

<b>A</b>	4																																
<b>R</b>	-1	5																															
<b>N</b>	-2	0	6																														
<b>D</b>	-2	-2	1	6																													
<b>C</b>	0	-3	-3	-3	9																												
<b>Q</b>	-1	1	0	0	-3	5																											
<b>E</b>	-1	0	0	2	-4	2	5																										
<b>G</b>	0	-2	0	-1	-3	-2	-2	6																									
<b>H</b>	-2	0	1	-1	-3	0	0	-2	8																								
<b>I</b>	-1	-3	-3	-3	-1	-3	-3	-4	-3	4																							
<b>L</b>	-1	-2	-3	-4	-1	-2	-3	-4	-3	2	4																						
<b>K</b>	-1	2	0	-1	-1	1	1	-2	-1	-3	-2	5																					
<b>M</b>	-1	-2	-2	-3	-1	0	-2	-3	-2	1	2	-1	5																				
<b>F</b>	-2	-3	-3	-3	-2	-3	-3	-3	-1	0	0	-3	0	6																			
<b>P</b>	-1	-2	-2	-1	-3	-1	-1	-2	-2	-3	-3	-1	-2	-4	7																		
<b>S</b>	1	-1	1	0	-1	0	0	0	-1	-2	-2	0	-1	-2	-1	4																	
<b>T</b>	0	-1	0	-1	-1	-1	-1	-2	-2	-1	-1	-1	-1	-2	-1	1	5																
<b>W</b>	-3	-3	-4	-4	-2	-2	-3	-2	-2	-3	-2	-3	-1	1	-4	-3	-2	11															
<b>Y</b>	-2	-2	-2	-3	-2	-1	-2	-3	2	-1	-1	-2	-1	3	-3	-2	-2	2	7														
<b>V</b>	0	-3	-3	-3	-1	-2	-2	-3	-3	3	1	-2	1	-1	-2	-2	0	-3	-1	4													
	<b>A</b>	<b>R</b>	<b>N</b>	<b>D</b>	<b>C</b>	<b>Q</b>	<b>E</b>	<b>G</b>	<b>H</b>	<b>I</b>	<b>L</b>	<b>K</b>	<b>M</b>	<b>F</b>	<b>P</b>	<b>S</b>	<b>T</b>	<b>W</b>	<b>Y</b>	<b>V</b>													

FIGURE 3.17. *The BLOSUM62 scoring matrix of Henikoff and Henikoff (1992). This matrix merges all proteins in an alignment that have 62% amino acid identity or greater into one sequence. BLOSUM62 performs better than alternative BLOSUM matrices or a variety of PAM matrices at detecting distant relationships between proteins. It is thus the default scoring matrix for most database search programs such as BLAST (Chapter 4). Used with permission.*