

Appendix 1: Active peptide fragments, the bound sites and properties based on the peptide lengths. (**Short peptides (2 – 5 amino acid residues)**)

Source	Peptide Sequence	Pepsite2 (p-value)	Active peptide fragment	Pepsite2 analysis		Hydrophobic/Hydrophilic analysis				Isoelectric point, pH	Ref.
				Bound sites	No. of hotspots	Hydrophobic (%)	Acidic (%)	Basic (%)	Neutral (%)		
<i>Aspergillus oryzae</i> N159-1 extract from traditional fermented Korean food	CL	0.01891	C1, L2	TRP375, TRP481, ASP616*, HE649*	2	50	0	0	50	2.91	(16)
Soybean protein hydrolysate	GSR	0.01278	G1, S2, R3	TRP376*, TRP481, ASP518*, MET519*, ARG600*, ASP616*, PHE649*	6	0	0	33.33	66.67	10.84	(17)
Soybean protein hydrolysate	EAK	0.03436	E1, A2, K3	TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, ARG600*, TRP613*, ASP616*, PHE649*, HIS674*	11	33.33	33.33	33.33	0	6.85	(17)
<i>Aspergillus oryzae</i> N159-1 extract from traditional fermented Korean food	PFP	0.0001747	P1, F2, P3	ASP282, TRP376*, ASP404*, ILE441*, TRP481, ASP518*, MET519*, PHE525, ASP616*	6	100	0	0	0	4.26	(16)
Soy protein	WLRL	0.02069	W1, L2, R3, L4	TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, ARG600*, TRP613*, ASP616*, PHE649*, HIS674*	10	75	0	25	0	10.72	(18)
Chinese giant salamander (<i>Andrias davidianus</i>) protein hydrolysate	CSSV	0.07312	C1, S2, S3, V4	TRP376*, TRP481, ASP518*, MET519*, PHE525	3	25	0	0	75	2.93	(19)
Chinese giant salamander (<i>Andrias davidianus</i>) protein hydrolysate	YSFR	0.01428	Y1, S2, F3, R4	ASP282, TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ASP616*, HIS674*	8	25	0	25	50	9.57	(19)
Chinese giant salamander (<i>Andrias davidianus</i>) protein hydrolysate	SAAP	0.003692	S1, A2, A3, P4	ASP282, TRP376*, ASP404*, ILE441*, TRP481, ASP518*, MET519*, PHE525	5	75	0	0	25	3.55	(19)
Chinese giant	PGGP	0.01177	P1, G2,	TRP376*, ASP404*, ILE441*,	7	50	0	0	50	4.26	(19)

salamander (<i>Andrias davidianus</i>) protein hydrolysate			P4	TRP481, ASP518*, PHE525, ARG600*, ASP616*, PHE649*								
In silico digestion of silkworm protein	QPGR	0.0002864	Q1, P2, G3, R4	ASP282, TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, ASP616*, PHE649*, HIS674*	10	25	0	25	50	10.55	(20)	
In silico digestion of silkworm protein	QPPT	0.00006857	Q1, P2, P3, T4	ASP282, TRP376*, ASP404*, ILE441*, TRP481, ASP518*, MET519*, PHE525, ARG600*, ASP616*	7	50	0	0	50	3.4	(20)	
In silico digestion of silkworm protein	NSPR	0.005659	N1, S2, P3, R4	ASP282, TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ASP616*, PHE649*, HIS674*	9	25	0	25	50	10.42	(20)	
Quinoa yoghurt beverage hydrolysate	KDLQL	0.01986	K1, L3, Q4, L5	ASP282, TRP376*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, TRP613*, GLY615, ASP616*, PHE649*	8	40	20	20	20	6.43	(21)	
Soy protein	SWLRL	0.034	S1, W2, L3, R4	TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, ASP616*, PHE649*, HIS674*	8	60	0	20	20	10.57	(18)	
Chinese giant salamander (<i>Andrias davidianus</i>) protein hydrolysate	LGGGN	0.02055	L1, G3, G4, N5	ASP282, TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, ASP616*, PHE649*, HIS674*	10	20	0	0	80	3.71	(19)	
In silico digestion of silkworm protein	SQSPA	0.001165	S1, Q2, P4, A5	ASP282, TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, TRP613*, ASP616*, PHE649*, HIS674*	11	40	0	0	60	3.36	(19)	
Albumin hydrolysate	KLPGF	0.004989	K1, L2, P3, F5	ASP282, TRP376*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, TRP613*, GLY615, ASP616*, PHE649*	8	60	0	20	20	9.91	(22)	
Albumin hydrolysate	EVSGL	0.09905	V2, S3, G4, L5	ASP282, TRP376*, TRP481, MET519*, PHE525, ASP616*, PHE649*	4	40	20	0	40	0.92	(22)	
Albumin hydrolysate	EAGVD	0.04794	A2, G3, V4, D5	ASP282, TRP376*, ASP404*, ILE441*, TRP481, ASP518*, MET519*, PHE525, ARG600*, ASP616*, PHE649*, HIS674*	9	40	40	0	20	0.81	(22)	
Egg white	TPSPR	0.0004057	T1, P2,	ASP282, TRP376*, ASP404*,	11	40	0	20	40	10.53	(23)	

protein hydrolysate			P4, R5	ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, TRP613*, ASP616*, PHE649*, HIS674*							
<i>Vaccaria hispanica</i> seeds	GFPFYF	0.002243	F2, P3, F4, Y5, P6	ASP282, TRP376*, ASP404*, ILE441*, TRP481, ASP518*, MET519*, PHE525, ASP616*	6	66.67	0	0	33.33	3.76	(24)
Albumin hydrolysate	NVLQPS	0.002657	N1, V2, L3, Q4, P5	ASP282, TRP376*, ASP404*, LEU405, ILE441*, ASP443, TRP481, TRP516*, ASP518*, MET519*, PHE525, ASP616*, PHE649*, HIS674*	9	50	0	0	50	3.3	(22)
Albumin hydrolysate	QITKPN	0.001887	Q1, I2, K4, P5, N6	TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, ASP616*, PHE649*, HIS674*	10	33.33	0	16.67	50	9.83	(22)
Albumin hydrolysate	AEAGVD	0.0207	A1, E2, A3, G4, V5	TRP376*, ASP404*, ILE441*, TRP481, ASP518*, MET519*, PHE525, ARG600*, ASP616*, PHE649*, HIS674*	9	50	33.33	0	16.67	0.81	(22)
Albumin hydrolysate	LEPINF	0.005689	E2, P3, I4, N5, F6	ASP282, TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, TRP613*, ASP616*, PHE649*, HIS674*	10	66.67	16.67	0	16.67	0.99	(22)
Albumin hydrolysate	ANENIF	0.01188	A1, N2, N4, I5, F6	ASP282, TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, TRP613*, ASP616*, PHE649*, HIS674*	10	50	16.67	0	33.33	0.99	(22)
Microalgae (<i>Spirulina platensis</i>) protein extract	GVPMPNK	0.000602	V2, P3, M4, P5, N6, K7	TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, TRP613*, GLY615, ASP616*, PHE649*, HIS674*	11	57.14	0	14.29	28.57	10.12	(25)
Quinoa yoghurt beverage hydrolysate	KLTPQMA	0.003334	K1, T3, P4, Q5, M6	ASP282, TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, TRP613*, GLY615, ASP616*	9	57.14	0	14.29	28.57	9.91	(21)
Black bean (<i>Phaseolus vulgaris</i>) proteins hydrolysate	GSPVSSR	0.005965	S2, P3, V4, S5, S6, R7	TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, PHE525, TRP613*, ASP616*, PHE649*, HIS674*	9	28.57	0	14.29	57.14	10.84	(26)
Black bean (<i>Phaseolus vulgaris</i>)	SGPFGPK	0.003293	P3, F4, G5, P6, K7	TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, PHE525, ARG600*, TRP613*,	9	42.86	0	14.29	42.86	9.86	(26)

proteins hydrolysate				GLY615, ASP616*, PHE649*							
Black bean (<i>Phaseolus vulgaris</i>) proteins hydrolysate	RKCLKMRQ	0.001332	R1, K2, K4, M5, R6, Q7	TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, TRP613*, GLY615, ASP616*, PHE649*, HIS674*	11	28.57	0	57.14	14.29	12.16	(26)
Quinoa yoghurt beverage hydrolysate	KSFGSSNI	0.02218	K1, S2, F3, G4, S5, S6	ASP282, TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, TRP613*, GLY615, ASP616*, PHE649*, HIS674*	11	25	0	12.5	62.5	9.91	(21)
Soy protein	LLPLPVLK	0.002893	P3, L4, P5, V6, L7, K8	TRP376*, ASP404*, LEU405, ILE441*, ASP443, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, TRP613*, GLY615, ASP616*, HIS674*	10	87.5	0	12.5	0	10.12	(18)
Oat (<i>Avena sativa</i>) globulin hydrolysate	LQAFEPLR	0.003451	Q2, A3, F4, E5, P6, R8	TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, ASP616*, PHE649*, HIS674*	10	62.5	12.5	12.5	12.5	6.86	(27)
Quinoa (<i>Chenopodium quinoa</i>) protein hydrolysate	IQAEGGLT	0.0569	I1, Q2, A3, E4, G5	ASP282, TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, TRP613*, ASP616*, PHE649*, HIS674*	11	37.5	12.5	0	50	0.97	(28)
Black bean (<i>Phaseolus vulgaris</i>) proteins hydrolysate	TTGGKGGK	0.1572	G3, K5, G7, K8	TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, ARG600*, TRP613*, GLY615, ASP616*, PHE649*, HIS674*	11	0	0	25	75	10.69	(26)
Quinoa yoghurt beverage hydrolysate	LAHMIVAGA	0.07043	H3, M4, I5, V6, A7	TRP376*, ASP404*, ILE441*, TRP481, ASP518*, MET519*, PHE525, ARG600*, ASP616*, PHE649*, HIS674*	9	77.78	0	11.11	11.11	7.81	(21)
Oat (<i>Avena sativa</i>) globulin hydrolysate	EFLLAGNNK	0.008787	L4, A5, G6, N7, N8, K9	ASP282, TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, TRP613*, GLY615, ASP616*, PHE649*, HIS674*	11	44.44	11.11	11.11	33.33	6.85	(27)
Microalgae (<i>Spirulina platensis</i>) protein extract	LRSELAAWSR	0.0386	L1, A6, A7, W8, S9, R10	ASP282, TRP376*, ASP404*, LEU405, ILE441*, ASP443, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, TRP613*, ASP616*, TRP618, PHE649*, HIS674*	11	50	10	20	20	10.68	(25)
Quinoa yoghurt beverage hydrolysate	MIKLRSTAKN	0.01589	M1, I2, T7, A8, K9, N10	ASP282, TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525,	10	40	0	30	30	11.57	(21)

Germinated soybean (<i>Glycine max</i>) protein isolate	QQQQQGGGSQSQ	0.004036	Q1, Q2, Q3, Q4, Q5, G6	ARG600*, ASP616*, TRP618, PHE649*, HIS674* ASP282, TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, TRP613*, ASP616*, PHE649*, HIS674*	11	0	0	0	100	3.41	(29)
Egg yolk protein hydrolysate	YINQMPQKSRE	0.00119	Q4, M5, P6, Q7, K8, R10	ASP282, TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, ASP616*, PHE649*, HIS674*	10	27.27	9.09	18.18	45.45	9.49	(30)
Germinated soybean (<i>Glycine max</i>) protein isolate	SDESTESETEQA	0.090185	S1, D2, S4, T5, E6, S7, E8, T9, E10, Q11, A12	ASP282, TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, TRP613*, ASP616*, TRP618, PHE649*, HIS674*	11	8.33	41.67	0	50	0.49	(29)
Germinated soybean (<i>Glycine max</i>) protein isolate	VVAEQAGEQGFE	0.03143	V1, V2, A3, E4, Q5, A6, G7, E8, Q9, E12	ASP282, TRP376*, ASP404*, ARG411, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, TRP613*, ASP616*, PHE649*, HIS674*	11	41.67	25	0	33.33	0.76	(29)
Egg yolk protein hydrolysate	YINQMPQKSREA	0.00119	Q4, M5, P6, Q7, K8, R10	ASP282, TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, ASP616*, PHE649*, HIS674*	10	33.33	8.33	16.67	41.67	9.49	(30)
Egg yolk protein hydrolysate	VTGRFAGHPAAQ	0.0116329	F5, A6, G7, H8, P9, A10, A11, Q12	ASP282, TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, TRP613*, ASP616*, PHE649*, HIS674*	10	50	0	16.67	33.33	10.81	(30)
Egg yolk protein by-product hydrolysate	LAPSLPGKPKPD	0.004422	L5, P6, G7, K8, P9, K10	ASP282, TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, TRP613*, GLY615, ASP616*, PHE649*, HIS674*	11	58.33	8.33	16.67	16.67	9.93	(31)
Germinated soybean (<i>Glycine max</i>) protein isolate	QQQQQGGGSQSQKG	0.0105465	Q1, Q2, Q3, Q4, Q5, G6, S8, Q9, Q11, K12	ASP282, TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, TRP613*, GLY615, ASP616*, PHE649*, HIS674*	11	0	0	7.69	92.31	9.83	(29)
Germinated soybean (<i>Glycine max</i>) protein isolate	RNLQGENEEEDSGA	0.115627	R1, N2, L3, Q4, G5, E6, N7, E8	ASP282, TRP376*, ASP404*, ARG411, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, TRP613*,	11	14.29	35.71	7.14	42.86	3.44	(29)

Germinated soybean (<i>Glycine max</i>) protein isolate	IMSDESTESETEQA	0.086435	D11, S12 I1, M2, S3, D4, S6, T7, E8, S9, E12, Q13, A14	ASP616*, TRP618, PHE649*, HIS674* ASP282, TRP376*, ASP404*, ILE441*, TRP481, ASP518*, MET519*, PHE525, ARG600*, ASP616*, TRP618, PHE649*	8	21.43	35.71	0	42.86	0.49	(29)
Germinated soybean (<i>Glycine max</i>) protein isolate	NALKPDNRIESEGG	0.00994	P5, D6, N7, R8, I9, E10	ASP282, TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, TRP613*, ASP616*, PHE649*, HIS674*	11	28.57	21.43	14.29	35.71	4.32	(29)
Germinated soybean (<i>Glycine max</i>) protein isolate	SSPDIYNPQAGSVT	0.007251	S1, Y6, N7, P8, Q9, A10, G11	ASP282, TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, TRP613*, ASP616*, TRP618, PHE649*, HIS674*	11	35.71	7.14	0	57.14	0.75	(29)
Sericin hydrolysate	SEDSSEVDIDLGNLG	0.109365	S4, S5, E6, V7, D8, I9, D10, L11, G12, N13	ASP282, TRP376*, ASP404*, ARG411, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, TRP613*, ASP616*, PHE649*, HIS674*	11	26.67	33.33	0	40	0.4	(32)
Microalgae (<i>Spirulina platensis</i>) protein extract	RNPFVFAPLLTVAAR	0.0151455	R1, N2, P3, F4, V5, A7, P8, T9, L10, L11, R16	ASP282, TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, TRP613*, ASP616*, TRP618, PHE649*, HIS674*	10	68.75	0	12.5	18.75	12.1	(25)
Germinated soybean (<i>Glycine max</i>) protein isolate	RQNIGQNSSPDIYNPQAG	0.009629	R1, Q2, N3, G5, Q6, N14, P15, Q16, A17, G18	ASP282, TRP376*, ASP404*, ILE441*, TRP481, TRP516*, ASP518*, MET519*, PHE525, ARG600*, ASP616*, PHE649*, HIS674*	10	27.78	5.56	5.56	61.11	6.34	(29)

Note: * Hotspot of AG

Appendix 2: Predicted binding interactions of selected α -glucosidase inhibitory peptides.

Peptides sequence	Binding affinity (kcal/mol)	Residues of α -glucosidase involve in protein-peptide interaction			
		Hydrophobic interaction (No. of interactions)	Salt bridge (No. of interactions)	Hydrogen bond	Hydrogen bond length (Å)
N Ultimate Position (N1)					
QITKPN	-8.7	Trp376* (3), Arg411 (1), Trp481 (2) Phe525 (1)	None	Arg411	2.87
QQQQQGGSSQSQ	-10.3	Asp282 (4), Trp481 (1), Met519* (1), Ser523 (1), Asn524 (1), Phe525 (4)	None	Ser523	2.90
SQSPA	-8.6	Trp481 (2), Phe525 (1)	None	None	None
SGPFGPK	-8.2	Trp376* (2), Trp481(3), Phe525 (1)	None	None	None
RKLKMRQ	-8.0	Trp376* (2), Trp481 (1), Leu677 (1)	None	None	None
RQNIGQNSSPDIYNPQAG	-10.7	Asp282 (2), Trp376* (2), Trp481 (1), Asp616* (2)	Asp282 (2) , Asp616* (1)	Asp282 , Asp616*	2.60, 2.81
KLPGF	-7.0	Asp282 (1), Phe525 (1), Asp616* (4)	Asp616* (1)	Asp616*	2.67
KLTPQMA	-7.6	Trp376* (2), Asp404* (3), Leu405 (1), Ile441* (1), Trp481 (2), Asp518* (3), Asp616* (1), Phe649* (2)	Asp404* (1)	Asp404* Asp518*	2.84 2.67
ANENIF	-7.8	Leu283 (1) Ala284 (1)	None	None	None
AEAGVD	-7.3	Trp376* (1)	None	None	None
C Ultimate Position (C1)					
TPSPR	-8.1	Trp376* (3) Trp481 (1) Asp518* (3) Trp613* (1) Asp616* (3) Phe649* (2) Ser676 (1) Leu677 (2)	Asp518* (1) Asp616* (1)	Asp518* Asp518* Asp616* Leu677	2.64 2.94 2.70 2.94
GSPVSSR	-9.7	Trp376* (4) Trp481 (3) Asp518* (3) Asp616* (3) Phe649* (2)	Asp518* (1) Asp616* (2)	Asp518* Asp518* Asp616*	2.67 2.91 2.67
GVPMPNK	-7.6	Asp282 (1) Asp616* (7)	Asp616* (2)	Asp282	3.11
LLPLPVLK	-7.6	Trp481 (2) Asp518* (4) Met519* (2) Arg600* (1) Asp616* (7)	Asp518* (1) Asp616* (2)	Asp518*	2.62
SQSPA	-8.6	Ser676 (1) Leu677 (1) Leu678 (5)	None	Leu678	2.85
IMSDESTESETEQA	-9.0	Arg527 (2)	None	None	None
N penultimate position (N2)					
SQSPA	-8.6	Asp282 (2) Asp616* (6) Leu650 (2)	None	Asp282 Asp616*	2.76 2.97
LQAFEPLR	-7.7	Asp282 (5) Leu283 (1) Trp481 (1) Asp616* (2)	None	Asp282	2.61
GVPMPNK	-7.6	Leu650 (1) Ser676 (1)	None	None	None
NVLQPS	-8.2	Ala284 (1) Asp616* (1) Leu650 (1)	None	None	None

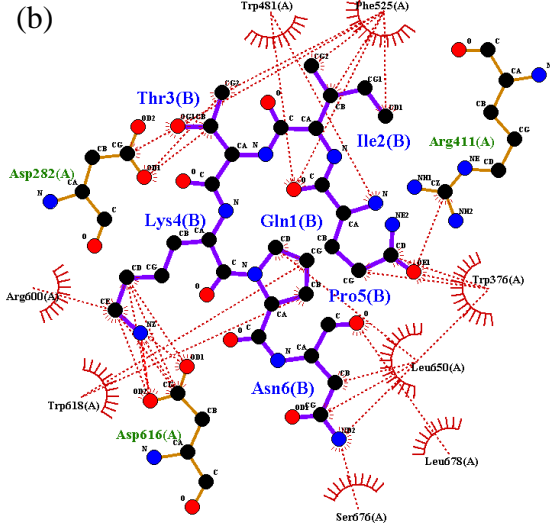
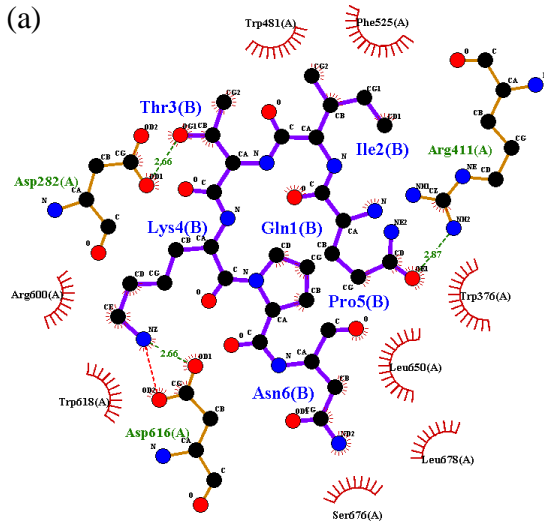
KSFGSSNI	-9.7	Asp282 (4) Phe525 (3)	None	Asp282	2.59
SSPDIYNPQAGSVT	-9.2	None	None	Lys479	2.73
ANENIF	-7.8	Asp282 (3) Trp481 (1) Arg600* (2) Asp616* (3)	None	Arg600* Asp616*	2.71 2.68
RNPVFVAPLLTVAAR	-9.5	None	None	None	None
RNLQGENEEEDSGA	-10.1	None	None	None	None
C penultimate position (C2)					
SQSPA	-8.6	Trp376* (4) Trp481 (2) Ser676 (1) Leu678 (2)	None	None	None
TPSPR	-8.1	Phe649* (1) Leu650 (4)	None	None	None
RQNIGQNSSPDIYNPQAG	-10.7	Phe525 (2)	None	None	None
RNPVFVAPLLTVAAR	-9.5	None	None	None	None
VTGRFAGHPAAQ	-8.5	None	None	None	None
KDLQL	-7.1	Trp376* (1) Leu650 (1) Ser676 (3) Leu677 (1) Leu678 (2) Ser679 (1)	None	None	None
SDESTESETEQA	-10.4	Leu650 (2) Ser676 (1)	None	None	None
IMSDESTESETEQA	-9.0	None	None	None	None
RKCLKMRQ	-8.0	Asp282 (2) Asp616* (3) Leu650 (1)	Asp282 (2)	Asp282 Asp616* Asp616*	2.63 2.59 3.04
SWLRL	-8.1	Trp376* (5) Trp481 (4) Asp518* (4) Met519* (1) Asp616* (1) Phe649* (1)	Asp518* (2) Asp616* (2)	Asp518*	2.63
N antepenultimate position (N3)					
GSPVSSR	-9.7	Asp282 (3) Ala284 (1) Tyr292 (1) Arg600* (2) Asp616* (7)	None	None	None
GFPFYP	-6.8	Trp481 (2) Met519* (2) Phe525 (3) Asp616* (1)	None	None	None
AEAGVD	-7.3	Asp282 (1) Trp481 (3) Arg600* (2) Asp616* (2)	None	Arg600*	2.82
VVAEQAGEQGFE	-8.7	Arg281 (5) Ala554 (1) Ala555 (2)	None	None	None
QQQQQGGQSQSQ	-10.3	Leu678 (1)	None	None	None
QQQQQGGQSQSQKG	-11.5	None	None	None	None
C antepenultimate position (C3)					
KLTPQMA	-7.6	Asp282 (3) Met519* (2) Phe525 (5)	None	Asp282	2.64
QQQQQGGQSQSQKG	-11.5	Leu678 (6)	None	None	None

SDESTESETEQA	-10.4	Trp481 (2)	None	None	None
NALKPDNRIESEGG	-8.7	Trp618 (1) Leu650 (1)	None	None	None
RNPFVFAPLLTVAAR	-9.5	None	None	None	None
VTGRFAGHPAAQ	-8.5	None	None	None	None
LAHMIVAGA	-7.3	Phe525 (3)	None	None	None
MIKLRSTAKN	-8.7	None	None	None	None
ANENIF	-7.8	None	None	None	None
EFLAGNNK	-7.5	Leu283 (1)	None	Arg281	2.99
SEDSSEVDIDLGNLG	-8.7	None	None	None	None
RNLQGENEEEDSGA	-10.1	Leu678 (3)	None	None	None
YINQMPQKSRE	-9.2	Arg411 (1) Trp481 (2) Phe525 (1)	None	Arg411	2.76
QITKPN	-8.7	Arg600* (1) Asp616* (7)	Asp616* (1)	Asp616*	2.66
LAPSLPGKPKPD	-7.9	Asp282 (3) Asn524 (2) Phe525 (2)	None	Asp282 Ser523 Asn524	2.63 2.77 3.02

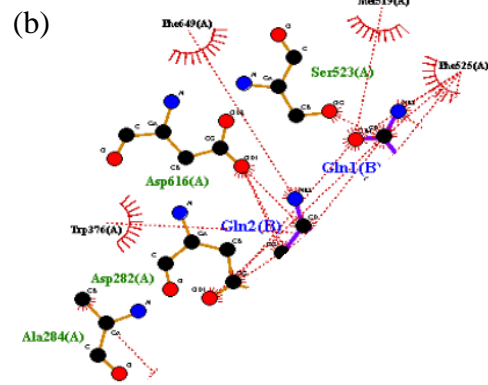
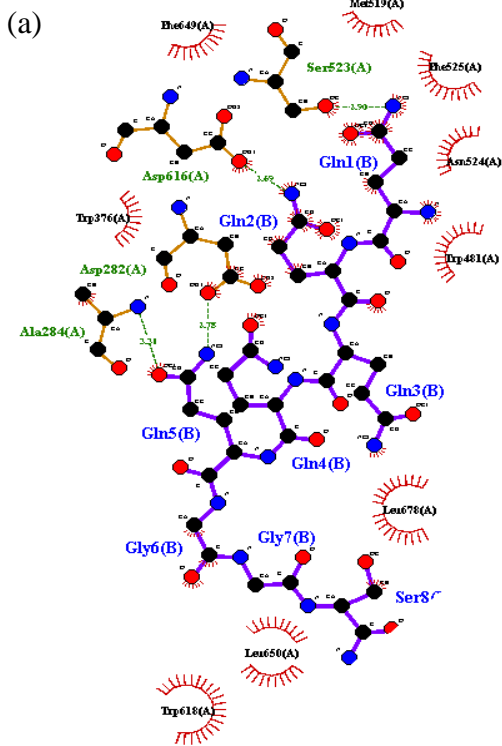
Note: * Hotspot of AG. The alphabate in **bold** is the studied amino acid residue

Binding interactions (i.e. (a) salt bridge and hydrogen bond, (b) hydrophobic interaction) between α -glucosidase and inhibitor peptides: (Appendix 3) QITKPN, (Appendix 4) QQQQQGGSQSQ, (Appendix5) RKLKMRQ, (Appendix6) RQNIGQNSSPDIYNPQAG, (Appendix7) SQSPA, (Appendix8) SGPFPGPK, (Appendix9) KLPGF, (Appendix10) KLTPQMA, (Appendix11) ANENIF, (Appendix12) AEAGVD, (Appendix13) TPSPR, (Appendix14) GSPVSSR, (Appendix15) GVPMPNK, (Appendix16) LLPLPVLK, (Appendix17) IMSDESTESETEQA, (Appendix18) LQAFEPLR, (Appendix19) NVLQPS, (Appendix20) KSGSSNI, (Appendix 21) SSPDIYNPQAGSVT, (Appendix22) RNPFVFAPLLTVAAR, (Appendix23) RNLQGENEEEDSGA, (Appendix24) SWLRL, (Appendix25) KDLQL, (Appendix 26) SDESTESETEQA, (Appendix 27)VTGRFAGHPAAQ, (Appendix 28) GFPFYP, (Appendix 29) VVAEQAGEQGFE, (Appendix 30) QQQQQGGSQSQKG, (Appendix31) NALKPDNRIESEGG, (Appendix 32) LAHMIVAGA, (Appendix 33) MIKLRSTAKN, (Appendix 34) EFLAGNNK, (Appendix 35) SEDSSEVDIDLGNLG, (Appendix 36) YINQMPQKSRE, and (Appendix 37) LAPSLPGKPKPD. Blue ball: nitrogen atom; red ball:

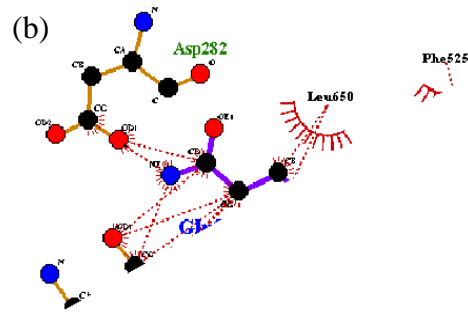
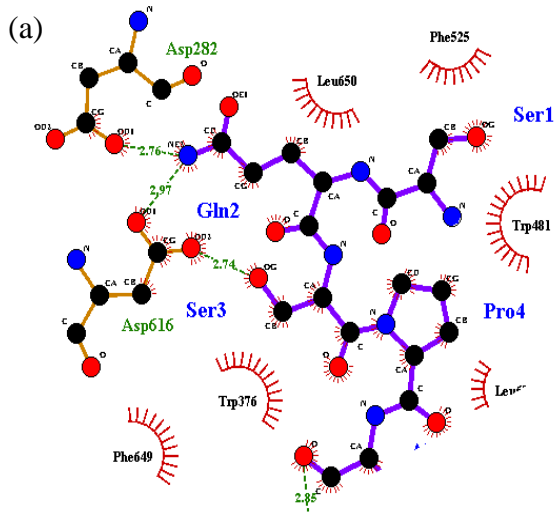
oxygen atom; black ball: carbon atom; yellow ball: sulphur atom; purple line: peptide bond;
orange line: non-peptide bond; green dotted line with number: hydrogen bond and the distance
(in Armstrong, Å); red dotted line: salt bridge; brick red dotted line: hydrophobic interaction;
brickred eyelashes: residue involved in hydrophobic interaction.



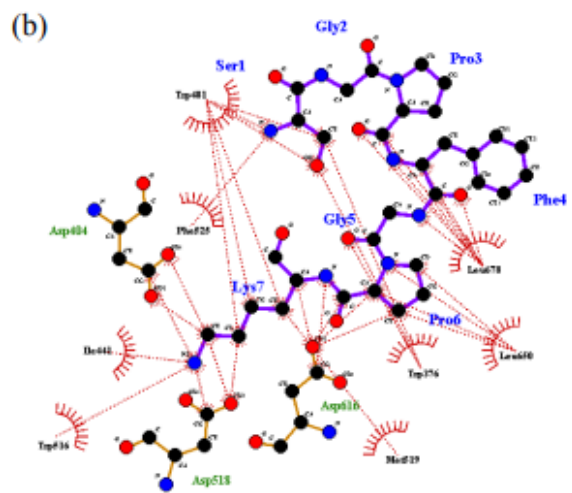
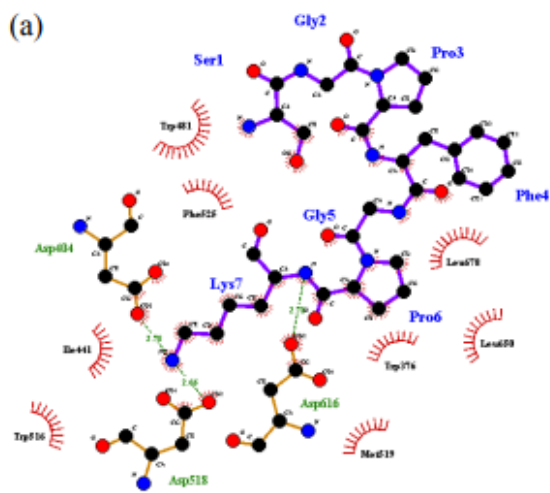
Appendix 3: QITKPN



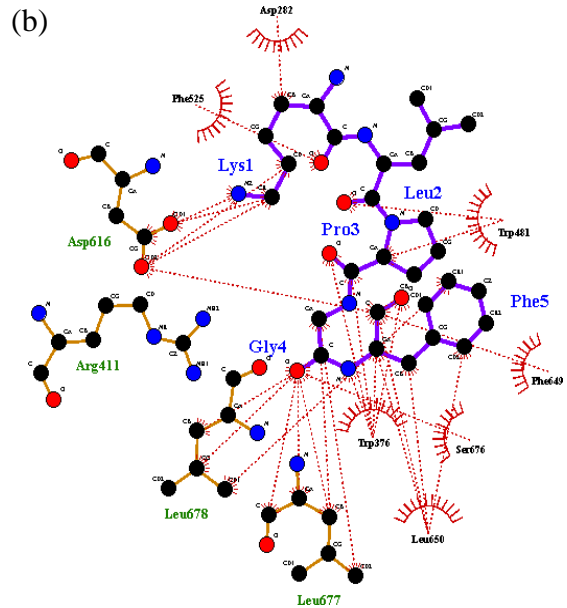
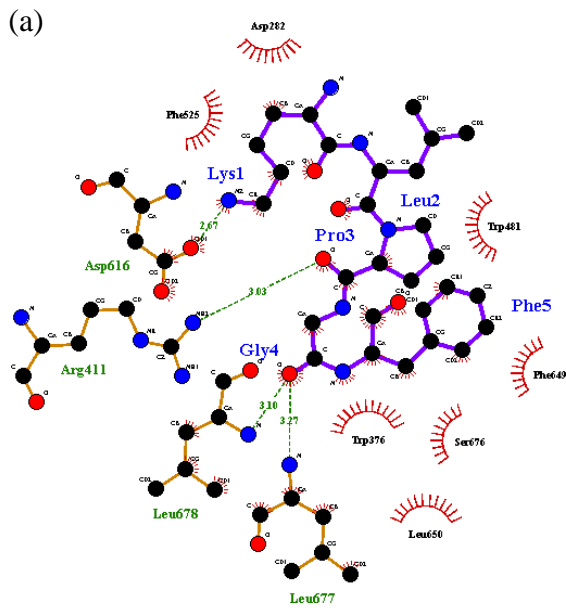
Appendix 4: QQQQQGGSQSQ



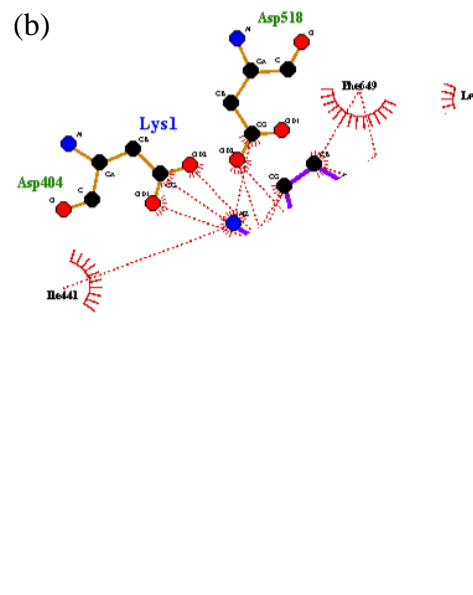
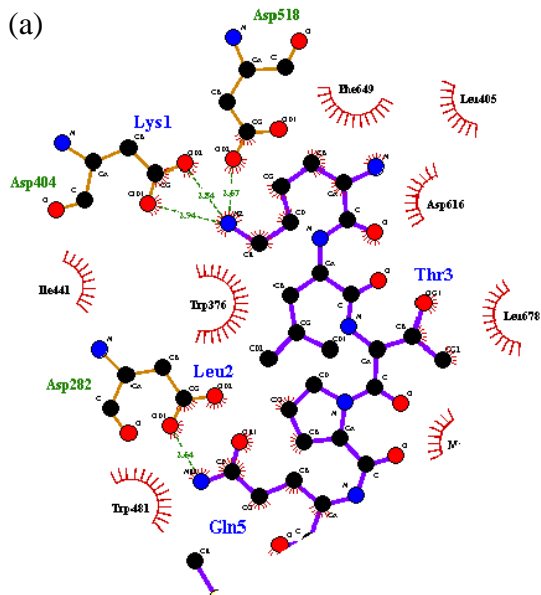
Appendix 7: SQSPA



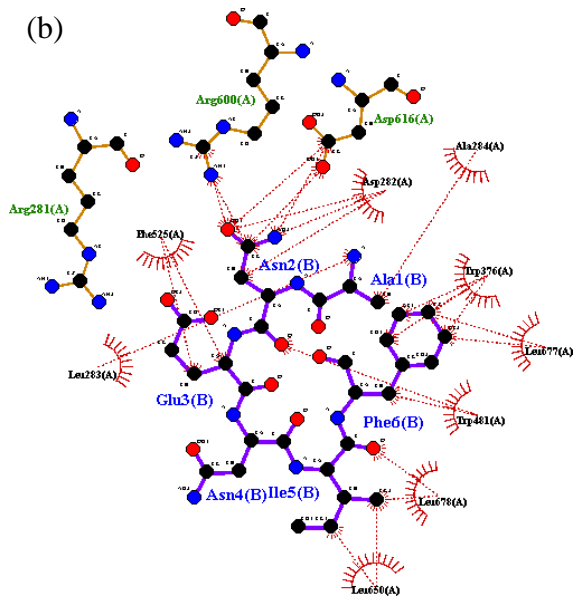
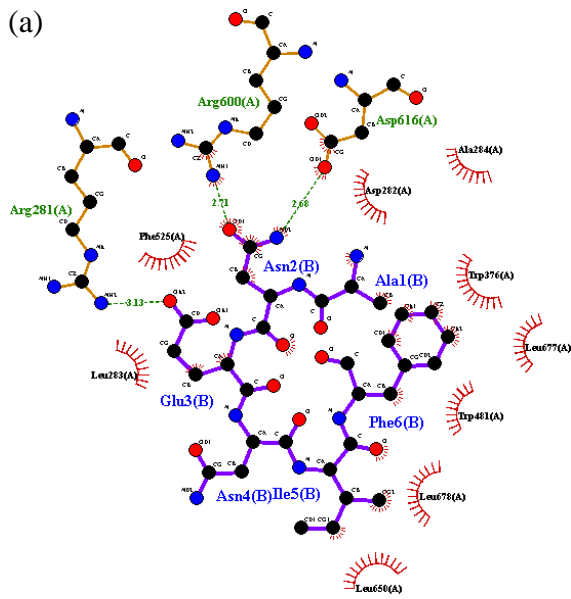
Appendix 8: SGPFPGPK



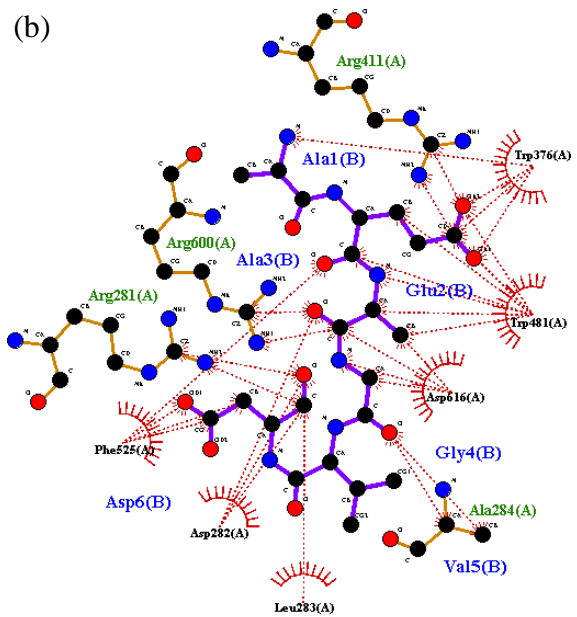
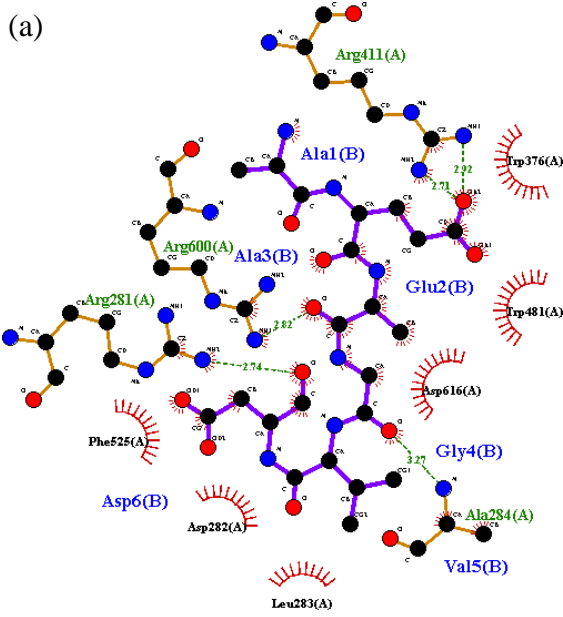
Appendix 9: KLPGF



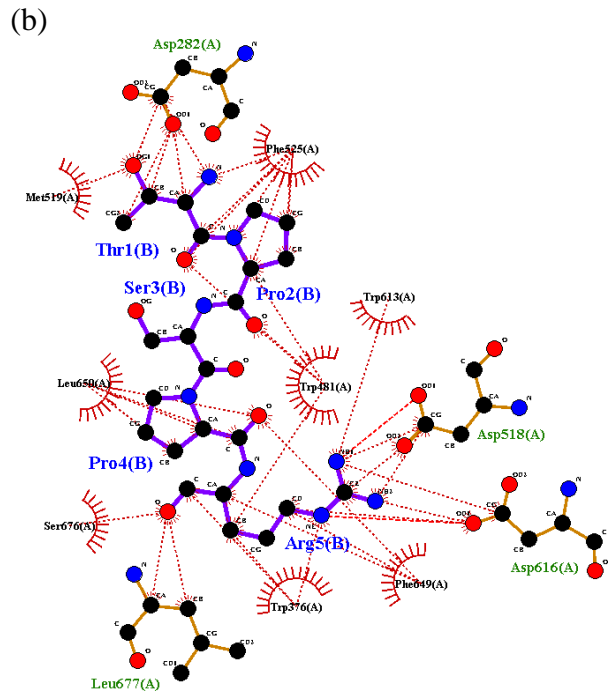
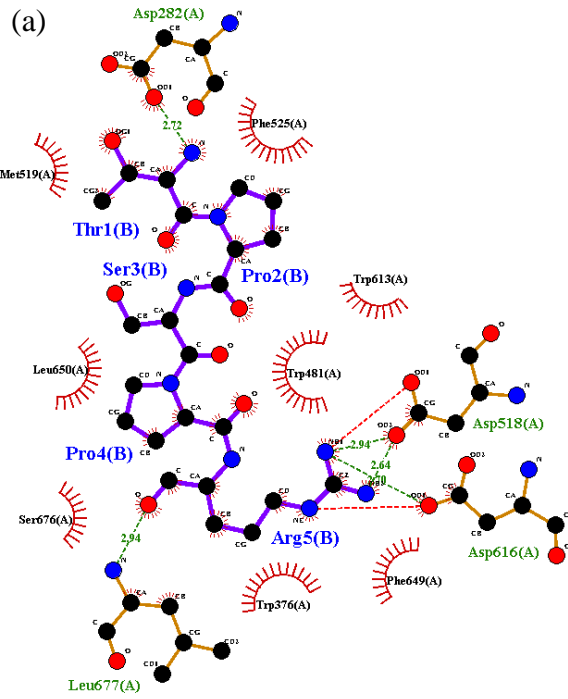
Appendix 10: KLTPQMA



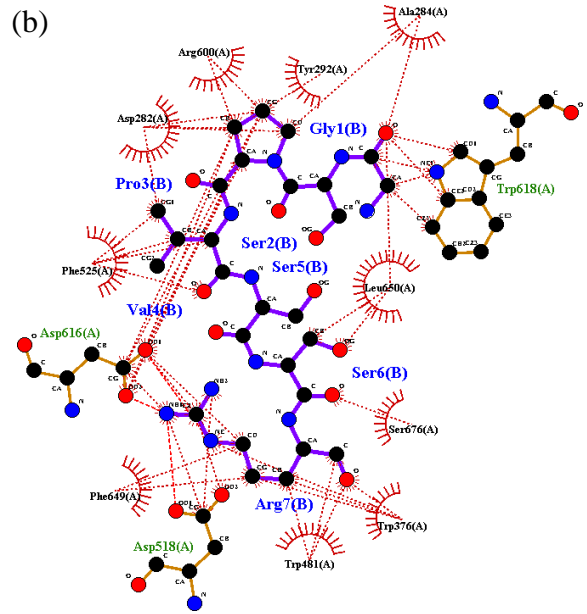
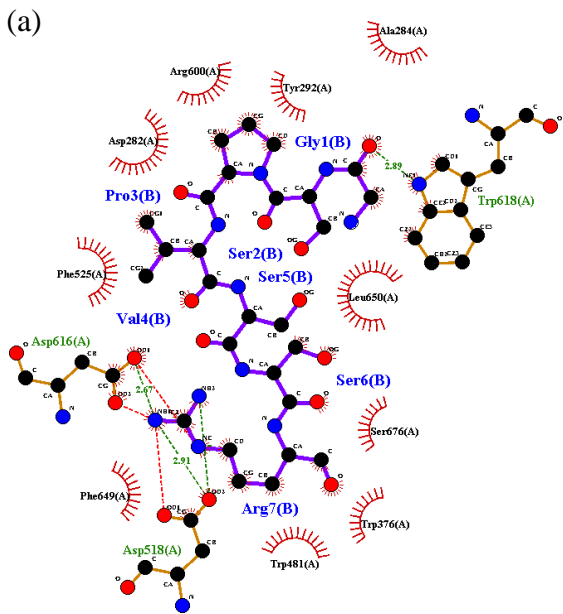
Appendix 11: ANENIF



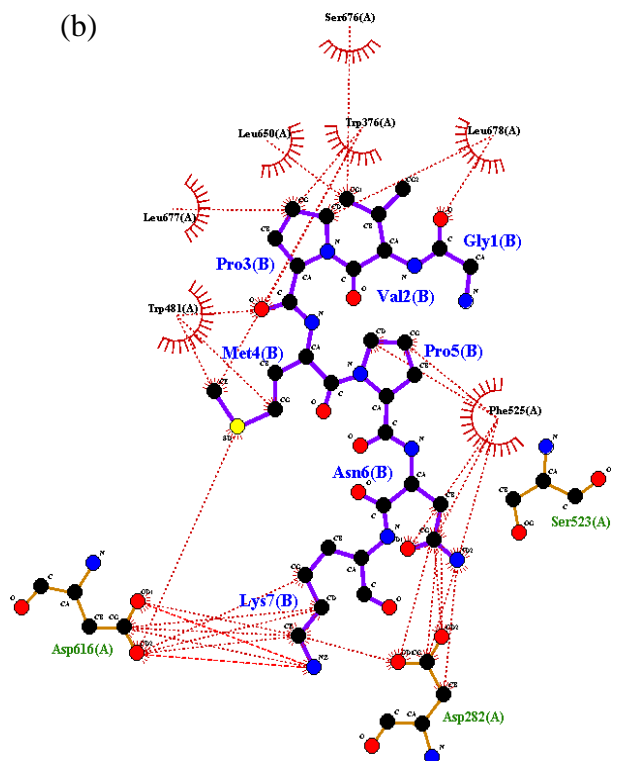
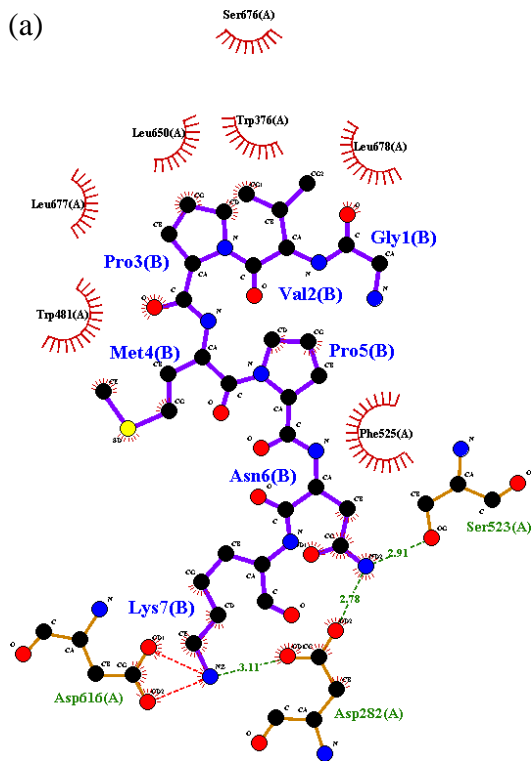
Appendix 12: AEAGVD



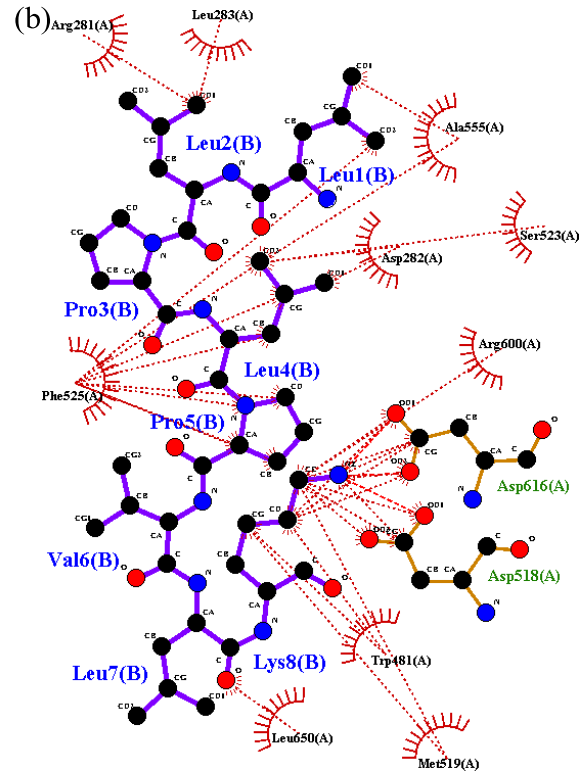
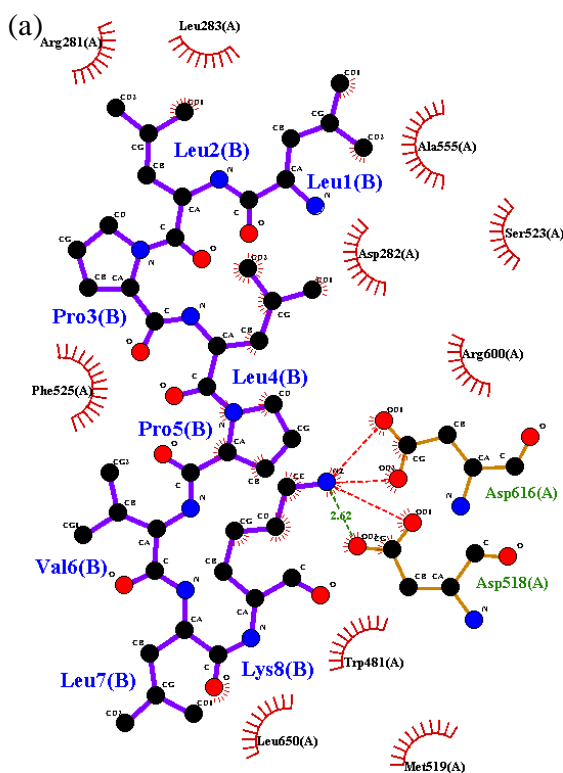
Appendix 13: TPSPR



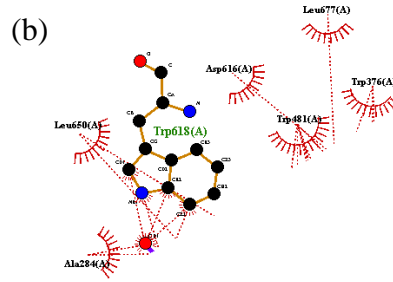
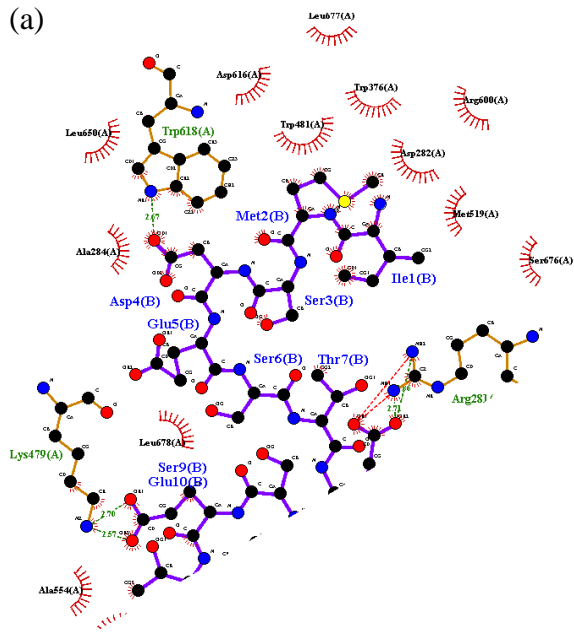
Appendix 14: GSPVSSR



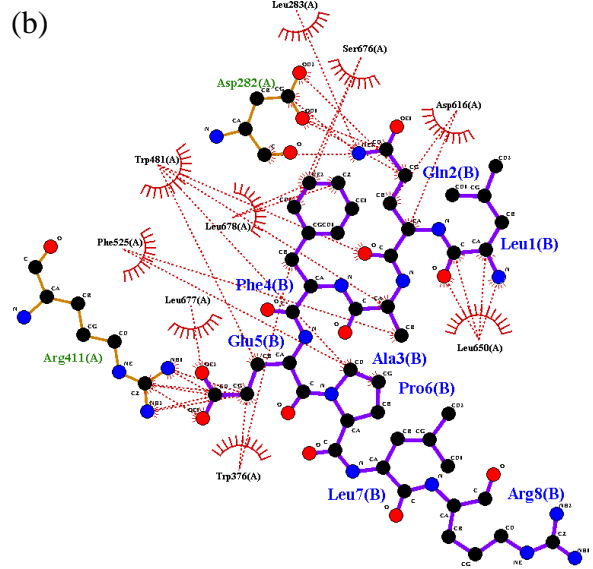
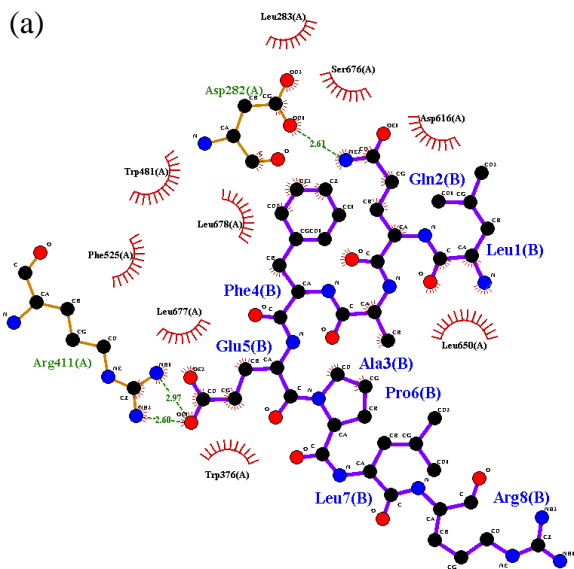
Appendix 15: GVPMPNK



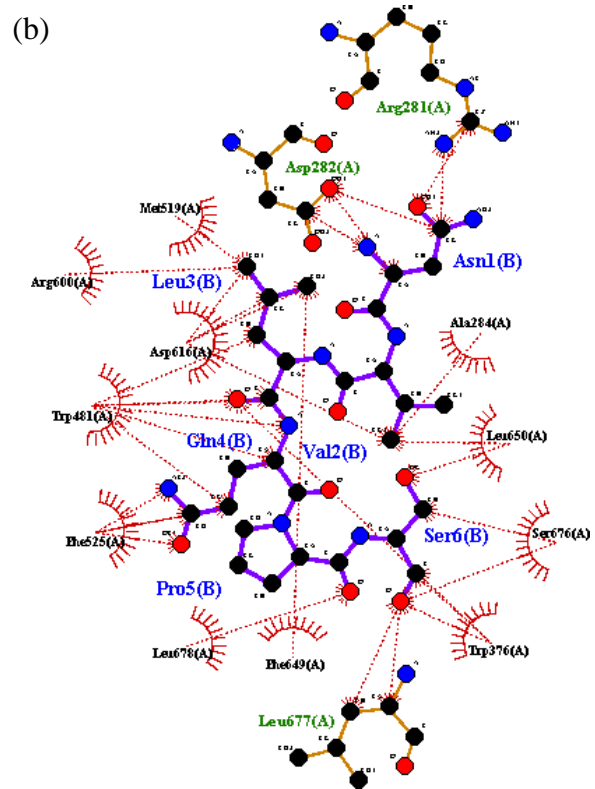
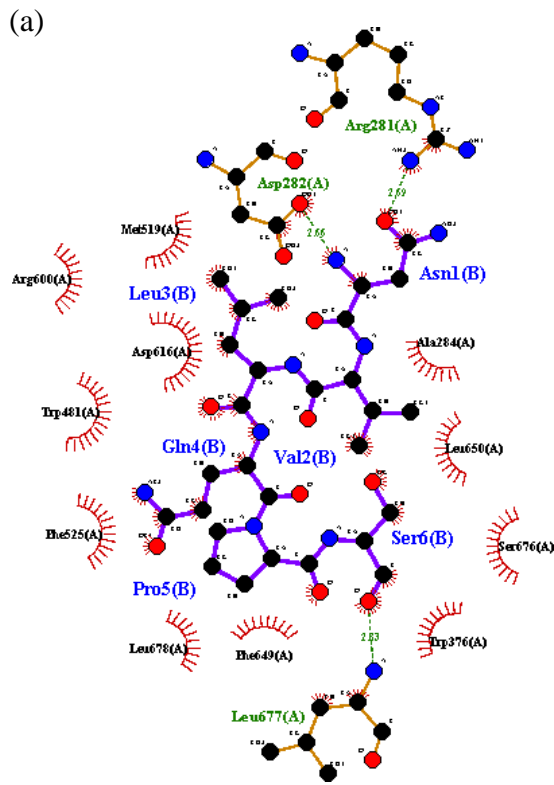
Appendix 16: LLPLPVLK



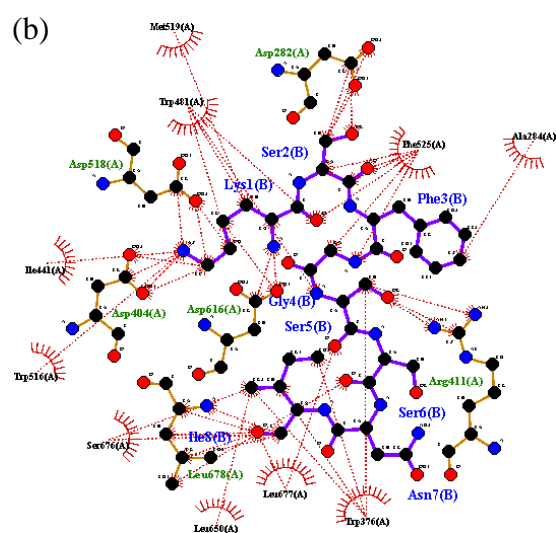
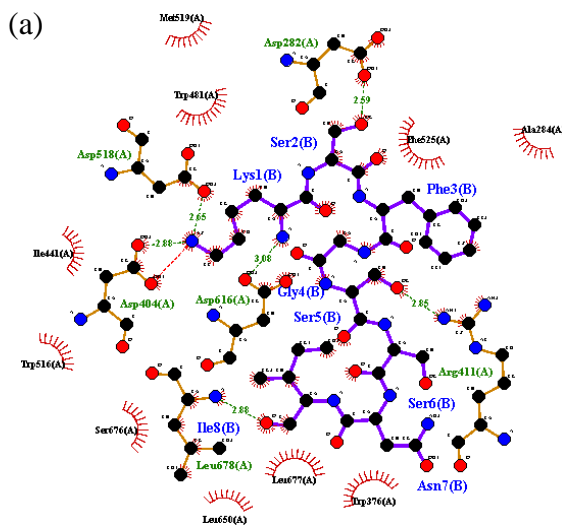
Appendix 17: IMSDESTESETEQA



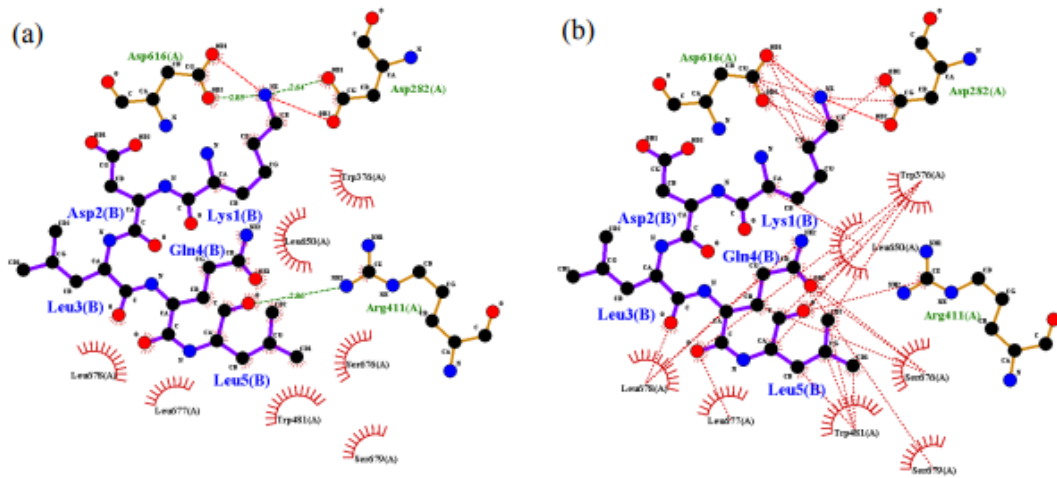
Appendix 18: LQAFEPLR



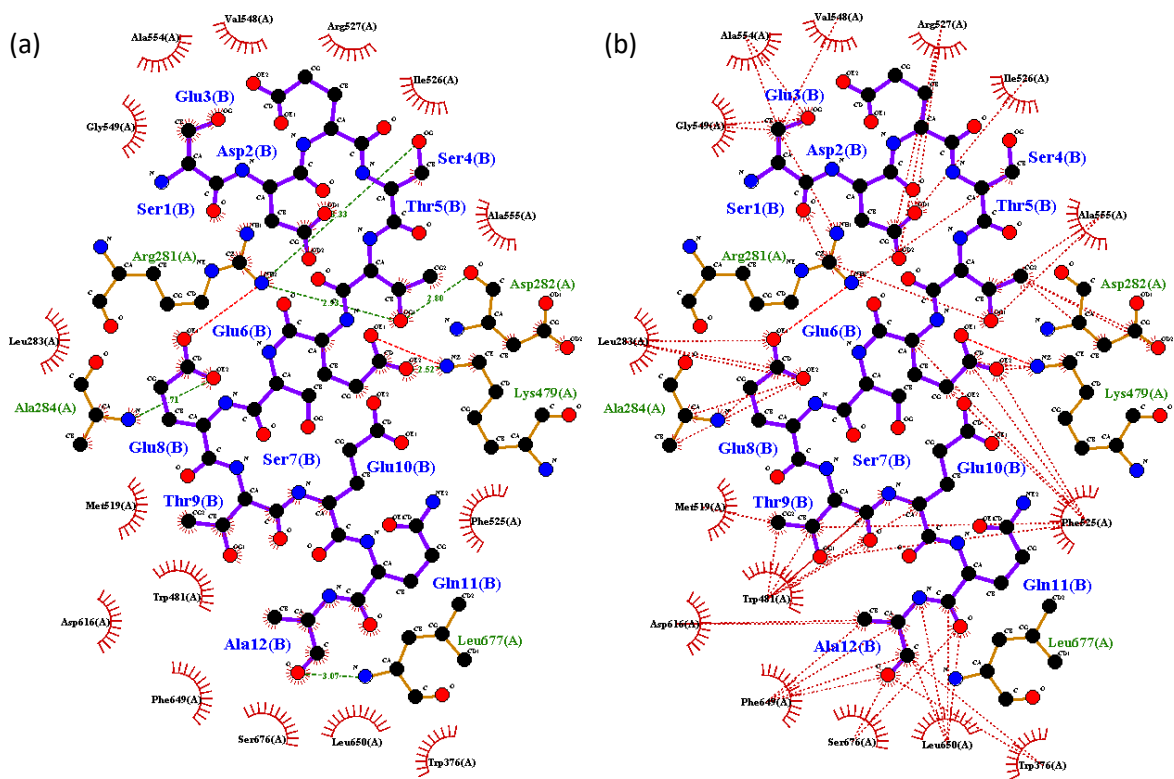
Appendix 19: NVLQPS



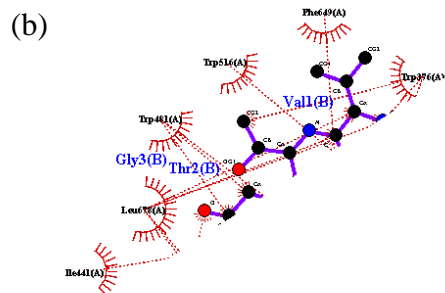
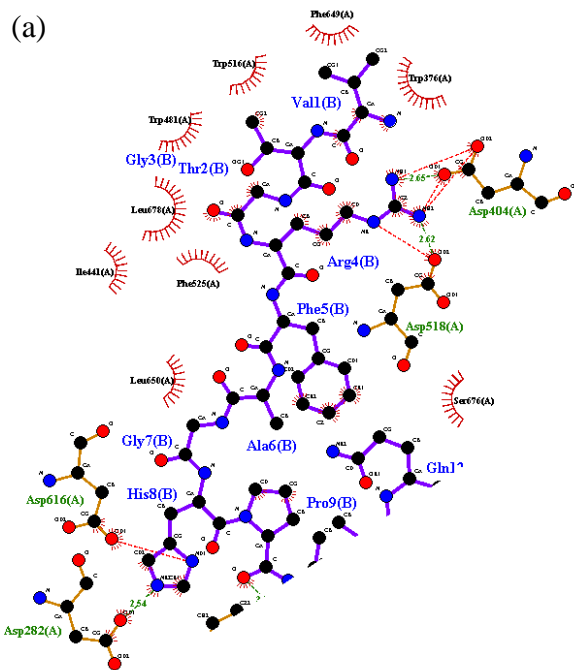
Appendix 20: KSGSSNI



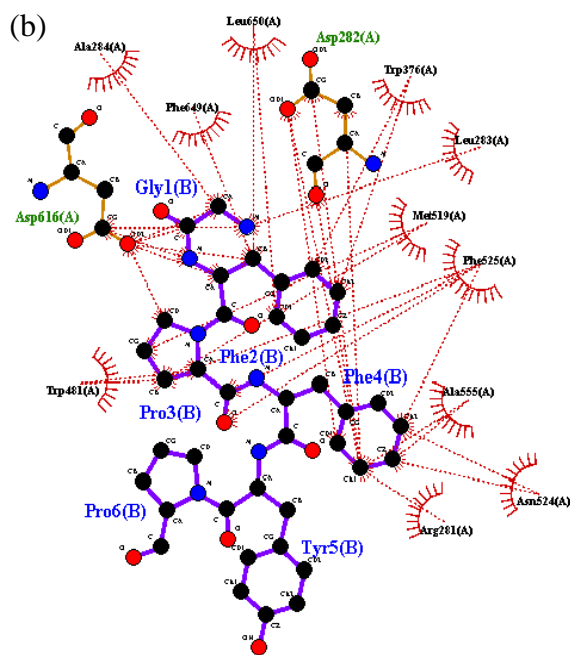
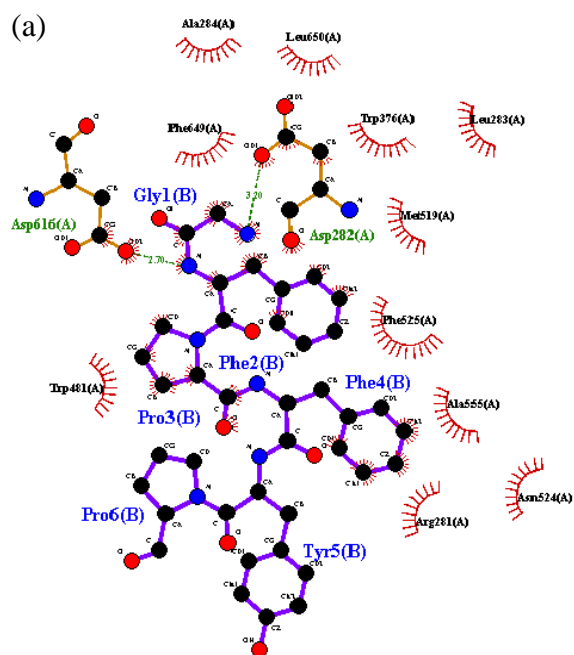
Appendix 25: KDLQL



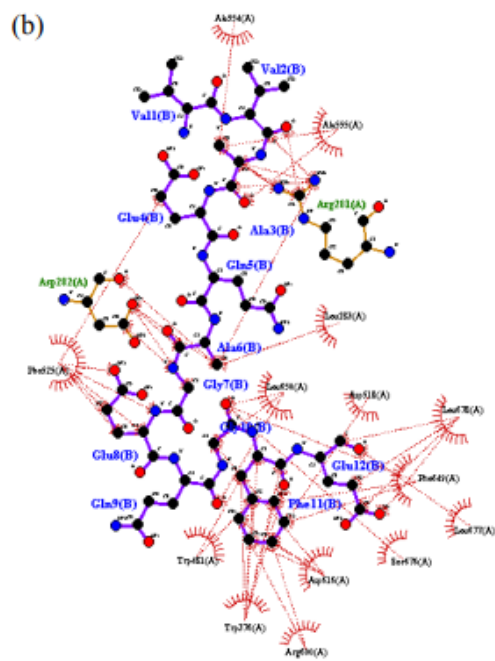
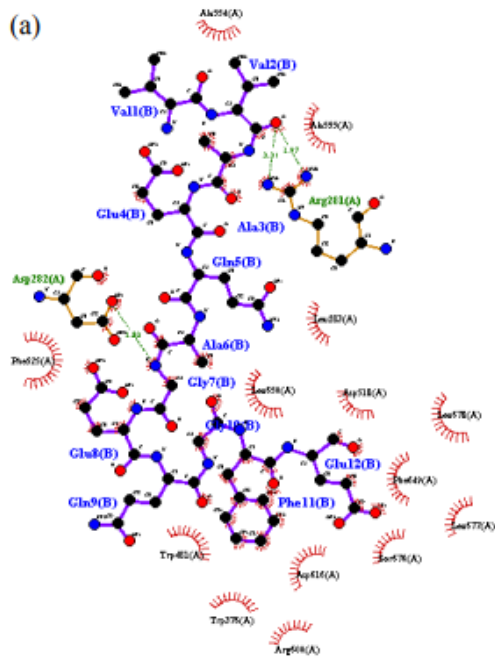
Appendix 26: SDESTESETEQA



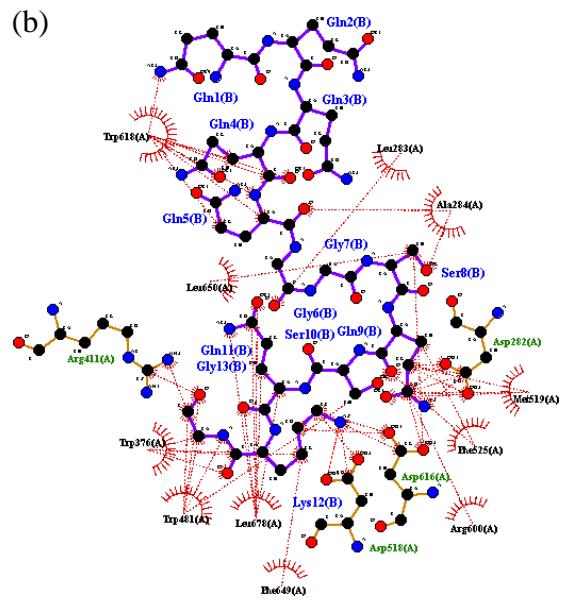
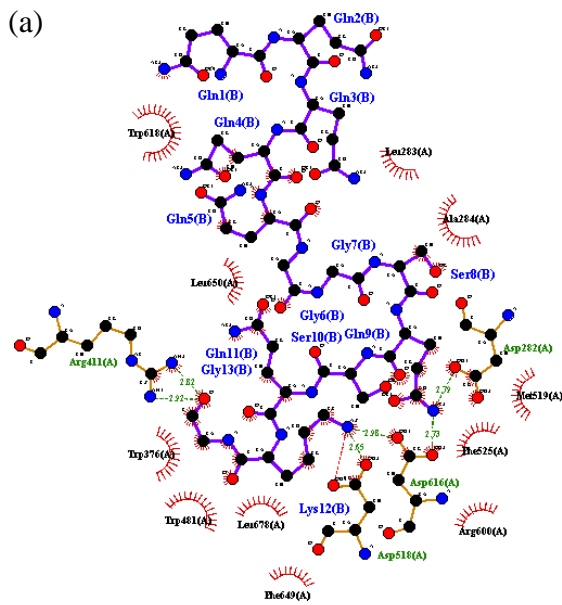
Appendix 27: VTGRFAGHPAAQ



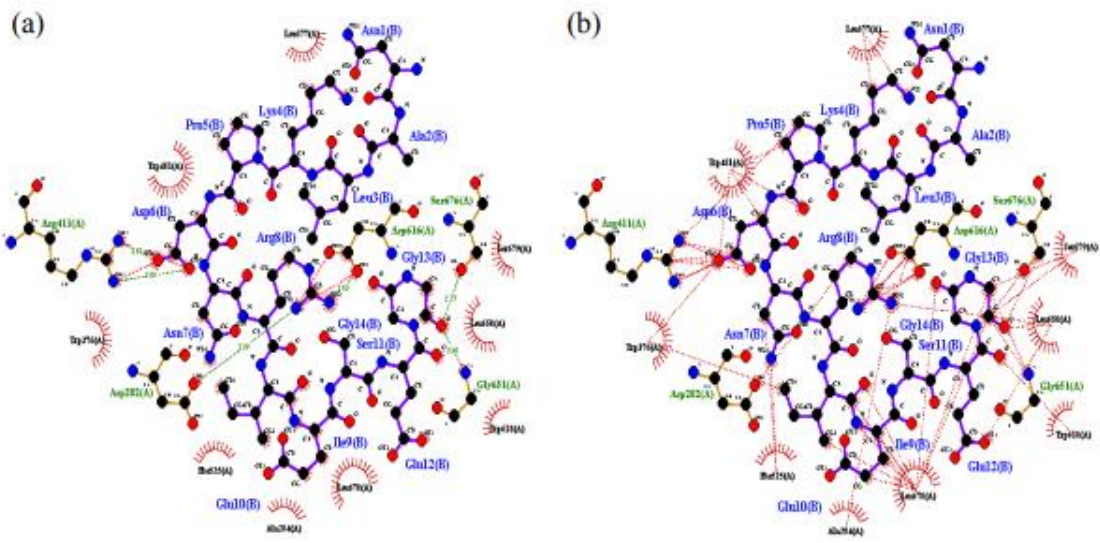
Appendix 28: GFPFYP



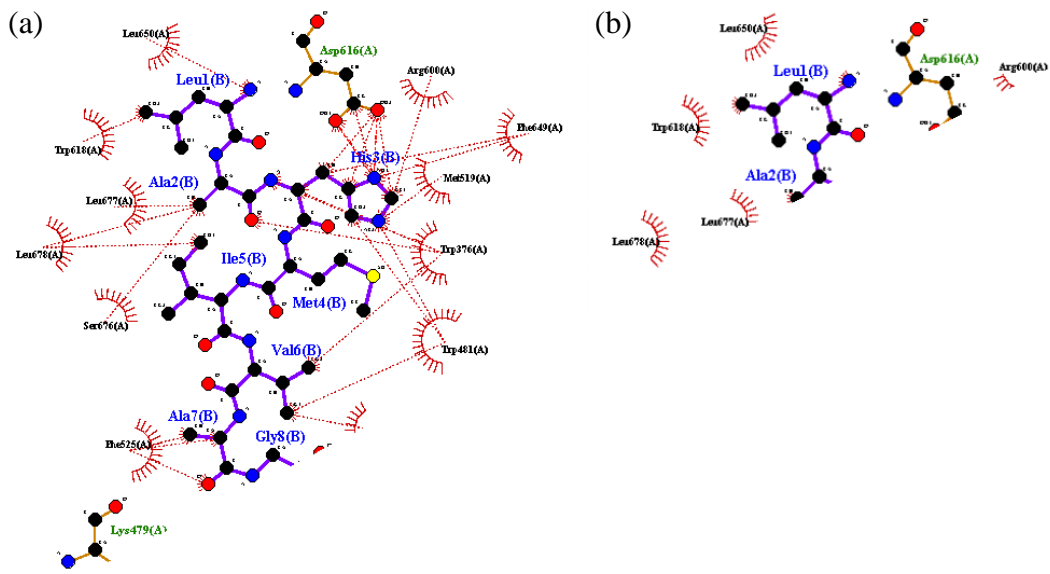
Appendix 29: VVAEQAGEQGFE



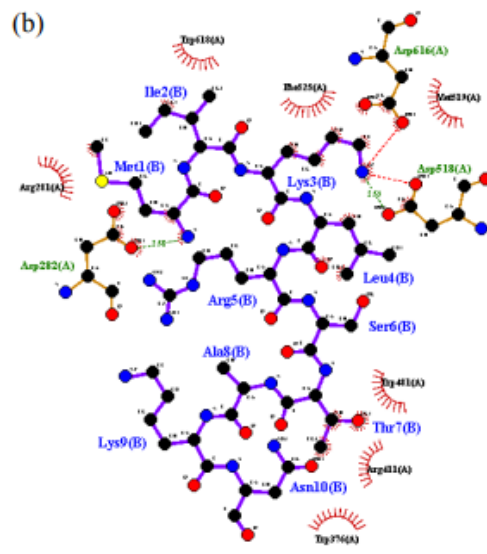
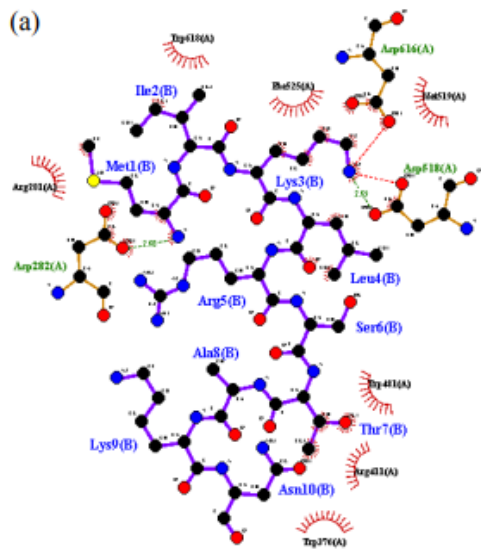
Appendix 30: QQQQQGGSQSQKG



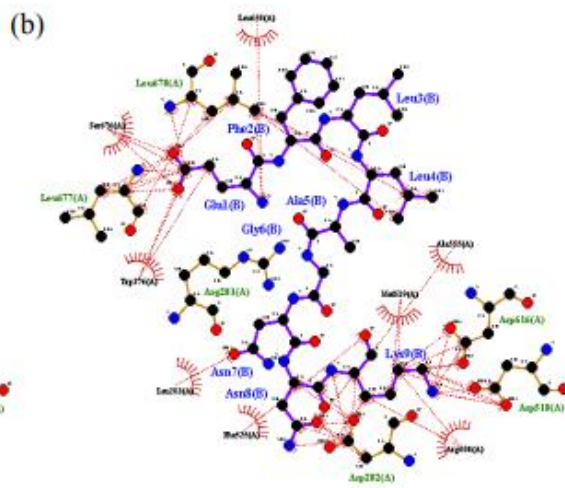
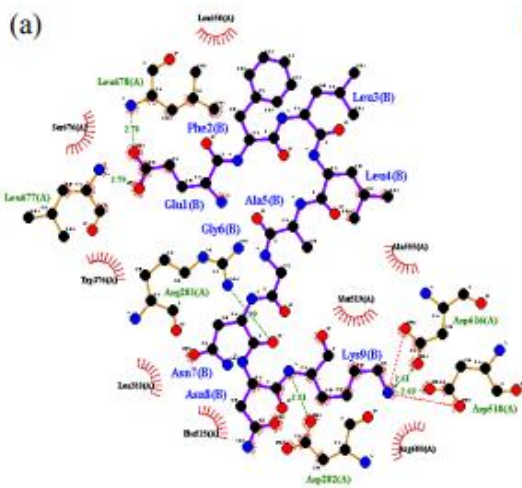
Appendix 31: NALKPDPNRIESEGG



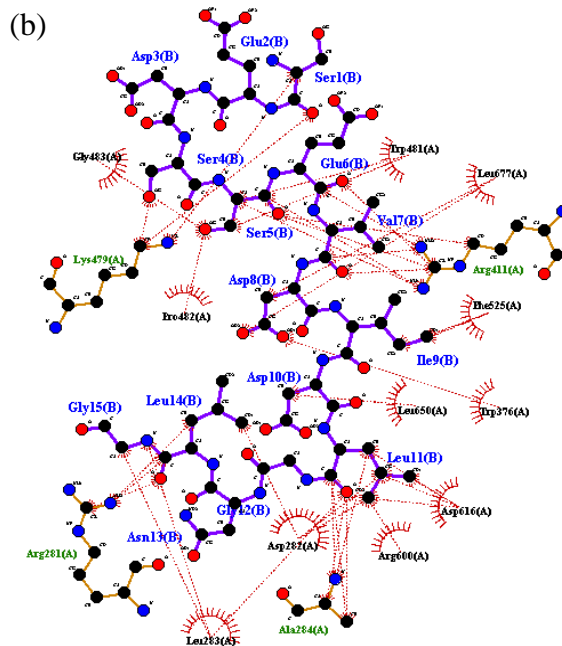
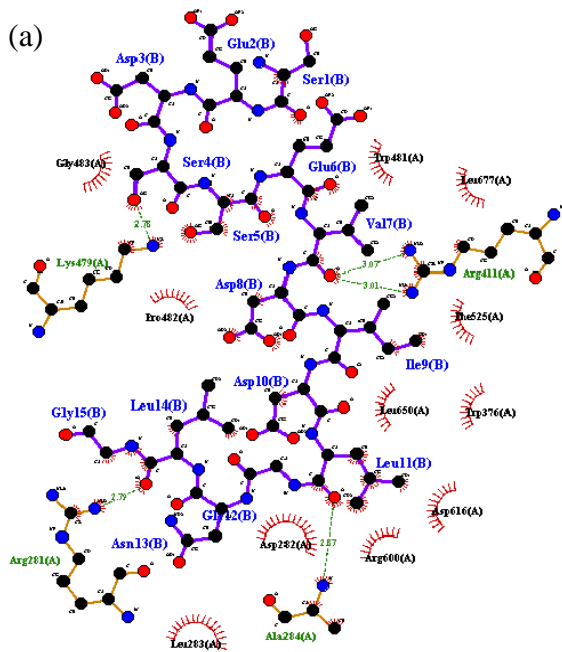
Appendix 32: LAHMIVAGA



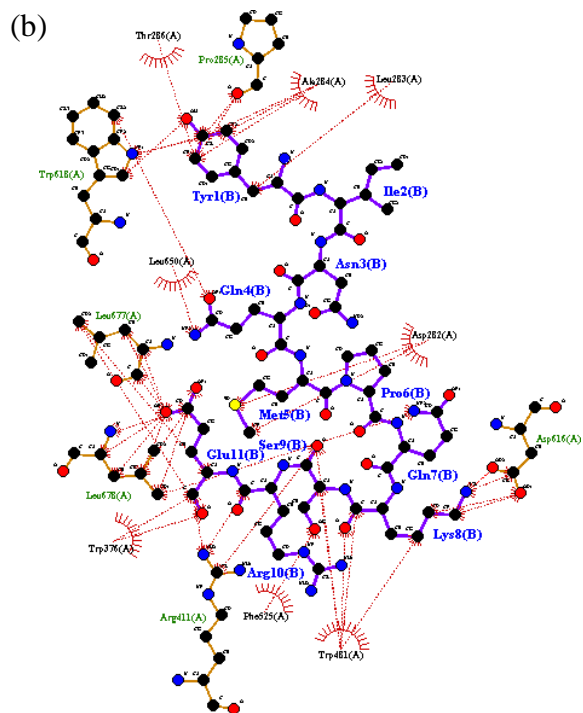
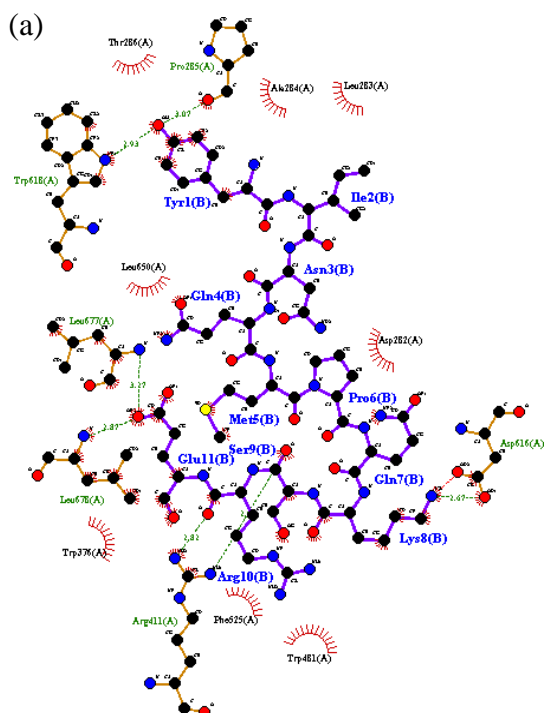
Appendix 33: MIKLRSTAKN



Appendix 34: EFLAGNNK



Appendix 35: SEDSSEVDIDLGNLG



Appendix 36: YINQMPQKSRE

