

# The effect of curcumin on the stability of A $\beta$ dimers

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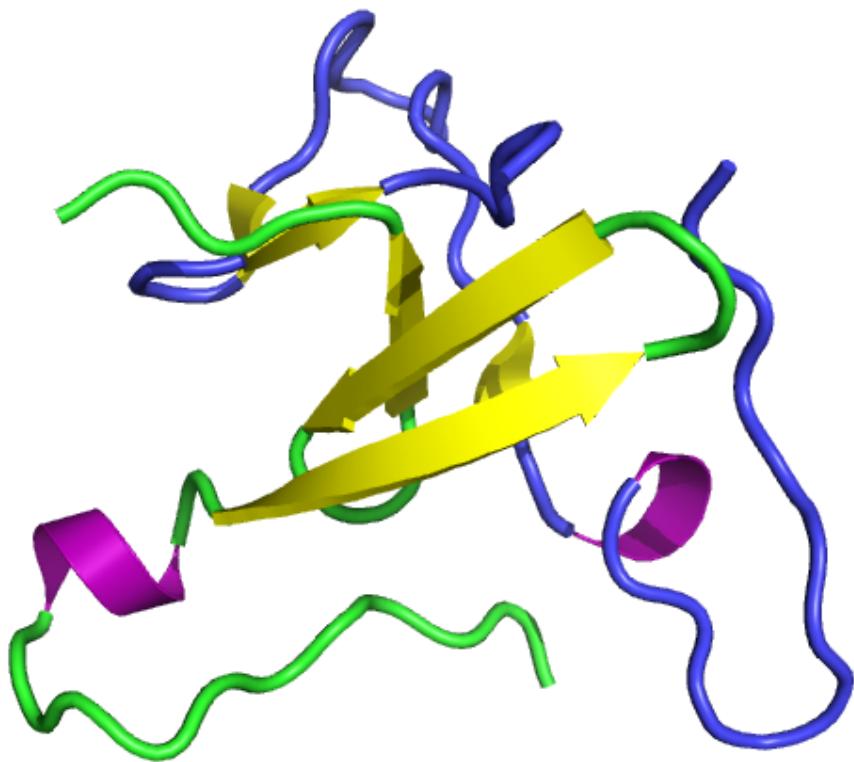
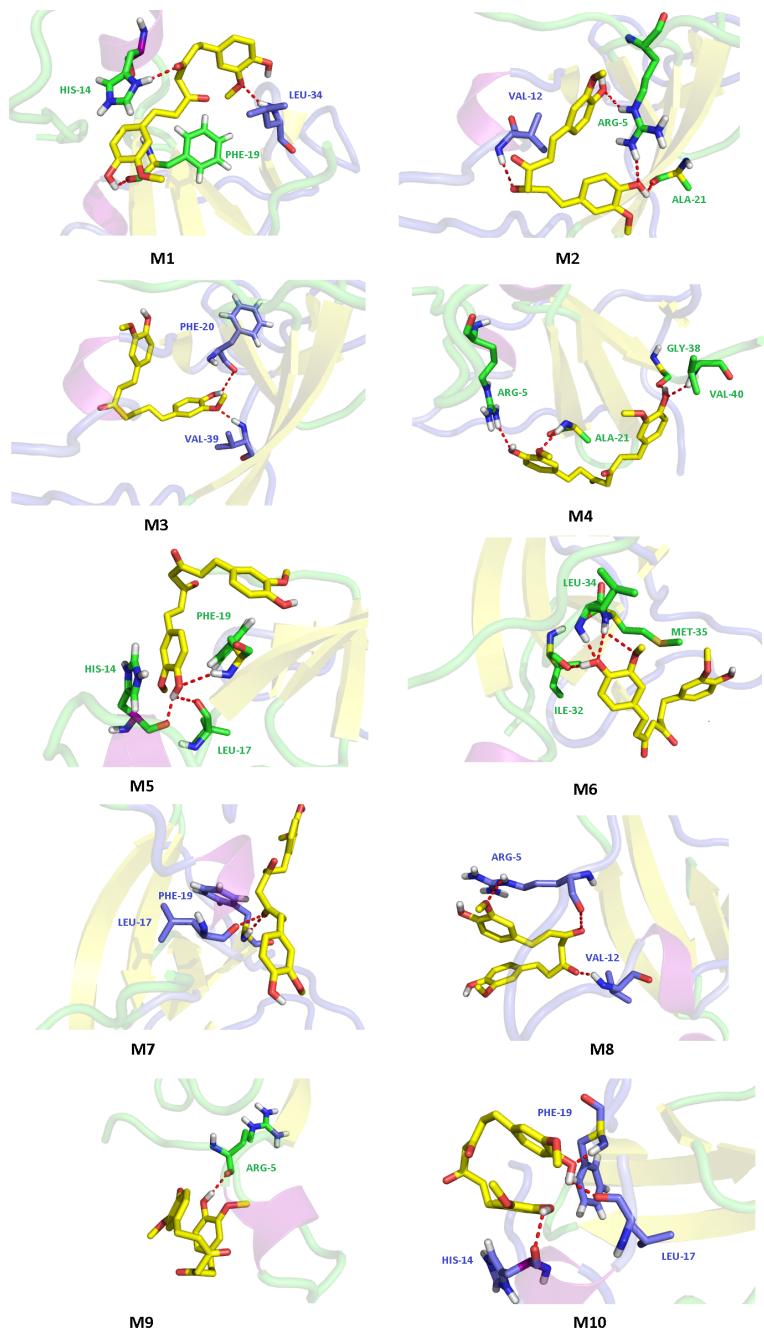


Figure S1: The snapshot of the dimer at the end of the set 2 simulation. The dimer was represented as cartoon ( $\beta$ -sheet: yellow; helix: purple; for the others from peptide A: tv\_green; for the others from peptide B: tv\_blue).



**Figure S2:** The initial M0-10 models. The secondary structure of dimer was represented as transparent cartoon ( $\beta$ -sheet: yellow;  $\alpha$ -helix: purple; others for peptide A: tv\_blue; others for peptide B: tv\_green). The curcumin was shown as stick and colored by element (C: yellow; H: grey; O: red). For the residues from peptide A involved in the contacts with curcumin was represented as stick and colored by element (C: marine; N: blue; H: grey; O: red). For the residues from peptide B involved in the direct contact with curcumin was also represented as stick and colored by the similar element except C atom was colored as green to distinguish from peptide A. Please note for those  $C_{\alpha}$  atom exists in the  $\beta$ -sheet part was colored as yellow, and purple for the  $C_{\alpha}$  atom in  $\alpha$ -helix part.

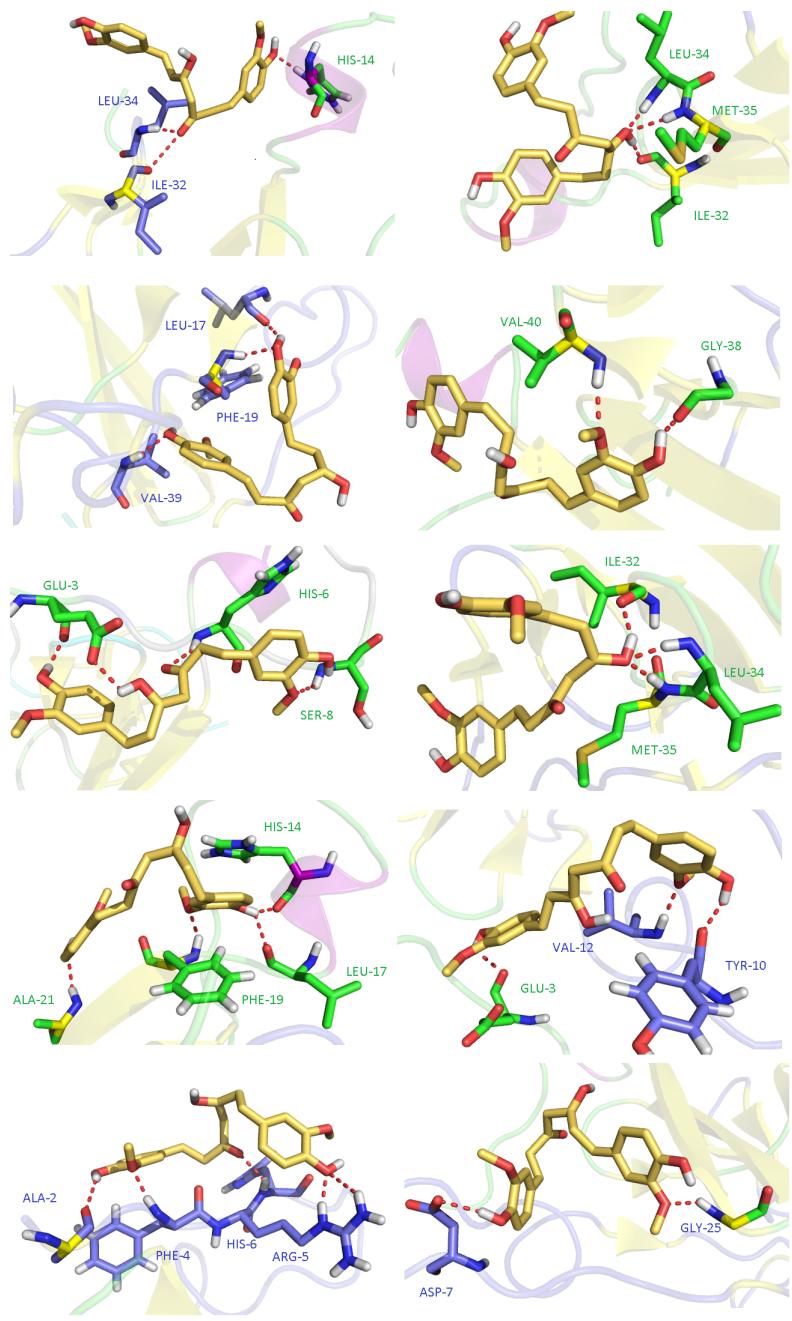


Figure S3: The initial M11-20 models. The secondary structure of dimer was represented as transparent cartoon ( $\beta$ -sheet: yellow;  $\alpha$ -helix: purple; others for peptide A: tv\_blue; others for peptide B: tv\_green). The curcumin was shown as stick and colored by element (C: yellow; H: grey; O: red). For the residues from peptide A involved in the contacts with curcumin was represented as stick and colored by element (C: marine; N: blue; H: grey; O: red). For the residues from peptide B involved in the direct contact with curcumin was also represented as stick and colored by the similar element except C atom was colored as green to distinguish from peptide A. Please note for those  $C_{\alpha}$  atom exists in the  $\beta$ -sheet part was colored as yellow, and purple for the  $C_{\alpha}$  atom in  $\alpha$ -helix part.

Table S1: Calculated pKa value for titratable residues.

Residues	pKa values
N-terminus	7.9
AspNT	2.4
Glu-3	4.2
Arg-5	12.2
His-6	6.0
Asp-7	4.2
Tyr-10	11.0
Glu-11	4.6
His-13	5.5
His-14	7.6
Lys-16	9.7
Glu-22	4.5
Asp-23	4.4
Lys-28	10.3
C-terminus	4.4

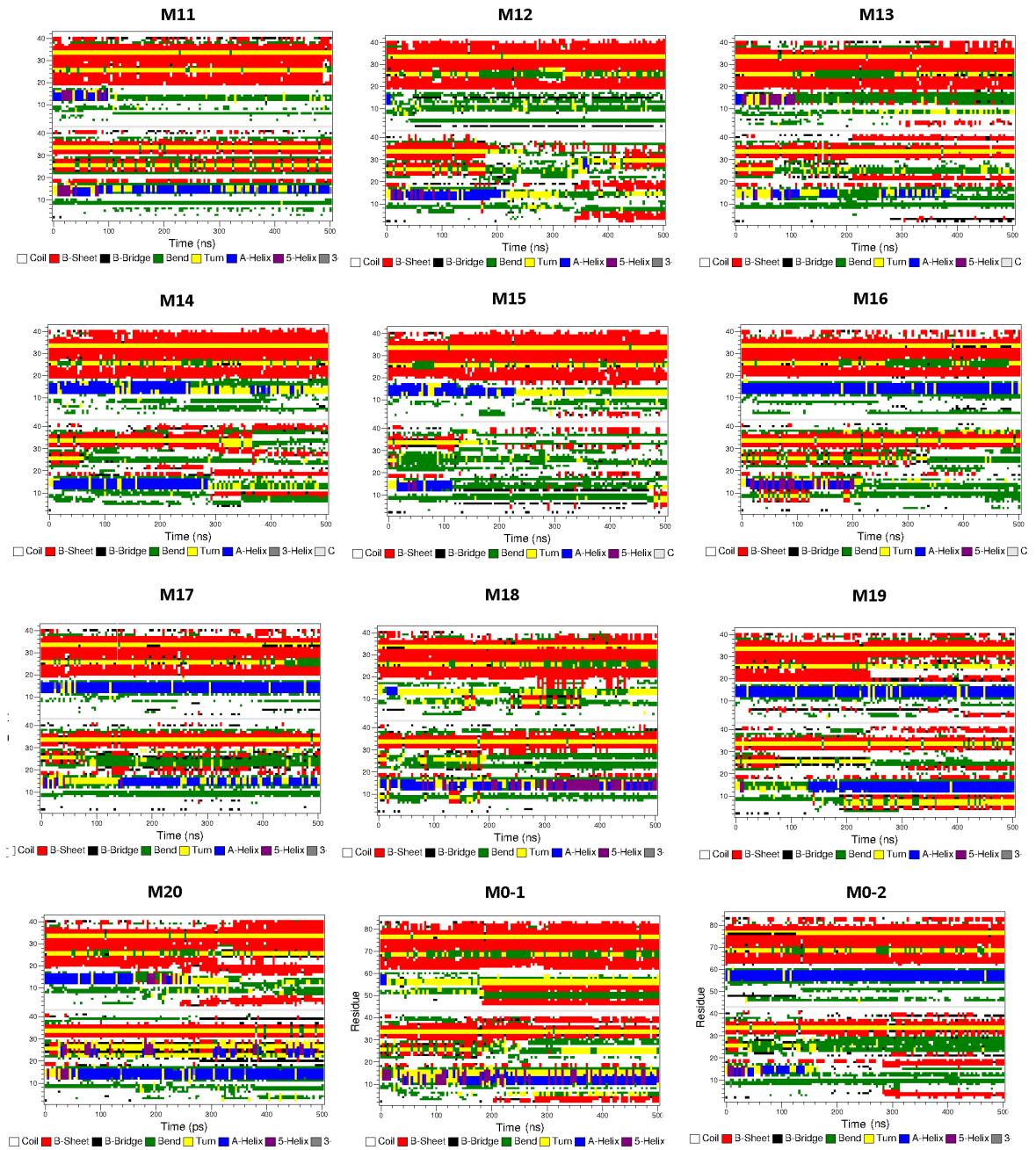


Figure S4: Evolution of the secondary structure of protein in the presence of keto-enol conformers and the controlled group M0.

Table S2: Simulation System

Model ID	$\beta$ -diketone tautomers					keto-enol tautomers				
	Potential binding sites	Binding Energy kcal/mol	Rank	Water molecules	Model ID	Potential binding sites	Binding Energy kcal/mol	Rank	Water molecules	
M1	A: LEU-34 B: HIS-14 $\alpha$ , PHE-19 $\beta$	-3.84	5	7475	M11	A: LEU-34, ILE-32 B: HIS-14 $\alpha$	-4.38	1	8111	
M2	A: VAL-12 B: ARG-5, ALA-21 $\beta$	-5.30	1	7471	M12	B: ILE-32 $\beta$ , LEU-34 MET-35 $\beta$	-4.14	2	7472	
M3	A: PHE-20, VAL-39	-2.82	9	7477	M13	A: LEU-17, PHE-19 $\beta$ VAL-39	-3.74	3	7474	
M4	B: ARG-5, ALA-21 $\beta$ GLY-38 $\beta$ , VAL-40	-3.04	8	7480	M14	B: GLY-38, VAL-40 $\beta$	-3.71	4	7478	
M5	B: HIS-14 $\alpha$ , LEU-17 PHE-19	-4.37	3	7478	M15	B: GLU-3, HIS-6 SER-8	-3.55	5	7468	
M6	B: ILE-32 $\beta$ , LEU-34 MET-35 $\beta$	-3.08	7	7474	M16	B: ILE-32 $\beta$ , LEU-34 MET-35 $\beta$	-3.53	6	7479	
M7	A: LEU-17, PHE-19 $\beta$	-4.79	2	7469	M17	A: HIS-14 $\alpha$ , LEU-17 PHE-19 $\beta$ , ALA-21 $\alpha$	-2.97	7	7475	
M8	A: ARG-5, VAL-12	-2.76	10	7472	M18	A: TYR-10, VAL-12 B: GLU-3	-2.88	8	7471	
M9	B: ARG-5	-4.04	4	7466	M19	A: ALA-2 $\beta$ , PHE-4 ARG-5, HIS-16	-2.77	9	7475	
M10	A: HIS-14, LEU-17 PHE-19	-3.66	6	7469	M20	A: ASP-7 B: GLY-25 $\beta$	-2.50	10	7471	
M0	-	-	-	7495						

- indicates NULL.

 $\alpha$  indicates residue sites on  $\alpha$ -helix. $\beta$  indicates residue sites on  $\beta$ -sheet.

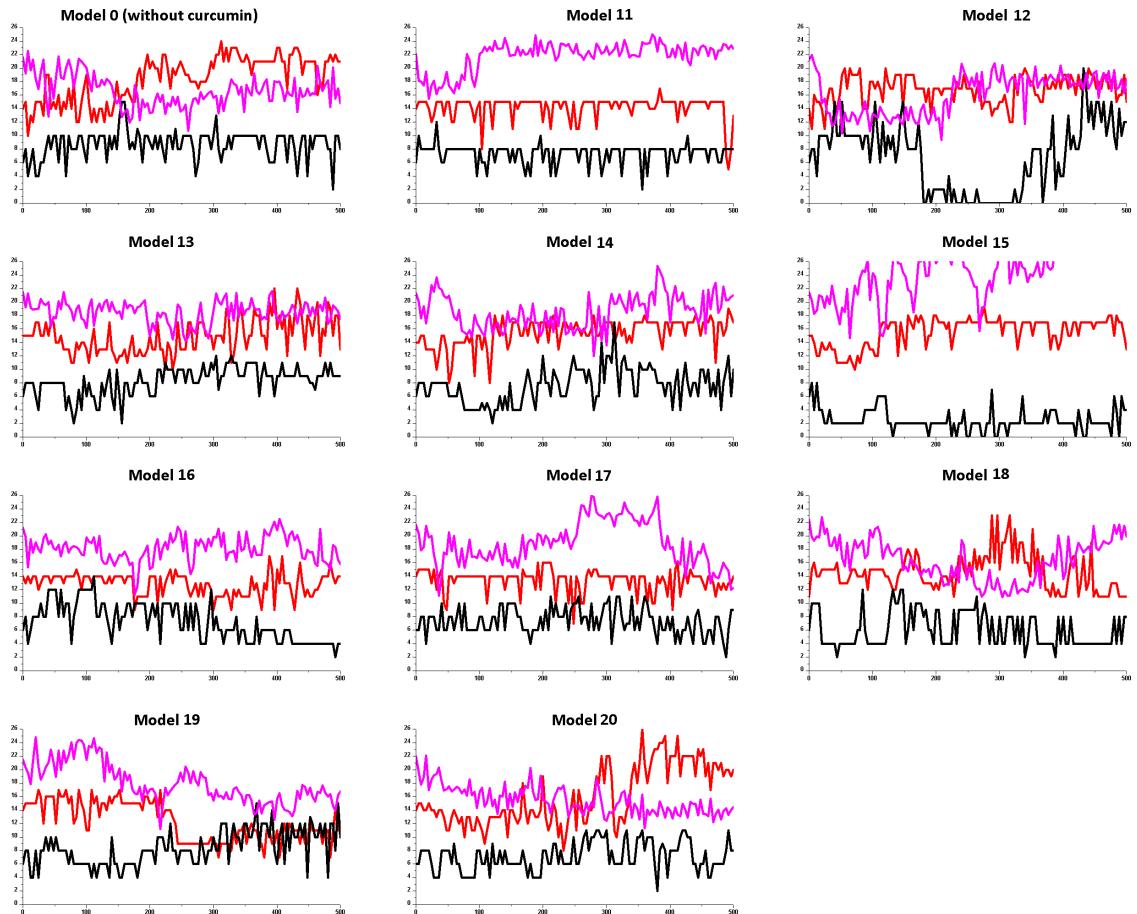


Figure S5: Time evolution of the number of residues in  $\beta$ -structure ( $\beta$ -sheet and  $\beta$ -bridge) of peptide A (black line) and B (colored by red) and the contact numbers between peptide A and B (colored by magenta). The data were extracted from each 11 model trajectories and averaged per 4 ns. The contact number were divided by 100.

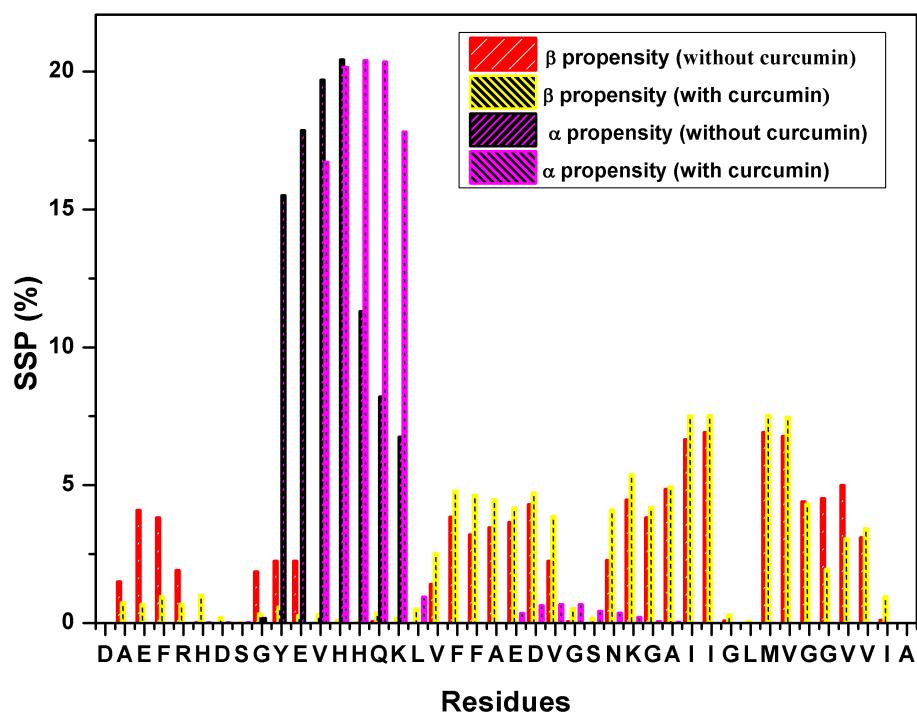


Figure S6: The secondary structure propensity of A $\beta$  residues in the presence and absence of curcumin.

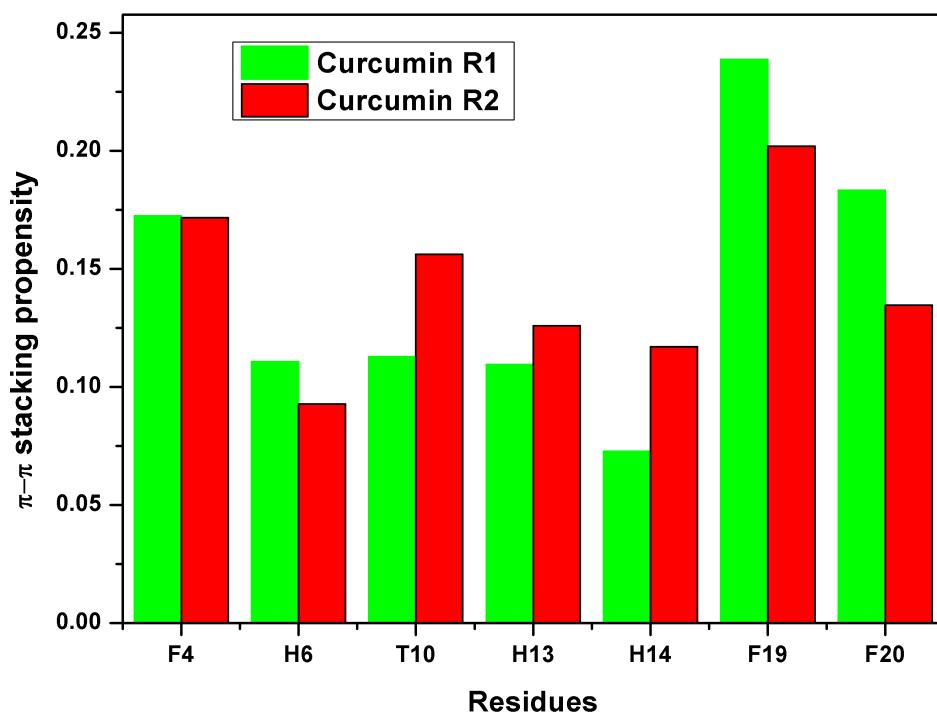


Figure S7: The  $\pi-\pi$  stacking propensity of  $\text{A}\beta$  residues His, Tyr and Phe with curcumin R1 and R2 respectively.

Table S3: The occurence of dehydron.

The occurence of dehydron	
pairs	occurence
B: (24V, 27N)	292
A: (24V, 27N)	222
B: (11E, 15Q)	157
B: (34L, 41I)	150
(A: 40V, B: 28K)	133
A:(30A, 37G)	124
A:(11E, 15Q)	110
B:(12V, 16K)	98
A:(22E, 29G)	89
A:(12V, 16K)	53
B:(22E, 29G)	52
A:(6H, 12V)	51
(A:38G, B:41I)	49
A:(23D, 27N)	45
A:(23D, 28K)	44
A:(5R, 9D)	42
(A:36V, B:39V)	37
B:(1D, 15Q)	35
A:(22E, 27N)	35
(A:3E, B:24V)	34
(A:41I, B:28K)	33
(A:1D, B:26S)	32
(A:1D, B:27N)	31
A:(7D, 10Y)	31
A:(28K, 35G)	31
...	< 30

Table S4: The curcumin topology

```
[ moleculetype ]
; Name nrexcl
CUR      3

[ atoms ]
;   nr      type    resnr resid   atom   cgnr   charge   mass
   1       CH3     1 CUR     C21     1    0.200  15.0350
   2       OA      1 CUR     O4      1   -0.400  15.9994
   3        C     1 CUR     C19     1    0.200  12.0110
   4      CR1     1 CUR     C20     1   -0.060  12.0110
   5       HC     1 CUR     H20     1    0.060  1.0080
   6        C     1 CUR     C18     1    0.265  12.0110
   7       OA     1 CUR     O5      1   -0.683  15.9994
   8        H     1 CUR     H52     1    0.418  1.0080
   9      CR1     1 CUR     C17     2   -0.060  12.0110
  10      HC     1 CUR     H17     2    0.060  1.0080
  11      CR1     1 CUR     C16     2   -0.060  12.0110
  12      HC     1 CUR     H16     2    0.060  1.0080
  13        C     1 CUR     C15     2   -0.000  12.0110
  14        C     1 CUR     C14     3    0.000  13.0190
  15        C     1 CUR     C13     3    0.000  13.0190
  16        C     1 CUR     C12     3    0.265  12.0110
  17       OA     1 CUR     O3      3   -0.683  15.9994
  18        H     1 CUR     H32     3    0.418  1.0080
  19        C     1 CUR     C11     3    0.000  13.0190
  20        C     1 CUR     C10     3    0.265  12.0110
  21        O     1 CUR     O6      3   -0.265  15.9994
  22        C     1 CUR     C9      4    0.000  13.0190
  23        C     1 CUR     C8      4    0.000  13.0190
  24        C     1 CUR     C4      4   -0.000  12.0110
  25      CR1     1 CUR     C3      4   -0.060  12.0110
  26      HC     1 CUR     H31     4    0.060  1.0080
  27      CR1     1 CUR     C5      5   -0.060  12.0110
  28      HC     1 CUR     H51     5    0.060  1.0080
  29      CR1     1 CUR     C6      6   -0.060  12.0110
  30      HC     1 CUR     H6      6    0.060  1.0080
  31        C     1 CUR     C7      6    0.265  12.0110
  32       OA     1 CUR     O2      6   -0.683  15.9994
  33        H     1 CUR     H22     6    0.418  1.0080
  34        C     1 CUR     C2      6    0.200  12.0110
  35       OA     1 CUR     O1      6   -0.400  15.9994
  36      CH3     1 CUR     C1      6    0.200  15.0350

[ bonds ]
;   ai    aj    fu      c0, c1, ...
  2     1    2  0.143  8180000.0  0.143  8180000.0 ;  O4  C21
  3     2    2  0.136 10200000.0  0.136 10200000.0 ;  C19 O4
  3     4    2  0.139 10800000.0  0.139 10800000.0 ;  C19 C20
  3     6    2  0.139 10800000.0  0.139 10800000.0 ;  C19 C18
  4     5    2  0.109 12300000.0  0.109 12300000.0 ;  C20 H20
 13     4    2  0.139 10800000.0  0.139 10800000.0 ;  C15 C20
  6     7    2  0.136 10200000.0  0.136 10200000.0 ;  C18 O5
  6     9    2  0.139 10800000.0  0.139 10800000.0 ;  C18 C17
  7     8    2  0.100 15700000.0  0.100 15700000.0 ;  O5  H52
  9    10    2  0.109 12300000.0  0.109 12300000.0 ;  C17 H17
  9    11    2  0.139 10800000.0  0.139 10800000.0 ;  C17 C16
 11    12    2  0.109 12300000.0  0.109 12300000.0 ;  C16 H16
 13    11    2  0.139 10800000.0  0.139 10800000.0 ;  C15 C16
 13    14    2  0.139 10800000.0  0.139 10800000.0 ;  C15 C14
 14    15    2  0.153  7150000.0  0.153  7150000.0 ;  C14 C13
 16    15    2  0.153  7150000.0  0.153  7150000.0 ;  C12 C13
 16    17    2  0.136 10200000.0  0.136 10200000.0 ;  C12 O3
 16    19    2  0.153  7150000.0  0.153  7150000.0 ;  C12 C11
 17    18    2  0.100 15700000.0  0.100 15700000.0 ;  O3  H32
 20    19    2  0.153  7150000.0  0.153  7150000.0 ;  C10 C11
 20    21    2  0.123 16600000.0  0.123 16600000.0 ;  C10 O6
 20    22    2  0.153  7150000.0  0.153  7150000.0 ;  C10 C9
 22    23    2  0.153  7150000.0  0.153  7150000.0 ;  C9  C8
 24    23    2  0.139 10800000.0  0.139 10800000.0 ;  C4  C8
 24    25    2  0.139 10800000.0  0.139 10800000.0 ;  C4  C3
 24    27    2  0.139 10800000.0  0.139 10800000.0 ;  C4  C5
 25    26    2  0.109 12300000.0  0.109 12300000.0 ;  C3  H31
```

34	25	2	0.139	10800000.0	0.139	10800000.0	;	C2	C3
27	28	2	0.109	12300000.0	0.109	12300000.0	;	C5	H51
27	29	2	0.139	10800000.0	0.139	10800000.0	;	C5	C6
29	30	2	0.109	12300000.0	0.109	12300000.0	;	C6	H6
31	29	2	0.139	10800000.0	0.139	10800000.0	;	C7	C6
31	32	2	0.136	10200000.0	0.136	10200000.0	;	C7	02
31	34	2	0.139	10800000.0	0.139	10800000.0	;	C7	C2
32	33	2	0.100	15700000.0	0.100	15700000.0	;	02	H22
34	35	2	0.136	10200000.0	0.136	10200000.0	;	C2	01
35	36	2	0.143	8180000.0	0.143	8180000.0	;	01	C1

[ pairs ]  
; ai aj fu c0, c1, ...

1	4	1					;	C21	C20
1	6	1					;	C21	C18
2	5	1					;	04	H20
2	7	1					;	04	05
2	9	1					;	04	C17
2	13	1					;	04	C15
3	8	1					;	C19	H52
3	10	1					;	C19	H17
3	11	1					;	C19	C16
3	14	1					;	C19	C14
4	7	1					;	C20	05
4	9	1					;	C20	C17
4	12	1					;	C20	H16
4	15	1					;	C20	C13
5	6	1					;	H20	C18
5	11	1					;	H20	C16
5	14	1					;	H20	C14
6	12	1					;	C18	H16
6	13	1					;	C18	C15
7	10	1					;	05	H17
7	11	1					;	05	C16
8	9	1					;	H52	C17
9	14	1					;	C17	C14
10	12	1					;	H17	H16
10	13	1					;	H17	C15
11	15	1					;	C16	C13
12	14	1					;	H16	C14
13	16	1					;	C15	C12
14	17	1					;	C14	03
14	19	1					;	C14	C11
15	18	1					;	C13	H32
15	20	1					;	C13	C10
16	21	1					;	C12	06
16	22	1					;	C12	C9
17	20	1					;	03	C10
18	19	1					;	H32	C11
19	23	1					;	C11	C8
20	24	1					;	C10	C4
21	23	1					;	06	C8
22	25	1					;	C9	C3
22	27	1					;	C9	C5
23	26	1					;	C8	H31
23	28	1					;	C8	H51
23	29	1					;	C8	C6
23	34	1					;	C8	C2
24	30	1					;	C4	H6
24	31	1					;	C4	C7
24	35	1					;	C4	01
25	28	1					;	C3	H51
25	29	1					;	C3	C6
25	32	1					;	C3	02
25	36	1					;	C3	C1
26	27	1					;	H31	C5
26	31	1					;	H31	C7
26	35	1					;	H31	01
27	32	1					;	C5	02
27	34	1					;	C5	C2
28	30	1					;	H51	H6
28	31	1					;	H51	C7
29	33	1					;	C6	H22
29	35	1					;	C6	01



29	27	31	30	2	0.0	167.4	0.0	167.4	; imp	C6	C5	C7	H6		
31	29	32	34	2	0.0	167.4	0.0	167.4	; imp	C7	C6	02	C2		
34	25	35	31	2	0.0	167.4	0.0	167.4	; imp	C2	C3	01	C7		
3	4	13	11	2	0.0	209.3	0.0	209.3	; imp	C19	C20	C15	C16		
4	13	11	9	2	0.0	209.3	0.0	209.3	; imp	C20	C15	C16	C17		
13	11	9	6	2	0.0	209.3	0.0	209.3	; imp	C15	C16	C17	C18		
11	9	6	3	2	0.0	209.3	0.0	209.3	; imp	C16	C17	C18	C19		
9	6	3	4	2	0.0	209.3	0.0	209.3	; imp	C17	C18	C19	C20		
6	3	4	13	2	0.0	209.3	0.0	209.3	; imp	C18	C19	C20	C15		
24	25	34	31	2	0.0	209.3	0.0	209.3	; imp	C4	C3	C2	C7		
25	34	31	29	2	0.0	209.3	0.0	209.3	; imp	C3	C2	C7	C6		
34	31	29	27	2	0.0	209.3	0.0	209.3	; imp	C2	C7	C6	C5		
31	29	27	24	2	0.0	209.3	0.0	209.3	; imp	C7	C6	C5	C4		
29	27	24	25	2	0.0	209.3	0.0	209.3	; imp	C6	C5	C4	C3		
27	24	25	34	2	0.0	209.3	0.0	209.3	; imp	C5	C4	C3	C2		
6	3	2	1	1	180.0	16.7	2	180.0	16.7	2	dih	C18	C19	04	C21
3	6	7	8	1	180.0	7.1	2	180.0	7.1	2	dih	C19	C18	05	H52
15	14	13	4	1	180.0	5.9	2	180.0	5.9	2	dih	C13	C14	C15	C20
16	15	14	13	1	180.0	5.9	2	180.0	5.9	2	dih	C12	C13	C14	C15
19	16	15	14	1	180.0	5.9	2	180.0	5.9	2	dih	C11	C12	C13	C14
15	16	17	18	1	180.0	16.7	2	180.0	16.7	2	dih	C13	C12	03	H32
20	19	16	15	1	180.0	5.9	2	180.0	5.9	2	dih	C10	C11	C12	C13
22	20	19	16	1	180.0	5.9	2	180.0	5.9	2	dih	C9	C10	C11	C12
23	22	20	19	1	180.0	5.9	2	180.0	5.9	2	dih	C8	C9	C10	C11
24	23	22	20	1	180.0	5.9	2	180.0	5.9	2	dih	C4	C8	C9	C10
27	24	23	22	1	180.0	5.9	2	180.0	5.9	2	dih	C5	C4	C8	C9
29	31	32	33	1	180.0	7.1	2	180.0	7.1	2	dih	C6	C7	02	H22
25	34	35	36	1	180.0	16.7	2	180.0	16.7	2	dih	C3	C2	01	C1