

Electronic Supplementary Materials

Proteochemometric Model for Predicting the Inhibition of Penicillin-Binding Proteins

Sunanta Nabu^{1,2,5}, Chanin Nantasenamat^{1,2*}, Wiwat Owasirikul^{1,3}, Ratana Lawung^{2,4}, Chartchalerm Isarankura-Na-Ayudhya², Maris Lapins⁵, Jarl E. S. Wikberg⁵, Virapong Prachayasittikul^{2*}

¹ *Center of Data Mining and Biomedical Informatics, Faculty of Medical Technology, Mahidol University, Bangkok 10700, Thailand*

² *Department of Clinical Microbiology and Applied Technology, Faculty of Medical Technology, Mahidol University, Bangkok 10700, Thailand*

³ *Department of Radiological Technology, Faculty of Medical Technology, Mahidol University, Bangkok 10700, Thailand*

⁴ *Center of Medical Laboratory Service, Faculty of Medical Technology, Mahidol University, Bangkok 10700, Thailand*

⁵ *Department of Pharmaceutical Biosciences, Uppsala University, Uppsala SE-751 24, Sweden*

***Corresponding author information:**

C. Nantasenamat;

Address: Center of Data Mining and Biomedical Informatics, Faculty of Medical Technology, Mahidol University. Tel.: +66 2 441 4371; Fax: +66 2 441 4380.

E-mail address: chanin.nan@mahidol.ac.th

V. Prachayasittikul;

Address: Department of Clinical Microbiology and Applied Technology, Faculty of Medical Technology, Mahidol University. Tel: +66 2 441 4376; Fax: +66 2 441 4380.

E-mail: virapong.pra@mahidol.ac.th

Table S1. The data set used for construction of proteochemometric model of penicillin binding protein 2 of *N. gonorrhoeae*.

Patterns	Penicillin		Cefixime		Ceftriaxone	
	MIC found	Modal MIC	MIC found	Modal MIC	MIC found	Modal MIC
wt	0.06	0.06	0.008, 0.016	0.008	0.008	0.008
I	0.06, 0.12, 0.25, 2	0.12	0.016	0.016	0.008	0.008
II	0.06, 0.12, 0.25	0.12	0.008, 0.016, 0.03	0.008	0.008	0.008
III	0.5	0.50	0.016	0.016	0.008	0.008
IV	0.25, 0.50, 2, 4	2	0.008, 0.06, 0.12, 0.25	0.25	0.008, 0.016, 0.06, 0.12, 0.25	0.12
V	1, 2, 4	2	0.008, 0.016, 0.03, 0.06, 0.12, 0.25	0.03	0.008, 0.016, 0.03, 0.06, 0.12, 0.25	0.03
VI	0.25	0.25	0.06	0.06	0.03	0.03
VII	1, 2	2	0.06, 0.12, 0.25	0.12	0.016, 0.06, 0.12, 0.25	0.12
VIII	0.5	0.50	0.12	0.12	0.03	0.03
IX	0.25, 1, 2	1	0.03, 0.12	0.12	0.008, 0.016, 0.03, 0.06, 0.12	0.06
XI	1	1	-	-	0.06	0.06
XII	0.06, 0.50, 1, 2	1	0.03, 0.06, 0.12	0.03	0.008, 0.016, 0.03, 0.06, 0.12	0.03
XIII	0.50, 1, 2, 4	1	0.06, 0.12, 0.25	0.12	0.06, 0.12, 0.25	0.06
XIV	0.25	0.25	0.008	0.008	0.008	0.008
XV	0.06	0.06	0.008	0.008	0.008	0.008
XVI	-	-	-	-	0.008	0.008
XVII	1, 2	1	0.12	0.12	0.008, 0.06, 0.12	0.12
XVIII	2	2	-	-	0.06, 0.12	0.06
XIX	1	1	-	-	0.008, 0.016	0.008
XX	-	-	-	-	0.06	0.06
XXI	0.25, 0.50	0.50	0.03	0.03	0.008	0.008
XXII	0.06, 0.50, 1	0.06	0.09	0.09	0.008, 0.016, 0.03	0.008
XXIV	2	2	0.12	0.12	0.12	0.12
XXV	-	-	-	-	0.12	0.12
XXVI	-	-	0.5	0.50	0.12	0.12
XXVII	0.25	0.25	0.016	0.016	0.008	0.008
XXVIII	-	-	-	-	0.12	0.12
XXIX	-	-	-	-	0.12	0.12
XXX nM	-	-	-	-	0.008	0.008
XXXIII	1	1	0.06	0.06	0.06	0.06
XXXVII	2	2	0.25	0.25	0.12	0.12
X	0.25, 0.50, 1.00, 2, 4, 8	2	0.12, 0.25, 0.50, 1	0.50	0.016, 0.03, 0.06, 0.12, 0.25, 0.50	0.12
XXIII	0.25	0.25	-	-	0.008	0.008
XXX	-	-	1	1	-	-
XXXI	-	-	0.25	0.25	-	-
XXXII	-	-	0.5	0.5	-	-
XXXIV	1, 2	2	0.12, 0.25	0.25	0.03, 0.06, 0.12	0.03
CII	-	-	1	1	0.5	0.50
CI	1	1	3	3	1.5	1.5
IIIg&Iva	1	1	0.09	0.09	0.02	0.02
IIIh	2	2	0.25	0.25	0.03	0.03
XXXVI	-	-	-	-	0.008	0.008
XXXVIII	0.25, 0.50, 1, 2, 4	1	0.008, 0.03, 0.06, 0.12	0.12	0.008, 0.03, 0.06	0.008
Mosaic2	4	4	0.25, 0.50	0.25	0.06	0.06
Mosaic3	-	-	0.25	0.25	-	-
Mosaic4	0.50, 1	1	0.06, 0.12, 0.25	0.25	0.008, 0.03	0.03
NG-3	2	2	0.5	0.5	0.06	0.06
30/02	2	2	0.25	0.25	0.09	0.09
35/02	2	2	0.25	0.25	0.09	0.09
C	4	4	8	8	2	2

Table S1. (Continued)

Patterns	Amino acid position																							
	35	41	70	83	100	101	144	160	173	201	202	203	204	214	230	241	262	279	285	288	291	311	312	316
wt	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
I	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
II	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
III	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
IV	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
V	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
VI	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
VII	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
VIII	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
IX	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
XI	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
XII	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
XIII	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
XIV	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
XV	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
XVI	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
XVII	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
XVIII	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
XIX	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
XX	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
XXI	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
XXII	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
XXIV	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
XXV	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
XXVI	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
XXVII	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
XXVIII	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
XXIX	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
XXX_nM	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
XXXIII	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	T	A	D	R	R	A	I	V
XXXVII	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	R	A	A	D	R	R	A	I	V
X	M	C	A	G	K	E	D	A	S	H	A	G	E	E	Q	Q	A	V	E	K	Q	A	M	T
XXIII	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	A	D	R	R	A	I	V
XXX	M	C	A	G	K	E	D	A	S	H	A	G	E	E	Q	Q	A	V	E	K	Q	A	M	T
XXXI	M	C	A	G	K	E	D	A	S	H	A	G	E	E	Q	Q	A	V	E	K	Q	A	M	T
XXXII	M	C	A	G	K	E	D	A	S	H	A	G	E	E	Q	Q	A	V	E	K	Q	A	M	T
XXXIV	M	C	A	G	K	E	D	A	S	H	A	G	E	E	Q	Q	A	V	E	K	Q	A	M	T
CII	M	C	A	G	K	E	D	A	S	H	A	G	E	E	Q	Q	A	V	E	K	Q	A	M	T
CI	M	C	A	G	K	E	D	A	S	H	A	G	E	E	Q	Q	A	V	E	K	Q	A	M	T
IIIg&Iva	M	C	A	G	K	E	D	A	S	H	A	G	E	E	Q	Q	A	V	E	K	Q	A	M	T
IIIh	M	C	A	G	K	E	D	A	S	H	A	G	E	E	Q	Q	A	V	E	K	Q	A	M	T
XXXVI	M	C	A	G	K	D	D	V	N	Y	G	E	D	Q	Q	Q	A	V	E	K	Q	A	I	V
XXXVIII	I	G	T	G	K	E	D	V	N	H	A	G	E	Q	K	Q	A	A	D	R	R	A	M	T
Mosaic2	M	C	A	G	K	D	D	A	S	H	A	G	E	E	Q	Q	A	V	E	K	Q	A	M	T
Mosaic3	M	C	A	G	K	E	D	A	S	H	A	G	E	Q	Q	Q	A	V	E	K	Q	A	M	T
Mosaic4	M	C	A	G	N	E	D	A	S	H	G	E	D	Q	K	Q	A	A	N	R	R	A	M	T
NG-3	M	C	A	V	K	E	D	A	S	H	A	G	E	E	Q	Q	A	V	E	K	Q	A	M	T
30/02	M	C	A	G	K	E	A	A	S	H	A	G	E	E	Q	Q	A	V	E	K	Q	A	M	T
35/02	M	C	A	G	K	E	D	A	N	H	A	G	E	E	Q	Q	A	V	E	K	Q	A	M	T
C	M	C	A	G	K	E	D	A	S	H	A	G	E	E	Q	Q	A	V	E	K	Q	V	M	P

Table S1. (Continued)

Patterns	Amino acid position																						
	323	324	326	327	328	329	330	331	332	335	341	342	343	345	45-34	352	373	375	376	377	382	385	388
wt	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	-	S	R	G	A	E	F	E	I
I	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
II	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
III	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
IV	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
V	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
VI	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
VII	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
VIII	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
IX	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
XI	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
XII	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
XIII	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
XIV	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
XV	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	-	S	R	G	A	E	F	E	I
XVI	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
XVII	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
XVIII	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
XIX	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
XX	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
XXI	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
XXII	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
XXIV	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
XXV	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
XXVI	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
XXVII	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
XXVIII	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
XXIX	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
XXX_nM	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
XXXIII	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
XXXVII	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
X	S	G	V	D	A	T	D	T	F	L	S	A	T	Q	-	T	M	T	P	K	F	D	V
XXIII	A	G	T	D	L	N	E	R	L	Q	P	S	P	R	D	S	R	G	A	E	F	E	I
XXX	S	G	V	D	A	T	D	T	F	L	S	A	T	Q	-	T	M	T	P	K	F	D	V
XXXI	S	G	V	D	A	T	D	T	F	L	S	A	T	Q	-	T	M	T	P	K	F	D	V
XXXII	S	G	V	D	A	T	D	T	F	L	S	A	T	Q	-	T	M	T	P	K	F	D	V
XXXIV	S	G	V	D	A	T	D	T	F	L	S	A	T	Q	-	T	M	T	P	K	F	D	V
CII	S	G	V	D	A	T	D	T	F	L	S	A	T	Q	-	T	M	T	P	K	F	D	V
CI	S	G	V	D	A	T	D	T	F	L	S	A	T	Q	-	T	M	T	P	K	F	D	V
IIIg&Iva	S	G	V	D	A	T	D	T	F	L	S	A	T	Q	-	T	M	T	P	K	F	D	V
IIIh	S	G	V	D	A	T	D	T	F	L	S	A	T	Q	-	T	M	T	P	K	F	D	V
XXXVI	A	E	T	N	L	N	E	R	L	Q	P	A	Q	R	-	S	R	S	S	K	L	S	I
XXXVIII	S	G	V	D	A	T	D	T	F	L	P	A	T	Q	-	T	M	T	P	K	F	D	V
Mosaic2	S	G	V	D	A	T	D	T	F	L	S	A	T	Q	-	T	M	T	P	K	F	D	V
Mosaic3	S	G	V	D	A	T	D	T	F	L	S	A	T	Q	-	T	M	T	P	K	F	D	V
Mosaic4	S	G	V	D	A	T	D	T	F	L	S	A	T	Q	-	T	M	T	P	K	F	D	V
NG-3	S	G	V	D	A	T	D	T	F	L	S	A	T	Q	-	T	M	T	P	K	F	D	V
30/02	S	G	V	D	A	T	D	T	F	L	S	A	T	Q	-	T	M	T	P	K	F	D	V
35/02	S	G	V	D	A	T	D	T	F	L	S	A	T	Q	-	T	M	T	P	K	F	D	V
C	S	G	V	D	T	T	D	T	F	L	P	A	T	Q	-	T	M	T	P	K	F	D	V

Table S1. (Continued)

Patterns	Amino acid position																						
	400	403	406	409	411	412	437	443	447	457	461	462	464	465	468	469	472	480	483	485	88-48	501	504
wt	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	A	F
I	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	A	F
II	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	A	L
III	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	A	L
IV	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	A	L
V	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	A	L
VI	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	A	L
VII	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	V	L
VIII	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	V	L
IX	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	A	L
XI	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	V	L
XII	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	A	L
XIII	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	V	L
XIV	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	A	L
XV	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	A	F
XVI	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	A	L
XVII	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	V	L
XVIII	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	T	L
XIX	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	A	L
XX	T	L	N	R	R	P	A	V	L	Q	I	F	E	L	R	E	N	P	T	T	-	A	L
XXI	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	V	L
XXII	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	A	L
XXIV	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	A	L
XXV	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	T	L
XXVI	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	V	L
XXVII	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	V	L
XXVIII	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	V	L
XXIX	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	V	L
XXX nM	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	T	L
XXXIII	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	V	L
XXXVII	T	L	N	R	R	P	A	V	L	Q	I	F	E	S	R	E	N	P	T	T	-	A	L
X	T	L	S	R	Q	K	V	E	V	K	V	I	A	S	K	K	E	A	T	T	-	A	L
XXIII	T	L	N	R	R	P	V	E	V	K	V	I	A	S	K	K	E	A	T	T	-	A	L
XXX	T	L	S	R	Q	K	V	E	V	K	V	I	A	S	K	K	E	A	T	T	-	V	L
XXXI	T	L	S	R	Q	K	V	E	V	K	V	I	A	S	K	K	E	A	T	T	-	A	L
XXXII	T	L	S	R	Q	K	V	E	V	K	V	I	A	S	K	K	E	A	T	T	-	A	L
XXXIV	T	L	S	R	Q	K	V	E	V	K	V	I	A	S	K	K	E	A	T	T	-	A	L
CII	T	L	S	R	Q	K	V	E	V	K	V	I	A	S	K	K	E	A	T	T	-	A	L
CI	T	L	S	R	Q	K	V	E	V	K	V	I	A	S	K	K	E	A	T	T	-	P	L
IIIg&Iva	T	L	S	R	Q	K	V	E	V	K	V	I	A	S	K	K	E	A	T	T	V	A	L
IIIh	T	L	S	R	Q	K	V	E	V	K	V	I	A	S	K	K	E	A	T	T	-	A	L
XXXVI	S	V	N	K	R	P	V	V	V	K	V	I	A	S	K	K	E	A	T	T	-	A	L
XXXVIII	T	L	N	R	R	P	A	V	V	Q	I	F	E	S	R	E	N	P	T	T	-	A	F
Mosaic2	T	L	S	R	Q	K	V	E	V	K	V	I	A	S	K	K	E	A	T	T	-	A	L
Mosaic3	T	L	S	R	Q	K	V	E	V	K	V	I	A	S	K	K	E	A	T	T	-	A	L
Mosaic4	T	L	S	R	Q	K	V	E	V	K	V	I	A	S	K	K	E	A	T	T	-	V	L
NG-3	T	L	S	R	Q	K	V	E	V	K	V	I	A	S	K	K	E	A	T	T	-	A	L
30/02	T	L	S	R	Q	K	V	E	V	K	V	I	A	S	K	K	E	A	T	T	-	A	L
35/02	T	L	S	R	Q	K	V	E	V	K	V	I	A	S	K	K	E	A	T	T	-	A	L
C	S	V	N	K	R	P	V	E	V	K	V	I	A	S	K	K	E	A	S	I	-	A	L

Table S1. (Continued)

Patterns	Amino acid position																	Source	
	510	512	515	516	532	534	541	542	545	549	551	552	555	556	563	566	73-57		574
wt	A	N	V	A	A	T	H	G	G	A	P	P	K	I	I	I	-	A	1-3
I	A	N	V	A	A	T	H	G	G	A	P	P	K	I	I	I	-	A	4,5
II	V	N	V	G	A	T	H	G	G	A	P	P	K	I	I	I	-	A	2-8
III	V	N	V	G	A	T	H	G	G	A	P	P	K	I	I	V	N	V	4
IV	V	N	V	G	A	T	H	S	G	A	P	P	K	I	I	I	-	A	1, 4, 5, 9, 10
V	V	N	V	G	A	T	H	S	G	A	P	P	K	I	I	V	N	V	1, 3-5, 9-11
VI	V	N	V	A	A	T	H	G	G	A	L	P	K	I	I	I	-	A	4
VII	V	N	V	G	A	T	H	S	G	A	P	P	K	I	I	I	-	A	4, 5, 7, 12
VIII	V	N	V	A	A	T	H	S	G	A	L	P	K	I	I	I	-	A	4
IX	V	N	V	G	A	T	H	G	G	A	L	P	K	I	I	I	-	A	4, 5, 10, 12
XI	V	N	V	G	A	T	H	G	G	A	L	P	K	I	I	I	-	A	5
XII	V	N	V	G	A	T	H	G	G	A	S	P	K	I	I	I	-	A	1, 5, 9, 13
XIII	V	N	V	G	A	T	H	G	G	A	S	P	K	I	I	I	-	A	5, 6, 9, 10, 12
XIV	V	N	V	G	A	T	N	G	G	A	P	P	K	I	I	I	-	A	5, 9
XV	A	N	V	A	A	T	N	G	G	A	P	P	K	I	I	I	-	A	5, 7
XVI	V	N	V	G	A	T	H	G	G	A	P	P	K	I	I	I	N	V	5
XVII	V	N	V	G	A	T	H	S	G	A	P	P	K	I	I	V	N	V	5, 9, 10
XVIII	V	N	V	G	A	T	H	S	G	A	P	P	K	I	I	V	N	V	5
XIX	V	N	V	G	A	T	N	G	G	A	P	P	K	I	I	V	N	V	5
XX	V	N	V	G	A	T	N	G	G	A	P	P	K	I	I	V	N	V	5
XXI	V	N	V	G	A	T	N	G	G	A	P	V	Q	V	I	V	N	V	1, 5, 10
XXII	V	N	V	G	A	T	N	G	G	A	P	V	Q	V	I	V	N	V	5, 12
XXIV	V	N	V	G	A	T	H	S	G	A	S	P	K	I	I	V	N	V	9
XXV	V	N	V	G	A	T	H	S	G	A	P	P	K	I	I	I	-	A	10
XXVI	V	N	V	G	A	T	H	S	G	A	S	P	K	I	I	V	-	A	10, 11
XXVII	V	N	V	G	A	T	H	G	G	A	P	P	K	I	I	I	-	A	10
XXVIII	V	N	V	G	A	T	H	G	G	A	P	P	K	I	I	V	-	A	10
XXIX	V	N	V	G	A	T	Y	G	G	A	P	P	K	I	I	I	-	A	10
XXX_nM	V	N	V	G	A	T	H	S	G	A	P	P	K	I	V	I	-	A	10
XXXIII	V	N	V	G	A	T	H	S	G	A	P	P	K	I	I	I	-	A	8, 12
XXXVII	V	N	V	G	A	T	H	G	G	A	S	P	K	I	I	I	-	A	13
X	V	Y	V	A	A	T	N	G	S	T	P	V	Q	V	I	V	N	V	1-9, 11-13
XXIII	V	Y	V	A	A	T	N	G	G	T	P	V	Q	V	I	V	N	V	5
XXX	V	Y	V	A	A	T	N	G	S	T	P	V	Q	V	I	V	N	V	11
XXXI	V	Y	V	A	V	T	N	G	S	T	P	V	Q	V	I	V	N	V	11
XXXII	V	Y	V	A	A	T	N	G	S	A	L	P	K	I	I	I	-	A	11
XXXIV	V	Y	V	A	A	T	N	G	S	A	P	P	K	I	I	I	-	A	6, 13-15
CII	V	Y	V	A	A	A	N	G	S	A	P	P	K	I	I	I	-	A	16
CI	V	Y	V	A	A	T	N	G	S	A	P	P	K	I	I	I	-	A	7, 17
IIIg&Iva	V	Y	V	A	A	T	N	G	S	A	P	P	K	I	I	I	-	A	3
IIIh	V	Y	V	A	A	T	N	G	S	T	P	P	K	I	I	I	-	A	3, 6
XXXVI	V	N	V	A	A	T	N	G	G	T	P	V	Q	V	I	V	N	V	8
XXXVIII	A	N	I	A	A	T	H	G	G	A	P	P	K	I	I	I	-	A	13-15
Mosaic2	V	Y	V	A	A	T	N	G	S	T	P	V	Q	V	I	V	N	V	1, 3
Mosaic3	V	Y	V	A	A	T	N	G	S	T	P	V	Q	V	I	V	N	V	1
Mosaic4	V	N	V	A	A	T	N	G	G	T	P	V	Q	V	I	V	N	V	1, 3
NG-3	V	Y	V	A	A	T	N	G	S	T	P	V	Q	V	I	V	N	V	6
30/02	V	Y	V	A	A	T	N	G	S	T	P	V	Q	V	I	V	N	V	12
35/02	V	Y	V	A	A	T	N	G	S	T	P	V	Q	V	I	V	N	V	12
C	V	Y	V	A	A	T	N	G	S	T	P	V	Q	V	I	V	N	V	8

Table S1. (Continued).

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Table S2. Ligand descriptors used for construction and validation of proteochemometric modeling of PBP2 *Neisseria gonorrhoeae*.

	Compound	Ligand descriptors												
		MW	nCIC	RBN	nHDon	nHAcc	TPSA	AlogP	Q _m	E	μ	HOMO	LUMO	GAP
Construction	Penicillin	334.4	3	4	2	6	112.01	1.312	0.266	-1429.14	5.335	-0.237	-0.018	0.219
	Cefixime	453.5	3	8	5	12	238.05	-0.195	0.336	-2215.34	2.722	-0.213	-0.055	0.158
	Ceftriaxone	552.6	4	8	3	15	299.72	-0.861	0.336	-2854.47	6.625	-0.209	-0.190	0.019
Validation	Cefdinir	395.5	3	5	5	10	211.75	-0.07	0.379	-1987.88	4.172	-0.224	-0.087	0.137
	Cefotaxime	455.5	3	8	4	12	227.05	-0.641	0.333	-2217.04	4.781	-0.222	-0.076	0.145
	Ceftibuten	410.5	3	6	5	10	216.46	-0.488	0.331	-2047.17	3.736	-0.225	-0.078	0.148
	Ceftizoxime	383.5	3	5	4	10	200.75	-0.376	0.335	-1949.77	3.521	-0.221	-0.076	0.145

Abbreviations:

MW	Molecular weight	nCIC	Number of rings
RBN	Number of rotatable bonds	nHDon	Number of hydrogen bond donors
nHAcc	Number of hydrogen bond acceptors	TPSA	Topological polar surface area
AlogP	Lipophilicities	E	The total energy of the molecule
Q_m	Mean absolute charge	μ	Dipole moment
HOMO	Highest occupied molecular orbital	LUMO	Lowest unoccupied molecular orbital
GAP	Gap between the energies of the HOMO and LUMO state		

Table S3. Number of significant PLS components used in each PCM model.

Models	Descriptor blocks	Number of PLS components	
		Models without VIP	Models applying VIP
1	L	1	1
2	P	1	1-2
3	LxP	1	1-2
4	LxL	2	2
5	PxP	1	1-2
6	L, P	4	2
7	L, P, LxP	7	4-6
8	L, P, LxL	4	3-5
9	L, P, PxP	4	4-5
10	L, P, LxP, LxL	5	4-5
11	L, P, LxP, PxP	5	4-6
12	L, P, LxL, PxP	5	4-5
13	L, P, LxP, LxL, PxP	5	4-5

Table S4. Model validation on predictions of pMIC and MIC values of known compounds.

Patterns	Penicillin		Cefixime		Ceftriaxone	
	pMIC	MIC, ($\mu\text{g/ml}$)	pMIC	MIC, ($\mu\text{g/ml}$)	pMIC	MIC, ($\mu\text{g/ml}$)
wt	6.746	0.06	7.753	0.008	7.839	0.008
I	6.445	0.12	7.452	0.016	7.839	0.008
II	6.445	0.12	7.753	0.01	7.839	0.008
III	5.825	0.50	7.452	0.02	7.839	0.008
IV	5.223	2.00	6.259	0.25	6.663	0.12
V	5.223	2.00	7.179	0.03	7.265	0.03
VI	6.126	0.25	6.878	0.06	7.265	0.03
VII	5.223	2.00	6.577	0.12	6.663	0.12
VIII	5.825	0.50	6.577	0.12	7.265	0.03
IX	5.524	1.00	6.577	0.12	6.964	0.06
XI	5.524	1.00	6.73	0.08	6.964	0.06
XII	5.524	1.00	7.179	0.03	7.265	0.03
XIII	5.524	1.00	6.577	0.12	6.964	0.06
XIV	6.126	0.25	7.753	0.008	7.839	0.008
XV	6.746	0.06	7.753	0.008	7.839	0.008
XVI	5.98	0.35	7.03	0.04	7.839	0.008
XVII	5.524	1.00	6.577	0.12	6.663	0.12
XVIII	5.223	2.00	6.47	0.15	6.964	0.06
XIX	5.524	1.00	7.19	0.03	7.839	0.01
XX	5.69	0.69	6.73	0.08	6.964	0.06
XXI	5.825	0.50	7.179	0.03	7.839	0.008
XXII	6.746	0.06	6.702	0.09	7.839	0.008
XXIV	5.223	2.00	6.577	0.12	6.663	0.12
XXV	5.58	0.89	6.63	0.11	6.663	0.12
XXVI	5.06	2.92	5.958	0.50	6.663	0.12
XXVII	6.126	0.25	7.452	0.02	7.839	0.01
XXVIII	5.78	0.55	6.83	0.07	6.663	0.12
XXIX	5.47	1.13	6.52	0.14	6.663	0.12
XXX_nM	6.02	0.32	7.08	0.04	7.839	0.01
XXXIII	5.524	1.00	6.878	0.06	6.964	0.06
XXXVII	5.223	2.00	6.259	0.25	6.663	0.12
X	5.223	2.00	5.958	0.50	6.663	0.12
XXIII	6.126	0.25	7.32	0.02	7.839	0.008
XXX	5.04	3.05	5.657	1.00	6.57	0.15
XXXI	5.32	1.60	6.259	0.25	6.84	0.08
XXXII	5.07	2.83	5.958	0.50	6.59	0.14
XXXIV	5.223	2.00	6.259	0.25	7.265	0.03
CII	4.88	4.45	5.657	1.00	6.043	0.50
CI	5.524	1.00	5.179	3.00	5.566	1.50
IIIg&Iva	5.524	1.00	6.702	0.09	7.441	0.02
IIIh	5.223	2.00	6.259	0.25	7.265	0.03
XXXVI	5.97	0.36	7.02	0.04	7.839	0.008
XXXVIII	5.524	1.00	6.577	0.12	7.839	0.01

Table S4. (Continued).

Patterns	Penicillin		Cefixime		Ceftriaxone	
	pMIC	MIC, ($\mu\text{g/ml}$)	pMIC	MIC, ($\mu\text{g/ml}$)	pMIC	MIC, ($\mu\text{g/ml}$)
Mosaic2	4.922	4.00	6.259	0.25	6.964	0.06
Mosaic3	5.24	1.94	6.259	0.25	6.76	0.10
Mosaic4	5.524	1.00	6.259	0.25	7.265	0.03
NG-3	5.223	2.00	5.958	0.50	6.964	0.06
30/02	5.223	2.00	6.259	0.25	6.788	0.09
35/02	5.223	2.00	6.259	0.25	6.788	0.09
C	4.922	4.00	4.753	8.01	5.441	2.00

Experimental susceptibility values are indicated in regular and predicted values are indicated in bold

Table S5. Predictions of MIC values of unknown compounds.

Patterns	Experimental MICs, ($\mu\text{g/ml}$)			Predicted MICs, ($\mu\text{g/ml}$)		
	Penicillin	Cefixime	Ceftriaxone	Cefotaxime	Ceftibuten	Ceftizoxime
	($S \leq 0.06$, $R \geq 2$)	($S \leq 0.25$) ^a	($S \leq 0.25$) ^a	($S \leq 0.5$) ^a	($S \leq 0.5$) ^a	($S \leq 0.5$) ^a
wt	0.06	0.008	0.008	0.01	0.02	0.02
I	0.12	0.02	0.008	0.01	0.02	0.02
II	0.12	0.008	0.008	0.04	0.05	0.06
III	0.50	0.02	0.008	0.06	0.08	0.09
IV	2.00	0.25	0.12	0.08	0.11	0.13
V	2.00	0.03	0.03	0.12	0.16	0.18
VI	0.25	0.06	0.03	0.05	0.07	0.08
VII	2.00	0.12	0.12	0.12	0.16	0.18
VIII	0.50	0.12	0.03	0.16	0.21	0.23
IX	1.00	0.12	0.06	0.07	0.09	0.10
XI	1.00	-	0.06	0.09	0.12	0.14
XII	1.00	0.03	0.03	0.10	0.14	0.16
XIII	1.00	0.12	0.06	0.15	0.20	0.23
XIV	0.25	0.008	0.008	0.02	0.03	0.03
XV	0.06	0.008	0.008	0.007	0.009	0.01
XVI	-	-	0.008	0.05	0.06	0.07
XVII	1.00	0.12	0.12	0.17	0.23	0.26
XVIII	2.00	-	0.06	0.17	0.22	0.25
XIX	1.00	-	0.008	0.03	0.04	0.05
XX	-	-	0.06	0.09	0.12	0.14
XXI	0.50	0.03	0.008	0.04	0.05	0.06
XXII	0.06	0.09	0.008	0.03	0.04	0.04
XXIV	2.00	0.12	0.12	0.31	0.41	0.46
XXV	-	-	0.12	0.12	0.16	0.18
XXVI	-	0.50	0.12	0.39	0.51	0.58
XXVII	0.25	0.02	0.008	0.06	0.08	0.09
XXVIII	-	-	0.12	0.07	0.10	0.11
XXIX	-	-	0.12	0.15	0.20	0.23
XXX_nM	-	-	0.008	0.04	0.06	0.06
XXXIII	1.00	0.06	0.06	0.13	0.18	0.20
XXXVII	2.00	0.25	0.12	0.25	0.33	0.38
X	2.00	0.50	0.12	0.29	0.38	0.43
XXIII	0.25	-	0.008	0.03	0.03	0.04
XXX	-	1.00	-	0.41	0.55	0.62
XXXI	-	0.25	-	0.21	0.28	0.32
XXXII	-	0.50	-	0.39	0.52	0.59
XXXIV	2.00	0.25	0.03	0.25	0.32	0.37
CII	-	1.00	0.50	0.62	0.82	0.93
CI	1.00	3.00	1.50	0.84	1.11	1.25
IIIg&Iva	1.00	0.09	0.02	0.09	0.11	0.13

Table S5. (Continued).

Patterns	Experimental MICs, ($\mu\text{g/ml}$)			Predicted MICs, ($\mu\text{g/ml}$)		
	Penicillin (S \leq 0.06, R \geq 2)	Cefixime (S \leq 0.25) ^a	Ceftriaxone (S \leq 0.25) ^a	Cefotaxime (S \leq 0.5) ^a	Ceftibuten	Ceftizoxime (S \leq 0.5) ^a
IIIh	2.00	0.25	0.03	0.24	0.31	0.36
XXXVI	-	-	0.008	0.16	0.21	0.24
XXXVIII	1.00	0.12	0.008	0.08	0.10	0.11
Mosaic2	4.00	0.25	0.06	0.28	0.37	0.42
Mosaic3	-	0.25	-	0.27	0.35	0.40
Mosaic4	1.00	0.25	0.03	0.13	0.17	0.20
NG-3	2.00	0.50	0.06	0.29	0.39	0.44
30/02	2.00	0.25	0.09	0.27	0.36	0.40
35/02	2.00	0.25	0.09	0.27	0.36	0.41
C	4.00	8.01	2.00	3.58	4.72	5.32

^a Interpretation criteria (S, susceptible; R, resistant) are according to the Clinical Laboratory and Standards Institute (CLSI)

Reference:

Clinical and Laboratory Standards Institute (2014). Performance standards for antimicrobial susceptibility testing, 24th informational supplement. CLSI document M100-S24. Clinical and Laboratory Standards Institute, Wayne, PA.

Figure S1. Alignment of 50 penicillin-binding protein 2 sequences used in the study. Amino acid numbering with respect to that of the wild-type PBP 2 sequence (GenBank accession no. M32091). Highlighted positions indicate selected amino acid positions for investigation in this study.

	10	20	30	40	50	
wt	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternI	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternII	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternIII	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternIV	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternV	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternVI	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternVII	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternVIII	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternIX	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXI	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXII	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXIII	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXIV	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXV	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXVI	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXVII	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXVIII	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXIX	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXX	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXXI	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXXII	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXXIV	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXXV	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXXVI	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXXVII	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXXVIII	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXXIX	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXXX_nM	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXXXIII	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXXXVII	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternX	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXXIII	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXXX	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXXXI	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXXXII	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXXXIV	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternCII	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternCI	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternIIlg&Iva	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternIIh	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXXXVI	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternXXXVIII	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	GLIAAGLYLQ	
mosaic2	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
mosaic3	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
mosaic4	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
NG-3	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
30/02	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
35/02	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
patternC	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISF	VLMAVAFLFA	CLIAAGLYLQ	
Consistency	*****	*****	*****	****9*****	9*****	

	60	70	80	90	100
wt	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternI	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternII	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternIII	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternIV	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternV	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternVI	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternVII	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternVIII	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternIX	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXI	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXII	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXIII	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXIV	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXV	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXVI	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXVII	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXVIII	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXIX	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXX	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXXI	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXXII	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXXIV	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXXV	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXXVI	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXXVII	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXXVIII	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXXIX	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXXX_nM	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXXXIII	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXXXVII	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternX	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXXIII	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXXX	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXXXI	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXXXII	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXXXIV	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternCII	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternCI	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternIIIg&Iva	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternIIIf	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXXXVI	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternXXXVIII	TVTYNFLKEQ	GDNRIVRTQT	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
mosaic2	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
mosaic3	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
mosaic4	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
NG-3	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
30/02	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
35/02	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
patternC	TVTYNFLKEQ	GDNRIVRTQA	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
Consistency	*****	*****9	*****	**9*****	*****9

	110	120	130	140	150
wt	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternI	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternII	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternIII	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternIV	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternV	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternVI	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternVII	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternVIII	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternIX	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXI	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXII	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXIII	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXIV	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXV	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXVI	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXVII	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXVIII	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXIX	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXX	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXXI	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXXII	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXXIV	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXXV	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXXVI	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXXVII	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXXVIII	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXXIX	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXXX_nM	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXXXIII	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXXXVII	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternX	EMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXXIII	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXXX	EMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXXXI	EMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXXXII	EMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXXXIV	EMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternCII	EMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternCI	EMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternIIIg&Iva	EMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternIIHh	EMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXXXVI	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternXXXVIII	EMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
mosaic2	DMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
mosaic3	EMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
mosaic4	EMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
NG-3	EMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
30/02	EMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
35/02	EMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
patternC	EMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIWIK	RQLDPKVAEE
Consistency	8*****	*****	*****	*****	***9*****

	160	170	180	190	200
wt	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternI	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternII	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternIII	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternIV	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternV	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternVI	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternVII	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternVIII	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternIX	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternXI	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternXII	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternXIII	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternXIV	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternXV	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternXVI	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternXVII	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternXVIII	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternXIX	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternXX	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternXXI	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternXXII	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternXXIV	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternXXV	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternXXVI	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternXXVII	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternXXVIII	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternXXX_nM	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternXXXIII	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternXXXVII	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternX	VKALGLENFA	FEKELKRHYP	MGSLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternXXIII	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternXXX	VKALGLENFA	FEKELKRHYP	MGSLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternXXXI	VKALGLENFA	FEKELKRHYP	MGSLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternXXXII	VKALGLENFA	FEKELKRHYP	MGSLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternXXXIV	VKALGLENFA	FEKELKRHYP	MGSLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternCII	VKALGLENFA	FEKELKRHYP	MGSLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternCI	VKALGLENFA	FEKELKRHYP	MGSLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternII Ig&Iva	VKALGLENFA	FEKELKRHYP	MGSLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternIIIh	VKALGLENFA	FEKELKRHYP	MGSLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternXXXVI	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternXXXVIII	VKALGLENFV	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
mosaic2	VKALGLENFA	FEKELKRHYP	MGSLFAHVIG	FTDIDGKGQE	GLELSLEDSL
mosaic3	VKALGLENFA	FEKELKRHYP	MGSLFAHVIG	FTDIDGKGQE	GLELSLEDSL
mosaic4	VKALGLENFA	FEKELKRHYP	MGSLFAHVIG	FTDIDGKGQE	GLELSLEDSL
NG-3	VKALGLENFA	FEKELKRHYP	MGSLFAHVIG	FTDIDGKGQE	GLELSLEDSL
30/02	VKALGLENFA	FEKELKRHYP	MGSLFAHVIG	FTDIDGKGQE	GLELSLEDSL
35/02	VKALGLENFA	FEKELKRHYP	MGNLFAHVIG	FTDIDGKGQE	GLELSLEDSL
patternC	VKALGLENFA	FEKELKRHYP	MGSLFAHVIG	FTDIDGKGQE	GLELSLEDSL
Consistency	*****7	*****8	*****8	*****8	*****8

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      ....|....| ....|....| ....|....| ....|....| ....|....|
      210      220      230      240      250
wt      YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternI      YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternII     YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternIII    YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternIV     YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternV      YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternVI     YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternVII    YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternVIII   YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternIX     YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXI     YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXII    YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXIII   YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXIV    YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXV     YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXVI    YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXVII   YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXVIII  YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXIX    YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXX     YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXXI    YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXXII   YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXXIII  YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXXIV   YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXXV    YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXXVI   YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXXVII  YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXXVIII YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXXIX   YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXXX_nM YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXXXIII YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXXXVII YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternX      HAGEGAEVVL RDREGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXXIII  YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXXX    HAGEGAEVVL RDREGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXXXI   HAGEGAEVVL RDREGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXXXII  HAGEGAEVVL RDREGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXXXIII HAGEGAEVVL RDREGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXXXIV  HAGEGAEVVL RDREGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternCII    HAGEGAEVVL RDREGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternCI     HAGEGAEVVL RDREGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternIIIg&Iva HAGEGAEVVL RDREGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternIIIh   HAGEGAEVVL RDREGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXXXVI  YGEDGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternXXXVIII HAGEGAEVVL RDROGNIVDS LDSPRNKAPK NGKDIIISLD QRIQTLAYEE
mosaic2      HAGEGAEVVL RDREGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
mosaic3      HAGEGAEVVL RDROGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
mosaic4      HGEDGAEVVL RDROGNIVDS LDSPRNKAPK NGKDIIISLD QRIQTLAYEE
NG-3        HAGEGAEVVL RDREGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
30/02      HAGEGAEVVL RDREGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
35/02      HAGEGAEVVL RDREGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
patternC     HAGEGAEVVL RDREGNIVDS LDSPRNKAPQ NGKDIIISLD QRIQTLAYEE
Consistency  7768***** **8***** *****9 *****9*****

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	260	270	280	290	300
wt	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternI	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternII	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternIII	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternIV	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternV	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternVI	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternVII	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternVIII	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternIX	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternXI	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternXII	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternXIII	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternXIV	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternXV	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternXVI	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternXVII	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternXVIII	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternXIX	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternXX	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternXXI	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternXXII	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternXXIV	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternXXV	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternXXVI	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternXXVII	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternXXVIII	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternXXIX	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternXXX_nM	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternXXXIII	LNKAVEYHQA	KTGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternXXXVII	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
patternX	LNKAVEYHQA	KAGTVVVLDA	RTGEILALVN	TPAYEPNKP	QADSEQRRNR
patternXXIII	LNKAVEYHQA	KAGTVVVLDA	RTGEILALVN	TPAYEPNKP	QADSEQRRNR
patternXXX	LNKAVEYHQA	KAGTVVVLDA	RTGEILALVN	TPAYEPNKP	QADSEQRRNR
patternXXXI	LNKAVEYHQA	KAGTVVVLDA	RTGEILALVN	TPAYEPNKP	QADSEQRRNR
patternXXXII	LNKAVEYHQA	KAGTVVVLDA	RTGEILALVN	TPAYEPNKP	QADSEQRRNR
patternXXXIV	LNKAVEYHQA	KAGTVVVLDA	RTGEILALVN	TPAYEPNKP	QADSEQRRNR
patternCII	LNKAVEYHQA	KAGTVVVLDA	RTGEILALVN	TPAYEPNKP	QADSEQRRNR
patternCI	LNKAVEYHQA	KAGTVVVLDA	RTGEILALVN	TPAYEPNKP	QADSEQRRNR
patternIIIg&Iva	LNKAVEYHQA	KAGTVVVLDA	RTGEILALVN	TPAYEPNKP	QADSEQRRNR
patternIIH	LNKAVEYHQA	KAGTVVVLDA	RTGEILALVN	TPAYEPNKP	QADSEQRRNR
patternXXXVI	LNKAVEYHQA	KAGTVVVLDA	RTGEILALVN	TPAYEPNKP	QADSEQRRNR
patternXXXVIII	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
mosaic2	LNKAVEYHQA	KAGTVVVLDA	RTGEILALVN	TPAYEPNKP	QADSEQRRNR
mosaic3	LNKAVEYHQA	KAGTVVVLDA	RTGEILALVN	TPAYEPNKP	QADSEQRRNR
mosaic4	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRRNR
NG-3	LNKAVEYHQA	KAGTVVVLDA	RTGEILALVN	TPAYEPNKP	QADSEQRRNR
30/02	LNKAVEYHQA	KAGTVVVLDA	RTGEILALVN	TPAYEPNKP	QADSEQRRNR
35/02	LNKAVEYHQA	KAGTVVVLDA	RTGEILALVN	TPAYEPNKP	QADSEQRRNR
patternC	LNKAVEYHQA	KAGTVVVLDA	RTGEILALVN	TPAYEPNKP	QADSEQRRNR
Consistency	*****	*9*****	*****7*	****8**8**	8*****

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...|...|...|...|...|...|...|...|...|...|
          310      320      330      340      349
wt      AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVR-DTHV
patternI AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternII AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternIII AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternIV AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternV AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternVI AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternVII AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternVIII AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternIX AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternXI AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternXII AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternXIII AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternXIV AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternXV AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVR-DTHV
patternXVI AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternXVII AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternXVIII AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternXIX AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternXX AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternXXI AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternXXII AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternXXIV AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternXXV AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternXXVI AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternXXVII AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternXXVIII AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternXXX_nM AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternXXXIII AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternXXXVII AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternX AVTDMIEPGS AMKPFTIAKA LDSGKVDATD TFNTLPYKIG SATVQ-DTHV
patternXXIII AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
patternXXX AVTDMIEPGS AMKPFTIAKA LDSGKVDATD TFNTLPYKIG SATVQ-DTHV
patternXXXI AVTDMIEPGS AMKPFTIAKA LDSGKVDATD TFNTLPYKIG SATVQ-DTHV
patternXXXII AVTDMIEPGS AMKPFTIAKA LDSGKVDATD TFNTLPYKIG SATVQ-DTHV
patternXXXIV AVTDMIEPGS AMKPFTIAKA LDSGKVDATD TFNTLPYKIG SATVQ-DTHV
patternCII AVTDMIEPGS AMKPFTIAKA LDSGKVDATD TFNTLPYKIG SATVQ-DTHV
patternCI AVTDMIEPGS AMKPFTIAKA LDSGKVDATD TFNTLPYKIG SATVQ-DTHV
patternIIIg&Iva AVTDMIEPGS AMKPFTIAKA LDSGKVDATD TFNTLPYKIG SATVQ-DTHV
patternIIIh AVTDMIEPGS AMKPFTIAKA LDSGKVDATD TFNTLPYKIG SATVQ-DTHV
patternXXXVI AVTDMIEPGS AIKPFVIAKA LDAEKTNLNE RLNTQPYKIG PAQVR-DTHV
patternXXXVIII AVTDMIEPGS AMKPFTIAKA LDSGKVDATD TFNTLPYKIG PATVQ-DTHV
mosaic2 AVTDMIEPGS AMKPFTIAKA LDSGKVDATD TFNTLPYKIG SATVQ-DTHV
mosaic3 AVTDMIEPGS AMKPFTIAKA LDSGKVDATD TFNTLPYKIG SATVQ-DTHV
mosaic4 AVTDMIEPGS AMKPFTIAKA LDSGKVDATD TFNTLPYKIG SATVQ-DTHV
NG-3 AVTDMIEPGS AMKPFTIAKA LDSGKVDATD TFNTLPYKIG SATVQ-DTHV
30/02 AVTDMIEPGS AMKPFTIAKA LDSGKVDATD TFNTLPYKIG SATVQ-DTHV
35/02 AVTDMIEPGS AMKPFTIAKA LDSGKVDATD TFNTLPYKIG SATVQ-DTHV
patternC AVTDMIEPGS VMKPFVIAKA LDSGKVDTTD TFNTLPYKIG PATVQ-DTHV
Consistency ***** 98***7**** **89*79778 67**6***** 786*73****

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	359	369	379	389	399
wt	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternI	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternII	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternIII	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternIV	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternV	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternVI	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternVII	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternVIII	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternIX	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternXI	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternXII	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternXIII	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternXIV	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternXV	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternXVI	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternXVII	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternXVIII	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternXIX	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternXX	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternXXI	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternXXII	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternXXIV	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternXXV	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternXXVI	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternXXVII	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternXXVIII	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternXXIX	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternXXX_nM	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternXXXIII	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternXXXVII	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternX	YPTLDVRGIM	QKSSNVGTSK	LSAMFTPKEEM	YDFYHDLGVG	VRMHSGFPPGE
patternXXIII	YPSLDVRGIM	QKSSNVGTSK	LSARFGAEEM	YDFYHELIG	VRMHSGFPPGE
patternXXX	YPTLDVRGIM	QKSSNVGTSK	LSAMFTPKEEM	YDFYHDLGVG	VRMHSGFPPGE
patternXXXI	YPTLDVRGIM	QKSSNVGTSK	LSAMFTPKEEM	YDFYHDLGVG	VRMHSGFPPGE
patternXXXII	YPTLDVRGIM	QKSSNVGTSK	LSAMFTPKEEM	YDFYHDLGVG	VRMHSGFPPGE
patternXXXIV	YPTLDVRGIM	QKSSNVGTSK	LSAMFTPKEEM	YDFYHDLGVG	VRMHSGFPPGE
patternCII	YPTLDVRGIM	QKSSNVGTSK	LSAMFTPKEEM	YDFYHDLGVG	VRMHSGFPPGE
patternCI	YPTLDVRGIM	QKSSNVGTSK	LSAMFTPKEEM	YDFYHDLGVG	VRMHSGFPPGE
patternII Ig&Iva	YPTLDVRGIM	QKSSNVGTSK	LSAMFTPKEEM	YDFYHDLGVG	VRMHSGFPPGE
patternIIIh	YPTLDVRGIM	QKSSNVGTSK	LSAMFTPKEEM	YDFYHDLGVG	VRMHSGFPPGE
patternXXXVI	YPSLDVRGIM	QKSSNVGTSK	LSARFSSKEM	YDLYHSLGIG	VRMHSGFPPGE
patternXXXVIII	YPTLDVRGIM	QKSSNVGTSK	LSAMFTPKEEM	YDFYHDLGVG	VRMHSGFPPGE
mosaic2	YPTLDVRGIM	QKSSNVGTSK	LSAMFTPKEEM	YDFYHDLGVG	VRMHSGFPPGE
mosaic3	YPTLDVRGIM	QKSSNVGTSK	LSAMFTPKEEM	YDFYHDLGVG	VRMHSGFPPGE
mosaic4	YPTLDVRGIM	QKSSNVGTSK	LSAMFTPKEEM	YDFYHDLGVG	VRMHSGFPPGE
NG-3	YPTLDVRGIM	QKSSNVGTSK	LSAMFTPKEEM	YDFYHDLGVG	VRMHSGFPPGE
30/02	YPTLDVRGIM	QKSSNVGTSK	LSAMFTPKEEM	YDFYHDLGVG	VRMHSGFPPGE
35/02	YPTLDVRGIM	QKSSNVGTSK	LSAMFTPKEEM	YDFYHDLGVG	VRMHSGFPPGE
patternC	YPTLDVRGIM	QKSSNVGTSK	LSAMFTPKEEM	YDFYHDLGVG	VRMHSGFPPGE
Consistency	**8*****	*****	***6*667**	**9**8**9*	*****


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      ....|....| ....|....| ....|....| ....|....| ....|....|
      409      419      429      439      449
wt      TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternI TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternII TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternIII TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternIV TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternV TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternVI TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternVII TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternVIII TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternIX TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternXI TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternXII TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternXIII TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternXIV TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternXV TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternXVI TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternXVII TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternXVIII TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternXIX TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternXX TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternXXI TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternXXII TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternXXIII TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternXXIV TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternXXV TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternXXVI TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternXXVII TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternXXVIII TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternXXIX TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternXXX_nM TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternXXXIII TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternXXXVII TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPLSF
patternX TAGLLRSWRR WQKIEQATMS FGYGLQSL SLL QLARAYTVLT HDGELLPVSF
patternXXIII TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTVLT HDGELLPVSF
patternXXX TAGLLRSWRR WQKIEQATMS FGYGLQSL SLL QLARAYTVLT HDGELLPVSF
patternXXXI TAGLLRSWRR WQKIEQATMS FGYGLQSL SLL QLARAYTVLT HDGELLPVSF
patternXXXII TAGLLRSWRR WQKIEQATMS FGYGLQSL SLL QLARAYTVLT HDGELLPVSF
patternXXXIII TAGLLRSWRR WQKIEQATMS FGYGLQSL SLL QLARAYTVLT HDGELLPVSF
patternXXXIV TAGLLRSWRR WQKIEQATMS FGYGLQSL SLL QLARAYTVLT HDGELLPVSF
patternCII TAGLLRSWRR WQKIEQATMS FGYGLQSL SLL QLARAYTVLT HDGELLPVSF
patternCI TAGLLRSWRR WQKIEQATMS FGYGLQSL SLL QLARAYTVLT HDGELLPVSF
patternIIIg&Iva TAGLLRSWRR WQKIEQATMS FGYGLQSL SLL QLARAYTVLT HDGELLPVSF
patternIIIh TAGLLRSWRR WQKIEQATMS FGYGLQSL SLL QLARAYTVLT HDGELLPVSF
patternXXXVI SAGVLRNWRK WRPIEQATMS FGYGLQSL SLL QLARAYTVLT HDGVLLPVSF
patternXXXVIII TAGLLRNWRR WRPIEQATMS FGYGLQSL SLL QLARAYTALT HDGVLLPVSF
mosaic2 TAGLLRSWRR WQKIEQATMS FGYGLQSL SLL QLARAYTVLT HDGELLPVSF
mosaic3 TAGLLRSWRR WQKIEQATMS FGYGLQSL SLL QLARAYTVLT HDGELLPVSF
mosaic4 TAGLLRSWRR WQKIEQATMS FGYGLQSL SLL QLARAYTVLT HDGELLPVSF
NG-3 TAGLLRSWRR WQKIEQATMS FGYGLQSL SLL QLARAYTVLT HDGELLPVSF
30/02 TAGLLRSWRR WQKIEQATMS FGYGLQSL SLL QLARAYTVLT HDGELLPVSF
35/02 TAGLLRSWRR WQKIEQATMS FGYGLQSL SLL QLARAYTVLT HDGELLPVSF
patternC SAGVLRNWRK WRPIEQATMS FGYGLQSL SLL QLARAYTVLT HDGELLPVSF
Consistency 9**9**8**9 *87***** *****7** ***6***8**

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	459	469	479	488	498	
wt	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternI	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternII	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternIII	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternIV	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternV	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternVI	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternVII	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternVIII	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternIX	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternXI	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternXII	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternXIII	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternXIV	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternXV	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternXVI	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternXVII	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternXVIII	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternXIX	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternXX	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternXXI	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternXXII	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternXXIV	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternXXV	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternXXVI	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternXXVII	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternXXVIII	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternXXX_nM	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternXXXIII	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternXXXVII	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
patternX	EKQAVAPK	GK RVIKAS	TAKK VR	ELMVSVTE	AGGTGTAG	- VDGFDVGA
patternXXIII	EKQAVAPK	GK RVIKAS	TAKK VR	ELMVSVTE	AGGTGTAG	- VDGFDVGA
patternXXX	EKQAVAPK	GK RVIKAS	TAKK VR	ELMVSVTE	AGGTGTAG	- VDGFDVGA
patternXXXI	EKQAVAPK	GK RVIKAS	TAKK VR	ELMVSVTE	AGGTGTAG	- VDGFDVGA
patternXXXII	EKQAVAPK	GK RVIKAS	TAKK VR	ELMVSVTE	AGGTGTAG	- VDGFDVGA
patternXXXIV	EKQAVAPK	GK RVIKAS	TAKK VR	ELMVSVTE	AGGTGTAG	- VDGFDVGA
patternCII	EKQAVAPK	GK RVIKAS	TAKK VR	ELMVSVTE	AGGTGTAG	- VDGFDVGA
patternCI	EKQAVAPK	GK RVIKAS	TAKK VR	ELMVSVTE	AGGTGTAG	- VDGFDVGA
patternII Ig&Iva	EKQAVAPK	GK RVIKAS	TAKK VR	ELMVSVTE	AGGTGTAG	- VDGFDVGA
patternIIIh	EKQAVAPK	GK RVIKAS	TAKK VR	ELMVSVTE	AGGTGTAG	- VDGFDVGA
patternXXXVI	EKQAVAPK	GK RVIKAS	TAKK VR	ELMVSVTE	AGGTGTAG	- VDGFDVGA
patternXXXVIII	EKQAVAPQ	GK RIFKE	STARE VR	NLMVSVTE	PGGTGTAG	- VDGFDVGA
mosaic2	EKQAVAPK	GK RVIKAS	TAKK VR	ELMVSVTE	AGGTGTAG	- VDGFDVGA
mosaic3	EKQAVAPK	GK RVIKAS	TAKK VR	ELMVSVTE	AGGTGTAG	- VDGFDVGA
mosaic4	EKQAVAPK	GK RVIKAS	TAKK VR	ELMVSVTE	AGGTGTAG	- VDGFDVGA
NG-3	EKQAVAPK	GK RVIKAS	TAKK VR	ELMVSVTE	AGGTGTAG	- VDGFDVGA
30/02	EKQAVAPK	GK RVIKAS	TAKK VR	ELMVSVTE	AGGTGTAG	- VDGFDVGA
35/02	EKQAVAPK	GK RVIKAS	TAKK VR	ELMVSVTE	AGGTGTAG	- VDGFDVGA
patternC	EKQAVAPK	GK RVIKAS	TAKK VR	ELMVSVTE	AGGSGLAG	- VDGFDVGA
Consistency	*****7**	*97*69**87	**7*****	6**9*9***0	*****	

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      ....|....| ....|....| ....|....| ....|....| ....|....|
      508      518      528      538      548
wt      GTARKEVNGR YADNKHVATF IGFAPAKNPR VIVAVTIDEP TAHGYYGQGVV
patternI      GTARKEVNGR YADNKHVATF IGFAPAKNPR VIVAVTIDEP TAHGYYGQGVV
patternII     GTARKLVNGR YVDNKHVGTG IGFAPAKNPR VIVAVTIDEP TAHGYYGQGVV
patternIII    GTARKLVNGR YVDNKHVGTG IGFAPAKNPR VIVAVTIDEP TAHGYYGQGVV
patternIV     GTARKLVNGR YVDNKHVGTG IGFAPAKNPR VIVAVTIDEP TAHSYYGGVV
patternV      GTARKLVNGR YVDNKHVGTG IGFAPAKNPR VIVAVTIDEP TAHSYYGGVV
patternVI     GTARKLVNGR YVDNKHVATF IGFAPAKNPR VIVAVTIDEP TAHGYYGQGVV
patternVII    GTVRKLVNGR YVDNKHVATF IGFAPAKNPR VIVAVTIDEP TAHSYYGGVV
patternVIII   GTVRKLVNGR YVDNKHVATF IGFAPAKNPR VIVAVTIDEP TAHSYYGGVV
patternIX     GTARKLVNGR YVDNKHVGTG IGFAPAKNPR VIVAVTIDEP TAHGYYGQGVV
patternXI     GTVRKLVNGR YVDNKHVGTG IGFAPAKNPR VIVAVTIDEP TAHGYYGQGVV
patternXII    GTARKLVNGR YVDNKHVGTG IGFAPAKNPR VIVAVTIDEP TAHGYYGQGVV
patternXIII   GTVRKLVNGR YVDNKHVGTG IGFAPAKNPR VIVAVTIDEP TAHGYYGQGVV
patternXIV    GTARKLVNGR YVDNKHVGTG IGFAPAKNPR VIVAVTIDEP TANGYYGGVV
patternXV     GTARKEVNGR YADNKHVATF IGFAPAKNPR VIVAVTIDEP TANGYYGGVV
patternXVI    GTARKLVNGR YVDNKHVGTG IGFAPAKNPR VIVAVTIDEP TAHGYYGQGVV
patternXVII   GTVRKLVNGR YVDNKHVGTG IGFAPAKNPR VIVAVTIDEP TAHSYYGGVV
patternXVIII  GTTRKLVNGR YVDNKHVGTG IGFAPAKNPR VIVAVTIDEP TAHSYYGGVV
patternXIX    GTARKLVNGR YVDNKHVGTG IGFAPAKNPR VIVAVTIDEP TANGYYGGVV
patternXX     GTARKLVNGR YVDNKHVGTG IGFAPAKNPR VIVAVTIDEP TANGYYGGVV
patternXXI    GTVRKLVNGR YVDNKHVATF IGFAPAKNPR VIVAVTIDEP TANGYYGGVV
patternXXII   GTARKLVNGR YVDNKHVGTG IGFAPAKNPR VIVAVTIDEP TANGYYGGVV
patternXXIII  GTARKLVNGR YVDNKHVGTG IGFAPAKNPR VIVAVTIDEP TAHSYYGGVV
patternXXIV   GTARKLVNGR YVDNKHVGTG IGFAPAKNPR VIVAVTIDEP TAHSYYGGVV
patternXXV    GTTRKLVNGR YVDNKHVGTG IGFAPAKNPR VIVAVTIDEP TAHSYYGGVV
patternXXVI   GTVRKLVNGR YVDNKHVGTG IGFAPAKNPR VIVAVTIDEP TAHSYYGGVV
patternXXVII  GTVRKLVNGR YVDNKHVGTG IGFAPAKNPR VIVAVTIDEP TAHGYYGQGVV
patternXXVIII GTVRKLVNGR YVDNKHVGTG IGFAPAKNPR VIVAVTIDEP TAHGYYGQGVV
patternXXIX   GTVRKLVNGR YVDNKHVGTG IGFAPAKNPR VIVAVTIDEP TAYGYGGVV
patternXXX_nM GTTRKLVNGR YVDNKHVGTG IGFAPAKNPR VIVAVTIDEP TAHSYYGGVV
patternXXXIII GTVRKLVNGR YVDNKHVGTG IGFAPAKNPR VIVAVTIDEP TAHSYYGGVV
patternXXXVII GTARKLVNGR YVDNKHVGTG IGFAPAKNPR VIVAVTIDEP TAHGYYGQGVV
patternX      GTARKLVNGR YVDYKHVATF IGFAPAKNPR VIVAVTIDEP TANGYYSGVV
patternXXIII  GTARKLVNGR YVDYKHVATF IGFAPAKNPR VIVAVTIDEP TANGYYSGVV
patternXXX    GTVRKLVNGR YVDYKHVATF IGFAPAKNPR VIVAVTIDEP TANGYYSGVV
patternXXXI   GTARKLVNGR YVDYKHVATF IGFAPAKNPR VIVAVTIDEP TANGYYSGVV
patternXXXII  GTARKLVNGR YVDYKHVATF IGFAPAKNPR VIVAVTIDEP TANGYYSGVV
patternXXXIII GTARKLVNGR YVDYKHVATF IGFAPAKNPR VIVAVTIDEP TANGYYSGVV
patternXXXIV  GTARKLVNGR YVDYKHVATF IGFAPAKNPR VIVAVTIDEP TANGYYSGVV
patternCII    GTARKEVNGR YVDYKHVATF IGFAPAKNPR VIVAVTIDEP TANGYYSGVV
patternCI     GTPRKLVNGR YVDYKHVATF IGFAPAKNPR VIVAVTIDEP TANGYYSGVV
patternIIIg&Iva GTARKLVNGR YVDYKHVATF IGFAPAKNPR VIVAVTIDEP TANGYYSGVV
patternIIUh   GTARKLVNGR YVDYKHVATF IGFAPAKNPR VIVAVTIDEP TANGYYSGVV
patternXXXVI  GTARKLVNGR YVDNKHVATF IGFAPAKNPR VIVAVTIDEP TANGYYGGVV
patternXXXVIII GTARKEVNGR YADNKHVATF IGFAPAKNPR VIVAVTIDEP TAHGYYGQGVV
mosaic2      GTARKLVNGR YVDYKHVATF IGFAPAKNPR VIVAVTIDEP TANGYYSGVV
mosaic3      GTARKLVNGR YVDYKHVATF IGFAPAKNPR VIVAVTIDEP TANGYYSGVV
mosaic4      GTVRKLVNGR YVDNKHVATF IGFAPAKNPR VIVAVTIDEP TANGYYGGVV
NG-3        GTARKLVNGR YVDYKHVATF IGFAPAKNPR VIVAVTIDEP TANGYYSGVV
30/02       GTARKLVNGR YVDYKHVATF IGFAPAKNPR VIVAVTIDEP TANGYYSGVV
35/02       GTARKLVNGR YVDYKHVATF IGFAPAKNPR VIVAVTIDEP TANGYYSGVV
patternC     GTARKLVNGR YVDYKHVATF IGFAPAKNPR VIVAVTIDEP TANGYYSGVV
Consistency  **7**9**** *9*6**97** ***** **9*9**** **78**7***

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      ....|....| ....|....| ....|....| ....
      558      568      577  581
wt      AGPPFKKIMG  GSLNILGISP  TKPLT-AAAV  KTPS
patternI      AGPPFKKIMG  GSLNILGISP  TKPLT-AAAV  KTPS
patternII     AGPPFKKIMG  GSLNILGISP  TKPLT-AAAV  KTPS
patternIII    AGPPFKKIMG  GSLNILGVSP  TKPLTNVA AV  KTPS
patternIV     AGPPFKKIMG  GSLNILGISP  TKPLT-AAAV  KTPS
patternV      AGPPFKKIMG  GSLNILGVSP  TKPLTNVA AV  KTPS
patternVI     AGLPFKKIMG  GSLNILGISP  TKPLT-AAAV  KTPS
patternVII    AGPPFKKIMG  GSLNILGISP  TKPLT-AAAV  KTPS
patternVIII   AGLPFKKIMG  GSLNILGISP  TKPLT-AAAV  KTPS
patternIX     AGLPFKKIMG  GSLNILGISP  TKPLT-AAAV  KTPS
patternXI     AGLPFKKIMG  GSLNILGISP  TKPLT-AAAV  KTPS
patternXII    AGSPFKKIMG  GSLNILGISP  TKPLT-AAAV  KTPS
patternXIII   AGSPFKKIMG  GSLNILGISP  TKPLT-AAAV  KTPS
patternXIV    AGPPFKKIMG  GSLNILGISP  TKPLT-AAAV  KTPS
patternXV     AGPPFKKIMG  GSLNILGISP  TKPLT-AAAV  KTPS
patternXVI    AGPPFKKIMG  GSLNILGISP  TKPLTNVA AV  KTPS
patternXVII   AGPPFKKIMG  GSLNILGVSP  TKPLTNVA AV  KTPS
patternXVIII  AGPPFKKIMG  GSLNILGVSP  TKPLTNVA AV  KTPS
patternXIX    AGPPFKKIMG  GSLNILGVSP  TKPLTNVA AV  KTPS
patternXX     AGPPFKKIMG  GSLNILGVSP  TKPLTNVA AV  KTPS
patternXXI    AGPVFKQVMG  GSLNILGVSP  TKPLTNVA AV  KTPS
patternXXII   AGPVFKQVMG  GSLNILGVSP  TKPLTNVA AV  KTPS
patternXXIII  AGSPFKKIMG  GSLNILGVSP  TKPLTNVA AV  KTPS
patternXXIV   AGPPFKKIMG  GSLNILGISP  TKPLT-AAAV  KTPS
patternXXV    AGPPFKKIMG  GSLNILGISP  TKPLT-AAAV  KTPS
patternXXVI   AGSPFKKIMG  GSLNILGVSP  TKPLT-AAAV  KTPS
patternXXVII  AGPPFKKIMG  GSLNILGISP  TKPLT-AAAV  KTPS
patternXXVIII AGPPFKKIMG  GSLNILGVSP  TKPLT-AAAV  KTPS
patternXXIX   AGPPFKKIMG  GSLNILGISP  TKPLT-AAAV  KTPS
patternXXX_nM AGPPFKKIMG  GSLNVLGISP  TKPLT-AAAV  KTPS
patternXXXIII AGPPFKKIMG  GSLNILGISP  TKPLT-AAAV  KTPS
patternXXXVII AGSPFKKIMG  GSLNILGISP  TKPLT-AAAV  KTPS
patternX      TGPVFKQVMG  GSLNILGVSP  TKPLTNVA AV  KTPS
patternXXIII  TGPVFKLVMG  GSLNILGVSP  TKPLTNVA AV  KTPS
patternXXX    TGPVFKQVMG  GSLNILGVSP  TKPLTNVA AV  KTPS
patternXXXI   TGPVFKQVMG  GSLNILGVSP  TKPLTNVA AV  KTPS
patternXXXII  AGLPFKKIMG  GSLNILGISP  TKPLT-AAAV  KTPS
patternXXXIII AGPPFKKIMG  GSLNILGISP  TKPLT-AAAV  KTPS
patternXXXIV  AGPPFKKIMG  GSLNILGISP  TKPLT-AAAV  KTPS
patternCII    AGPPFKKIMG  GSLNILGISP  TKPLT-AAAV  KTPS
patternCI     AGPPFKKIMG  GSLNILGISP  TKPLT-AAAV  KTPS
patternIIIg&Iva AGPPFKKIMG  GSLNILGISP  TKPLT-AAAV  KTPS
patternIIIfh  TGPVFKKIMG  GSLNILGISP  TKPLT-AAAV  KTPS
patternXXXVI  TGPVFKQVMG  GSLNILGVSP  TKPLTNVA AV  KTPS
patternXXXVIII AGPPFKKIMG  GSLNILGISP  TKPLT-AAAV  KTPS
mosaic2      TGPVFKQVMG  GSLNILGVSP  TKPLTNVA AV  KTPS
mosaic3      TGPVFKQVMG  GSLNILGVSP  TKPLTNVA AV  KTPS
mosaic4      TGPVFKQVMG  GSLNILGVSP  TKPLTNVA AV  KTPS
NG-3        TGPVFKQVMG  GSLNILGVSP  TKPLTNVA AV  KTPS
30/02       TGPVFKQVMG  GSLNILGVSP  TKPLTNVA AV  KTPS
35/02       TGPVFKQVMG  GSLNILGVSP  TKPLTNVA AV  KTPS
patternC     TGPVFKQVMG  GSLNILGVSP  TKPLTNVA AV  KTPS
Consistency  7*76**79**  ****9**9**  *****17***  ****

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