



HAL
open science

Co-immunoprecipitation: Protein–RNA and Protein–DNA Interaction

Tobias Sahr, Carmen Buchrieser

► **To cite this version:**

Tobias Sahr, Carmen Buchrieser. Co-immunoprecipitation: Protein–RNA and Protein–DNA Interaction. Carmen Buchrieser; Hubert Hilbi. Legionella: Methods and Protocols , 954, Humana Press, pp.583-593, 2013, Methods in Molecular Biology (MIMB), 978-1-62703-160-8 (Hardcover), 978-1-4939-6274-7 (Softcover), 978-1-62703-161-5 (eBook). 10.1007/978-1-62703-161-5_36 . pasteur-01333974

HAL Id: pasteur-01333974

<https://pasteur.hal.science/pasteur-01333974>

Submitted on 6 Feb 2018

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

1 **Co-Immunoprecipitation: protein-RNA and protein-DNA interaction**

2
3 Tobias Sahr and Carmen Buchrieser*

4
5 *Institut Pasteur, Biologie des Bactéries Intracellulaires, 75724 Paris, France and ²CNRS*
6 *UMR 3525, 75724 Paris, France*

7
8
9
10
11
12
13
14
15
16 **Running title:** ChIPseq and RIPseq of *Legionella*

17
18
19
20 **Key words:** *Legionella pneumophila*, next generation sequencing, co-immunoprecipitation,
21 protein-RNA, protein-DNA interaction

22
23
24
25

1 **Summary**

2 Transcriptional and post-transcriptional regulators play a critical role in allowing a bacterium
3 to adapt to the diverse environments and conditions it encounters. In order to characterize the
4 role of these regulators the identification of their specific interaction partners is of utmost
5 importance. Co-Immunoprecipitation (IP) is based on antigen/antibody complex formation to
6 purify a protein of interest from the rest of the samples together with its interaction partner.
7 This method allows us to study direct interaction of a regulator with its specific binding
8 partners like protein-RNA, protein-DNA or protein-protein interactions. IP typically requires
9 careful optimization and troubleshooting depending on the varying physicochemical
10 characteristics of the protein of interest. In the following chapter we present a starting point
11 and the basic guidelines to obtain the best possible results from an IP experiment with
12 subsequent use of new generation sequencing (NGS) techniques to detect mRNA or ncRNA-
13 targets (RIPseq) and protein-DNA interactions (ChIPseq).

14

15 **1. Introduction**

16 Bacteria have developed a variety of strategies with which they adapt their genetic expression
17 to meet the challenges of their ever-changing surrounding environment. These include
18 specific sigma factors, two-component systems, peptide or chemical-based quorum sensing
19 systems, repressors, positive regulators, as well as small regulatory RNAs. Alone or in
20 combination, these mechanisms enable bacterial cells to communicate with their environment,
21 their hosts, and with each other, allowing the bacteria to adopt specific responses, express
22 specific proteins (toxins, adhesins, invasins, siderophores) or develop specialized structures
23 such as biofilms or spores to ensure survival, colonization of their ecological niches and
24 dissemination. Expression profiles of *Legionella* lacking transcriptional regulators have been
25 used successfully to broadly define genes impacted by the deleted regulator (1-7). Although
26 providing informative data, transcriptional analysis alone cannot distinguish between direct
27 and indirect regulatory effects or identify regulated genes that may be transcriptionally silent
28 under the test conditions. Furthermore, in these experiments additional non-specific results
29 like stress response or activation of subsequent regulatory cascades cannot be avoided and
30 sometimes these secondary effects even overwhelm and hide original regulator-specific
31 effects and only vague conclusions about primary/direct responses can be drawn from the
32 experiments.

33 Co-Immunoprecipitation (IP) enables the purification of a protein based on antigen/antibody
34 complex formation. Therefore, isolates of the protein purified from the rest of the samples can

1 be achieved to study direct interaction between the protein and specific binding partners like
2 nucleotides or other proteins. The most critical factor for the success of these experiments is
3 the quality of the antibody used, but also many other factors during the different steps from
4 lysis to elution are influencing the outcome of the IP (8). ChIP coupled with next-generation
5 sequencing (ChIP-seq) has revolutionized whole-genome mapping of DNA-binding protein
6 sites. Although ChIP-seq rapidly gained support in eukaryotic systems (9), it remains
7 underused in the mapping of bacterial transcriptional regulator-binding sites, and only three
8 studies have been published to date (10-12). However, no study using *L. pneumophila* as
9 model has been reported yet.

10 The following protocols should be seen only as starting points for conducting these
11 experiments, as protocol optimization for each protein studied and each antibody used is
12 indispensable. Here we describe two different methods i) RIPseq to characterize protein-RNA
13 interactions and ii) ChIPseq to characterize protein-Chromatin/DNA interactions. Both of
14 them lead to the construction of DNA-libraries optimized for Next Generation Sequencing
15 (NGS) techniques. Alternatively, the library screening can be performed with hybridization to
16 Microarrays (on Chip) for which additional steps for DNA dye labeling after PCR
17 amplification are necessary.

18
19

20 **2. Materials**

21 **2.1. Strains and growth media**

22 1. *Legionella pneumophila* e.g. strains Paris, JR32 or Philadelphia-1

23

24 2. AYE medium. For 1 liter dissolve 12 g yeast extract and 10 g ACES, adjust pH to 6.9 with
25 1 M KOH. Add 10 mL of cysteine 40 g/L and 10 mL of iron pyrophosphate 30 g/L. Fill
26 volume to 1 L with distilled water and filter sterilize.

27

28 3. CYE plates. For 1 liter dissolve 10 g yeast extract and 10 g ACES, adjust pH to 6.9 with
29 1M KOH, add 15 g of agar, 2 g of activated charcoal and autoclave. Add 10mL of filter
30 sterilized cysteine 40 g/L and 10 mL of filter sterilized ferric nitrate 25 g/L. Poor plates.

31

32 **2.2 RIP library construction**

33

34 1. Formaldehyde 37%

- 1
- 2 2. Disposable 50 mL polypropylene tubes
- 3
- 4 3. Rotating wheel
- 5
- 6 4. Protease inhibitor cocktail (e.g. SigmaFast, Sigma, S8830-20TAB)
- 7
- 8 5. Lysis buffer: 50 mM HEPES-KOH pH7.5, 150mM NaCl, 1 mM EDTA, 1% Triton X-100,
- 9 0.1% Na-deoxycholate, protease inhibitor
- 10
- 11 6. Sonicator
- 12
- 13 7. Specific antibody against protein of interest or alternatively antibody against Tag (e.g.
- 14 Flag- or Strep-Tag)
- 15
- 16 8. Dynabeads® Protein A or G (Invitrogen, 100-01D or 100-03D),
- 17
- 18 9. Magnet for separation
- 19
- 20 10. Wash buffer RIPseq: 10 mM Tris-HCl pH 7.5, **250 mM NaCl**, 0.5% NP40, 0.5% Na-
- 21 deoxycholate, 1 mM EDTA
- 22
- 23 11. TE buffer : 10mM Tris, 1mM EDTA, pH 7.5
- 24
- 25 12. Elution buffer: 50mM Tris, 1mM EDTA, 1% SDS, pH8.0
- 26
- 27 13. Proteinase K 20µg/µl
- 28 14. DNase I recombinant, RNase free (10U/µl)
- 29
- 30 15. RNA fragmentation kit (Ambion, AM8740)
- 31
- 32 16. Alkaline Phosphatase
- 33
- 34 17. 3'-RNA adapter P-UCGUAUGCCGUCUUCYGCUUGUidT (idT = inverted deoxyT)

- 1
- 2 18. T4 Polynucleotide Kinase
- 3
- 4 19. 5'-RNA adapter GUUCAGAGUUCUACAGUCCGACGAU
- 5
- 6 20. Reverse Transcription Specific primer CAAGCAGAAGACGGCATAACGA
- 7
- 8 21. Phenol solution, pH4.3
- 9
- 10 22. Chloroform:Isoamyl alcohol 24:1
- 11
- 12 23. RNase inhibitor
- 13
- 14 24. 3M Sodium Acetate, pH5.2
- 15
- 16 25. Ethanol p.a.; Etanol 75%
- 17
- 18 26. Glycogen (20mg/ml)
- 19
- 20 27. Tobacco acid pyrophosphatase 10U/ μ l, TAP
- 21
- 22 28. 5'-RNA adapter (25 μ M) GUUCAGAGUUCUACAGUCCGACGAU
- 23
- 24 29. T4 RNA Ligase 5U/ μ l
- 25
- 26 30. Superscript II Reverse Transcriptase Kit (Invitrogen, 18064014)
- 27
- 28 31. 10mM dNTP mix
- 29
- 30 32. Certified Low Range Ultra Agarose
- 31
- 32 33. Agarose gel electrophoresis equipment
- 33
- 34 34. 0.5M EDTA pH8.0

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33

35. Distilled water DNase/RNase free

36. Thermocycler

37. High Fidelity DNA Polymerase

38. Primer 1 (25 μ M) CAAGCAGAAGACGGCATAACGA

39. Primer 2 (25 μ M) AATGATACGGCGACCACCGACAGGTTTCAG
AGTTCTACAGTCCGA

40. PCR Clean-up kit

41. Bionalyzer 2100 (Agilent);

42. DNA 1000 Chips (Agilent, 5067-1504)

43. Bradford reagent

2.2 ChIPseq library construction

1. Formaldehyde 37%

2. Disposable 50 mL polypropylene tubes

3. Protease inhibitor cocktail

4. Lysis buffer: 50 mM HEPES-KOH pH7.5, 150mM NaCl, 1 mM EDTA, 1% Triton X-100,
0.1% Na-deoxycholate, protease inhibitor

5. Sonicator

- 1 6. Specific antibody against protein of interest or alternatively antibody against Tag (e.g.
- 2 Flag- or Strep-Tag)
- 3
- 4 7. Dynabeads® Protein A or G (Invitrogen, 100-01D or 100-03D),
- 5
- 6 8. Magnet for separation
- 7
- 8 9. Wash buffer ChIPseq: 10 mM Tris-HCl pH 7.5, **250 mM LiCl**, 0.5% NP40, 0.5% Na-
- 9 deoxycholate, 1 mM EDTA
- 10
- 11 10. TE buffer : 10mM Tris, 1mM EDTA, pH 7.5
- 12
- 13
- 14 11. Elution buffer: 50mM Tris, 1mM EDTA, 1% SDS, pH8.0
- 15
- 16 12. Proteinase K 20µg/µl
- 17
- 18 13. RNase A, DNase free (0.35µg/µl in PBS)
- 19
- 20 14. Genomic DNA Sample Prep Kit (Illumina, FC-102-1001)
- 21

22 **3. RIPseq and ChIP-seq library construction (common steps; Note 1)**

- 23 1. Inoculate 50 mL fresh AYE media to $OD_{600} = 0.1$ from an overnight culture and allow
- 24 bacteria to grow to an optimal OD (depending on the expression of desired protein).
- 25 2. Transfer each culture to separate disposable 50 mL polypropylene tubes and add 1.4 mL
- 26 of 37% Formaldehyde (Note 2).
- 27 3. Incubate the formaldehyde-treated cells for 20 minutes at room temperature on a
- 28 rotating platform, and transfer to a rotating platform overnight at 4°C.
- 29 4. Spin the 50 mL polypropylene tubes containing the formaldehyde-treated cells for 5min
- 30 at 5000g (4°C), pour off the supernatant and wash the cells 3 times in cold 1X PBS (if
- 31 not using the cells immediately, store cell pellet at -80°C).
- 32 5. Resuspend the cell pellets using 1ml Lysis Buffer + protease inhibitor
- 33 And pulse-sonicate them with around 60 watt five times for 20sec

34 **For ChIP-seq additional DNA fragmentation:**

- 1 **sonication on ice for 15 min 30sec ON/ 30sec OFF (avoid raising temperature!!) or**
2 **nebulization necessary**
- 3 6. Centrifuge at max speed for 20min and transfer supernatant in a new tube, quantify the
4 total protein with Bradford and adjust it to 1mg protein/ml (Note 3)
- 5 7. Preparation of magnetic beads
- 6 - Aliquot 100µL of Dynabeads ProteinG for each sample to be immunoprecipitated
7 and wash them 3 times in 1XPBS + 1%BSA solution, resuspend them in 250µl
8 PBS/BSA + add 5-10µg of antibody and incubate them over night at 4°C on a
9 rotating platform (Note 4)
- 10 - do the same with 200µl of beads, but incubate them over night without antibody or
11 with an unspecific antibody)
- 12 - Wash the beads 3 times in cold PBS/BSA and resuspend them in 100µl PBS/BSA
13 per sample
- 14 8. Co-Immunoprecipitation
- 15 - Add 100µl of magnetic beads (**without antibody or with an unspecific antibody**)
16 to the protein solution (prepared in step 6) and incubate for 4h at 4°C on a rotating
17 platform (pre-clearing of solution from unspecific protein-beads interaction); place
18 them on a magnet and transfer the supernatant into a fresh tube
- 19 - Divide the fraction in two equal aliquots.
20 Add in one 100µl of magnetic beads **with specific antibody**. For the second part,
21 add 100µl of magnetic beads **without antibody or with an unspecific antibody**
22 (negative control). Incubate samples over night at 4°C on a rotating platform
- 23 9. Place samples on a magnet and wash the beads twice with cold Lysis buffer containing
24 additional 350mM NaCl
- 25 10. Wash the beads five times in cold Wash buffer (**important for RIPseq use NaCl**
26 **instead of LiCl!!!**)
- 27 11. Wash once with cold TE buffer
- 28 12. Resuspend beads in 150µl Elution buffer and incubate them for 15min at 65°C with
29 brief vortexing every 2min
- 30 13. Place the solution on a magnet and transfer supernatant into a new tube (discard the
31 beads!)
- 32 14. Reverse cross-linking (by incubation over night at 65°C)
- 33 15. P/C/I extraction and NaAc precipitation (Note 5 and 6), resuspend pellet in 50µl
34 distilled water

1 16. Add 140µl TE buffer + 3µl Glycogen + 7µl Proteinase K (20µg/µl) and incubate 2h at
2 37°C

3 17. Extract again with P/C/I and resuspend after NaAc precipitation in 44µl distilled H₂O.
4 Continue with step 3.1 for RNA-Immunoprecipitation or with 3.2 for DNA/Chromatin-
5 IP
6

7 **3.1. RIPseq (continuation)**

8 1. DNase I digestion: add 5µl of DNase 10xbuffer and 1µl of DNase I and incubate
9 reaction for 30min at 25°C. Extract with P/C/I and precipitate samples with NaAc.
10 Resuspend the dry pellet in 10µl distilled RNase-free water

11 2. Fragmentation: the RNA was metal-catalyzed heat fragmented to sizes of around 100-
12 200nt using the RNA fragmentation kit

13 1.1µl 10x fragmentation reagent (buffered zinc solution)

14 10µl RNA

15 Incubation at 70°C for 5min

16 Terminate reaction by putting on ice and add 1.1µl stop solution

17 After NaAc precipitation, resuspend the dry pellet in 26µl RNase-free distilled H₂O
18

19 3. RNA dephosphorylation:

20 a) TAP treatment

21 Denature the RNA from step 2 for 10min at 65°C

22 After 1min on ice, add 3µl TAP buffer and 1µl TAP (10U) and incubate for 1h at 37°C

23 b) Alkaline Phosphatase treatment

24 Add 14µl distilled H₂O, 5µl 10x Dephosphorylation buffer and 1µl Alkaline

25 Phosphatase (10U) and incubate for 30min at 37°C
26

27 Phenol/Chloroform/IAA extraction, NaAc precipitation; resuspend the dry pellet in 5.9
28 µl distilled water
29

30 4. 3'-RNA adapter ligation

31 5.9µl RNA

32 0.6µl 3' adapter (100µM)

33 Incubate mix for 10min at 65°C, put on ice for 1min and add

34 1µl T4 RNA ligase buffer

1 1µl ATP solution
2 0.5µl RNase inhibitor
3 1µl RNA ligase
4 Incubate for 6h at 20°C, following 4°C over night, purify with columns (e.g.
5 NucleoSpin) and resuspend RNA after NaAc precipitation in 10µl distilled water
6
7 5. Re-phosphorylation of 5' end
8 10µl RNA
9 2µl PK buffer
10 1µl ATP solution
11 0.5µl RNase inhibitor
12 1µl Polynucleotide Kinase
13 5.5µl RNase free H₂O
14
15 P/C/I extraction and precipitation with NaAc; resuspend pellet in 5.3µl distilled H₂O
16
17 6. 5'-RNA adapter ligation:
18 5.3µl RNA
19 1.2µl 5'-RNAadapter (25µM)
20 Incubate 10min at 65°C, on ice for 1min and add
21 1µl T4 RNA ligase buffer
22 1µl ATP solution
23 0.5µl RNase inhibitor
24 1µl RNA ligase
25 And incubate for 6h at 20°C, following 4°C over night
26
27 7. Reverse Transcription using RT Specific primer
28 10µl RNA +0.5µl RT Specific primer (100µM)
29 Denature at 65°C for 10min, on ice 1min and add
30 6µl first strand buffer
31 1.5µl DTT (100mM)
32 1.5µl dNTP
33 1µl RNase inhibitor
34 8µl RNase-free H₂O

1 1.5µl Superscript II RT
2 Incubate 1h at 42°C and purify on columns (e.g. NucleoSpin), recover with 30µl of
3 distilled water
4

5 8. PCR amplification (see also Note 7)

6 30µl template cDNA
7 10µl Phusion HF buffer
8 8µl H₂O
9 0.5µl Primer 1 (25µM)
10 0.5µl Primer 2 (25µM)
11 0.5µl dNTP (25mM)
12 0.5µl Phusion DNA Polymerase
13

14 98°C 1min
15

16 98°C 10sec

17 60°C 30sec

18 72°C 30sec

19 15 cycles
20

21 72°C 10min

22 4°C
23

24 9. Size fractionation

25 Run samples of step 8 on a low range ultra 2% agarose gel. Cut the zones between 100-
26 170nt and 170-250nt and purify independently with columns (e.g. Nucleospin).

27 Combine the samples of the two “zones”, precipitate and resuspend pellet in 30µl-
28 distilled water

29 Purify with columns (e.g. Nucleospin), precipitate and resuspend pellets in 10µl-
30 distilled water
31

32 10. Check quality and quantity with the Bioanalyzer (DNA 1000) (Note 8)

33 11. Ready for Sequencing with Illumina
34

3.2. ChIP-seq library construction (continuation)

1. RNase digestion: add add 56µl of RNase A (final concentration 0.2 µg/µl) and incubate reaction for 2h at 37°C. Extract with P/C/I and precipitate samples with NaAc.
Resuspend the dry pellet in 30µl distilled RNase-free water
2. blunt end-DNA by incubation with T4 DNA Polymerase
 - 30µl DNA sample
 - 45µl water
 - 10µl T4 DNA Ligase Buffer (with 10mM ATP)
 - 4µl dNTP (10mM)
 - 5µl T4 DNA Polymerase
 - 1µl Klenow Enzyme
 - 5µl T4 Polynucleotide KinaseIncubate 30min at 20°C and purify with columns (e.g. NucleoSpin)
3. Adenylation of 3' ends
 - 32µl DNA sample
 - 5µl Klenow buffer
 - 10µl dATP (1mM)
 - 3µl Klenow Exo-Incubate 30min at 37°C, purification with columns (e.g. NucleoSpin)
4. Adapter Ligation
 - 18µl DNA sample
 - 25µl Ligase Buffer
 - 2µl PE Adapter Oligo Mix (Illumina)
 - 5µl DNA LigaseIncubate 15min at 20°C, purification and resuspend in 30µl distilled water
5. PCR amplification (as described in 3.1. step 8)
6. Size fractionation on a low range ultra 2% agarose gel (see also 3.1. step 9)
7. Check quality and quantity with the Bioanalyzer (DNA 1000) (Note 8)

4. Notes

- 1
- 2 1. Keep aliquots of the different stages and test them by western blot to monitor the
- 3 efficiency of your lysis, binding, washing and elution steps.
- 4 2. Formaldehyde step is optional, but usually necessary as the protein-nucleotide
- 5 interactions are weak and unstable resulting in too small quantities. Alternative to wild
- 6 type cultures, cultures overexpressing the protein of interest can be used to increase
- 7 quantity.
- 8 3. For IP experiments an amount of at least 3-5mg of total protein is recommended
- 9 (depending on abundance of the protein of interest).
- 10 4. Specific antibodies or antibodies against Tags can be used similarly; test quality of
- 11 antibodies in western blot experiments before use.
- 12 5. Phenol/Chloroform/IAA (P/C/I) extraction: Add 50% of Phenol to the sample and mix
- 13 vigorously by vortexing. Add the same amount of Chloroform/Isoamyl alcohol and mix
- 14 well. Centrifuge at max speed for 5 min, transfer the supernatant to a new tube and add
- 15 1 vol of Chloroform/Isoamyl alcohol, mix vigorously, centrifuge and transfer
- 16 supernatant into a new tube.
- 17 6. NaAc precipitation: Add 10% 3M sodium acetate (pH5.2), 2% glycogen and 2.5vol of
- 18 ethanol p.a. to the sample and store it min 2h (better over night) at -20°C. Centrifuge at
- 19 4°C for 15min at max speed and discard supernatant. Wash RNA pellet with 500µl ice-
- 20 cold 75% ethanol centrifuge again for 5min, discard supernatant and let the pellet dry
- 21 for 10min at RT. Resuspend the dry pellet RNase-free distilled H₂O.
- 22 7. Number of cycles during PCR amplification can differ between experiments depending
- 23 on the amount of cDNA obtained in previous step. Typically are 12 to maximal 17
- 24 cycles. More cycles are not recommended as additional PCR steps may introduce a
- 25 significant amplification bias in cDNA representation.
- 26 8. DNA amounts are typically in nM range; anyhow, for the hybridization on the Cluster
- 27 Station concentrations of 1–10 pM are recommended.
- 28

29 **Acknowledgements**

30

31 This work received support from the Institut Pasteur, the Centre national de la recherche
32 scientifique (CNRS) and the Institut Carnot-Pasteur MI and from the ANR-10-PATH-004
33 project, in the frame of ERA-Net PathoGenoMics

1

2 5. References

3

- 4 1. Albert-Weissenberger, C., Sahr, T., Sismeiro, O., Hacker, J., Heuner, K., and
5 Buchrieser, C. (2010) Control of flagellar gene regulation in *Legionella pneumophila*
6 and its relation to growth phase, *J Bacteriol* 192, 446-455.
- 7 2. Bruggemann, H., Hagman, A., Jules, M., Sismeiro, O., Dillies, M. A., Gouyette, C.,
8 Kunst, F., Steinert, M., Heuner, K., Coppee, J. Y., and Buchrieser, C. (2006)
9 Virulence strategies for infecting phagocytes deduced from the in vivo transcriptional
10 program of *Legionella pneumophila*, *Cell Microbiol* 8, 1228-1240.
- 11 3. Hovel-Miner, G., Faucher, S. P., Charpentier, X., and Shuman, H. A. (2010) ArgR-
12 regulated genes are derepressed in the *Legionella*-containing vacuole, *J Bacteriol* 192,
13 4504-4516.
- 14 4. Hovel-Miner, G., Pampou, S., Faucher, S. P., Clarke, M., Morozova, I., Morozov, P.,
15 Russo, J. J., Shuman, H. A., and Kalachikov, S. (2009) SigmaS controls multiple
16 pathways associated with intracellular multiplication of *Legionella pneumophila*, *J*
17 *Bacteriol* 191, 2461-2473.
- 18 5. Sahr, T., Bruggemann, H., Jules, M., Lomma, M., Albert-Weissenberger, C., Cazalet,
19 C., and Buchrieser, C. (2009) Two small ncRNAs jointly govern virulence and
20 transmission in *Legionella pneumophila*, *Mol Microbiol* 72, 741-762.
- 21 6. Tiaden, A., Spirig, T., Carranza, P., Bruggemann, H., Riedel, K., Eberl, L.,
22 Buchrieser, C., and Hilbi, H. (2008) Synergistic contribution of the *Legionella*
23 *pneumophila* lqs genes to pathogen-host interactions, *J Bacteriol* 190, 7532-7547.
- 24 7. Tiaden, A., Spirig, T., Weber, S. S., Bruggemann, H., Bosshard, R., Buchrieser, C.,
25 and Hilbi, H. (2007) The *Legionella pneumophila* response regulator LqsR promotes
26 host cell interactions as an element of the virulence regulatory network controlled by
27 RpoS and LetA, *Cell Microbiol* 9, 2903-2920.
- 28 8. Waldminghaus, T., and Skarstad, K. (2010) ChIP on Chip: surprising results are often
29 artifacts, *BMC Genomics* 11, 414.
- 30 9. Park, P. J. (2009) ChIP-seq: advantages and challenges of a maturing technology, *Nat*
31 *Rev Genet* 10, 669-680.
- 32 10. Davies, B. W., Bogard, R. W., and Mekalanos, J. J. (2011) Mapping the regulon of
33 *Vibrio cholerae* ferric uptake regulator expands its known network of gene regulation,
34 *Proc Natl Acad Sci U S A* 108, 12467-12472.
- 35 11. Kahramanoglou, C., Seshasayee, A. S., Prieto, A. I., Ibberson, D., Schmidt, S.,
36 Zimmermann, J., Benes, V., Fraser, G. M., and Luscombe, N. M. (2011) Direct and
37 indirect effects of H-NS and Fis on global gene expression control in *Escherichia coli*,
38 *Nucleic Acids Res* 39, 2073-2091.
- 39 12. Lun, D. S., Sherrid, A., Weiner, B., Sherman, D. R., and Galagan, J. E. (2009) A blind
40 deconvolution approach to high-resolution mapping of transcription factor binding
41 sites from ChIP-seq data, *Genome Biol* 10, R142.

42

43