Table S1. Crystallographic Data

	Native	Thimerosal	Mercury Acetate	Sodium Tungstate
a (Å)	52.2	52.3	52.6	52.1
b (Å)	121.4	121.7	121.8	120.8
c (Å)	127.5	127.6	127.8	127.4
Resolution (Å)	20-1.7 (1.76-1.7)	20-2.7 (2.8-2.7)	20-2.7 (2.8-2.7)	20-2.6 (2.69-2.6)
# total reflections	388,243	228,747	54,141	120,441
# unique reflections	82,849	22,696	20,785	25,089
Completeness (%)	92.3 (62.5)	100 (100)	89.7 (87.9)	99.5 (99.8)
Mosaicity (˚)	0.5	0.6	0.7	0.7
I/σ(I)	35.2 (5.0)	21.2 (9.3)	10.9 (4.6)	8.7 (2.9)
R_{merge} [a]	3.9 (25.9)	13.4 (26.9)	9.2 (19.4)	11.2 (26.8)

Numbers in parenthesis are for the high-resolution bin

[a] $R_{merge} = 100x\Sigma|I-<I>|/\Sigma I$

Table S2. Refinement statistics

R_{cryst} (%) [a]	17.4
R_{free} (%) [b]	20.7
# Protein residues modeled	741
# Solvent molecules	670
RMSD bonds (Å)	0.015
RMSD angles (˚)	1.554
ϕ, ψ Most favored (%)	92.7
ϕ, ψ Additional Allowed (%)	6.4
<B> Overall (Å^2)	19.9
<B> Main Chain (Å^2)	17.8
<B> Side Chains (Å^2)	20.2
<B> Water (Å^2)	28.0
<B> IP_6 (Å^2)	14.6

[a] $R_{cryst} = 100x\Sigma||F_{obs}|-k|F_{calc}||/\Sigma|F_{obs}|$

[b] R_{free} = The R_{factor} against 5% of the data removed prior to refinement

Stereochemistry was analyzed using PROCHECK (*S17*)