	Y	G	D	T	D	S	T L I V	M F	L A I V M	Y A I T K E R L S	H V F C	P G Y V K R
hHSV1	TAC	GGG	GAC	ACG	GAC	TCC	ATA	TTT	GTG	CTG	TGC	CGC
hVZV	TAT	GGA	GAT	ACG	GAT	TCT	GTG	TTT	ATC	CGA	TTC	AAG
eHV1	TAC	GGA	GAC	ACC	GAC	TCC	GTG	TTT	ATC	AAG	TTT	GTG
hHV6	TAT	GGT	GAT	ACG	GAT	AGC	ATC	TTT	ATG	TCT	GTC	AGA
hHV7	TAT	GGT	GAT	ACT	GAC	AGT	CTT	TTT	GTT	ACT	TTC	AAA
hCMV	TAC	GGG	GAC	ACG	GAC	TCC	ATA	TTT	GTG	CTG	TGC	CGC
gpCMV	TAC	GGG	GAC	ACG	GAC	AGC	GTC	TTT	GTC	ATA	TGC	GGC
mCMV	TAC	GGC	GAC	ACC	GAC	AGT	GTG	TTT	GCG	GCT	TTC	TAC
HVS	TAT	GGA	GAC	ACA	GAC	TCT	CTA	TTT	GTA	GAA	TGT	GTT
hEBV	TAC	GGG	GAC	ACG	GAC	TCG	CTG	TTT	ATC	GAG	TGC	CGG
iHV1	TAT	GGG	GAT	ACG	GAT	AGT	ACG	ATG	CTG	TAC	CAC	CCA
5′–TAY	GGN	GAY	CAN	GAY–3′								
3′–ATR	CCN	CTR	GTN	CTR–5′								

FIGURE 27.2. Designing PCR primers. Alignment of a region of the DNA polymerase genes from a sample of herpesviruses (abbreviations of the virus names given in leftmost column). The different amino acids present at each position in these samples (e.g., the first amino acid is Y in all of the viruses, the seventh varies among TLIV) are shown above the *top horizontal bar*. The amino acid abbreviations are as in Figure 2.23. An alignment of the DNA sequences encoding these proteins is shown with conserved nucleotides highlighted in *blue* and with each codon separated. Note that even related viruses frequently use different codons for the same amino acid. "Degenerate" PCR primers could be designed from this alignment that take into account the variation in codon usage and even the choice of amino acid. Such primers would include a mixture of all the possible sequences. Even when a protein's amino acid sequence is 100% conserved between species, the degeneracy of the genetic code usually prevents the use of nondegenerate primers. This is an important consideration because PCR works better with less degenerate primers. (Modified from Rose T.M. *Nucleic Acids Res.* **26:** 1628–1635, Fig. 2, © 1998 Oxford University Press.)