

Figure S1 a) B-factor distributions of the backbone atoms. B-factors were scaled between 1 and 100 by unity-based normalization. Top row: 165 structures with resolution better than 1.9 Å (bin R1). Middle row: 357 structures with resolution 1.9-2.5 Å (bin R2). Bottom row: 187 structures with resolution 2.5-3.0 Å (bin R3). Water bridges considered between amino acids and DNA phosphates.

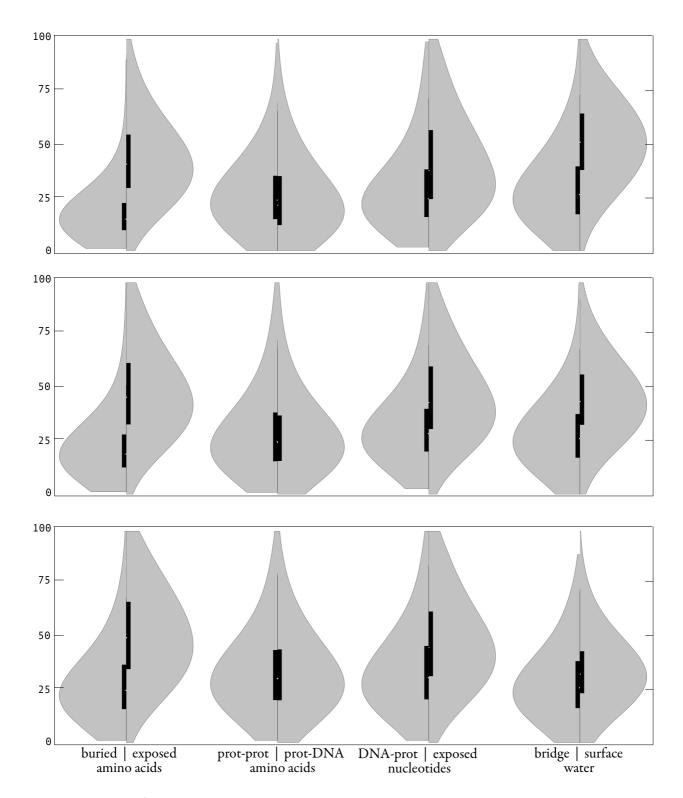


Figure S1 b) B-factor distributions of the side chain atoms. B-factors were scaled between 1 and 100 by unity-based normalization. Top row: 165 structures with resolution better than 1.9 Å (bin R1). Middle row: 357 structures with resolution 1.9-2.5 Å (bin R2). Bottom row187 structures with resolution 2.5-3.0 Å (bin R3). Water bridges considered between amino acids and DNA bases.

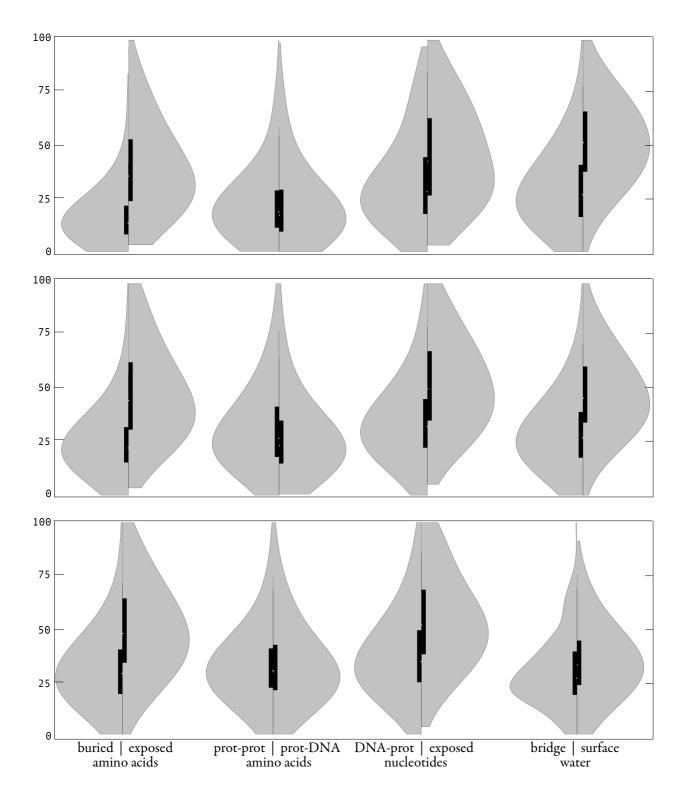


Figure S1 c) B-factor distributions of the backbone atoms of the protein-DNA complexes containing transcription factors.

B-factors were scaled between 1 and 100 by unity-based normalization.

Top row: 56 structures with resolution better than 1.9 Å (bin R1).

Middle row: 132 structures with resolution 1.9-2.5 Å (bin R2).

Bottom row: 89 structures with resolution 2.5-3.0 Å (bin R3).

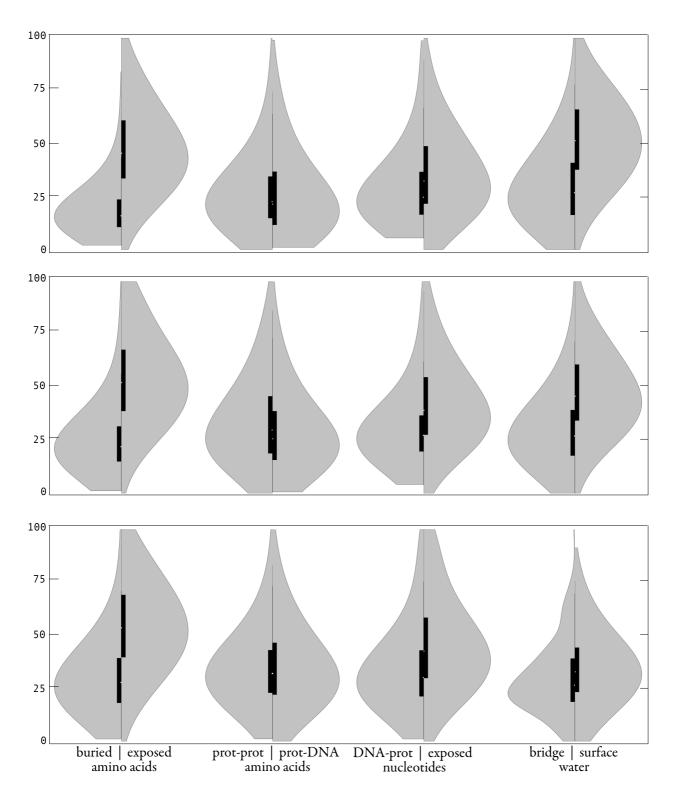


Figure S1 d) B-factor distributions of the side chain atoms of the protein-DNA complexes containing transcription factors.
B-factors were scaled between 1 and 100 by unity-based normalization.
Top row: 56 structures with resolution better than 1.9 Å (bin R1).

Middle row: 132 structures with resolution 1.9-2.5 Å (bin R2). Bottom row: 82 structures with resolution 2.5-3.0 Å (bin R3).

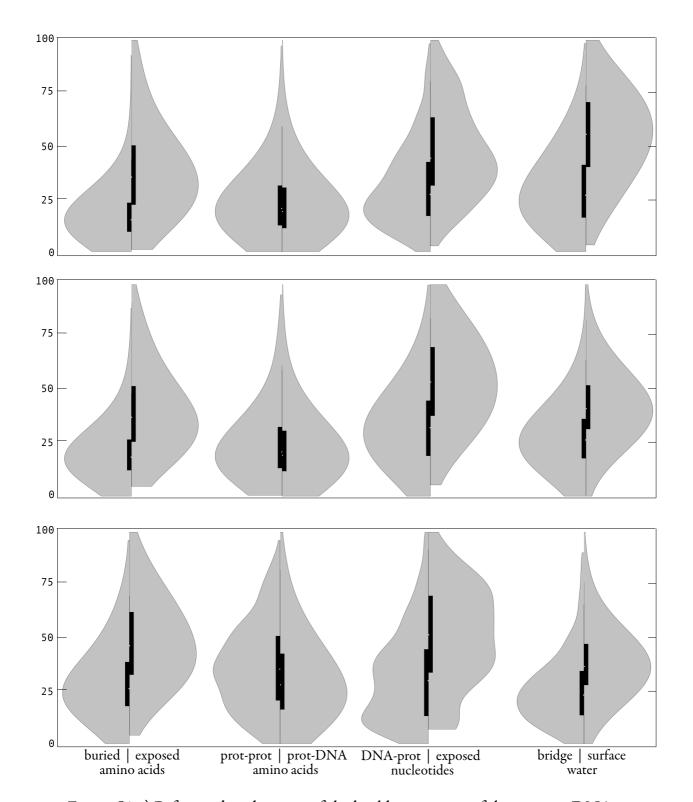


Figure S1 e) B-factor distributions of the backbone atoms of the protein-DNA complexes containing nucleases.

B-factors were scaled between 1 and 100 by unity-based normalization.

Top row: 41 structures with resolution better than 1.9 Å (bin R1).

Middle row: 59 structures with resolution 1.9-2.5 Å (bin R2).

Bottom row: 21 structures with resolution 2.5-3.0 Å (bin R3).

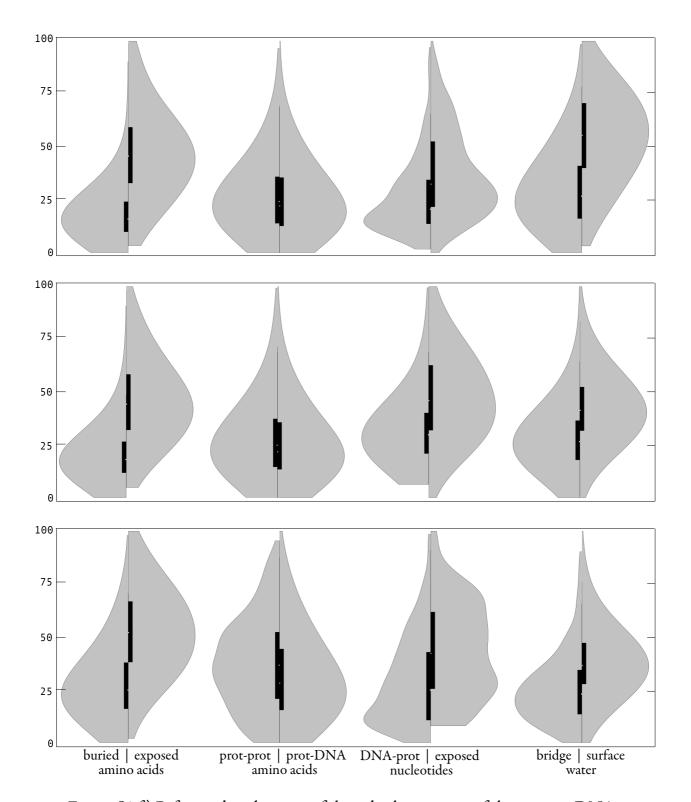


Figure S1 f) B-factor distributions of the side chain atoms of the protein-DNA complexes containing nucleases.

B-factors were scaled between 1 and 100 by unity-based normalization.

Top row: 41 structures with resolution better than 1.9 Å (bin R1).

Middle row: 59 structures with resolution 1.9-2.5 Å (bin R2).

Bottom row: 21 structures with resolution 2.5-3.0 Å (bin R3).