

**S3 Table.** Hydrogen bonds between FH20 and OspE in the CFI interaction.

FH residue	Distance (Å)	OspE residue	Analyzed from the crystal structure PDB 4J38*
Arg <sup>1182</sup> (N <sup>η2</sup> )	3.10	Asp <sup>73</sup> (O <sup>δ2</sup> )	3.02
Arg <sup>1182</sup> (N <sup>η2</sup> )	2.81	Glu <sup>68</sup> (O <sup>ε2</sup> )	2.97
Arg <sup>1182</sup> (N <sup>ε</sup> )	n.d.	Thr <sup>84</sup> (O <sup>γ1</sup> )	3.75
Arg <sup>1182</sup> (O)	2.76	Arg <sup>66</sup> (N <sup>η1</sup> )	2.67
Trp <sup>1183</sup> (N <sup>ε1</sup> )	n.d.	Thr <sup>84</sup> (O <sup>γ1</sup> )	n.d.
Trp <sup>1183</sup> (O)	2.81	Asn <sup>77</sup> (N <sup>δ2</sup> )	3.08
Thr <sup>1184</sup> (O <sup>δ1</sup> )	n.d.	Asn <sup>77</sup> (O <sup>δ1</sup> )	3.73
Ser <sup>1191</sup> (OG)	3.10	Gly <sup>80</sup> (O)	2.61
Glu <sup>1195</sup> (O <sup>ε2</sup> )	3.77	Tyr <sup>114</sup> (N <sup>ζ</sup> )	n.d.
Glu <sup>1195</sup> (O <sup>ε2</sup> )	n.d.	Gly <sup>80</sup> (N)	3.70
Ser <sup>1196</sup> (O)	3.04	Ser <sup>82</sup> (N)	n.d.
Ser <sup>1196</sup> (O)	3.34	His <sup>81</sup> (N <sup>δ1</sup> )	3.02
Ser <sup>1196</sup> (O <sup>γ</sup> )	3.83	Val <sup>120</sup> (O)	n.d.
Glu <sup>1198</sup> (N)	2.81	Ser <sup>82</sup> (O)	2.82
Glu <sup>1198</sup> (O <sup>ε1</sup> )	n.d.	Thr <sup>84</sup> (O <sup>γ1</sup> )	2.90
Glu <sup>1198</sup> (O <sup>ε1</sup> )	3.62	Thr <sup>84</sup> (N)	2.68
Arg <sup>1215</sup> (N <sup>η1</sup> )	2.88	Thr <sup>84</sup> (O)	3.71
Arg <sup>1215</sup> (N <sup>ε</sup> )	2.92	Val <sup>120</sup> (O)	2.83
Arg <sup>1215</sup> (N <sup>η1</sup> )	n.d.	Ile <sup>121</sup> (O)	3.46

- Bhattacharjee A, Oeemig JS, Kolodziejczyk R, Meri T, Kajander T, Lehtinen MJ, et al. Structural basis for complement evasion by Lyme disease pathogen *Borrelia burgdorferi*. *J Biol Chem.* 2013;288(26):18685-95. doi: 10.1074/jbc.M113.459040. PubMed PMID: 23658013; PubMed Central PMCID: PMC3696643.