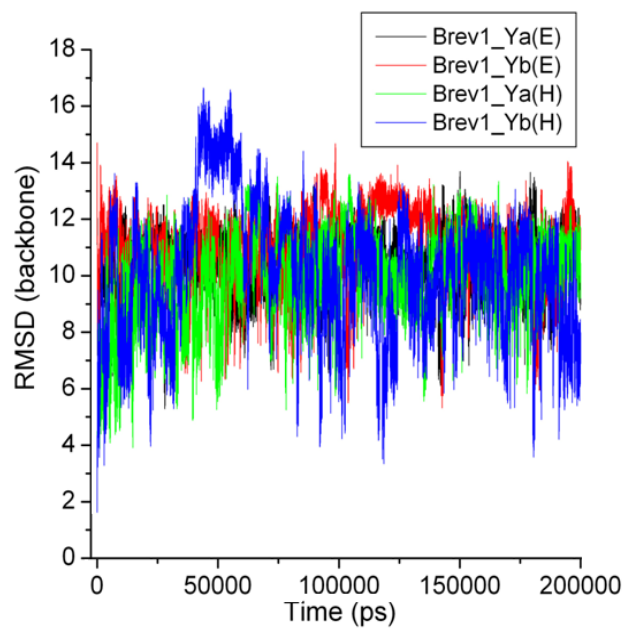
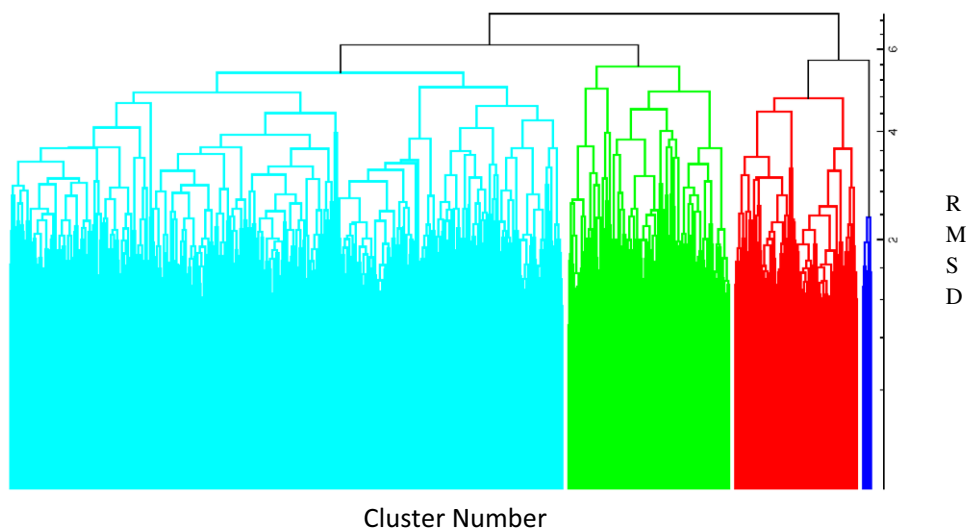


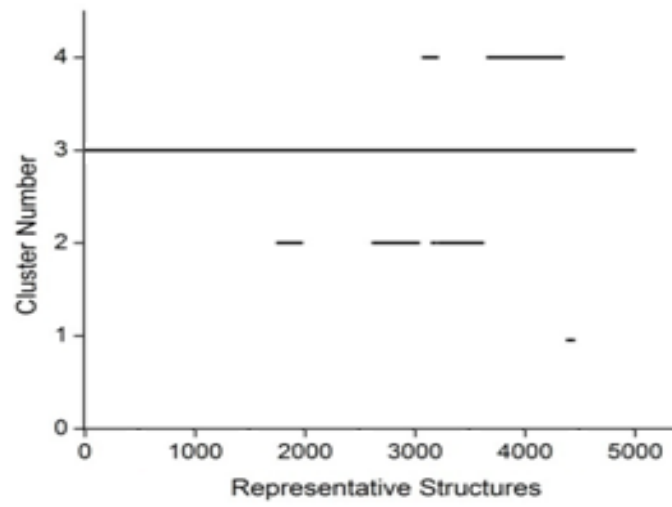
## Supplementary data



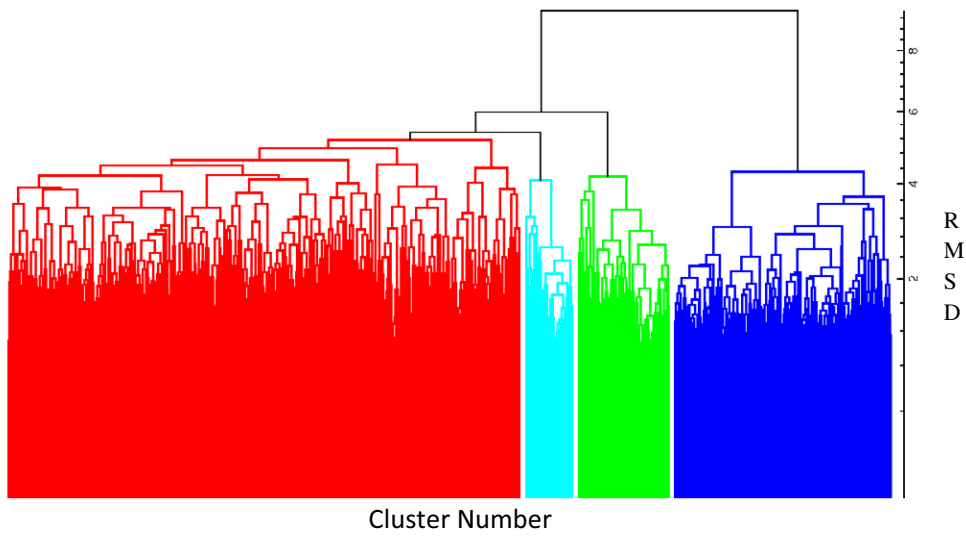
**Figure S(A):** The root mean square deviation (RMSD, Å) of sampled conformations in different simulations relative to their  $\alpha$ -helical starting structures.



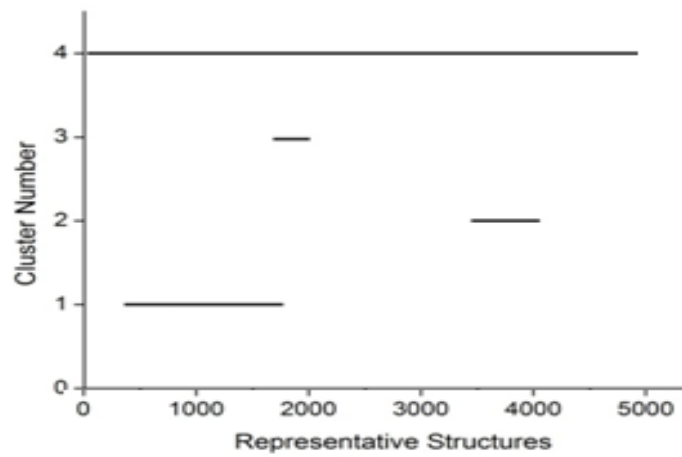
**Figure S(B):** Dendrogram showing different clusters in simulation Brev1\_Ya<sup>(H)</sup>.



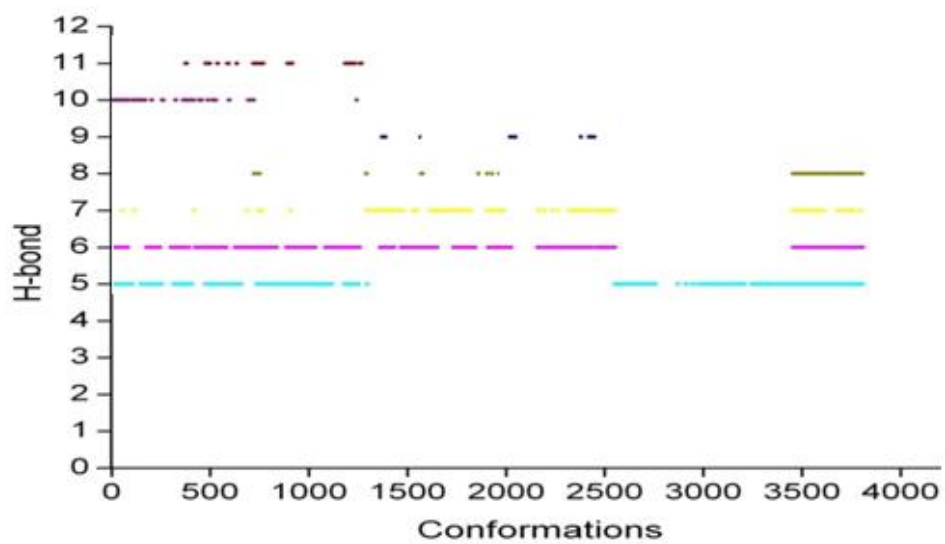
**Figure S(C):** The evolution of 4 clusters across the representative structures for simulation Brev1\_Ya<sup>(H)</sup>.



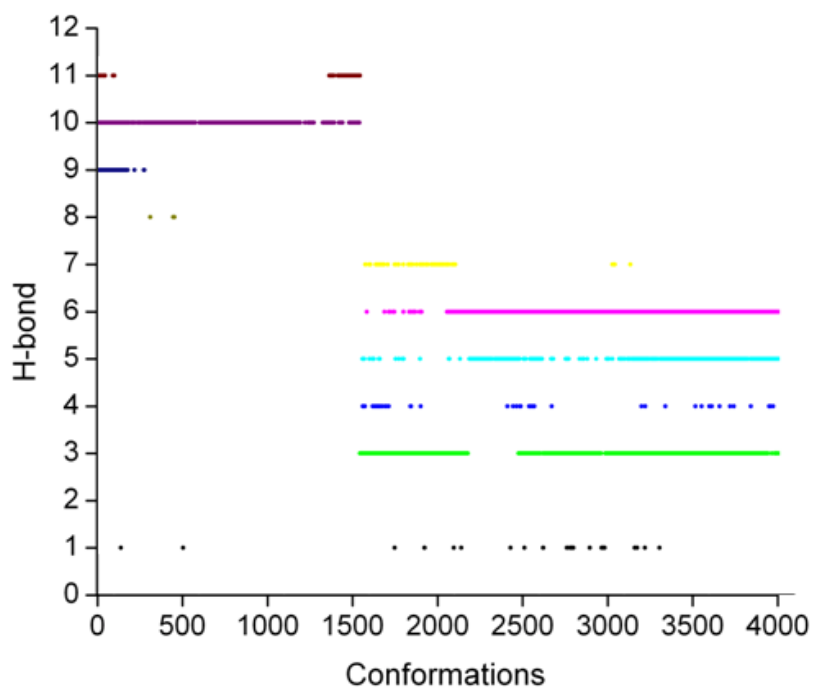
**Figure S(D):** Dendrogram showing different clusters in simulation Brev1\_Yb<sup>(H)</sup>.



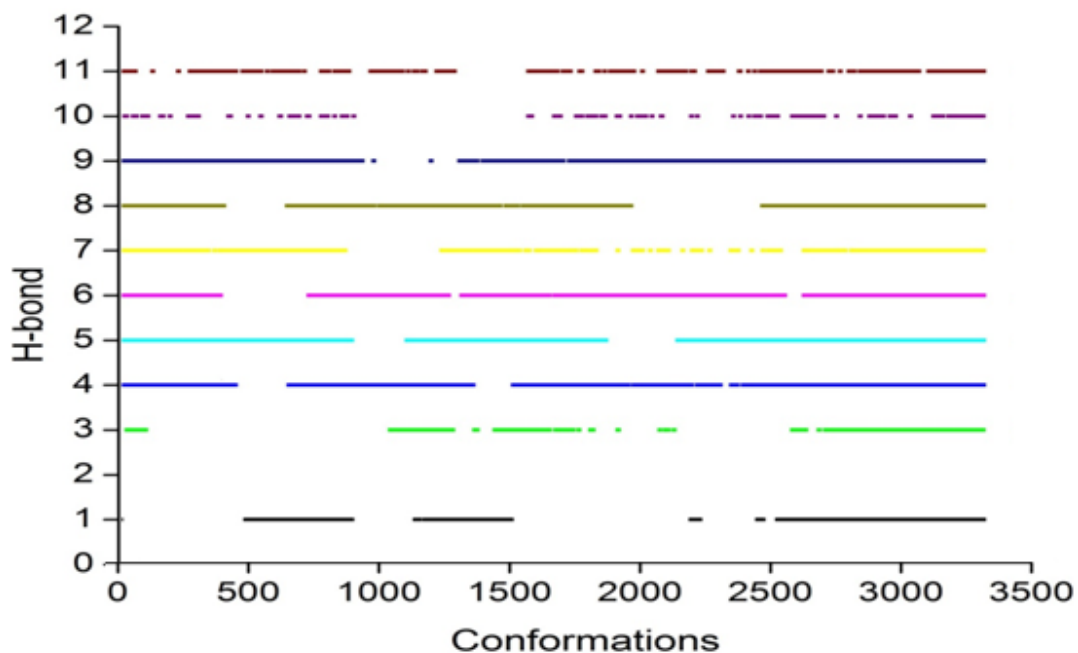
**Figure S(E):** The evolution of 4 clusters across the representative structures in simulation Brev1\_Yb<sup>(H)</sup>.



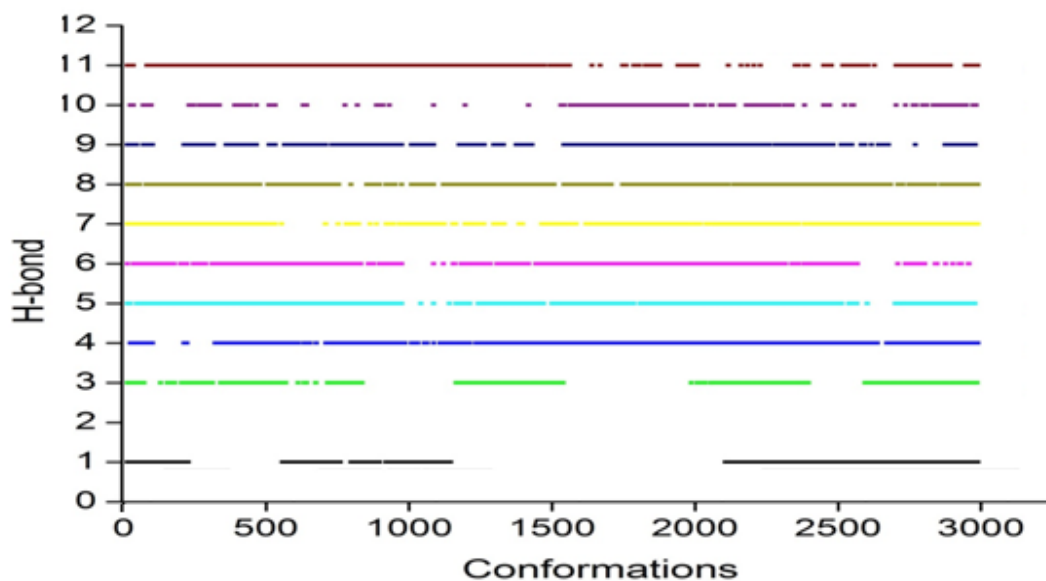
**Figure S(F):** The evolution of intramolecular hydrogen bonds for  $\alpha$ -helicity between important residues in the simulation Brev1\_Ya<sup>(E)</sup>.



**Figure S(G):** The evolution of intramolecular hydrogen bonds for  $\alpha$ -helicity between important residues in the simulation Brev1\_Yb<sup>(E)</sup>.



**Figure S(H):** The evolution of intramolecular hydrogen bonds for  $\alpha$ -helicity between important residues in the simulation Brev1\_Ya<sup>(H)</sup>.

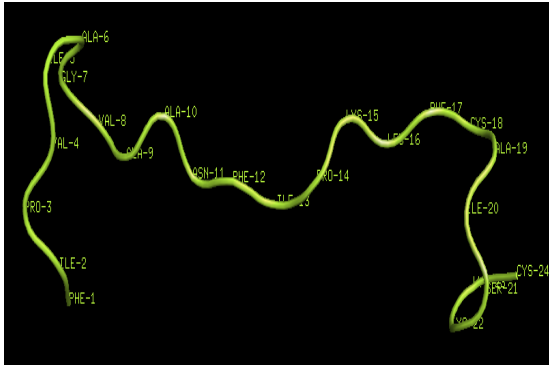


**Figure S(I):** The evolution of intramolecular hydrogen bonds for  $\alpha$ -helicity between important residues in the simulation Brev1\_Yb<sup>(H)</sup>.

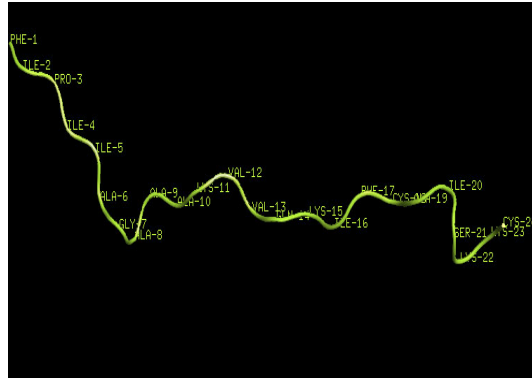
**Table S1:** The  $\alpha$ -helical propensities observed due to backbone-backbone hydrogen bond interactions and their percentages in the largest cluster of each trajectory performed.

Hbond Number	Donor-acceptor	C1 (Brev1_Ya <sup>(E)</sup> )	C1 (Brev1_Yb <sup>(E)</sup> )	C3 (Brev1_Ya <sup>(H)</sup> )	C4 (Brev1_Yb <sup>(H)</sup> )
1	(10)O....N(14)	----	7.2	18.5	19.2
2	(11)O....N(15)	----	----	----	----
3	(12)O....N(16)	----	32.2	38.8	39.2
4	(13)O....N(17)	----	6.1	33.1	36.3
5	(14)O....N(18)	23.1	27.2	29.4	29.8
6	(15)O....N(19)	29.9	30.1	35.1	35.4
7	(16)O....N(20)	11.2	5.3	24.7	27.2
8	(17)O....N(21)	3.2	1.5	22.9	19.5
9	(18)O....N(22)	3.6	4.3	18.3	20.0
10	(19)O....N(23)	10.8	19.4	17.1	18.1
11	(20)O....N(24)	3.9	3.5	15.2	16.3

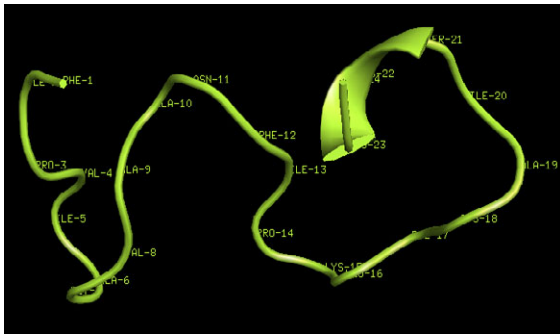
C2 (Brev1\_Ya<sup>(E)</sup>)



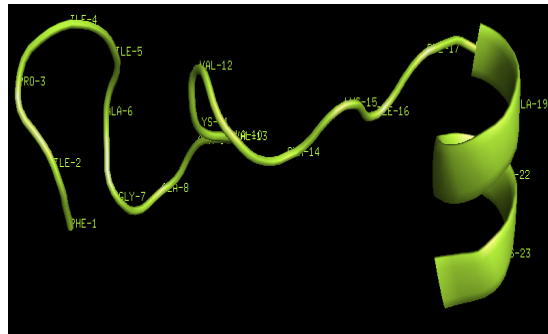
C2 (Brev1\_Yb<sup>(E)</sup>)



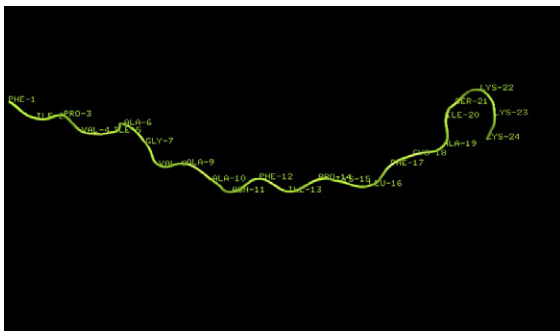
C3 (Brev1\_Ya<sup>(E)</sup>)



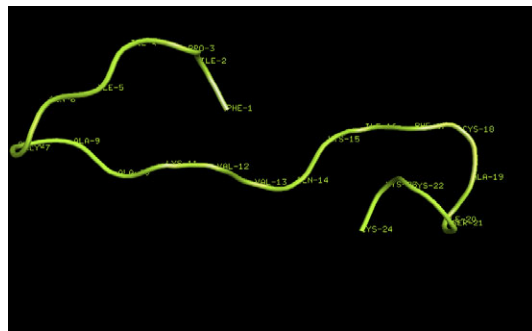
C3 (Brev1\_Yb<sup>(E)</sup>)



C4 (Brev1\_Ya<sup>(E)</sup>)



C4 (Brev1\_Yb<sup>(E)</sup>)

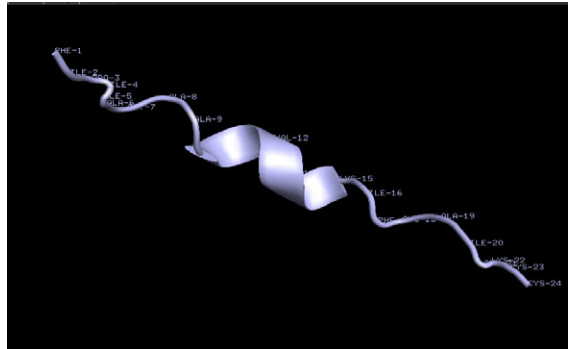
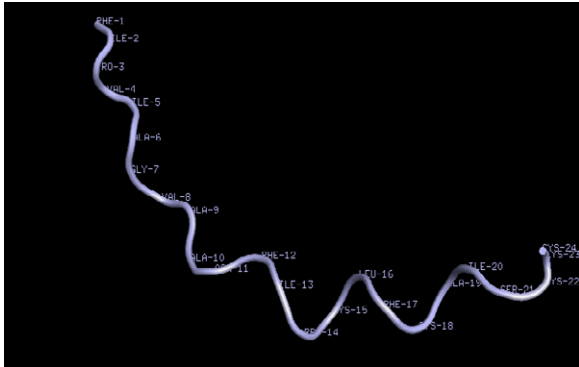


C1 (Brev1\_Ya<sup>(H)</sup>)

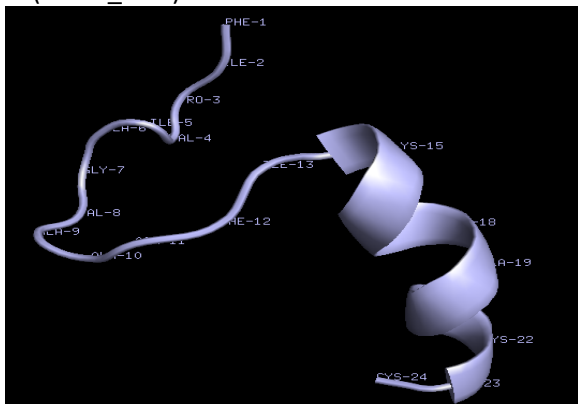


C1 (Brev1\_Yb<sup>(H)</sup>)

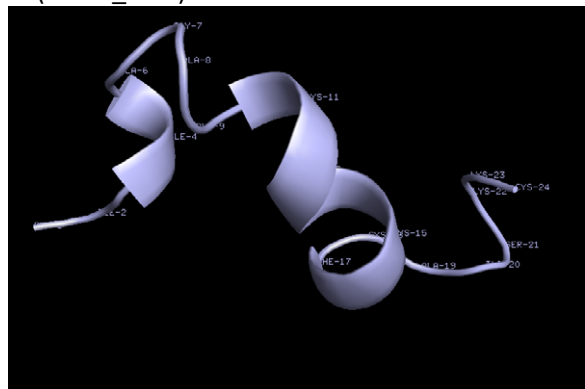




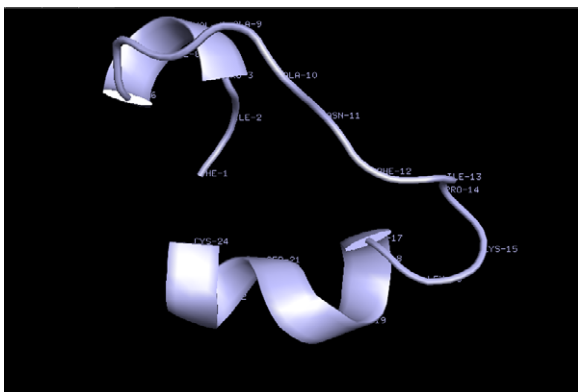
C2 (Brev1\_Ya<sup>(H)</sup>)



C1 (Brev1\_Yb<sup>(H)</sup>)



C4 (Brev1\_Ya<sup>(H)</sup>)



C3 (Brev1\_Yb<sup>(H)</sup>)

