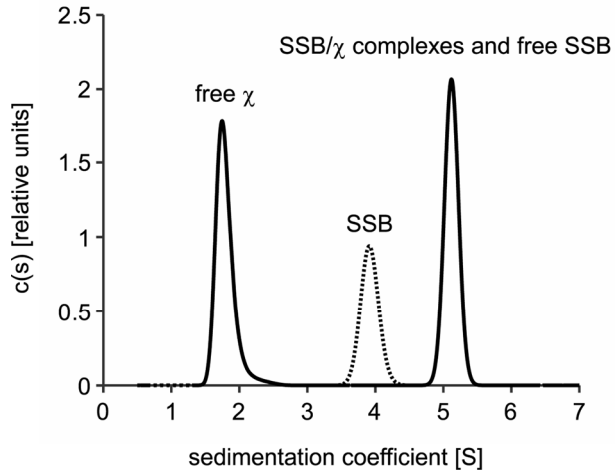
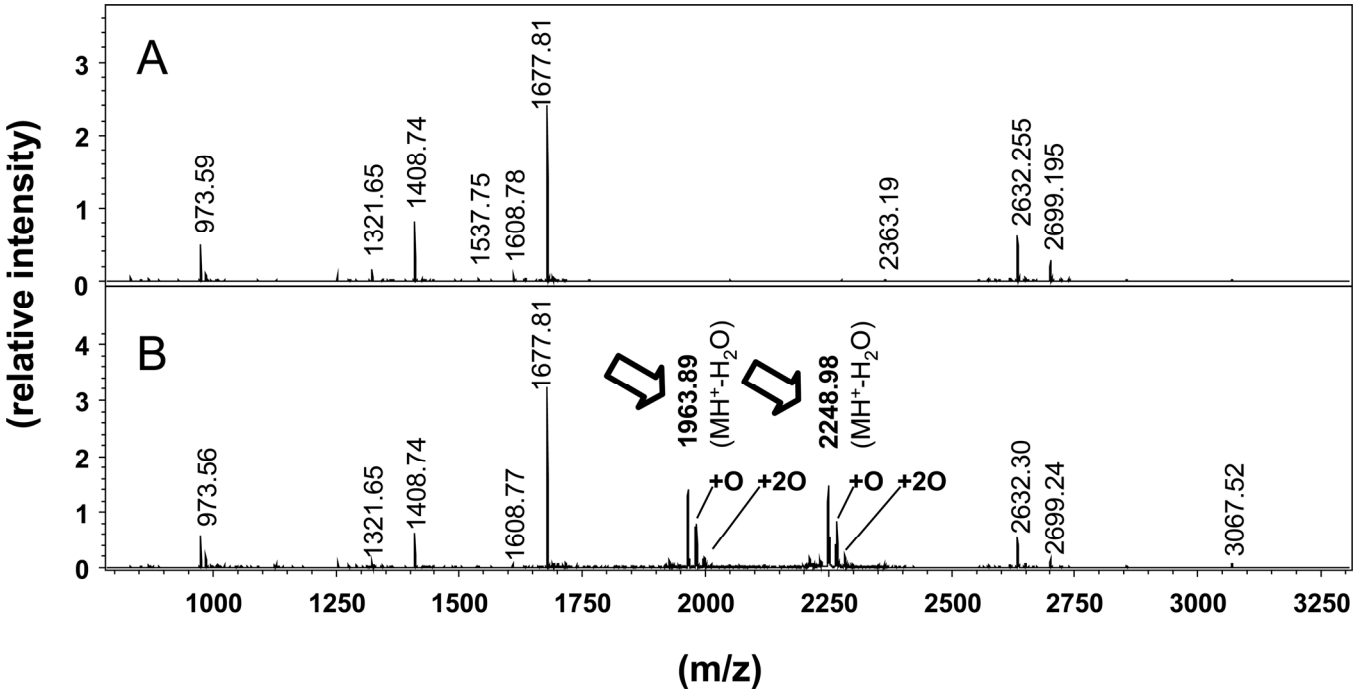
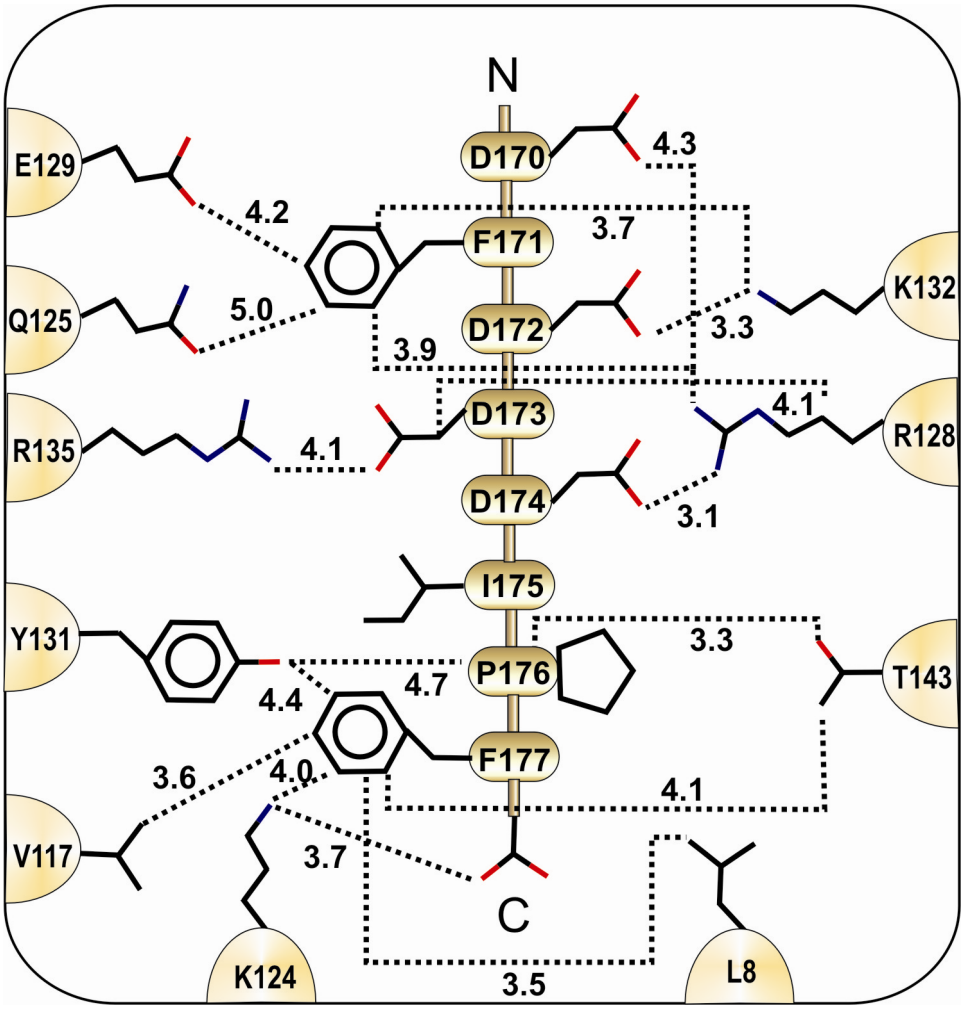
Supporting material



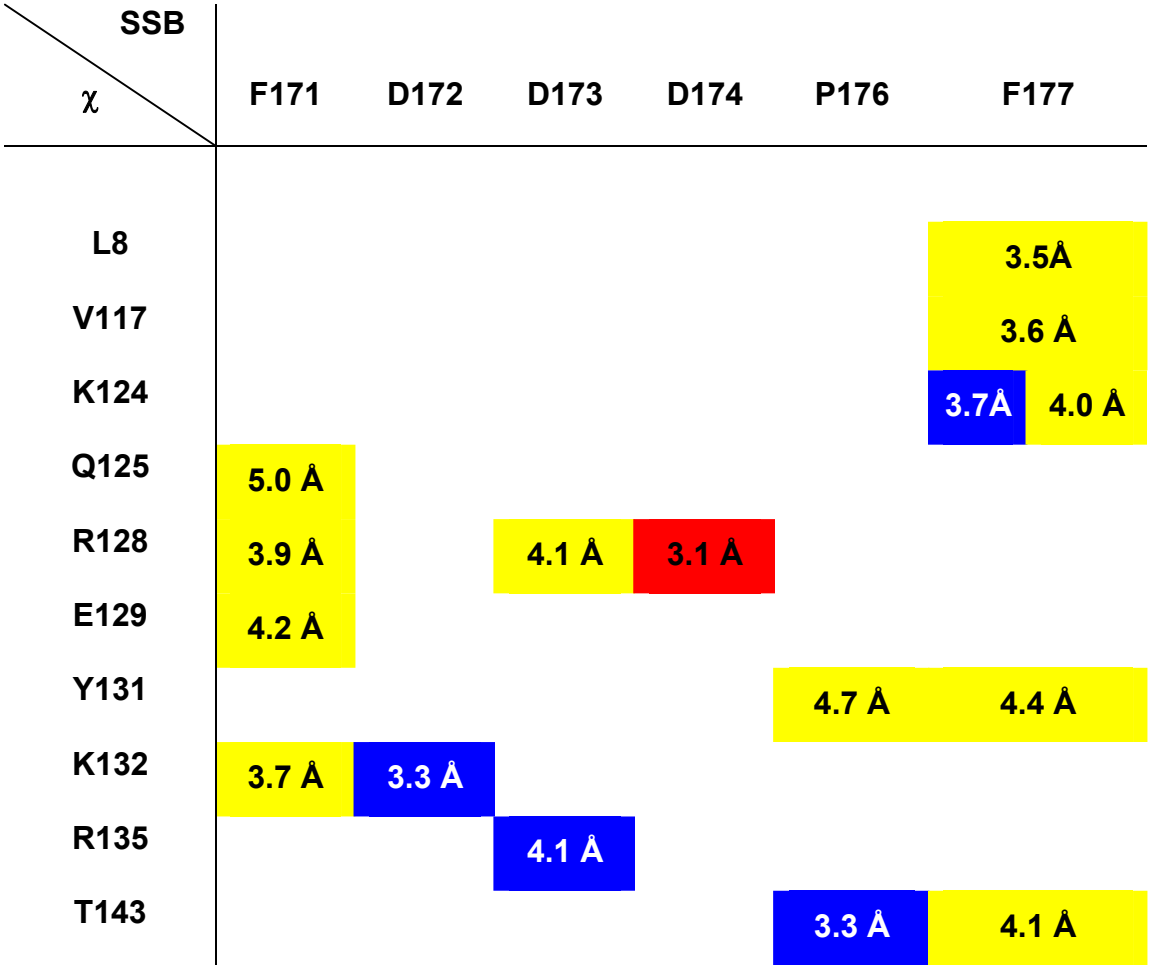
Supplementary Figure S1: Interaction of EcoSSB and Ecoχ at 20°C in 0.3 M NaCl, 0.5 mM DTT, 20 mM potassium phosphate pH 7.4. *c*(*s*) distributions of sedimentation velocity experiments in the analytical ultracentrifuge for 2.5 µM wild-type EcoSSB in the absence (dashed curve) or presence (solid curve) of 30 µM Ecoχ.



Supplementary Figure S2: MS analysis of untreated and cross-linked χ protein. χ protein untreated (A) or cross-linked with EDC to the SSB-Carb peptide (B) was digested with trypsin. Peptide masses were analysed by MALDI-MS and peptide mass fingerprints were generated. χ protein cross-linked to the SSB-Carb peptide exhibited two additional mass signals of m/z 1963.89 and 2248.98 (arrows) that correspond to the cross-linked peptide Y131-R135 and E129-R135, respectively. Additional oxygen adducts were identified (+O; +2O).



Supplementary Figure S3: Schematic representation of the C-terminal residues of SSB (centre) interacting with χ as predicted by our experimental data and molecular modelling. Distances in angstroms are indicated by dotted lines.



Supplementary Table S1: Distances of selected residues in the new model of SSB/χ interaction as shown in Figure 5. In the final model of SSB/χ interaction, distances between important amino acid residues of SSB and χ were measured with Coot (1). The colour labelling in the table refers to the type of interaction. Yellow: hydrophobic interaction; blue: electrostatic interaction and red: hydrogen bond.

	ExoI (A site) [2]	ExoI (B site) [2]	RecQ [3]	χ subunit of DNA polymerase III
Residues of hydrophobic pocket to accommodate C-terminal residues of SSB	L147 L204 Y207	W245 L264 C330	L420 I423 L494 A498	L8 V117 Y131 T143

Supplementary Table S2: Residues of ExoI, RecQ and the χ subunit of DNA polymerase III involved in hydrophobic pocket formation at the SSB-binding sites. All SSB-binding sites identified so far share common surface features (2, 3), such as a hydrophobic pocket to accommodate the ultimate C-terminus of SSB.

References

1. Emsley,P. and Cowtan,K. (2004) Coot: model-building tools for molecular graphics. *Acta Crystallogr. D Biol. Crystallogr.,* **60,** 2126-2132.

2. Lu,D. and Keck,J.L. (2008) Structural basis of *Escherichia coli* single-stranded DNA-binding protein stimulation of exonuclease I. *Proc. Natl. Acad. Sci. U. S. A.,* **105,** 9169-9174.

3. Shereda,R.D., Reiter,N.J., Butcher,S.E. and Keck,J.L. (2009) Identification of the SSB binding site on *E. coli* RecQ reveals a conserved surface for binding SSB's C terminus. *J. Mol. Biol.,* **386,** 612-625.