



## รายการอ้างอิง

### ภาษาไทย

- ณัฐรศ จันทขุม ยุง ใน ปาราสิตวิทยาทางการแพทย์ พิสัย กรัยวิเชียรและคณะ  
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ตารางผนวก ก. The Genetic Code

		Second Position							
		U		C		A		G	
U	UUU	<b>Phe</b>	UCU	<b>SER</b>	UAU	<b>Tyr</b>	UGU	<b>Cys</b>	U
	UUC		UCC		UAC		UGC		C
	UUA	<b>Leu</b>	UCA		UAA*	<b>Stop</b>	UGA*	<b>Stop</b>	A
	UUG		UCG		UAG*		UGG		<b>Trp</b>
C	CUU	<b>Leu</b>	CCU	<b>Pro</b>	CAU	<b>His</b>	CGU	<b>Arg</b>	U
	CUC		CCC		CAC		CGC		C
	CUA		CCA		CAA	CGA	A		
	CUG		CCG		CAG	CGG	G		
A	AUU	<b>Ile</b>	ACU	<b>Thr</b>	AAU	<b>Asn</b>	AGU	<b>Ser</b>	U
	AUC		ACC		AAC		AGC		C
	AUA		ACA		AAA	AGA	A		
	AUG <sup>+</sup>		ACG		AAG	AGG	<b>Arg</b>		G
G	GUU	<b>Val</b>	GCU	<b>Ala</b>	GAU	<b>Asp</b>	GGU	<b>Gly</b>	U
	GUC		GCC		GAC		GGC		C
	GUA		GCA		GAA	GGA	A		
	GUG <sup>+</sup>		GCG		GAG	GGG	G		

\* Chain-terminating, or "nonsense," codons.

+ Also used to specify the initiator formyl-Met-tRNA<sup>Met</sup>. The Val triplet GUG is therefore "ambiguous" in that it codes both valine and methionine

ภาคผนวก ข. Hydropathy scale and information used in the assignments (Kyte & Doolittle, 1982)

Side-chain	Hydropathy index	$G^{\circ}_{\text{transfer}}$ (water-vapor) <sup>a</sup>	Fraction of side-chains 100% buried <sup>b</sup>	Fraction of side-chains 95% buried <sup>c</sup>
Isoleucine	4.5	4.4	4.5	5.2
Valine	4.2	4.2	4.3	4.2
Leucine	3.8	4.5	3.2	2.8
Phenylalanine	2.8	2.5	2.5	3.5
Cysteine/cystine	2.5	1.9	6.0	3.2
Methionine	1.9	1.9	1.0	1.9
Alanine	1.8	3.9	5.3	1.6
Glycine	-0.4	-	4.2	1.3
Threonine	-0.7	-0.6	-0.5	-1.0
Tryptophan	-0.9	-0.9	-2.4	-0.3
Serine	-0.8	-0.8	-0.7	-1.0
Tyrosine	-1.3	-1.1	-3.3	-2.2
Proline	-1.6	-	-2.4	-1.8
Histidine	-3.2	-4.2	-3.6	-1.9
Glutamic acid	-3.5	-3.9	-2.8	-1.7
Glutamine	-3.5	-3.5	-4.0	-3.6
Aspartic acid	-3.5	-4.5	-2.5	-2.3
Asparagine	-3.5	-3.8	-3.1	-2.7
Lysine	-3.9	-3.2	-	-4.2
Arginine	-4.5	-	-	-

All values in the last 3 columns result from arbitrary normalization to spread them between -4.5 and +4.5. the normalization functions were:

<sup>a</sup>  $-0.679 (G^{\circ}_{\text{transfer}}; \text{Table 1}) + 2.32$ .

<sup>b</sup>  $48.1 (\text{fraction } 100\% \text{ buried; Chothia, 1976}) - 4.50$

<sup>c</sup>  $16.45 (\text{fraction } 95\% \text{ buried; Chothia, 1976}) - 4.71$

ภาคผนวก ค. Amino acid pair distance (Miyata et al., 1979)

CYS	PRO	ALA	GLY	SER	THR	GLN	GLU	ASN	ASP	HIS	LYS	ARG	VAL	LEU	ILE	MET	PHE	TYR	TRP	
	1.33	1.39	2.22	1.84	1.45	2.48	3.26	2.83	3.48	2.56	3.27	3.06	0.86	1.65	1.63	1.46	2.24	2.38	3.34	CYS
		0.06	0.97	0.56	0.87	1.92	2.48	1.80	2.40	2.15	2.94	2.90	1.79	2.70	2.62	2.36	3.17	3.12	4.17	PRO
			0.91	0.51	0.90	1.92	2.46	1.78	2.37	2.17	2.96	2.92	1.85	2.76	2.69	2.42	3.23	3.18	4.23	ALA
				0.85	1.70	2.48	2.78	1.96	2.37	2.78	3.54	3.58	2.76	3.67	3.60	3.34	4.14	4.08	5.13	GLY
					0.89	1.65	2.06	1.31	1.87	1.94	2.71	2.74	2.15	3.04	2.95	2.67	3.45	3.33	4.38	SER
						1.12	1.83	1.40	2.05	1.32	2.10	2.03	1.42	2.25	2.14	1.86	2.60	2.45	3.50	THR
							0.84	0.99	1.47	0.32	1.06	1.13	2.13	2.70	2.57	2.30	2.81	2.48	3.42	GLN
								0.85	0.90	0.96	1.14	1.45	2.97	3.53	3.39	3.13	3.59	3.22	4.08	GLU
									0.65	1.29	1.84	2.04	2.76	3.49	3.37	3.08	3.70	3.42	4.39	ASN
										1.72	2.05	2.34	3.40	4.10	3.98	3.69	4.27	3.95	4.88	ASP
											0.79	0.82	2.11	2.59	2.45	2.19	2.63	2.27	3.16	HIS
												0.40	2.70	2.98	2.84	2.63	2.85	2.42	3.11	LYS
													2.43	2.62	2.49	2.29	2.47	2.02	2.72	ARG
														0.91	0.85	0.62	1.43	1.52	2.51	VAL
															0.14	0.41	0.63	0.94	1.73	LEU
																0.29	0.61	0.86	1.72	ILE
																	0.82	0.93	1.89	MET
																		0.48	1.11	PHE
																			1.06	TYR
																				TRP

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ตารางที่ ๑. Codon usage per 100 codons of the *P.vivax* Pv200 gene of Sal-1 strain

	T*	R**	NR***	T	R	NR	T	R	NR	T	R	NR			
TTT	0.59	0.00	0.89	TCT	0.29	0.00	0.45	TAT	0.88	0.00	1.35	TGT	0.29	0.00	0.45
TTC	1.47	0.00	2.24	TCC	1.77	0.86	2.24	TAC	2.95	0.00	4.48	TGC	0.29	0.00	0.45
TTA	0.59	0.00	0.89	TCA	0.59	1.72	0.00	TAA	0.00	0.00	0.00	TGA	0.00	0.00	0.00
TTG	1.47	0.00	2.24	TCG	0.59	1.72	0.00	TAG	0.00	0.00	0.00	TGG	0.00	0.00	0.00
CTT	1.77	0.86	2.24	CCT	1.18	2.58	0.45	CAT	0.59	1.72	0.00	CGT	0.00	0.00	0.00
CTC	1.77	0.00	2.69	CCC	0.59	0.00	0.89	CAC	0.59	0.00	0.89	CGC	0.00	0.00	0.00
CTA	1.18	0.00	1.79	CCA	3.24	6.03	1.79	CAA	5.31	12.93	1.35	CGA	0.29	0.00	0.45
CTG	1.47	0.00	2.24	CCG	0.29	0.86	0.00	CAG	2.36	1.72	2.69	CGG	0.00	0.00	0.00
ATT	2.99	0.86	4.04	ACT	1.18	1.72	0.89	AAT	2.65	3.45	2.24	AGT	0.29	0.86	0.00
ATC	1.47	0.00	2.24	ACC	1.47	0.86	1.79	AAC	3.83	0.86	5.38	AGC	1.18	0.86	1.35
ATA	1.18	0.86	1.35	ACA	3.83	9.48	0.89	AAA	3.83	0.00	5.83	AGA	0.29	0.86	0.00
ATG	2.06	0.00	3.14	ACG	0.88	1.72	0.45	AAG	6.49	1.72	8.97	AGG	0.29	0.00	0.45
GTT	1.18	0.86	1.35	GCT	2.06	1.72	2.24	GAT	1.78	0.86	2.24	GGT	0.29	0.86	0.00
GTC	1.18	0.86	1.35	GCC	2.95	5.17	1.79	GAC	2.65	0.00	4.03	GGC	0.59	1.72	0.00
GTA	3.54	7.76	1.35	GCA	4.42	10.34	1.35	GAA	5.01	3.45	5.83	GGA	2.06	6.03	0.00
GTG	1.47	1.72	1.35	GCG	0.88	2.58	0.00	GAG	2.36	0.00	3.59	GGG	0.59	0.86	0.45

\* T = total codon; \*\* R = codon for repeats; \*\*\* NR = codon for nonrepeats.

Figure 9. Codon usage per 100 codons of the *P.vivax* Pv200 gene of allele 439B

	T*	R**	NR***	T	R	NR	T	R	NR	T	R	NR			
TTT	0.31	0.00	0.45	TCT	0.31	0.00	0.45	TAT	0.92	0.00	1.37	TGT	0.31	0.00	0.45
TTC	1.84	0.00	2.74	TCC	2.15	0.93	2.74	TAC	3.07	0.00	4.57	TGC	0.31	0.00	0.45
TTA	0.61	0.00	0.91	TCA	0.92	2.80	0.00	TAA	0.00	0.00	0.00	TGA	0.00	0.00	0.00
TTG	1.53	0.00	2.28	TCG	0.31	0.93	0.00	TAG	0.00	0.00	0.00	TGG	0.00	0.00	0.00
CTT	1.84	0.93	2.28	CCT	0.92	1.87	0.45	CAT	0.00	0.00	0.00	CGT	0.00	0.00	0.00
CTC	1.84	0.00	2.74	CCC	0.61	0.00	0.91	CAC	0.61	0.00	0.91	CGC	0.00	0.00	0.00
CTA	1.23	0.00	1.83	CCA	3.07	5.61	1.83	CAA	6.75	17.76	1.37	CGA	0.31	0.00	0.45
CTG	1.53	0.00	2.28	CCG	0.61	1.87	0.00	CAG	2.76	3.74	2.28	CGG	0.00	0.00	0.00
ATT	1.84	0.00	2.74	ACT	0.92	1.87	0.45	AAT	2.45	1.87	2.74	AGT	0.61	1.87	0.00
ATC	2.15	0.93	2.74	ACC	1.53	0.93	1.83	AAC	3.37	0.93	4.57	AGC	0.92	0.00	1.37
ATA	1.23	0.93	1.37	ACA	2.45	5.61	0.91	AAA	4.29	0.00	6.39	AGA	0.31	0.00	0.45
ATG	2.15	0.00	3.20	ACG	0.31	0.00	0.45	AAG	6.75	1.87	9.13	AGG	0.31	0.00	0.45
GTT	1.23	0.00	1.83	GCT	2.15	2.80	1.83	GAT	1.84	1.87	1.83	GGT	0.00	0.00	0.00
GTC	1.23	0.93	1.37	GCC	3.99	5.61	3.20	GAC	3.07	0.00	4.57	GGC	0.92	1.87	0.45
GTA	2.76	5.61	1.37	GCA	4.29	10.28	1.37	GAA	0.31	0.93	0.00	GGA	0.61	1.87	0.00
GTG	1.53	1.87	1.37	GCG	0.61	1.87	0.00	GAG	0.00	0.00	0.00	GGG	0.61	0.93	0.45

\* T = total codon; \*\* R = codon for repeats; \*\*\* NR = codon for nonrepeats.

ภาคผนวก จ. Codon usage per 100 codons of the *P.vivax* Pv200 gene of allele 414A

	T*	R**	NR***	T	R	NR	T	R	NR	T	R	NR			
TTT	0.60	0.00	0.90	TCT	0.30	0.00	0.45	TAT	0.90	0.00	1.34	TGT	0.30	0.00	0.45
TTC	1.50	0.00	2.24	TCC	1.80	0.91	2.24	TAC	3.00	0.00	4.48	TGC	0.30	0.00	0.45
TTA	0.60	0.00	0.90	TCA	0.90	2.73	0.00	TAA	0.00	0.00	0.00	TGA	0.00	0.00	0.00
TTG	1.50	0.00	2.24	TCG	0.30	0.91	0.00	TAG	0.00	0.00	0.00	TGG	0.00	0.00	0.00
CTT	1.80	0.91	2.24	CCT	1.20	2.73	0.45	CAT	0.90	2.73	0.00	CGT	0.00	0.00	0.00
CTC	1.80	0.00	2.69	CCC	0.60	0.00	0.90	CAC	0.60	0.00	0.90	CGC	0.00	0.00	0.00
CTA	1.20	0.00	1.79	CCA	1.80	1.82	1.79	CAA	5.10	12.73	1.34	CGA	0.30	0.00	0.45
CTG	1.50	0.00	2.24	CCG	0.30	0.91	0.00	CAG	2.40	1.82	2.69	CGG	0.00	0.00	0.00
ATT	2.70	0.00	4.03	ACT	1.20	1.82	0.90	AAT	2.70	3.64	2.24	AGT	0.60	1.82	0.00
ATC	1.50	0.00	2.24	ACC	1.80	1.82	1.79	AAC	3.60	0.00	5.38	AGC	0.90	0.00	1.34
ATA	1.20	0.91	1.34	ACA	4.20	10.91	0.90	AAA	3.90	0.00	5.83	AGA	0.30	0.91	0.00
ATG	2.10	0.00	3.14	ACG	0.90	1.82	0.45	AAG	6.60	1.82	8.99	AGG	0.30	0.00	0.45
GTT	1.20	0.91	1.34	GCT	2.10	1.82	2.24	GAT	1.80	0.91	2.24	GGT	0.30	0.91	0.00
GTC	1.20	0.91	1.34	GCC	2.10	2.73	1.79	GAC	2.70	0.00	4.03	GGC	0.90	2.73	0.00
GTA	3.60	9.09	0.90	GCA	4.80	11.82	1.34	GAA	4.80	2.73	5.83	GGA	2.10	6.36	0.00
GTG	1.80	1.82	1.79	GCG	0.90	2.73	0.00	GAG	2.40	0.00	3.57	GGG	0.60	0.91	0.45

\* T = total codon; \*\* R = codon for repeats; \*\*\* NR = codon for nonrepeats.

ตารางที่ ๗. Codon usage per 100 codons of the *P.vivax* Pv200 gene of allele 439A

	T*	R**	NR***	T	R	NR	T	R	NR	T	R	NR			
TTT	0.65	0.00	0.90	TCT	0.33	1.19	0.00	TAT	0.65	0.00	0.90	TGT	0.33	0.00	0.45
TTC	1.64	0.00	2.26	TCC	2.29	1.19	2.71	TAC	3.61	0.00	4.98	TGC	0.33	0.00	0.45
TTA	0.65	0.00	0.90	TCA	1.31	4.76	0.00	TAA	0.00	0.00	0.00	TGA	0.00	0.00	0.00
TTG	1.97	1.97	2.26	TCG	0.00	0.00	0.00	TAG	0.00	0.00	0.00	TGG	0.00	0.00	0.00
CTT	1.97	1.19	2.26	CCT	0.98	2.38	0.45	CAT	0.00	0.00	0.00	CGT	0.00	0.00	0.00
CTC	1.97	0.00	2.71	CCC	0.65	0.00	0.90	CAC	0.65	0.00	0.90	CGC	0.00	0.00	0.00
CTA	1.31	0.00	1.81	CCA	2.95	5.95	1.81	CAA	6.23	19.04	1.36	CGA	0.65	1.19	0.45
CTG	1.64	0.00	2.26	CCG	0.65	2.38	0.00	CAG	2.62	2.38	2.71	CGG	0.00	0.00	0.00
ATT	2.29	0.00	3.17	ACT	0.65	1.19	0.45	AAT	2.29	1.19	2.71	AGT	0.65	2.38	0.00
ATC	1.97	1.19	2.26	ACC	1.64	2.38	1.36	AAC	3.28	0.00	4.52	AGC	1.31	1.19	1.36
ATA	0.98	0.00	1.36	ACA	2.95	8.33	0.90	AAA	4.26	0.00	5.88	AGA	0.33	1.19	0.00
ATG	2.29	0.00	3.17	ACG	0.33	0.00	0.45	AAG	7.21	1.19	9.50	AGG	0.33	0.00	0.45
GTT	1.31	0.00	1.81	GCT	1.64	1.19	1.81	GAT	1.97	1.19	2.26	GGT	0.00	0.00	0.00
GTC	1.31	1.19	1.36	GCC	3.61	4.76	3.17	GAC	2.95	0.00	4.07	GGC	0.65	1.19	0.45
GTA	2.95	7.14	1.36	GCA	2.62	5.95	1.36	GAA	4.59	2.38	5.43	GGA	0.98	3.57	0.00
GTG	1.31	1.19	1.36	GCG	0.98	3.57	0.00	GAG	3.28	1.19	4.07	GGG	0.33	0.00	0.45

\* T = total codon; \*\* R = codon for repeats; \*\*\* NR = codon for nonrepeats.

ภาคผนวก ๓ Hydropathy index for each amino acid and average hydropathy values for a span setting of 9 amino acids of Pv200 blocks 4 to 6 among different alleles.

AMINO ACID RESIDUE NUMBER	HYDROPATHY index	HYDROPATHY index	HYDROPATHY index	HYDROPATHY index
1				
2				
3				
4				
5				
6				
7				
8				
9	(0.08)	(0.08)	(0.08)	(0.08)
10	(0.19)	(0.19)	(0.19)	(0.19)
11	(1.08)	(1.08)	(1.08)	(1.08)
12	(1.32)	(1.32)	(1.32)	(1.32)
13	(1.32)	(1.32)	(1.32)	(1.32)
14	(2.13)	(2.13)	(2.13)	(2.13)
15	(2.72)	(2.72)	(2.72)	(2.72)
16	(1.91)	(1.91)	(1.91)	(1.91)
17	(1.60)	(1.60)	(1.60)	(1.60)
18	(1.60)	(1.63)	(1.60)	(1.63)
19	(1.49)	(1.52)	(1.49)	(1.52)
20	(1.49)	(1.52)	(1.49)	(1.52)
21	(1.49)	(1.52)	(1.49)	(1.52)
22	(1.49)	(1.52)	(1.49)	(1.52)
23	(0.79)	(0.82)	(0.79)	(0.82)
24	(0.79)	(0.82)	(0.79)	(0.82)
25	(0.90)	(0.93)	(0.90)	(0.93)
26	(0.91)	(0.94)	(0.91)	(0.94)
27	(1.46)	(1.46)	(1.46)	(1.46)
28	(0.60)	(0.60)	(0.60)	(0.60)
29	0.26	0.26	0.26	0.26
30	0.26	0.26	0.26	0.26
31	1.07	1.07	1.07	1.07
32	0.37	0.37	0.37	0.37
33	1.22	1.22	1.22	1.22
34	0.52	0.52	0.52	0.52
35	0.22	0.22	0.22	0.22
36	0.73	0.73	0.73	0.73
37	0.69	0.69	0.69	0.69
38	0.72	0.72	0.72	0.72
39	1.61	1.61	1.61	1.61
40	0.80	0.80	0.80	0.80
41	0.80	0.80	0.80	0.80
42	0.83	0.83	0.83	0.83
43	0.83	0.83	0.83	0.83
44	1.42	1.42	1.42	1.42
45	1.38	1.38	1.38	1.38



AMINO ACID RESIDUE NUMBER	HYDROPATHY index	HYDROPATHY index	HYDROPATHY index	HYDROPATHY index
46	0.57	0.57	0.57	0.57
47	(0.32)	(0.32)	(0.32)	(0.32)
48	(0.36)	(0.36)	(0.36)	(0.36)
49	(0.36)	(0.36)	(0.36)	(0.36)
50	(0.36)	(0.36)	(0.36)	(0.36)
51	(0.43)	(0.43)	(0.43)	(0.43)
52	0.38	0.38	0.38	0.38
53	(0.21)	(0.21)	(0.21)	(0.21)
54	(1.02)	(1.02)	(1.02)	(1.02)
55	(0.43)	(0.43)	(0.43)	(0.43)
56	(0.43)	(0.43)	(0.43)	(0.43)
57	(0.43)	(0.43)	(0.43)	(0.43)
58	(0.43)	(0.43)	(0.43)	(0.43)
59	(0.43)	(0.43)	(0.43)	(0.43)
60	(1.24)	(1.24)	(1.24)	(1.24)
61	(1.24)	(1.24)	(1.24)	(1.24)
62	(1.00)	(1.00)	(1.00)	(1.00)
63	(0.11)	(0.14)	(0.11)	(0.14)
64	(0.49)	(0.52)	(0.49)	(0.52)
65	(0.49)	(0.52)	(0.49)	(0.52)
66	(0.49)	(0.52)	(0.49)	(0.52)
67	(0.24)	(0.28)	(0.24)	(0.28)
68	0.53	0.50	0.53	0.50
69	0.84	0.81	0.84	0.81
70	0.33	0.34	0.33	0.34
71	0.09	0.10	0.09	0.10
72	(0.80)	(0.76)	(0.80)	(0.76)
73	(0.80)	(0.76)	(0.80)	(0.76)
74	(0.80)	(0.76)	(0.80)	(0.76)
75	(1.44)	(1.40)	(1.44)	(1.40)
76	(1.44)	(1.40)	(1.44)	(1.40)
77	(1.98)	(1.93)	(1.98)	(1.93)
78	(1.48)	(1.43)	(1.48)	(1.43)
79	(1.18)	(1.18)	(1.18)	(1.18)
80	(0.66)	(0.66)	(0.66)	(0.66)
81	0.16	0.16	0.16	0.16
82	(0.06)	(0.06)	(0.06)	(0.06)
83	(0.17)	(0.17)	(0.17)	(0.17)
84	(0.38)	(0.38)	(0.38)	(0.38)
85	0.27	0.27	0.27	0.27
86	0.02	0.02	0.02	0.02
87	(0.79)	(0.79)	(0.79)	(0.79)
88	(0.58)	(0.58)	(0.58)	(0.58)
89	(1.10)	(1.10)	(1.10)	(1.10)
90	(1.91)	(1.91)	(1.91)	(1.91)

AMINO ACID RESIDUE NUMBER	HYDROPATHY index	HYDROPATHY index	HYDROPATHY index	HYDROPATHY index
91	(1.21)	(1.21)	(1.21)	(1.21)
92	(0.21)	(0.21)	(0.21)	(0.21)
93	(0.00)	(0.00)	(0.00)	(0.00)
94	(0.89)	(0.89)	(0.89)	(0.89)
95	(0.00)	(0.00)	(0.00)	(0.00)
96	(0.00)	(0.00)	(0.00)	(0.00)
97	(0.33)	(0.33)	(0.33)	(0.33)
98	0.27	0.27	0.27	0.27
99	1.16	1.16	1.16	1.16
100	1.04	1.04	1.04	1.04
101	0.47	0.47	0.47	0.47
102	0.26	0.26	0.26	0.26
103	0.26	0.26	0.26	0.26
104	(0.63)	(0.63)	(0.32)	(0.04)
105	(0.63)	(0.63)	(0.32)	(0.04)
106	(0.90)	(0.90)	(0.59)	(0.31)
107	(1.19)	(1.19)	(0.88)	(0.60)
108	(1.22)	(1.22)	(0.91)	(0.90)
109	(1.22)	(1.22)	(0.91)	(1.28)
110	(0.94)	(0.94)	(0.63)	(0.73)
111	(0.36)	(0.36)	(0.04)	(0.42)
112	(0.36)	(0.36)	(0.04)	(0.12)
113	0.53	0.53	0.53	(0.37)
114	1.39	1.39	1.39	(0.37)
115	1.77	1.77	1.77	0.23
116	1.46	1.46	1.46	0.73
117	0.94	0.94	0.94	0.03
118	0.36	0.36	0.36	0.17
119	0.07	0.07	0.07	(0.39)
120	0.29	0.29	0.29	(0.40)
121	0.18	0.18	0.18	(0.70)
122	(0.37)	(0.37)	(0.37)	(1.16)
123	(0.63)	(0.63)	(0.63)	(0.57)
124	(0.92)	(0.92)	(0.92)	(1.07)
125	(0.92)	(0.92)	(0.92)	(1.88)
126	(0.96)	(0.96)	(0.96)	(0.91)
127	(0.61)	(0.61)	(0.61)	(0.94)
128	(0.60)	(0.60)	(0.60)	(0.93)
129	(1.10)	(1.10)	(1.10)	(1.23)
130	(0.64)	(0.64)	(0.64)	(0.64)
131	(0.99)	(0.99)	(0.99)	0.32
132	(1.27)	(1.27)	(1.27)	0.04
133	(0.71)	(0.71)	(0.71)	0.03
134	(0.71)	(0.71)	(0.71)	0.03
135	(0.43)	(0.43)	(0.43)	0.03

AMINO ACID RESIDUE NUMBER	HYDROPATHY index	HYDROPATHY index	HYDROPATHY index	HYDROPATHY index
136	(0.78)	(0.78)	(0.78)	(0.28)
137	(0.78)	(0.78)	(0.78)	(0.59)
138	(0.50)	(0.50)	(0.50)	(0.59)
139	0.01	0.01	0.01	(1.18)
140	0.87	0.87	0.87	(2.03)
141	0.56	0.56	0.56	(2.34)
142	(0.09)	(0.30)	(0.27)	(2.64)
143	(0.09)	(0.30)	(0.27)	(2.64)
144	(0.64)	(0.89)	(0.82)	(3.50)
145	(0.64)	(0.89)	(0.82)	(3.50)
146	(0.10)	(1.20)	(0.28)	(3.50)
147	0.17	(1.79)	(0.01)	(3.50)
148	(0.69)	(2.64)	(0.28)	(3.20)
149	(0.96)	(3.50)	(0.54)	(3.20)
150	(0.10)	(3.50)	0.31	(2.34)
151	0.00	(3.50)	0.59	(1.49)
152	0.86	(3.50)	1.44	(1.28)
153	0.82	(3.50)	1.41	(0.69)
154	1.03	(3.50)	1.62	(0.48)
155	0.52	(3.50)	1.11	0.11
156	(0.02)	(3.50)	0.57	0.46
157	0.29	(3.50)	0.29	0.16
158	0.04	(3.50)	0.04	0.74
159	(0.78)	(3.50)	(0.78)	(0.11)
160	(1.09)	(3.50)	(1.09)	(0.97)
161	(1.36)	(3.50)	(1.36)	(0.32)
162	(1.36)	(3.20)	(1.36)	(0.02)
163	(1.22)	(3.20)	(1.22)	0.07
164	(1.22)	(2.34)	(1.22)	(0.21)
165	(1.53)	(1.49)	(1.53)	(0.56)
166	(1.26)	(1.28)	(1.26)	(0.34)
167	(1.60)	(0.69)	(1.60)	(0.62)
168	(1.32)	(0.48)	(1.32)	(0.32)
169	(1.32)	0.11	(1.32)	(0.32)
170	(1.60)	0.46	(1.60)	(0.88)
171	(1.60)	0.16	(1.60)	(1.18)
172	(1.64)	0.74	(1.64)	(0.89)
173	(1.13)	(0.11)	(1.13)	(0.99)
174	(1.13)	(0.97)	(1.13)	(0.64)
175	(1.13)	(0.32)	(1.13)	0.00
176	(0.54)	(0.02)	(0.54)	(0.01)
177	(0.86)	0.07	(0.86)	0.28
178	0.00	(0.21)	0.00	0.59
179	(0.31)	(0.56)	(0.31)	0.50
180	(0.31)	(0.34)	(0.31)	0.50



AMINO ACID RESIDUE NUMBER	HYDROPATHY index	HYDROPATHY index	HYDROPATHY index	HYDROPATHY index
181	(0.30)	(0.63)	(0.30)	0.12
182	(0.94)	(0.63)	(0.94)	0.22
183	(0.36)	(0.33)	(0.36)	0.09
184	(0.60)	(0.60)	(0.60)	(0.18)
185	(0.60)	(0.90)	(0.60)	0.11
186	(0.26)	(0.99)	(0.26)	0.11
187	(0.77)	(0.96)	(0.77)	0.39
188	(0.77)	(0.10)	(0.77)	0.77
189	0.09	(0.01)	0.09	0.39
190	0.37	0.28	0.37	0.77
191	0.46	0.59	0.46	0.67
192	0.18	0.50	0.18	1.04
193	0.61	0.22	0.61	1.06
194	0.33	(0.16)	0.33	0.77
195	0.88	0.22	0.30	0.18
196	0.83	0.47	0.26	0.40
197	0.83	0.20	0.26	(0.19)
198	0.57	0.49	(0.30)	(0.16)
199	0.19	0.49	(0.30)	0.07
200	0.48	0.39	(0.01)	(0.14)
201	0.38	0.77	(0.11)	(0.73)
202	(0.09)	0.67	(0.54)	(0.52)
203	(0.40)	0.77	0.00	(0.01)
204	(0.70)	0.39	(0.01)	(0.01)
205	(0.70)	0.39	0.28	(0.12)
206	(0.49)	0.39	0.59	0.69
207	(1.08)	0.39	0.50	0.44
208	(1.08)	0.39	0.50	(0.07)
209	(1.08)	0.77	0.12	0.52
210	(1.08)	0.39	0.22	0.77
211	(0.80)	0.77	0.09	0.54
212	(0.21)	0.67	(0.18)	0.40
213	(0.59)	1.04	0.11	0.43
214	(0.68)	1.06	0.11	(0.27)
215	(0.59)	0.77	0.66	(1.04)
216	(0.28)	0.18	1.03	(0.16)
217	(0.28)	0.40	0.66	0.24
218	(0.28)	(0.19)	1.03	0.51
219	0.10	(0.16)	0.93	0.58
220	0.10	0.07	1.03	(0.01)
221	0.37	(0.14)	1.04	(0.38)
222	0.74	(0.73)	0.76	(0.10)
223	0.74	(0.52)	0.17	0.50
224	1.03	(0.01)	0.12	0.47
225	0.93	(0.01)	(0.47)	(0.42)

AMINO ACID RESIDUE NUMBER	HYDROPATHY index	HYDROPATHY index	HYDROPATHY index	HYDROPATHY index
226	1.03	(0.12)	(0.43)	(1.12)
227	1.04	0.69	(0.21)	(1.17)
228	0.76	0.44	(0.42)	(0.67)
229	0.17	(0.07)	(0.73)	(0.67)
230	0.12	0.52	(0.52)	(0.97)
231	(0.47)	0.77	(0.01)	(1.03)
232	(0.43)	0.54	(0.01)	(1.63)
233	(0.21)	0.40	(0.12)	(0.82)
234	(0.42)	0.43	0.69	(0.82)
235	(0.73)	(0.27)	0.44	(0.23)
236	(0.52)	(1.04)	(0.07)	(1.04)
237	(0.01)	(0.16)	0.52	(1.86)
238	(0.01)	0.24	0.77	(1.86)
239	(0.12)	0.51	0.54	(1.86)
240	0.69	0.58	0.40	(2.10)
241	0.44	(0.01)	0.43	(1.21)
242	(0.07)	(0.38)	(0.27)	(2.02)
243	0.52	(0.10)	(1.04)	(2.02)
244	0.77	0.50	(0.16)	(2.61)
245	0.54	0.47	0.24	(2.61)
246	0.40	(0.42)	0.51	(1.94)
247	0.43	(1.12)	0.58	(1.94)
248	(0.27)	(1.17)	(0.01)	(1.94)
249	(1.04)	(0.67)	(0.38)	(1.13)
250	(0.16)	(0.67)	(0.10)	(2.02)
251	0.24	(0.97)	0.50	(1.21)
252	0.51	(1.03)	0.47	(0.40)
253	0.58	(1.63)	(0.42)	0.30
254	(0.01)	(0.82)	(1.12)	0.30
255	(0.38)	(0.82)	(1.17)	0.49
256	(0.10)	(0.23)	(0.67)	0.49
257	0.50	(1.04)	(0.67)	0.49
258	0.47	(1.86)	(0.97)	(0.32)
259	(0.42)	(1.86)	(1.03)	0.49
260	(1.12)	(1.86)	(1.63)	(0.11)
261	(1.17)	(2.10)	(0.82)	(0.33)
262	(0.67)	(1.21)	(0.82)	(0.43)
263	(0.67)	(2.02)	(0.23)	(0.19)
264	(0.97)	(2.02)	(1.04)	(0.74)
265	(1.03)	(2.61)	(1.86)	0.14
266	(1.63)	(2.61)	(1.86)	0.39
267	(0.82)	(1.94)	(1.86)	0.39
268	(0.82)	(1.94)	(2.10)	(0.12)
269	(0.23)	(1.94)	(1.21)	0.27
270	(1.04)	(1.13)	(2.02)	(0.02)

AMINO ACID RESIDUE NUMBER	HYDROPATHY index	HYDROPATHY index	HYDROPATHY index	HYDROPATHY index
271	(1.86)	(2.02)	(2.02)	(0.32)
272	(1.86)	(1.21)	(2.30)	(0.57)
273	(1.86)	(0.40)	(2.30)	(0.06)
274	(2.10)	0.30	(1.63)	(0.94)
275	(1.21)	0.30	(1.63)	(1.19)
276	(2.02)	0.49	(1.63)	(0.38)
277	(2.02)	0.49	(0.82)	(0.43)
278	(2.30)	0.49	(1.71)	(0.14)
279	(2.30)	(0.32)	(0.90)	(0.44)
280	(1.63)	0.49	(0.09)	0.07
281	(1.63)	(0.11)	0.30	0.31
282	(1.63)	(0.33)	0.30	(0.50)
283	(0.82)	(0.43)	0.49	(0.50)
284	(1.71)	(0.19)	0.49	(0.50)
285	(0.90)	(0.74)	0.49	(0.71)
286	(0.09)	0.14	(0.32)	(0.10)
287	0.30	0.39	0.49	(0.74)
288	0.30	0.39	(0.11)	(0.74)
289	0.49	(0.12)	(0.33)	(0.67)
290	0.49	0.27	(0.43)	(0.67)
291	0.49	(0.02)	(0.19)	(0.67)
292	(0.32)	(0.32)	(0.74)	(0.67)
293	0.49	(0.57)	0.14	(0.67)
294	(0.11)	(0.06)	0.39	(1.27)
295	(0.33)	(0.94)	0.39	(1.81)
296	(0.43)	(1.19)	(0.12)	(2.06)
297	(0.19)	(0.38)	0.27	(2.06)
298	(0.74)	(0.43)	(0.02)	(2.94)
299	0.14	(0.14)	(0.62)	(2.30)
300	0.39	(0.44)	(0.87)	(2.30)
301	0.39	0.07	(0.36)	(1.71)
302	(0.12)	0.31	(1.24)	(1.01)
303	0.27	(0.50)	(1.49)	(0.20)
304	(0.02)	(0.50)	(0.68)	(0.51)
305	(0.62)	(0.50)	(0.73)	(0.20)
306	(0.87)	(0.71)	(0.44)	
307	(0.36)	(0.10)	(0.74)	
308	(1.24)	(0.74)	0.07	
309	(1.49)	(0.74)	0.31	
310	(0.68)	(0.67)	(0.50)	
311	(0.73)	(0.67)	(0.50)	
312	(0.44)	(0.67)	(0.50)	
313	(0.74)	(0.67)	(0.71)	
314	0.07	(0.67)	(0.10)	
315	0.31	(1.27)	(0.74)	

AMINO ACID RESIDUE NUMBER	HYDROPATHY index	HYDROPATHY index	HYDROPATHY index	HYDROPATHY index
316	(0.50)	(1.81)	(0.74)	
317	(0.50)	(2.06)	(0.67)	
318	(0.50)	(2.06)	(0.67)	
319	(0.71)	(2.94)	(0.67)	
320	(0.10)	(2.30)	(0.67)	
321	(0.74)	(2.30)	(0.67)	
322	(0.74)	(1.71)	(1.27)	
323	(0.67)	(1.01)	(1.81)	
324	(0.67)	(0.20)	(2.06)	
325	(0.67)	(0.51)	(2.06)	
326	(0.67)	(0.20)	(2.94)	
327	(0.67)		(2.30)	
328	(1.27)		(2.30)	
329	(1.81)		(1.71)	
330	(2.06)		(1.01)	
331	(2.06)		(0.20)	
332	(2.94)		(0.51)	
333	(2.30)		(0.20)	
334	(2.30)			
335	(1.71)			
336	(1.01)			
337	(0.20)			
338	(0.51)			
339	(0.20)			

ศูนย์วิทยทรัพยากร  
จุฬาลงกรณ์มหาวิทยาลัย

## ประวัติผู้เขียน



นาย จตุรงค์ พุทธิพิทย เกิดวันที่ 4 กุมภาพันธ์ พ.ศ. 2512 ที่ ตำบลบางไผ่ อำเภอเมือง จังหวัดฉะเชิงเทรา สำเร็จการศึกษาปริญญาตรีวิทยาศาสตร์บัณฑิต ภาควิชาวาริชศาสตร์ คณะวิทยาศาสตร์ มหาวิทยาลัยบูรพา ในปีการศึกษา 2534 และเข้าศึกษาต่อในหลักสูตรวิทยาศาสตรมหาบัณฑิต ที่ จุฬาลงกรณ์มหาวิทยาลัย เมื่อ พ.ศ. 2535 ในภาควิชาชีววิทยา คณะวิทยาศาสตร์ และ ภาควิชาปรสิตวิทยา คณะแพทยศาสตร์



ศูนย์วิทยทรัพยากร  
จุฬาลงกรณ์มหาวิทยาลัย