Table 3. Summary of interaction energies in molecular models of 1,25D or CF in VDRwt and the receptor mutants S278A and Y143F/S278A

Ligand	Chair/ seco-B ring orientation	VDR pocket	VDRwt I_E, kcal/mol	VDR wt, ΔI_E	VDR S278A I_E, kcal/mol	VDR S278A, ΔI_E	VDR Y143F/ S278A I_E, kcal/mol	VDR Y143F/ S278A, ΔI_E
1,25D	β/trans	G	-108	17	-106	17	-101	13
	β/cis	A	-93		-89		-87	
	α/trans	A	-88		-88		-89	
CF*	β/trans	G	-98	16	-99	18	-96	21
	β/cis	A	-85		-81		*-73*	
	α/trans	A	*-76*		-83†		*-76*	

The I_Es and the ΔI_Es were calculated as described in Table 1. Complexes where no A-ring H-bonds are formed with S237, R274, Y143, or S278 are indicated in italics.

*CF has an α/β-chair ratio of ≈35:65 in chloroform (based on known 1,25D and 25D A-ring chair equilibria) and therefore has been factored into the ΔI_E value; see ¶, Table 1.

†In the VDR S278A mutant, the 1 α-OH of CF formed an H-bond with S237 in the α/trans complex.