

Cancer gene expression illuminated

Stellaris® RNA FISH Probes for cancer research

Visualisation and quantification of single RNA transcripts, using RNA fluorescent *in situ* hybridisation (FISH), offers the unique ability to observe altered disease-specific expression in fixed cells or intact tissue. Gene expression profiles are complex and can vary immensely between regions of tissue, cells, regions of a single nucleus, and therefore require advanced methods of analysis.

Custom or DesignReady probe sets

LGC, Biosearch Technologies™ offers a free, online probe designer (www.biosearchtech.com/stellarisdesigner) which allows you to craft Stellaris RNA FISH probes with optimal binding properties for your target RNA sequence. A custom Stellaris RNA FISH probe set is a blend of up to 48 oligos each labeled with a fluorophore.

We also offer DesignReady probe sets which are professionally designed and go through rigorous bioinformatics analysis to ensure specificity. These made-to-order probe sets include cancer specific targets across a wide range of model organisms.

More information and current protocols are available online (www.biosearchtech.com/stellaris).

Detect, localise, and quantify RNA molecules in cells or intact tissue

Biosearch Technologies' Stellaris RNA FISH probes, can quantify and localise RNA within cells, tissue sections, or whole mount tissue where the morphology is preserved. A Stellaris FISH probe set comprises multiple oligonucleotides targeting a single RNA target. The fluorescently labeled probes bind along the target transcript, and combine to produce a punctate signal for an individual RNA molecule.

DesignReady cancer sets include:			
ADAM17	EGFR	HOTAIR	MYC
AKT1	ERBB2 & 3	HOXA5	NCOA3
AR	ERG	JAG1	PCA3
BCL2	EZH2	JUN	PIK3CA
BRAF	FOS	KIT	MTOR
BRCA1 & 2	GREB1	KLK3	TERT
CDK4	H19	MALAT1	TERC
CTNNB1	HIF1A	MKI67	TP53

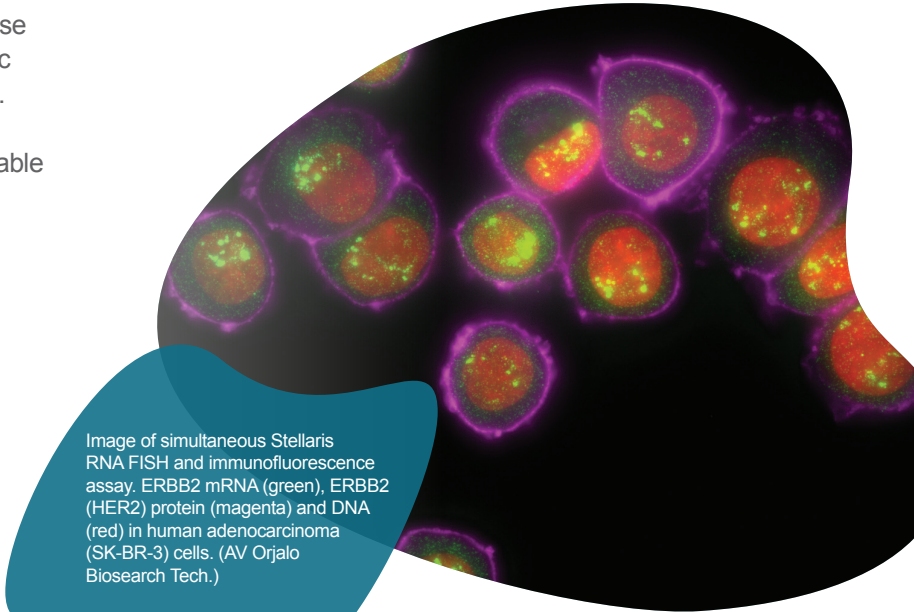
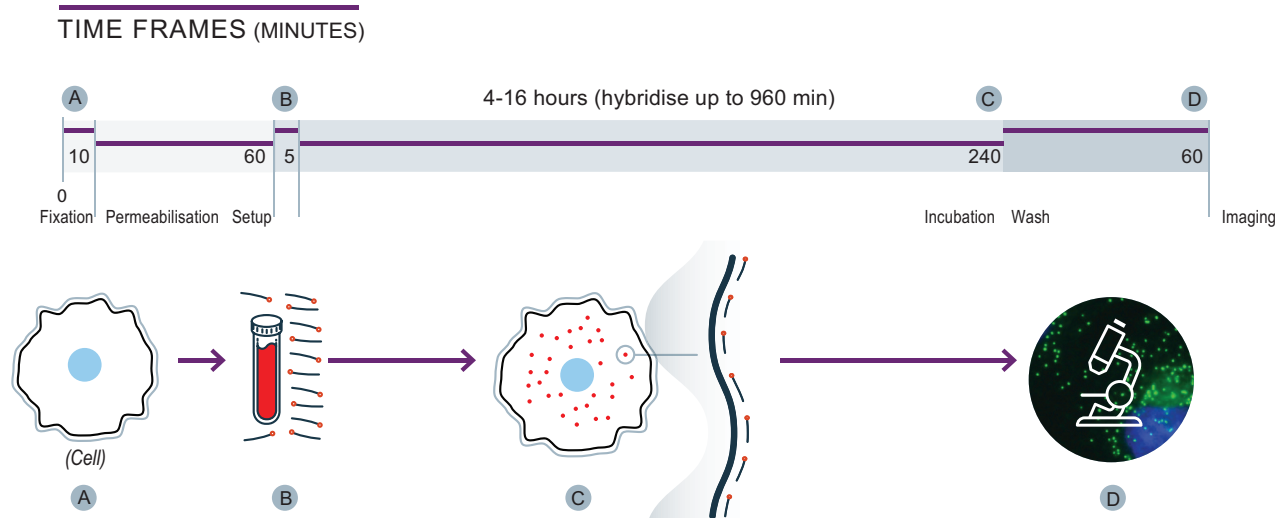


Image of simultaneous Stellaris RNA FISH and immunofluorescence assay. ERBB2 mRNA (green), ERBB2 (HER2) protein (magenta) and DNA (red) in human adenocarcinoma (SK-BR-3) cells. (AV Orjalo Biosearch Tech.)

The Stellaris RNA FISH method



Publication highlights

Over 33% of publications citing Stellaris RNA FISH publish in Cell, Nature, or Science journals. Visit our Citation Center for the complete list.

Post-transcriptional modifications contribute to the upregulation of Cyclin D2 in multiple myeloma. Misiewicz-Krzeminska *et al.* Clinical Cancer Research. 2016. Url: <https://dx.doi.org/10.1158/1078-0432.CCR-14-2796>

G1/S inhibitors and the SWI/SNF complex control cell-cycle exit during muscle differentiation. Ruijtenberg *et al.* Cell. 2015. Url: <https://dx.doi.org/10.1016/j.cell.2015.06.013>

Genome-wide profiling of p53-regulated enhancer RNAs uncovers a subset of enhancers controlled by a lncRNA. Leveille *et al.* Nature Communications. 2015. Url: <https://dx.doi.org/10.1038/ncomms7520>

Niche appropriation by Drosophila intestinal stem cell tumors. Patel *et al.* Nature Cell Biology. 2015. Url: <https://dx.doi.org/10.1038/ncb3214>

FuseFISH: robust detection of transcribed gene fusions in single cells. Semrau *et al.* Cell reports. 2014. Url: <https://dx.doi.org/10.1016/j.celrep.2013.12.002>

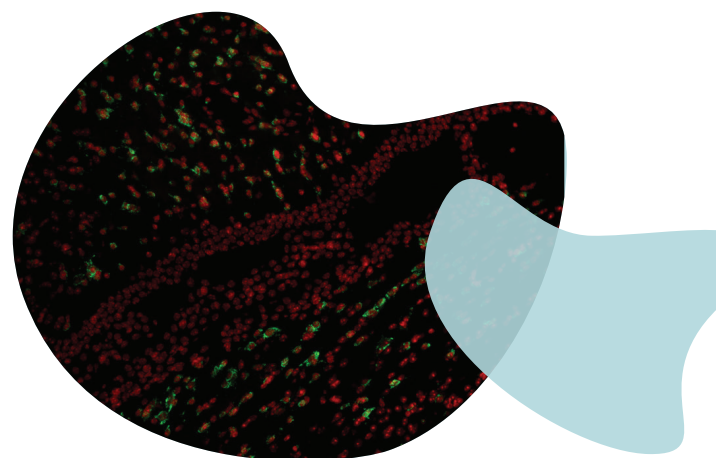
Proteostatic control of telomerase function through TRiC-mediated folding of TCAB1. Freund *et al.* Cell. 2014. Url: <https://dx.doi.org/10.1016/j.cell.2014.10.059>

Single-molecule transcript counting of stem-cell markers in the mouse intestine. Itzkovitz *et al.* Nature Cell Biology. 2011. Url: <https://dx.doi.org/10.1038/ncb2384>

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