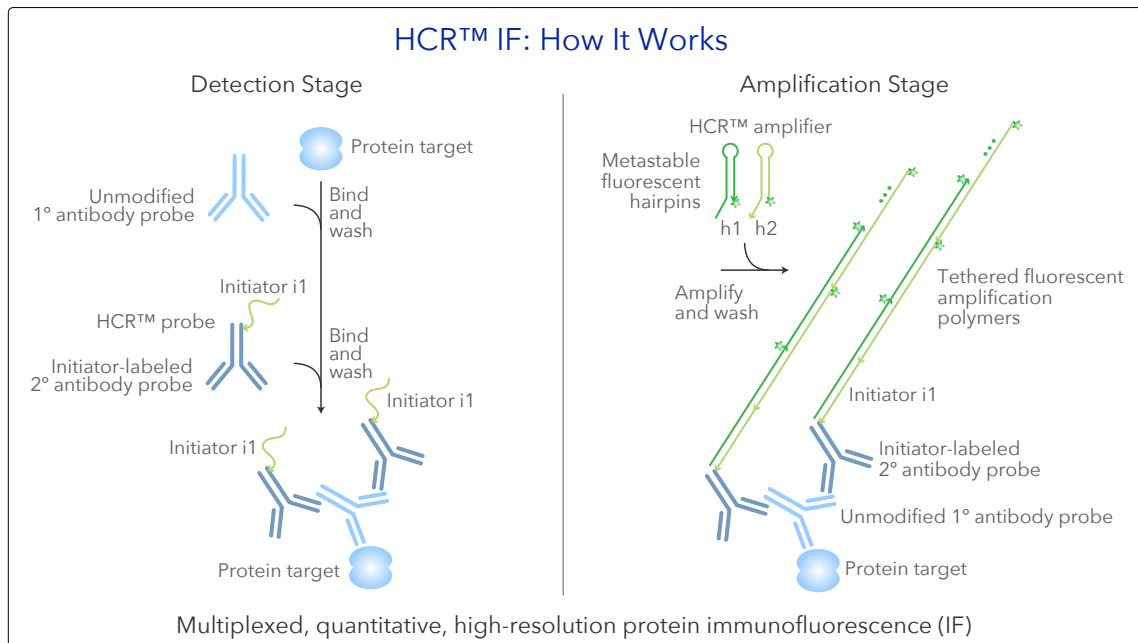
[support@molecularinstruments.com](mailto:support@molecularinstruments.com)

### Safety data sheets (SDS)

[www.molecularinstruments.com/safety](http://www.molecularinstruments.com/safety)

### Patents

Molecular Instruments® products are protected by and for use under patents: [www.molecularinstruments.com/patents](http://www.molecularinstruments.com/patents)



## **HCR™ IF**

*Multiplexed, quantitative, high-resolution protein imaging*

### **Multiplexed Experiment**

- Order one HCR™ IF bundle per target protein

### **Example 2-Plex Experiment**

- HCR™ IF bundle for target Protein1
  - 1° Ab: Rabbit Anti-Protein1 (your own 1° antibody)
  - HCR™ IF 2° Ab probe: Donkey Anti-Rabbit for use with amplifier B1
  - HCR™ amplifier: B1-647
  - HCR™ IF buffers: antibody buffer, amplification buffer (for use with all bundles)
- HCR™ IF bundle for target Protein2
  - 1° Ab: Mouse Anti-Protein2 (your own 1° antibody)
  - HCR™ IF 2° Ab probe: Donkey Anti-Mouse for use with amplifier B2
  - HCR™ amplifier: B2-488

### **Storage conditions**

- Store HCR™ IF antibody probes and HCR™ amplifiers at -20 °C.
- Store HCR™ IF antibody buffer and HCR™ amplification buffer at 4 °C.
- On the bench top, keep stock solutions on ice.
- Make sure all solutions are well mixed before use.

## Sample preparation

Samples should be prepared in the same manner as for a traditional immunohistochemistry, up to the primary antibody application step. This may include permeabilization and antigen retrieval. Then proceed with the protocol described below.

## Multiplexed HCR™ IF protocol

### Detection stage

1. Block tissue by applying 200  $\mu\text{L}$  of antibody buffer on top of the sample. Incubate at room temperature for 1 h in a humidified chamber.
2. Prepare working concentration of primary antibodies in antibody buffer. Prepare 100  $\mu\text{L}$  per section.  
*NOTE: follow manufacturer's guidelines for primary antibody working concentration.*
3. Drain slide by blotting edges on a Kimwipe and wipe around the section with another Kimwipe.
4. Add primary antibody solution to each section and incubate overnight ( $>12$  h) at 4 °C in a humidified chamber.  
*NOTE: Incubation may be optimized (e.g., 1–2 h at room temperature) depending on sample type and thickness.*
5. Remove excess antibodies by immersing slide in 1 $\times$  PBST at room temperature for 3  $\times$  5 min.
6. Prepare 1  $\mu\text{g}/\text{mL}$  working concentration of initiator-labeled secondary antibodies in antibody buffer. Prepare 100  $\mu\text{L}$  per section.  
*NOTE: Concentration may be optimized depending on protein target and primary antibody.*
7. Drain slide by blotting edges on a Kimwipe and wipe around the section with another Kimwipe.
8. Add secondary antibody solution to each section and incubate for 1 h at room temperature in a humidified chamber.
9. Remove excess antibodies by immersing slide in 1 $\times$  PBST at room temperature for 3  $\times$  5 min.

## Amplification stage

1. Immerse slide in  $5\times$  SSCT at room temperature for 5 min.
2. Drain slide by blotting edges on a Kimwipe and wipe around the section with another Kimwipe.
3. Add 200  $\mu\text{L}$  of amplification buffer on top of the tissue sample and pre-amplify in a humidified chamber for 30 min at room temperature.  
*NOTE: equilibrate amplification buffer to room temperature before use.*
4. Separately prepare 6 pmol of hairpin h1 and 6 pmol of hairpin h2 by snap cooling 2  $\mu\text{L}$  of 3  $\mu\text{M}$  stock (heat at 95 °C for 90 seconds and cool to room temperature in a dark drawer for 30 min).  
*NOTE: Hairpins h1 and h2 are provided in hairpin storage buffer ready for snap cooling. h1 and h2 should be snap cooled in separate tubes. This is the amount of hairpins needed for each target on a single slide using 100  $\mu\text{L}$  of incubation volume.*
5. Prepare a 60 nM hairpin solution by adding all snap-cooled h1 hairpins and snap-cooled h2 hairpins to 100  $\mu\text{L}$  of amplification buffer at room temperature per section.
6. Remove the pre-amplification solution and drain excess buffer on slide by blotting edges on a Kimwipe.
7. Add 100  $\mu\text{L}$  of the hairpin solution on top of the tissue sample.
8. Incubate overnight ( $>12$  h) in a dark humidified chamber at room temperature.
9. Remove excess hairpins by immersing slide in  $5\times$  SSCT at room temperature for:
  - (a)  $2\times 5$  min
  - (b)  $2\times 15$  min
  - (c)  $1\times 5$  min
10. Drain slide by blotting edges on a Kimwipe and dry around the section with another Kimwipe.
11. Add 50–100  $\mu\text{L}$  of antifade mounting reagent on top of the sample.
12. Place a coverslip on top for microscopy.

## Buffer recipe

### PBST

1 $\times$  PBS  
0.1% Tween 20

### For 50 mL of solution

5 mL of 10 $\times$  PBS  
500  $\mu\text{L}$  of 10% Tween 20  
Fill up to 50 mL with ultrapure H<sub>2</sub>O

### 5 $\times$ SSCT

5 $\times$  sodium chloride sodium citrate (SSC)  
0.1% Tween 20

### For 40 mL of solution

10 mL of 20 $\times$  SSC  
400  $\mu\text{L}$  of 10% Tween 20  
Fill up to 40 mL with ultrapure H<sub>2</sub>O

*NOTE: avoid using calcium chloride and magnesium chloride in PBS as this leads to increased autofluorescence in the samples.*

## HCR™ Technology Citation Notes

For citation, please select from the list below as appropriate for your application:

- **HCR™ IF + HCR™ RNA-FISH**

[HCR™ IF + HCR™ RNA-FISH](#) enables a unified approach to multiplexed, quantitative, high-resolution protein immunofluorescence (IF) and RNA fluorescence in situ hybridization (RNA-FISH), with quantitative 1-step enzyme-free signal amplification performed for all protein and RNA targets simultaneously ([Schwarzkopf et al., 2021](#)).

- **HCR™ IF**

[HCR™ IF](#) enables multiplexed, quantitative, high-resolution protein immunofluorescence (IF) in highly autofluorescent samples (e.g., FFPE brain tissue sections) ([Schwarzkopf et al., 2021](#)).

- **HCR™ RNA-FISH (v3.0)**

Third-generation [HCR™ RNA-FISH \(v3.0\)](#) enables multiplexed, quantitative, high-resolution RNA fluorescence in situ hybridization (RNA-FISH) with [automatic background suppression throughout the protocol](#) for dramatically enhanced performance (signal-to-background, subcellular quantitative RNA imaging precision, single-molecule quantitative RNA imaging fidelity) and ease-of-use (no probe set optimization for new targets and organisms) ([Choi et al., 2018](#)). Quantitative analysis modes:

- [Subcellular quantitative RNA imaging](#): analog mRNA relative quantitation with subcellular resolution in the anatomical context of thick autofluorescent samples.
- [Single-molecule quantitative RNA imaging](#): digital mRNA absolute quantitation with single-molecule resolution in the anatomical context of thick autofluorescent samples.
- [Quantitative RNA flow cytometry](#): analog mRNA relative quantitation for high-throughput expression profiling of mammalian cells and bacteria.

[Protocols for HCR™ RNA-FISH \(v3.0\)](#) in diverse organisms are adapted from the Zoo paper.

- **Subcellular quantitative RNA imaging**

[Subcellular quantitative RNA imaging](#) enables mRNA relative quantitation with subcellular resolution in the anatomical context of thick autofluorescent samples (e.g., whole-mount vertebrate embryos). The [read-out/read-in analysis framework](#) enables bidirectional quantitative discovery in an anatomical context ([Trivedi et al., 2018](#)).

- **Zoo paper**

Protocols for multiplexed mRNA imaging in diverse sample types ([Choi et al., 2016](#)):

- bacteria in suspension
- FFPE human tissue sections
- generic sample in solution
- generic sample on a slide
- mammalian cells on a slide
- mammalian cells in suspension
- whole-mount chicken embryos
- whole-mount fruit fly embryos
- whole-mount mouse embryos
- whole-mount nematode larvae
- whole-mount sea urchin embryos
- whole-mount zebrafish embryos and larvae

- **Single-molecule quantitative RNA imaging**

[Single-molecule quantitative RNA imaging](#) enables RNA absolute quantitation with single-molecule resolution in the anatomical context of thick autofluorescent samples (e.g., 0.5 mm adult mouse brain sections) ([Shah et al., 2016](#)).

- **HCR™ northern blots**

[HCR™ northern blots](#) enable multiplexed quantification of RNA target size and abundance for up to 5 target RNAs ([Schwarzkopf & Pierce, 2016](#)).

- **HCR™ RNA-FISH (v2.0)**

Second-generation in situ HCR™ RNA-FISH technology (v2.0) using DNA HCR™ probes and DNA HCR™ amplifiers: 10× increase in signal, 10× reduction in cost, dramatic increase in reagent durability ([Choi et al., 2014](#)).

- **HCR™ RNA-FISH (v1.0)**

First-generation HCR™ RNA-FISH technology (v1.0) using RNA HCR™ probes and RNA HCR™ amplifiers: multiplexed mRNA imaging in whole-mount vertebrate embryos with simultaneous signal amplification for up to 5 target mRNAs ([Choi et al., 2010](#)).

- **HCR™ technology**

[HCR™ amplifiers](#) enable multiplexed, quantitative, 1-step, isothermal, enzyme-free signal amplification in diverse technological settings ([Dirks & Pierce, 2004](#)).