

Evaluation of Propolis Activity as Sucrose-Dependent and Sucrose-Independent of *Streptococcus mutans* Inhibitor to Treat Dental Caries Using In Silico Approach

Muhammad Miftah Jauhar¹, Putri Hawa Syaifie¹, Adzani Gaisani Arda¹, Donny Ramadhan², Dwi Wahyu Nugroho¹, Nofa Mardia Ningsih Kaswati¹, Etik Mardliyati*³, Alfian Noviyanto¹, Nurul Taufiqu Rochman⁴

¹Nano Center Indonesia, Jl. PUSPIPTEK, South Tangerang, Banten, 15314, Indonesia

²Research Center for Pharmaceutical Ingredients and Traditional Medicine, National Research and Innovation Agency (BRIN), Cibinong, Bogor, Jawa Barat, 16911, Indonesia

³Research Center for Vaccine and Drug, National Research and Innovation Agency (BRIN), Cibinong, Bogor, Jawa Barat, 16911, Indonesia

⁴Research Center for Metallurgy and Materials, National Research and Innovation Agency (BRIN), PUSPIPTEK, South Tangerang, Banten, 15314, Indonesia

doi: <http://doi.org/10.7324/JAPS.2023.45365>

Supplementary Material

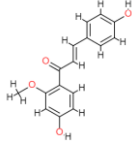
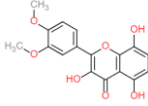
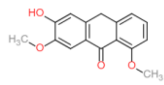
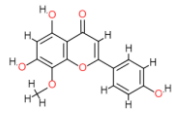
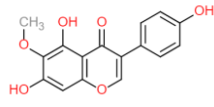
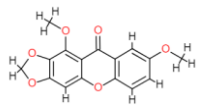
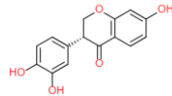
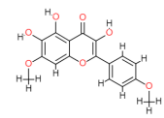
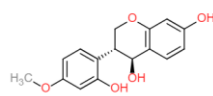
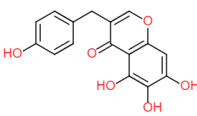
Table S1. Docking validation between acarbose and 3AIC protein

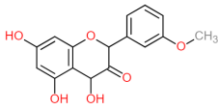
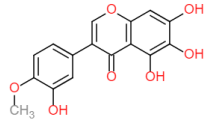
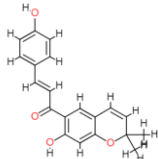
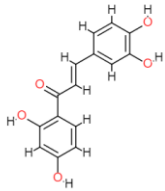
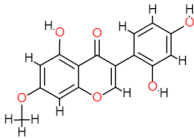
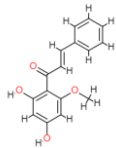
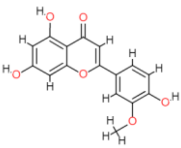
Rank	Sub-Rank	Run	Binding Energy	Cluster RMSD	Reference RMSD	Grep Pattern
1	1	3	-7.16	0.00	1.00	RANKING
1	2	10	-7.13	0.50	0.77	RANKING
1	3	4	-7.11	0.47	0.81	RANKING
1	4	6	-7.10	0.54	0.82	RANKING
1	5	9	-7.08	0.49	0.73	RANKING
1	6	2	-7.07	0.55	0.85	RANKING
1	7	7	-7.00	0.41	0.97	RANKING
1	8	1	-6.95	1.93	1.90	RANKING
1	9	8	-6.87	0.30	0.87	RANKING
2	1	5	-6.53	0.00	2.61	RANKING

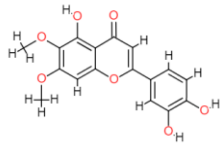
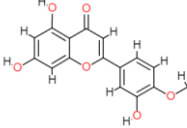
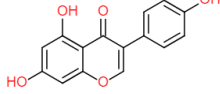
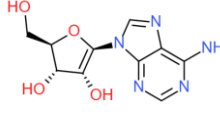
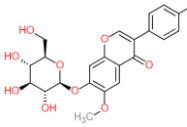
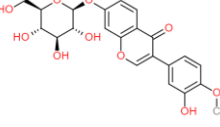
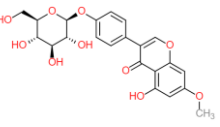
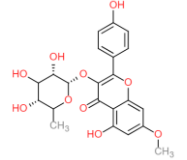
Table S2. Docking validation between Phenylmethanesulfonic Acid (PMS) and 3IPK protein

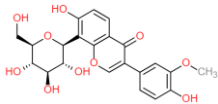
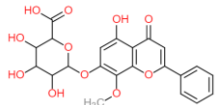
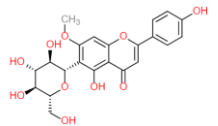
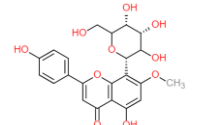
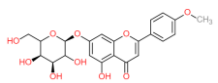
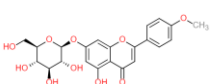
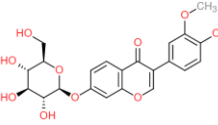
Rank	Sub-Rank	Run	Binding Energy	Cluster RMSD	Reference RMSD	Grep Pattern
1	1	3	-4.75	0.00	1.24	RANKING
1	2	10	-4.74	0.54	1.04	RANKING
1	3	6	-4.73	0.21	1.14	RANKING
1	4	5	-4.70	0.56	1.21	RANKING
1	5	7	-4.70	0.52	1.17	RANKING
1	6	4	-4.70	0.33	1.19	RANKING
1	7	8	-4.66	0.68	1.16	RANKING
1	8	1	-4.65	0.52	0.94	RANKING
1	9	2	-4.63	0.92	1.09	RANKING
1	10	9	-4.60	0.90	1.10	RANKING

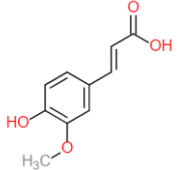
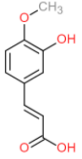
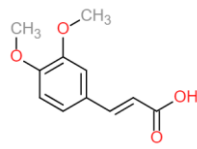
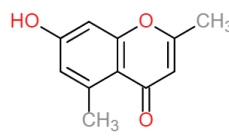
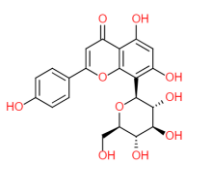
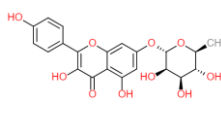
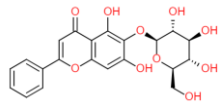
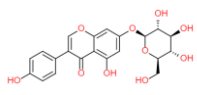
Table S3. Ligands from propolis screening

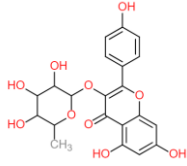
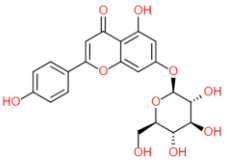
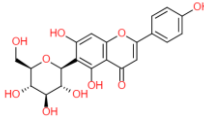
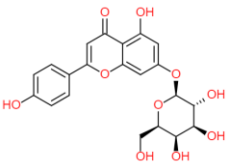
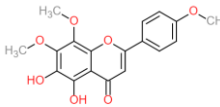
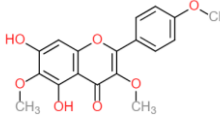
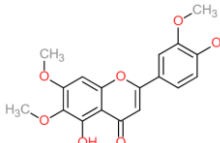
No	Compound	Formula	Structure	PubChem ID	Classification
1	2'-O-Methylisoliquiritigenin	C ₁₆ H ₁₄ O ₄		5319688	chalcones
2	3,5,8-Trihydroxy-3',4'-dimethoxyflavone	C ₁₇ H ₁₄ O ₇			flavonols
3	3-Hydroxy-2,8-dimethoxyxanthone	C ₁₅ H ₁₂ O ₅			simple oxygenated xanthone
4	4'-Hydroxywogonin	C ₁₆ H ₁₂ O ₆		5322078	flavones
5	Tectorigenin	C ₁₆ H ₁₂ O ₆		5281811	isoflavones
6	1,7-Dimethoxy-2,3-methylenedioxyxanthone	C ₁₆ H ₁₂ O ₆		85670503	simple oxygenated xanthone
7	3',4',7-Trihydroxy flavanone	C ₁₅ H ₁₀ O ₅		5281611	flavones
8	3,5,6-Trihydroxy-4',7'-dimethoxyflavone	C ₁₇ H ₁₄ O ₇		5322058	flavones
9	4,7,2'-Trihydroxy-4'-methoxyisoflavanol	C ₁₆ H ₁₆ O ₅			flavonols
10	5,6,7-Trihydroxy-3-(4'-hydroxybenzyl) chromone	C ₁₆ H ₁₂ O ₆			Homoisoflavanones

11	5,7,4'-Trihydroxy flavanone	C ₁₅ H ₁₂ O ₅		129847910	flavones
12	Alpinetin	C ₁₆ H ₁₄ O ₄		154279	flavonols
13	Bavachromene	C ₂₀ H ₁₈ O ₄		5321800	chalcones
14	Butein	C ₁₅ H ₁₂ O ₅		5281222	chalcones
15	Cajanin	C ₁₆ H ₁₂ O ₆		5281706	flavones
16	Cardamonin	C ₁₆ H ₁₄ O ₄		641785	chalcones
17	Chrysoeriol	C ₁₆ H ₁₂ O ₆		5280666	flavones

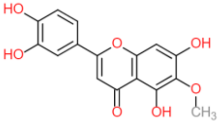
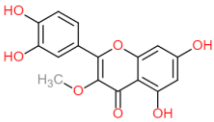
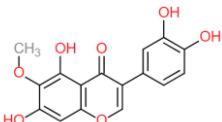
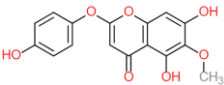
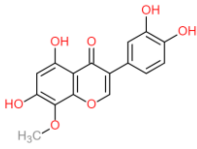
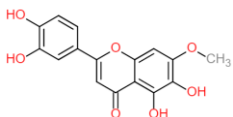
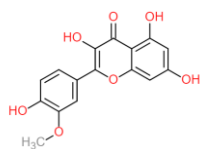
18	Cirsiliol	C17H14O7		160237	flavonols
19	Diosmetin	C16H12O6		5281612	flavonols
20	genistein_1	C15H12O5		25201420	isoflavones
21	Adenosin	C10H13N5O4		60961	Purines base
22	Glycitin	C22H22O10		187808	isoflavones
23	Calycosin-7-O-β-D-glucopyranoside	C22H22O10		5318267	isoflavones
24	Prunetin 4 glucoside	C22H22O10		5918474	isoflavones
25	Rhamnocitrin 3 rhamnoside	C22H22O10		44259556	flavones

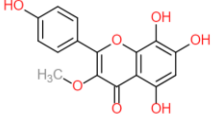
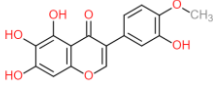
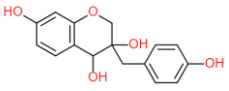
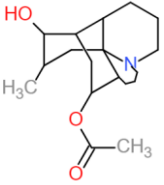
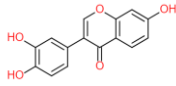
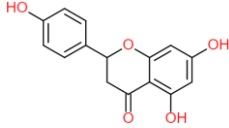
26	3 methoxypuerarin	C22H22O10		5319485	isoflavones
27	Wogonoside	C22H22O10		12004622	flavones
28	Swertisin	C22H22O10		124034	flavones
29	Isoswertisin	C22H22O10		44258317	flavones
30	Acacetin 7 galactoside	C22H22O10		44257885	flavones
31	Tilianin	C22H22O10		5321954	flavones
32	3-methoxydaidzin	C22H22O10		10527347	isoflavones

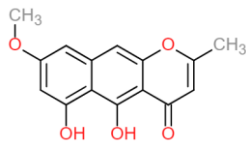
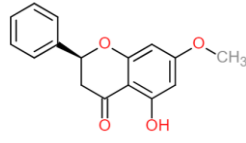
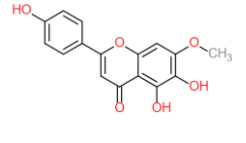
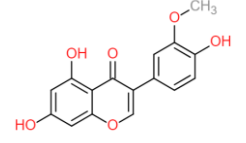
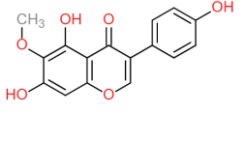
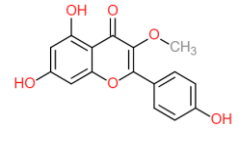
33	Ferulic acid	C ₁₀ H ₁₀ O ₄		445858	Phenolic acids
34	Isoferulic acid	C ₁₀ H ₁₀ O ₄		736186	Phenolic acids
35	3,4-Dimethoxy-cinnamic acid	C ₁₀ H ₁₀ O ₄		717531	Phenolic acids
36	2,5-Dimethyl-7-hydroxychromone	C ₁₁ H ₁₀ O ₃		5316891	isoflavones
37	Vitexin	C ₂₁ H ₂₀ O ₁₀		5280441	flavones
38	Kaempferol-7-O-α-L-rhamnoside	C ₂₁ H ₂₀ O ₁₀		25079965	flavonols
39	Baicalein-7-O-β-D-glucopyranoside	C ₂₁ H ₂₀ O ₁₀		5321896	flavones
40	Genistin	C ₂₁ H ₂₀ O ₁₀		5281377	isoflavones

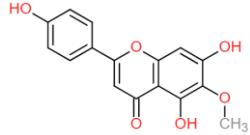
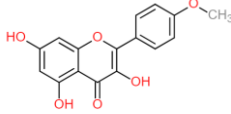
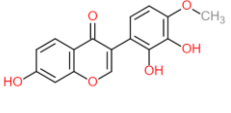
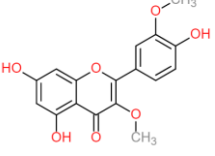
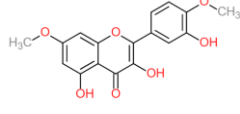
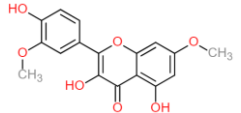
41	Kaempferol 3 rhamnoside	C ₂₁ H ₂₀ O ₁₀		5835713	flavonols
42	Cosmosiin	C ₂₁ H ₂₀ O ₁₀		5280704	flavones
43	Isovitexin	C ₂₁ H ₂₀ O ₁₀		162350	flavones
44	Apigenin-7-O-galactopyranoside	C ₂₁ H ₂₀ O ₁₀			flavones
45	5,6-Dihydroxy-7,8,4'-trimethoxyflavone	C ₁₈ H ₁₆ O ₇		44258635	flavonols
46	Santin	C ₁₈ H ₁₆ O ₇		5281695	flavonols
47	Cirsilineol	C ₁₈ H ₁₆ O ₇		162464	flavonols

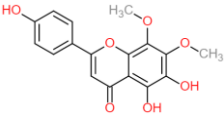
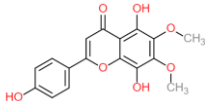
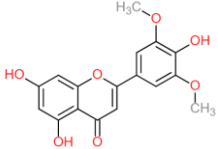
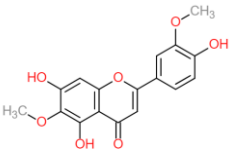
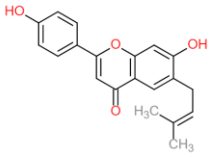
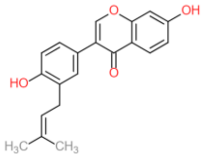
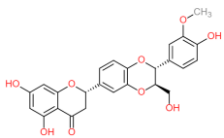
48	Pachypodol	C18H16O7		5281677	flavonols
49	3',5-Dihydroxy-3,4',7-trimethoxy flavone	C18H16O7		319310128	flavones
50	Eupatilin	C18H16O7		5273755	flavonols
51	Nevadensin	C18H16O7		160921	flavonols
52	Penduletin	C18H16O7		5320462	flavonols
53	5,4'-Dihydroxy-6,7,8-trimethoxyflavone	C18H16O7		73207	flavonols
54	Isoaloeresin D	C29H32O11		76332505	Phenolic compounds

55	Eupafolin	C ₁₆ H ₁₂ O ₇		5317284	flavones
56	Quercetin-3-methyl ether	C ₁₆ H ₁₂ O ₇		5280681	flavonols
57	Irilin D	C ₁₆ H ₁₂ O ₇		10495590	isoflavones
58	Capillarisin	C ₁₆ H ₁₂ O ₇		5281342	Phenolic compounds
59	3',4',5,7-Tetrahydroxy-8-methoxyisoflavone	C ₁₆ H ₁₂ O ₇		5493449	isoflavones
60	Pedalitin	C ₁₆ H ₁₂ O ₇		31161	isoflavones
61	Isoharmentin	C ₁₆ H ₁₂ O ₇		5281654	flavonols

62	3-Methoxyherbacetin	C ₁₆ H ₁₂ O ₇		51642537	flavonols
63	3',5,6,7-Tetrahydroxy-4'-methoxyisoflavone	C ₁₆ H ₁₂ O ₇		10543410	isoflavones
64	3'-Deoxysappanol	C ₁₆ H ₁₆ O ₅		13846660	isoflavones
65	Fawcettiine	C ₁₈ H ₂₉ NO ₃		50841427	alkaloid
66	3',4',7-Trihydroxyisoflavanone	C ₁₅ H ₁₂ O ₅		22065265	isoflavones
67	Naringenin	C ₁₅ H ₁₂ O ₅		932	flavonols

68	Rubrofusarin	C ₁₅ H ₁₂ O ₅		72537	simple oxygenated xanthone
69	Pinostrobin	C ₁₆ H ₁₄ O ₄		73201	flavonols
70	Sorbifolin	C ₁₆ H ₁₂ O ₆		3084390	flavonols
71	3'-O-Methylrobol	C ₁₆ H ₁₂ O ₆		5319744	flavones
72	Hydroxygenkwanin	C ₁₆ H ₁₂ O ₆		5318214	flavones
73	Isokaempferide	C ₁₆ H ₁₂ O ₆		5280862	flavonols

74	Hispidulin	C ₁₆ H ₁₂ O ₆		5281628	flavonols
75	Kaempferide	C ₁₆ H ₁₂ O ₆		5281666	flavonols
76	Koparin	C ₁₆ H ₁₂ O ₆		5318834	flavones
77	Quercetin-3,3'-dimethyl-ether	C ₁₇ H ₁₄ O ₇		5316900	flavonols
78	Ombuine	C ₁₇ H ₁₄ O ₇		5320287	flavonols
79	Rhamnazin	C ₁₇ H ₁₄ O ₇		5320945	flavonols

80	Thymusin	C17H14O7		628895	flavonols
81	Isothymusin	C17H14O7		630253	flavonols
82	Tricin	C17H14O7		5281702	flavonols
83	Jaceosidin	C17H14O7		5379096	flavonols
84	Licoflavone A	C20H18O4		5319000	flavonols
85	Neobavaisoflavone	C20H18O4		5320053	isoflavones
86	Silandrin	C25H22O9		441663	flavonols

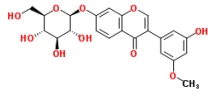
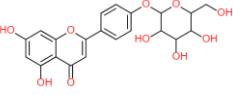
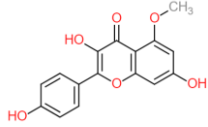
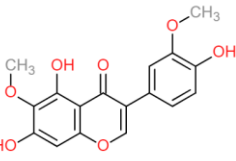
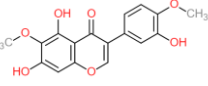
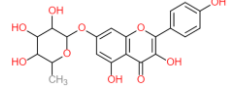
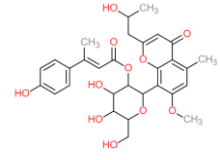
87	3'-methoxy-5'-hydroxyisoflavone-7-O-β-D-glucoside	C ₂₂ H ₂₂ O ₁₀			isoflavones
88	Flavone,5,7-dihydroxy-4'-O-α-D-glucoside	C ₂₁ H ₂₀ O ₁₀			isoflavones
89	5-Methyl kaempferol	C ₁₆ H ₁₂ O ₆		5319694	flavonols
90	Iristectorigenin A	C ₁₇ H ₁₄ O ₇		5491637	isoflavones
91	Iristectorigenin B	C ₁₇ H ₁₄ O ₇		5488781	isoflavones
92	7-O-α-L-Rhamnopyranosyl-kaempferol	C ₂₁ H ₂₀ O ₁₀			flavonols
93	Coumaroyl	C ₂₉ H ₃₂ O ₁₁			Phenolic acids

Table S4. Interaction and residue involving diosmetin and cosmosiin to 3AIC protein. Bold-black word as the key residue among potential and native ligands, while bold-purple word as the similar binding residue between diosmetin and genistin.

Protein		Interaction		Ligand	
Name	Residue	Category	Type		
3AIC	ASP 477	Hydrogen Bond	Conventional Hydrogen Bond	Diosmetin	
	TRP 517		Conventional Hydrogen Bond		
	GLU 515		Carbon-Hydrogen Bond		
	ASP 909		Carbon-Hydrogen Bond		
	ASN 481		Carbon-Hydrogen Bond		
	TYR 916	Hydrophobic	Pi-Pi T Shaped		
	HIS 587		Pi-Alkyl		
	ALA 478				
	LEU 433				
	ASN 914	Van Der Waals			Cosmosiin
	ARG 475	Van Der Waals			
	ASN 862	Van Der Waals			
	ASP 480	Van Der Waals			
	ASP 588	Electrostatic	Pi-Anion		
	ASP 480	Hydrogen Bond	Conventional Hydrogen Bond		
	ASP 588			Conventional Hydrogen Bond	
	GLU 515				
	ASP 477		Carbon-Hydrogen Bond		
	GLN 960		Carbon-Hydrogen Bond		
	ASP 909	Hydrophobic	Pi-Pi T Shaped		
ASN 481	Pi-Sigma				
TRP 517			Pi-Alkyl		
LEU 433					
LEU 382					
ALA 478					
TYR 430	Van Der Waals				
PHE 907	Van Der Waals				
GLN 592	Van Der Waals				
LEU 434	Van Der Waals				
TYR 916	Van Der Waals				
ARG 475	Van Der Waals				
HIS 587	Van Der Waals				

Table S5. Interaction and residue involving genistin and 3'-methoxy-5'-hydroxyisoflavone-7-O- β -D glucoside to 3IPK protein. Bold-black word as the key residue among potential and native ligands, while bold-purple word as the similar binding residue between genistin and 3'-methoxy-5'-hydroxyisoflavone-7-O- β -D glucoside.

Protein		Interaction		Ligand
Name	Residue	Category	Type	
3IPK	ASP 512	Hydrogen Bond	Conventional Hydrogen Bond	Genistin
	ARG 824			
	ASP 760			
	TRP 816			
	THR 586			
	SER 697	Carbon-Hydrogen Bond		
	LYS 822	Hydrophobic	Pi-Alkyl	
	TRP 816		Pi-Pi Stacked	
	LEU 653	Van Der Waals		
	ASN 820			
	SER 762			
	VAL 587			
	THR 652	Hydrogen Bond	Conventional Hydrogen Bond	3'-Methoxy-5'-Hydroxyisoflavone-7-O- β -D Glucoside
	ASN 820			
	ARG 824			
	TRP 816			
THR 586				
ASP 909 ASN 481	Carbon-Hydrogen Bond			
TRP 816	Hydrophobic	Pi-Pi stacked		
LEU 653		Alkyl		
LYS 822		Pi-Alkyl		
ASP 512	Van Der Waals			
SER 762				
VAL 587				

Description	Scientific Name	Max Score	Query Cover	E value	Per. ident
LPXTG cell wall anchor domain-containing protein	Limosilactobacillus reuteri	79.3	83%	9.00E-15	27.88
LPXTG cell wall anchor domain-containing protein	Limosilactobacillus reuteri	70.5	35%	5.00E-12	30.96
hypothetical protein	Limosilactobacillus reuteri	68.2	87%	1.00E-11	24.9
KxYKxGKxW signal peptide domain-containing protein	Limosilactobacillus reuteri	68.6	34%	1.00E-11	32.29
hypothetical protein	Limosilactobacillus reuteri	67	51%	2.00E-11	28
hypothetical protein	Limosilactobacillus reuteri	66.6	50%	3.00E-11	27.31
LPXTG cell wall anchor domain-containing protein	Limosilactobacillus reuteri	67.8	35%	4.00E-11	31.5
LPXTG cell wall anchor domain-containing protein	Limosilactobacillus reuteri	67.8	35%	4.00E-11	31.5
hypothetical protein	Limosilactobacillus reuteri	66.2	35%	4.00E-11	30.96

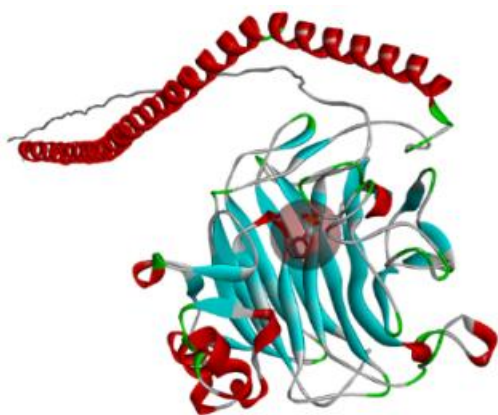
Figure S1. BLAST-P result between 3IPK protein and *Lactobacillus reuteri* protein

Description	Scientific Name	Max Score	Query Cover	E value	Per. ident
KxYKxGKxW signal peptide domain-containing protein	Limosilactobacillus reuteri	82	40%	4.00E-16	28.67
glycosyl hydrolase 53 family protein	Limosilactobacillus reuteri	82.8	40%	2.00E-15	28.57
glycosyl hydrolase 53 family protein	Limosilactobacillus reuteri	82	40%	3.00E-15	27.36
glycosyl hydrolase 53 family protein	Limosilactobacillus reuteri	81.6	40%	3.00E-15	27.36
KxYKxGKxW signal peptide domain-containing protein	Limosilactobacillus reuteri	79.7	50%	4.00E-15	26.33
KxYKxGKxW signal peptide domain-containing protein	Limosilactobacillus reuteri	80.1	50%	4.00E-15	25.61
KxYKxGKxW signal peptide domain-containing protein	Limosilactobacillus reuteri	79.3	40%	5.00E-15	28.47
Arabinogalactan endo-1,4-beta-galactosidase precursor	Limosilactobacillus reuteri subsp. porcinus	80.9	40%	7.00E-15	28.38
glycosyl hydrolase 53 family protein	Limosilactobacillus reuteri	80.5	40%	9.00E-15	28.38

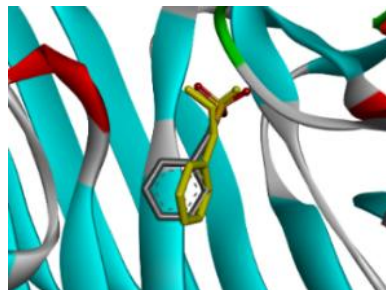
Figure S2. BLAST-P result between 3AIC protein and *Lactobacillus reuteri* protein

Description	Scientific Name	Max Score	Query Cover	E value	Per. ident
zonadhesin isoform 3 precursor	Homo sapiens	43.9	16%	0.003	36.26
zonadhesin splice variant 3	Homo sapiens	43.9	16%	0.003	36.26
zonadhesin variant 3	Homo sapiens	43.9	16%	0.003	36.26
zonadhesin splice variant 6	Homo sapiens	43.9	16%	0.003	36.26
zonadhesin isoform 6 precursor	Homo sapiens	43.9	16%	0.003	36.26
zonadhesin variant 6	Homo sapiens	43.9	16%	0.003	36.26
zonadhesin splice variant 5	Homo sapiens	43.9	16%	0.003	36.26
zonadhesin variant 5	Homo sapiens	43.9	16%	0.003	36.26
zonadhesin variant 1	Homo sapiens	43.9	16%	0.003	36.26

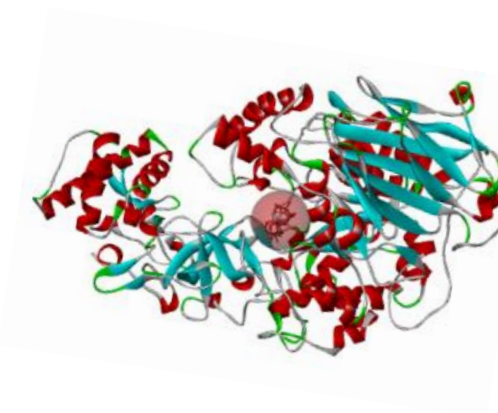
Figure S3. BLAST-P result between 3AIC protein and *Homo sapiens* protein



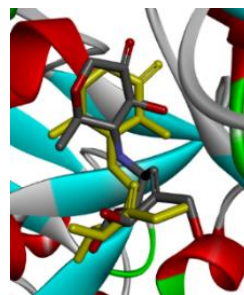
(A)



(B)



(C)



(D)

Figure S4. Protein-ligand binding site. 3AIC binding site (A), acarbose before and after (yellow) validation (B). 3IPK binding site (C), PMS before and after (yellow) validation (D)

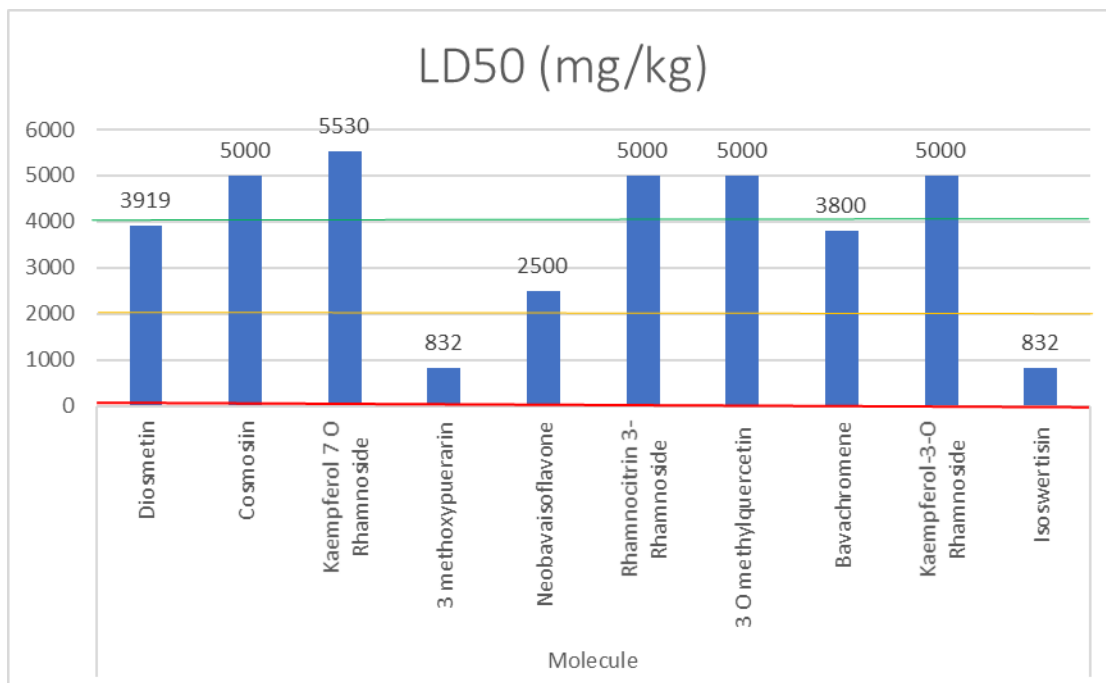


Figure S5. Lethal dose top ten ligands of 3AIC protein. Class 1 fatal if swallowed (red line), class IV harmful if swallowed (yellow line), and Class V may be harmful if swallowed (green line)

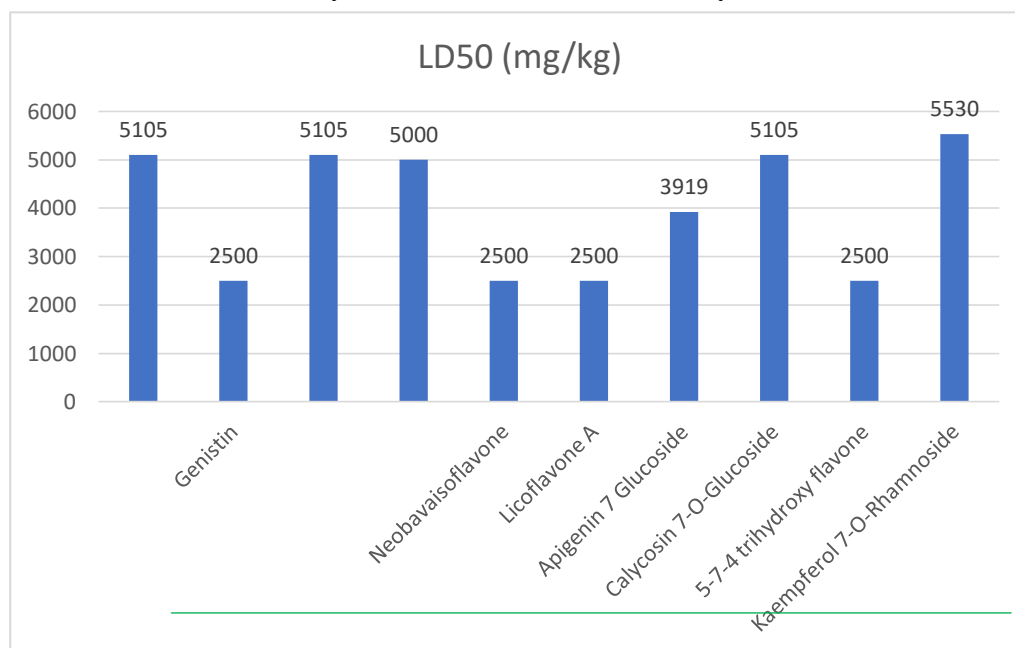


Figure S6. Lethal dose top ten ligands of 3IPK protein. Class 1 fatal if swallowed (red line), class IV harmful if swallowed (yellow line), and Class V may be harmful if swallowed (green line)

001 Input_pdb_SEQRES_A	V	D	A	D	L	L	Q	I	A	G	D	Y	L	K	A	A	K	G	I	H	K	N	D	K	A	A	N	D	H	L	S	I	L	E	A	W	S	Y	-	N	D	T	P	Y	L	H	D	-	D	G
002 UniRef90_B0M1N9_201_1044	V	D	A	D	L	L	Q	I	S	S	D	Y	L	K	S	A	Y	K	I	D	K	N	N	K	N	A	N	D	H	V	S	I	V	E	A	W	S	D	-	N	D	T	P	Y	L	N	D	-	D	G
003 UniRef90_A0A2X3VGA6_186_1039	V	N	A	D	L	L	Q	I	A	S	D	Y	F	K	S	Y	Y	G	V	D	K	S	E	S	N	A	I	N	H	L	S	I	L	E	A	W	S	D	-	N	D	P	Y	Y	N	Q	D	-	T	K
004 UniRef90_F8LHX2_277_1116	V	N	A	D	L	L	Q	I	A	S	D	Y	F	K	A	K	Y	G	A	D	Q	S	Q	D	Q	A	I	K	H	L	S	I	L	E	A	W	S	H	-	N	D	A	Y	Y	N	E	D	-	T	K
005 UniRef90_P08987_219_1062	V	D	A	D	L	L	Q	I	A	G	D	Y	L	K	A	A	K	G	I	H	K	N	D	K	A	A	N	D	H	L	S	I	L	E	A	W	S	D	-	N	D	T	P	Y	L	H	D	-	D	G
006 UniRef90_Q03VD8_320_1157	V	D	A	D	L	L	Q	I	A	A	D	Y	F	K	L	A	Y	G	V	D	Q	N	D	A	T	A	N	Q	H	L	S	I	L	E	D	W	S	H	-	N	D	P	L	Y	V	T	D	-	Q	G
007 UniRef90_A0A0R2DQ27_313_1167	V	D	A	D	L	L	Q	I	A	A	S	Y	F	K	D	A	Y	K	V	N	K	N	D	K	N	A	N	Q	H	I	S	I	L	E	D	W	S	D	-	N	D	A	Q	Y	V	K	D	-	Q	G
008 UniRef90_A0A652NDY6_352_1188	V	D	A	D	L	L	Q	I	A	S	D	Y	F	K	L	A	Y	G	V	N	K	N	D	E	T	A	N	K	H	L	S	I	L	E	D	W	S	H	-	N	D	P	L	Y	V	T	D	-	K	G
009 UniRef90_A0A3S4LN26_329_1168	V	D	A	D	L	L	Q	I	A	S	D	Y	F	K	E	K	Y	R	V	A	D	N	E	A	N	A	I	A	H	L	S	I	L	E	A	W	S	Y	-	N	D	H	Q	Y	N	K	D	-	T	K
010 UniRef90_A0A0R1M1B8_222_1078	V	D	A	D	L	L	Q	I	A	A	D	Y	F	K	D	A	Y	K	V	D	Q	N	D	Q	N	A	N	Q	H	L	S	I	L	E	D	W	S	D	-	N	D	A	Q	Y	V	Q	D	-	H	G

(A)

001 Input_pdb_SEQRES_A	Q	A	N	S	-	-	N	Y	R	I	L	N	R	T	P	T	N	Q	-	T	G	K	K	D	P	R	Y	T	-	-	-	A	D	R	T	-	-	-	I	G	G	Y	E	F	L	L	A	N	D	V
002 UniRef90_B0M1N9_201_1044	D	T	Q	S	-	-	G	Y	R	I	L	N	R	T	P	T	N	Q	-	T	G	S	L	D	P	R	F	T	-	F	N	Q	N	D	P	-	-	-	L	G	G	Y	E	Y	L	L	A	N	D	V
003 UniRef90_A0A2X3VGA6_186_1039	Y	A	N	S	-	-	D	Y	R	L	L	N	R	T	P	T	S	Q	-	T	G	E	Q	-	-	K	Y	F	-	-	-	V	D	N	S	-	-	-	I	G	G	Y	E	F	L	L	A	N	D	I
004 UniRef90_F8LHX2_277_1116	H	A	N	S	-	-	D	Y	R	L	L	N	R	T	P	T	S	Q	-	T	G	K	H	N	P	K	Y	T	-	-	-	K	D	T	S	-	-	-	N	G	G	F	E	F	L	L	A	N	D	I
005 UniRef90_P08987_219_1062	Y	A	N	S	-	-	N	Y	R	I	L	N	R	T	P	T	N	Q	-	T	G	K	K	D	P	R	Y	T	-	-	-	A	D	N	T	-	-	-	I	G	G	Y	E	F	L	L	A	N	D	V
006 UniRef90_Q03VD8_320_1157	D	A	N	S	-	-	N	F	R	L	L	N	R	T	P	T	N	Q	-	T	G	E	Q	-	-	A	Y	N	-	-	-	L	D	N	S	-	-	-	K	G	G	F	E	L	L	A	N	D	V	
007 UniRef90_A0A0R2DQ27_313_1167	S	A	N	S	-	-	D	Y	R	L	L	N	R	T	P	T	N	Q	-	L	G	Y	P	-	-	S	Y	T	-	-	-	I	D	S	-	-	-	L	G	G	Y	E	F	L	L	A	N	D	V	
008 UniRef90_A0A652NDY6_352_1188	D	A	N	S	-	-	N	F	R	L	L	N	R	T	P	T	N	Q	-	T	G	K	Q	-	-	A	Y	N	-	-	-	L	D	N	S	-	-	-	K	G	G	F	E	L	L	A	N	D	V	
009 UniRef90_A0A3S4LN26_329_1168	H	A	N	S	-	-	D	F	R	L	M	N	R	T	P	T	N	Q	-	T	G	T	R	-	-	K	Y	H	-	-	-	I	D	R	S	-	-	-	N	G	G	Y	E	L	L	A	N	D	I	
010 UniRef90_A0A0R1M1B8_222_1078	K	A	N	S	-	-	N	Y	R	L	L	N	R	T	P	T	N	Q	-	Q	G	H	P	-	-	A	Y	T	-	-	-	T	D	N	S	-	-	-	L	G	G	Y	E	F	L	L	A	N	D	V

(B)

001 Input_pdb_SEQRES_A	D	N	S	N	P	V	V	Q	A	E	Q	L	N	W	L	H	F	L	M	N	F	G	N	I	Y	-	-	A	N	-	-	D	P	D	-	-	-	A	N	F	D	S	I	R	V	D	A	V	D	N
002 UniRef90_B0M1N9_201_1044	D	N	S	N	P	V	V	Q	A	E	S	L	N	W	L	H	Y	L	L	N	F	G	S	I	Y	-	-	A	N	-	-	D	P	E	-	-	-	A	N	F	D	S	I	R	V	D	A	V	D	N
003 UniRef90_A0A2X3VGA6_186_1039	D	N	S	N	P	A	V	Q	A	E	Q	L	N	W	L	H	Y	L	M	N	F	G	T	I	V	-	-	A	N	-	-	D	P	E	-	-	-	A	N	F	D	G	V	R	V	D	A	V	D	N
004 UniRef90_F8LHX2_277_1116	D	N	S	N	P	A	V	Q	A	E	Q	L	N	W	L	H	Y	I	M	N	I	G	T	I	T	-	-	G	G	-	-	S	E	D	-	-	-	E	N	F	D	G	V	R	V	D	A	V	D	N
005 UniRef90_P08987_219_1062	D	N	S	N	P	V	V	Q	A	E	Q	L	N	W	L	H	F	L	M	N	F	G	N	I	Y	-	-	A	N	-	-	D	P	D	-	-	-	A	N	F	D	S	I	R	V	D	A	V	D	N
006 UniRef90_Q03VD8_320_1157	D	N	S	N	P	V	V	Q	A	E	Q	L	N	W	L	Y	Y	L	M	N	F	G	T	I	T	-	-	A	N	-	-	D	A	D	-	-	-	A	N	F	D	G	I	R	V	D	A	V	D	N
007 UniRef90_A0A0R2DQ27_313_1167	D	N	S	N	P	V	V	Q	A	E	Q	L	N	W	M	Y	Y	L	L	N	F	G	S	I	V	-	-	N	H	-	-	D	A	N	-	-	-	G	N	F	D	S	I	R	V	D	A	V	D	N
008 UniRef90_A0A652NDY6_352_1188	D	N	S	N	P	V	V	Q	A	E	Q	L	N	W	L	Y	Y	L	M	N	F	G	S	I	T	-	-	A	N	-	-	D	A	D	-	-	-	A	N	F	D	G	I	R	V	D	A	V	D	N
009 UniRef90_A0A3S4LN26_329_1168	D	N	S	N	P	T	V	Q	A	E	Q	L	N	W	L	H	Y	I	M	N	I	G	S	I	L	-	-	G	N	-	-	D	P	S	-	-	-	A	N	F	D	G	V	R	I	D	A	V	D	N
010 UniRef90_A0A0R1M1B8_222_1078	D	N	S	N	P	V	V	Q	A	E	Q	L	N	W	M	Y	Y	L	L	N	F	G	S	I	V	-	-	K	H	-	-	D	A	A	-	-	-	G	N	F	D	S	I	R	V	D	A	V	D	N

(C)

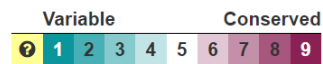
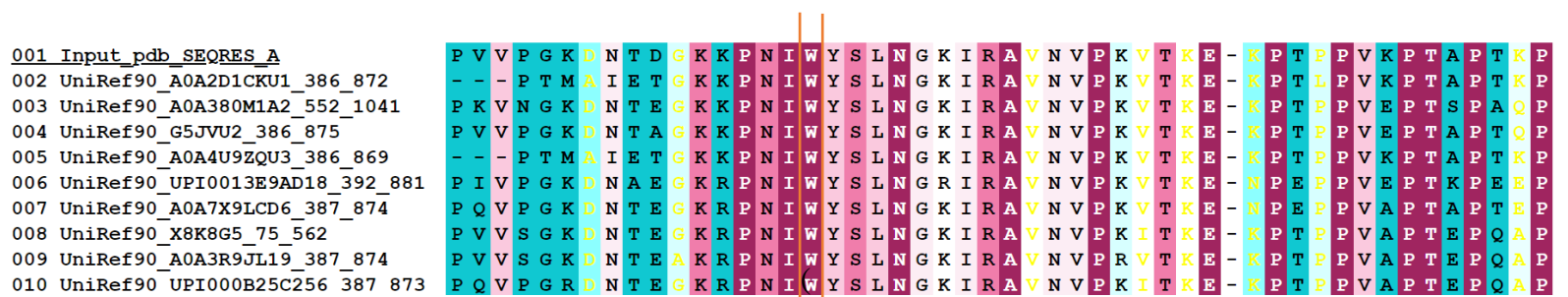


Figure S7. Partial 3AIC protein sequence. Conserved amino acid shows within the blue line.

Amino acid of glutamic acid 515 (A), leucine 433 (B), aspartic acid 477 and asparagine 481 (C).



(A)



(B)

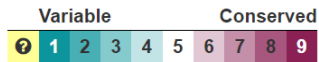


Figure S8. Partial 3IPK protein sequence. Conserved amino acid shows within the orange line.

The amino acid of tryptophan 816 (A), and arginine 824 (B).

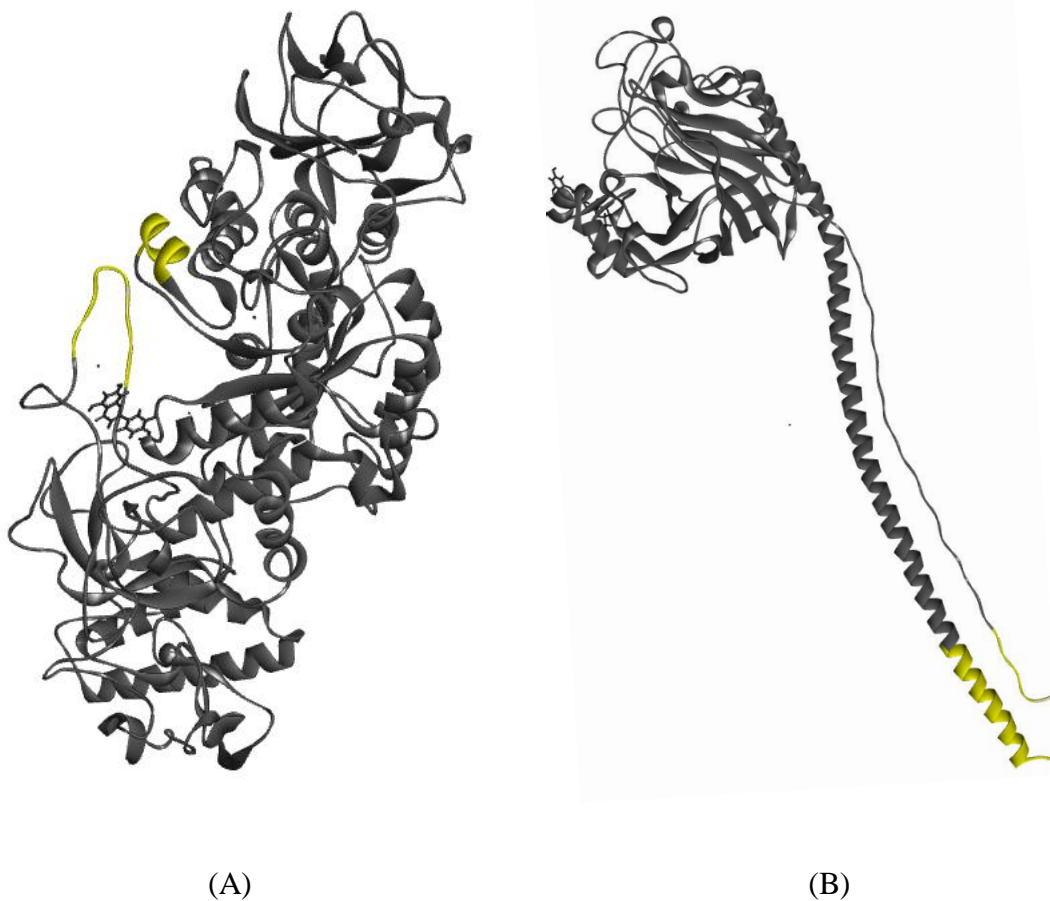
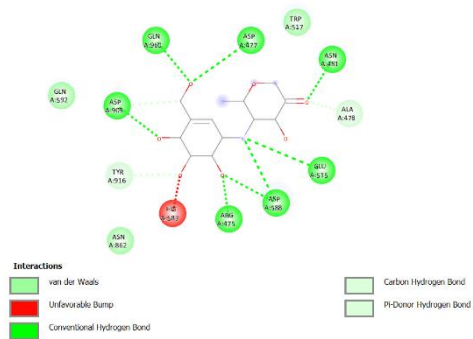
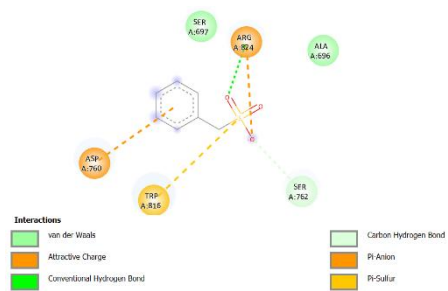


Figure S9. 3AIC and 3IPK crystal protein. The fluctuating residue is shown by yellow color. The fluctuating residue of 173-182 (left) and 276-283 (right) from diosmetin and cosmosiin in 3AIC protein (A). The fluctuating residue of 1-23 (left) and 482-489 (right) from genistin and 3'-Methoxy-5'-hydroxyisoflavone-7-O- β -D glucoside in 3IPK protein (B)



(A)



(B)

Figure S10. Protein and native ligand interaction between 3AIC-acarbose (A) and 3IPK-Phenylmethanesulfonic Acid (PMS) (B)