Supplementary Table 1.

Metal Contents of purified Nur proteins[a].

	Number of Ni/ Nur monomer			Number Zn/ Nur monomer		
	1st	2nd	Avg	1st	2nd	Avg
WT	**0.56**	**0.48**	**0.52**	**0.55**	**0.69**	**0.62**
H72A	**0.35**	**0.18**	**0.27**	**0.6**	**0.58**	**0.59**
H90A	**0.49**	**0.35**	**0.42**	**0.47**	**0.57**	**0.52**

[a] Purified Nur proteins were subjected to ICP-AES to estimate metal contents (See Supplementary Methods). Analyzed values obtained from two separate preparations of three Nur proteins (wild type, H72A mutant, and H90A mutant) were presented. Amount of other metals, such as iron, manganese, and copper were under the detection limit (< 0.1 ppm). In the buffer solution, the amount of Ni and Zn were below the detection limit (< 0.1 ppm). The exact amount of detected metals in wild type Nur somewhat varies depending on purification conditions. Therefore, we purified two sets of three Nur proteins concomitantly for metal analysis and present values for each set of three.

Supplementary Table 2. Data collection and Refinement

Data sets, Space group	Peak, $P3_1$	Inflection, $P3_1$	Remote, $P3_1$
Wavelength (Å)	1.4847	1.4857	1.4510
Resolution (Å)	50-2.4	50-2.4	50-2.4
Completeness (%)[1]	99.8 (99.8)	99.8 (98.3)	99.8 (98.8)
R_{sym} (%)[1,2]	5.5 (54.0)	5.6 (58.1)	5.4 (57.8)
Number of unique reflections	18,205	18,186	18,240
Average Redundancy	3.7 (3.1)	3.7 (3.1)	3.7 (3.1)
Mosaicity	0.300	0.558	0.566
Refinement statistics			
Resolution range (Å)	20-2.4		
Number of hetero atoms			
Water	82		
Malonate	3		
Chloride	5		
Ethylene glycol	4		
R^3 (R_{free}) (%)	22.4(27.0)		
R.m.s. deviations[4]			
Bonds (Å)	0.007		
Angles (°)	1.3		

[1]The number in parentheses is for the outer shell

[2]$R_{sym} = \Sigma_{\Sigma h}\Sigma_{\Sigma I} |I_{h,i}-I_h| / \Sigma_{\Sigma h}\Sigma_{\Sigma I}\Sigma\Sigma I_{h,i}$, where I_h is the mean intensity of the i observations of symmetry related reflections of h.

[3] $R = \Sigma |F_o - F_c| / \Sigma F_o$, where $F_o = F_p$, and F_c is the calculated protein structure factor from the atomic model. R_{free} was calculated with 10 % of the reflections.
[4] R.m.s. deviations in bond length and angles are the deviations from ideal values.