Table S1. Statistics of data sets and structure refinement		
	GR/Cortisol	GR/Mometasone
PDB code	4P6X	4P6W
Data collection		
APS beam line	APS-21ID	APS-21ID
Space group	P61	P23
Resolution, Å	30-2.5	30-1.95
Cell parameters, Å, °	a=b=220.8, c=74.2; α=β=90, γ=120	a=b=c=130.2; α=β=γ=90
Total/Unique reflections	650426 /71878	545016/53521
Completeness, %	100 (100)	99.4 (98.0)
I/σ	19.9 (5.2)	23.5 (2.0)
Redundancy	9.0 (7.6)	10.2 (3.7)
Rsym	0.10 (0.32)	0.128 (0.51)
Structure determination		
Resolution, Å	40-2.5	30-1.95
No. reflections	71517	53320
NCS molecules	6	1
No. residues	1362	264
No. solvent molecules	487	130
No. of non-H atoms	13695	2315
Rcryst	24.9%	20.8%
Rfree	29.2%	22.7%
rmsd bonds, Å	0.004	0.008
rmsd angles, °	0.886	1.671
Average B factor, $Å^2$	53.0	33.5
Ramachandran statistics	Favored 94.6%, Allowed 4.5%, Outliers 0.9%	Favored 97.7%, Allowed 2.3%, Outliers 0.0%
Rmsd is for root-mean-square deviation from ideal geometry of protein.		