

A	2																								
R	-2	6																							
N	0	0	2																						
D	0	-1	2	4																					
C	-2	-4	-4	-5	12																				
Q	0	1	1	2	-5	4																			
E	0	-1	1	3	-5	2	4																		
G	1	-3	0	1	-3	-1	0	5																	
H	-1	2	2	1	-3	3	1	-2	6																
I	-1	-2	-2	-2	-2	-2	-2	-3	-2	5															
L	-2	-3	-3	-4	-6	-2	-3	-4	-2	-2	6														
K	-1	3	1	0	-5	1	0	-2	0	-2	-3	5													
M	-1	0	-2	-3	-5	-1	-2	-3	-2	2	4	0	6												
F	-3	-4	-3	-6	-4	-5	-5	-5	-2	1	2	-5	0	9											
P	1	0	0	-1	-3	0	-1	0	0	-2	-3	-1	-2	-5	6										
S	1	0	1	0	0	-1	0	1	-1	-1	-3	0	-2	-3	1	2									
T	1	-1	0	0	-2	-1	0	0	-1	0	-2	0	-1	-3	0	1	3								
W	-6	2	-4	-7	-8	-5	-7	-7	-3	-5	-2	-3	-4	0	-6	-2	-5	17							
Y	-3	-4	-2	-4	0	-4	-4	-5	0	-1	-1	-4	-2	7	-5	-3	-3	0	10						
V	0	-2	-2	-2	-2	-2	-2	-1	-2	4	2	-2	2	-1	-1	-1	0	-6	-2	4					
	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V					

FIGURE 3.14. Log-odds matrix for PAM250. High PAM values (e.g., PAM250) are useful for aligning very divergent sequences. A variety of algorithms for pairwise alignment, multiple sequence alignment, and database searching (e.g., BLAST) allow you to select an assortment of PAM matrices such as PAM250, PAM70, and PAM30.