For all you seq...

RNA

RNA Transcription

CaptureSeq
RASL-seq
ClickSeq
3Seq
3-Seq
3′-end-seq
PAS-Seq
SS3-Seq
3′T-fill
cP-RNA-Seq
3P-Seq
2P-seq
3′-Seq
TIF-Seq
PEAT
SMORE-Seq
TL-seq
TATL-seq
RARseq
TAIL-seq
PAL-seq
FRT-Seq
ChIRP
CHART
RAP
GRO-seq
BRIC-Seq
Bru-Seq
BruChase-Seq
5′-GRO-seq
BruDRB-seq
4sUDRB-seq
PRO-seq
PRO-cap
CAGE
DeepCAGE
3′NT method
NET-Seq
mNET-seq
PARE-Seq
GMUCT 1.0
GMUCT 2.0

Key

Yellow highlights indicate the target of the protocol

3′-azido-2′,3′-dideoxynucleotide triphosphate (AzNTP)

Copper-catalysed cycloaddition of 3′-azido blocked cDNA to 5′-hexynyl DNA adaptor

Biotin

Psoralen

Photoactivatable Nucleosides

4-thiouridine (4SU)

5-iodouridine (SIU)

4-bromo uridine (SBrU)

6-Thioguanosine (6SG)

1,6-Hexanediol

Br-UTP

5,6-dichlorobenzimidazole 1-b-D-ribofuranoside (DRB)

5′-Bromo-uridine (BrdU)

EDTA

3′ Terminal structure of RNA

Display methods on mobile device

RNA-Protein Interactions

Ribo-Seq
GTI-Seq
ARTseq™
RIP-Seq
CLIP
HITS-CLIP
Pol II CLIP
MiR-CLIP
eCLIP
irCLIP
PAR-CLIP
iCLIP
BrdU-CLIP
AGO-CLIP
PIP-Seq
hiCLIP
RBNS
TRIBE
HiTS-RAP
TRAP-Seq
DLAF
miTRAP
CLASH

Uridine

Pseudouridine (Ψ)

p-benzoylphenylalanine (Bpa)

1-cyclohexyl-(2-morpholino-ethyl)carbodiimide-metho-p-toluene sulfonate (CMCT)

Display methods on mobile device

Ψ-CMC adduct

Inosine

Acrylonitrile

N1-cyanoethyl inosine

N^6-Methyladenosine (m6A)

1-methyl-7-nitroisatoic anhydride (1M7)

RNA + Acylation

DIBO-biotin "click"

Preparation of acylated RNA for biotin–streptavidin purification. DIBO, dibenzocyclooctyne

Dimethyl sulfate (DMS)

5-ethynyl-2′-deoxyuridine (EdU)

Locked nucleic acid (LNA)

RNA Low-Level Detection

scRNA-seq
SUPeR-seq
UMI Method
Digital RNA
HiRes-Seq
FREQ-Seq
RNAtag-Seq
MARS-Seq
Quartz-Seq
DP-Seq
Smart-seq
NanoCAGE
CAGEscan
Smart-seq2
snRNA-seq
FRISCR
CEL-Seq
STRT
TCR Chain Pairing
TCR-LA-MC PCR

RNA Structure

SHAPE-Seq
icSHAPE
CIRS-seq
SHAPE-MaP
Struc-ture-Seq
DMS-Seq
SPARE
PARS
dsRNA-Seq
PARTE
Frag-seq
CapSeq
CIP-TAP

RNA Modifications

MeRIP-Seq
m6A-seq
m6A-RIP
miCLIP-m6A
Ψ-seq
PSI-seq
Pseudo-seq
ICE

TruSeq PCR Free

Double-stranded DNA
Fractionate Size select
End repair Phosphorylate
A-overhang
Add Adaptors
Adaptor ligation
Product ready for cluster generation

TruSeq Nano

Double-stranded DNA
Fractionate Size select
End repair Phosphorylate
A-overhang
Add Adaptors
Adaptor ligation
Denature and amplify
Product ready for cluster generation

TruSeq Custom Amplicon

Double-stranded DNA
Region of interest
Custom Probe 1
Custom Probe 2
Add custom probes
Extension and ligation
Add sequencing primers
PCR
Product ready for cluster generation

TruSeq RNA

mRNA
polyA select
Fragment
Random hexamer
First and second strand synthesis

TruSeq Small RNA

Small RNA fragment
Ligate adaptors
Add primer
Reverse transcription
Denature and amplify
Product ready for cluster generation

TruSeq RNA Stranded

RNA
Random primer
Create cDNA
Create second strand cDNA
End repair Phosphorylate A-overhang
Adaptor ligation
Denature and amplify
Product ready for cluster generation

TruSeq RNA Access

Target
Pool stranded RNA-Seq libraries
Biotinylated target probe
Hybridize probes to targets
Capture on streptavidin magnetic beads
Elute
Product ready for cluster generation

TruSeq Targeted RNA Expression

Target
Total RNA
cDNA
Add custom primers
Hybridization
Extension-Ligation
Denature and amplify
Product ready for cluster generation

Nextera Library Preparation

Transposase
DNA
Tagmentation
~300bp
Amplification
Product ready for cluster generation

Nextera Rapid Capture

Target
Denatured and pooled fragments from Nextera library
Biotinylated target probe
Hybridize probes to targets
Capture on magnetic beads
Elute
Product ready for cluster generation

Nextera Mate Pair

Transposase
Biotinylated junction adapter
DNA
Tagmentation
Circularize
Fragment
Isolate biotinylated fragment
Adaptor ligation
Denature and amplify
Product ready for cluster generation

Sequencing by Synthesis

Adapter hybrid-izes to flowcell
Reverse strand syntesis
Remove forward strand
Fold over and hybridize to second primer
Synthesize second strand
Forward strand
Reverse strand
Bridge amplification
Thousands of molecules are amplified in parallel
Sequence primer
Index 1 primer
Read 2 primer
The reverse strand is cleaved and washed away
With each cycle, four fluores-cently tagged nucleotides compete for addition to the growing chain. Only one is incorporated based on the sequence of the template.
The read product is washed away
Sequence Index1
The read product is washed away
Fold over and hybridize to first primer
Deblock P5 primer and add unlabeled bases
Sequence Index2
Synthesize second strand
The forward-strand is cleaved and washed away
The second read is sequenced

Moleculo

~10kb Sheared genomic DNA
End repair
Adapter ligation
Generate clonal pools
Amplify
Transposase
Tagmentation
~600bp
Add indices
Prepared fragments
Pool and purify

References

2P-Seq Spies N. et al. (2013) Genome Res 23: 2078-2090
3′-end-seq Haenni S. et al. (2012) Nucleic Acids Res 40: 6304-6318
3′NT method Weber C. M. et al. (2014) Mol Cell 53: 819-830
3′-Seq Lianoglou S. et al. (2013) Genes Dev 27: 2380-2396
3P-Seq Jan C. H. et al. (2011) Nature 469: 97-101
3Seq or 3-Seq Beck A. H. et al. (2010) PLoS One 5: e8768
3′T-fill Wilkening S. et al. (2013) Nucleic Acids Res 41: e65
4sUDRB-seq Fuchs G. et al. (2014) Genome Biol 15: R69
5′-GRO-seq Lam M. T. et al. (2013) Nature 498: 511-515
AGO-CLIP Grosswendt S. et al. (2014) Mol Cell 54: 1042-1054
BrdU-CLIP Weyn-Vanhentenryck SM et al. (2014) Cell Rep 6:1139-52
BRIC-seq Tani H. et al. (2012) Genome Res 22: 947-956
BruChase-Seq Paulsen M. T. et al. (2013) Proc Natl Acad Sci U S A 110: 2240-2245
BruDRB-seq Bru-Seq Veloso A. et al. (2014) Genome Res 24: 896-905
Paulsen M. T. et al. (2013) Proc Natl Acad Sci U S A 110: 2240-2245
CAGE Takahashi H. et al. (2012) Nat Protoc 7: 542-561
CAGEscan Plessy C. et al. (2010) Nat Methods 7: 528-534
CapSeq Gu W. et al. (2012) Cell 151: 1488-1500
CaptureSeq Mercer T. R. et al. (2014) Nat Protoc 9: 989-1009
CEL-Seq Hashimshony T. et al. (2012) Cell Rep 2: 666-673
ChIRP Simon M. D. et al. (2011) Proc Natl Acad Sci U S A 108: 20497-20502
CIP-TAP Chu C. et al. (2011) Mol Cell 44: 667-678
CirSeq Gu W. et al. (2012) Cell 151: 1488-1500
CIRS-seq Acevedo A. et al. (2014) Nature 505: 686-690
Incarnato D. et al. (2014) Genome Biol 15: 491
CLaP CLASH ClickSeq CLIP-seq cP-RNA-Seq CytoSeq DeepCAGE Digital RNA Div-Seq DLAF DMS-Seq Binan L. et al. (2016) Nat Commun 7:11636
Kudla G. et al. (2011) Proc Natl Acad Sci U S A 108: 10010-10015
Routh A. et al. (2015) J Mol Biol 427: 2610-2616
Yeo GW et al. (2009) Nat Struct Mol Biol 16:130-7
Honda S et al. (2015) Proc Natl Acad Sci U S A 112:E3816-25
Fan H. C. et al. (2015) Science 347: 1258367
Valen E. et al. (2009) Genome Res 19: 255-265
Shirokguch K. et al. (2012) Proc Natl Acad Sci U S A 109: 1347-1352
Habib N. et al. (2016) bioriv
Agarwal S. et al. (2015) Nat Commun 6: 6002
Rouskin S. et al. (2014) Nature 505: 701-705
DP-Seq Drop-Seq DR-Seq dsRNA-Seq eCLIP Frag-seq FREQ-Seq FRISCR FRT-Seq G&T-seq GMUCT 1.0 GMUCT 2.0 GRO-Seq Bhargava V. et al. (2013) Sci Rep 3: 1740
Macosko E. Z. et al. (2015) Cell 161: 1202-1214
Dey SS et al. (2015) Nat Biotechnol 33:285-9
Zheng Q. et al. (2010) PLoS Genet 6: e1001141
Van Nostrand EL et al. (2016) Nat Methods advance online publication
Underwood J. G. et al. (2010) Nat Methods 7: 995-1001
Chubiz L. M. et al. (2012) PLoS One 7: e47959
Thomsen ER et al. (2016) Nat Methods 13:87-93
Mamanova L. et al. (2011) Nat Protoc 6: 1736-1747
Macaulay I. C. et al. (2015) Nat Methods 12: 519-522
Gregory B. D. et al. (2008) Dev Cell 14: 854-866
Willmann M. R. et al. (2014) Methods 67: 64-73
Core L. J. et al. (2008) Science 322: 1845-1848
GTI-Seq hi-CLIP HiRes-Seq Hi-SCL HITS-CLIP HITS-RAP ICE iCLIP icSHAPE inDrop irCLIP M6A-RIP Wan J. et al. (2014) Nucleic Acids Res 42: D845-850
Sugimoto Y. et al. (2015) Nature 519: 491-494
Imashimizu M. et al. (2013) Nucleic Acids Res 41: 9090-9104
Rotem A. et al. (2015) PLoS One 10: e0116328
Chi S. W. et al. (2009) Nature 460: 479-486
Tome J. M. et al. (2014) Nat Methods 11: 683-688
Sakurai M. et al. (2010) Nat Chem Biol 6: 733-740
Konig J. et al. (2010) Nat Struct Mol Biol 17: 909-915
Spitale R. C. et al. (2015) Nature 519: 486-490
Klein AM et al. (2015) Cell 161:1187-201
Zarnegar BJ et al. (2016) Nat Meth advance online publication
Batista P. J. et al. (2014) Cell Stem Cell 15: 707-719
m6A-seq MARS-seq MeRIP-Seq miCLIP-m6A MiR-CLIP miTRAP mNET-Seq NanoCAGE NET-Seq Nuc-Seq PAIR PAL-seq PAR-CLIP Dominissini D. et al. (2012) Nature 485: 201-206
Jaitin DA et al. (2014) Science 343:776-9
Meyer K. D. et al. (2012) Cell 149: 1635-1646
Linder B. et al. (2015) Nat Methods 12: 767-772
Imig J et al. (2015) Nat Chem Biol 11:107-14
Braun J. et al. (2014) Nucleic Acids Res 42: e66
Nojima T. et al. (2015) Cell 161: 526-540
Plessy C. et al. (2010) Nat Methods 7: 528-534
Chunchman L. S. et al. (2011) Nature 469: 368-373
Habib N et al. (2016) bioRxiv
Bell TJ et al. (2015) Methods Mol Biol 1324:457-68
Subtelny A. O. et al. (2014) Nature 508: 66-71
Hafner M. et al. (2010) Cell 141: 129-141
PARE-Seq PARS PARTE PAS-Seq PEAT PIP-Seq Pol II CLIP PRO-cap PRO-seq Pseudo-seq PSI-seq Quartz-Seq RAP German M. A. et al. (2008) Nat Biotechnol 26: 941-946
Wan Y. et al. (2013) Nat Protoc 8: 849-869
Wan Y. et al. (2012) Nat Cell 48: 169-181
Shepard P. J. et al. (2011) RNA 17: 761-772
Ni T. et al. (2010) Nat Methods 7: 521-527
Silverman IM et al. (2014) Genome Biol 15:R3
Li Z. et al. (2015) Nat Struct Mol Biol 22: 256-264
Kwak H. et al. (2013) Science 339: 950-954
Kwak H. et al. (2013) Science 339: 950-953
Carlile T. M. et al. (2014) Nature 515: 143-146
Lovejoy A. F. et al. (2014) PLoS One 9: e110799
Sasagawa Y. et al. (2013) Genome Biol 14: R31
Engreitz J. M. et al. (2013) Science 341: 1237973
RARseq RASL-seq RBNS RIP-Seq RNA-Seq RNAtag-Seq scM&T-seq SCRB-Seq scRNA-seq scTrio-seq SHAPE-MaP Alabady MS et al. (2015) PLoS One 10:e0134855
Li H. et al. (2012) Curr Protoc Mol Biol Chapter 4: Unit 4 13 11-19
Lambert N. et al. (2014) Mol Cell 54: 887-900
Zhao J. et al. (2010) Mol Cell 40: 939-953
Mortazavi A. et al. (2008) Nat Methods 5: 621-628. See TruSeq RNA.
Shishkin A. A. et al. (2015) Nat Methods 12: 323-325
Angermueller C et al. (2016) Nat Methods advance online publication
Soumillon M et al. (2014) bioRxiv
Tang F et al. (2009) Nat Methods 6:377-82
Hou Y et al. (2016) Cell Res 26:304-19
Siegfried N. A. et al. (2014) Nat Methods 11: 959-965
SHAPE-Seq Smart-Seq Smart-seq2 SMORE-Seq snRNA-seq SPARE SS3-Seq STRT Structure-Seq SUPeR-seq TAIL-seq Lucks J. B. et al. (2011) Proc Natl Acad Sci U S A 108: 11063-11068
Ramskold D. et al. (2012) Nat Biotechnol 30: 777-782
Picelli S. et al. (2013) Nat Methods 10: 1096-1098v
Park D. et al. (2014) Nucleic Acids Res 42: 3736-3749
Grindberg RV et al. (2013) Proc Natl Acad Sci U S A 110:19802-7
Schapire A. L. et al. (2013) Methods 64: 283-291
Yoon O. K. et al. (2010) RNA 16: 1256-1267
Islam S. et al. (2011) Genome Res 21: 1160-1167
Ding Y. et al. (2014) Nature 505: 696-700. See also DMS-Seq
Fan X. et al. (2015) Genome Biol 16: 148
Chang H. et al. (2014) Mol Cell 53: 1044-1052
TATL-seq TCR Chain Pairing TCR-LA-MC PCR TIF-Seq TIVA TRAP-Seq TRIBE UMI Method ψ-seq Arribere J. A. et al. (2013) Genome Res 23: 977-987
Turchaninova M. A. et al. (2013) Eur J Immunol 43: 2507-2515
Ruggiero E et al. (2015) Nat Commun 6:8081
Pelechano V. et al. (2013) Nature 497: 127-131
Lovatt D. et al. (2014) Nat Methods 11: 190-196
Arribere J. A. et al. (2013) Genome Res 23: 977-987
Jiao X. et al. (2010) Mol Syst Biol 6: 419
McMahon AC et al. (2016) Cell 165:742-53
Kivioja T. et al. (2012) Nat Methods 9: 72-74
Schwartz S. et al. (2014) Cell 159: 148-162