Supplementary Table 2 List of the major hydrophobic interactions and H-bonds in the off7/MBP complex.

off7 interaction residue (repeat module #)[a]	H-bond[b]	MBP interaction residue (helix #)[a]
THR 48 *[c] (1)		**LYS 216 (H9)**
TYR 56 * (1)		**LYS 216 (H9)**
TYR 56 * (1)	OH<-NZ (3.11 Å)	**LYS 154 (H7)**
VAL 78 * (2)		**SER 366 (H17)**
VAL 78 * (2)		**GLY 367 (H17)**
PHE 79 * (2)		**LYS 214 (H9)**
PHE 79 * (2)		VAL 210 (H9)
PHE 79 * (2)		ALA 365 (H17)
TYR 81 * (2)		**LYS 214 (H9)**
TYR 81 * (2)	OH<-ND2 (2.80 Å)	**ASN 215 (H9)**
LEU 86 (2)		**LYS 216 (H9)**
TYR 89 * (2)		**ASN 215 (H9)**
TYR 89 * (2)		HIS 217 (H9)
TYR 89 * (2)	O<-NZ (2.85 Å)	**LYS 151 (H7)**
TRP 90 * (2)	NE1->O (3.08 Å)	**ASN 215 (H9)**
TRP 90 * (2)		HIS 217 (H9)
TRP 90 * (2)		ASP 150 (H7)
ASP 110 (3)	OD2<-NZ (2.68 Å)	**LYS 214 (H9)**
ASP 112 * (3)		**LYS 214 (H9)**
TRP 123 * (3)		**LYS 151 (H7)**
TRP 123 * (3)		ALA 148 (H7)
TYR 125 (3)	OH<-NZ (2.48 Å)	**LYS 151 (H7)**

[a] A cut-off of 3.9 Å was applied for hydrophobic interactions. Bold entries denote residues contributing with more than 5% to the total buried surface area.

[b] A cut-off of 3.9 Å for donor-acceptor and 2.5 Å for hydrogen-acceptor was applied.

[c] A star indicates that this amino acid is located in a randomized library position of off7.