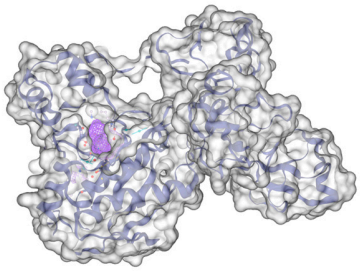
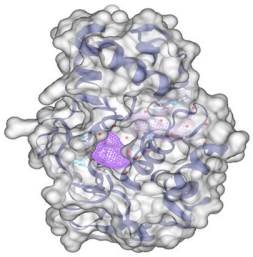
SUPPLEMENTARY MATERIAL

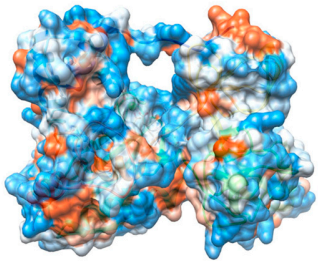
A



B



C



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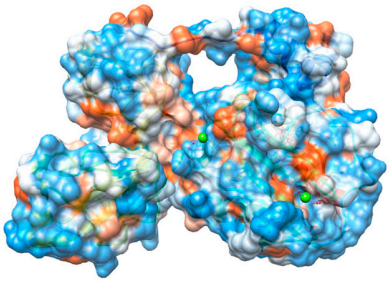

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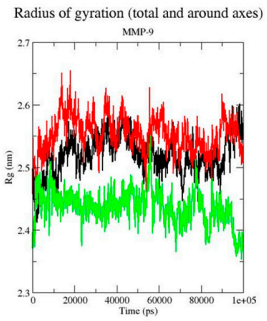

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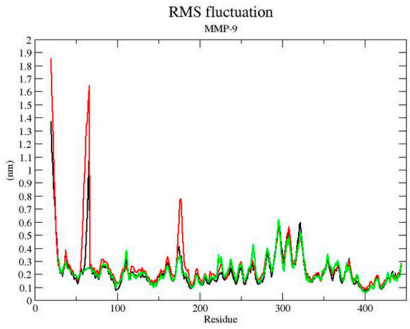

Figure S1.- Protein pockets calculated with Protein Plus server: (A) Binding site 1 and (B) Binding site 2.
Protein hydrophobic surface calculated with UCSF Chimera: (C) Back, Allosteric binding site region and (D) front, showing binding site 1 region. (blue=hydrophilic and orange=hydrophobic).
(E) Radius of gyration from MMP-9 calculated by molecular dynamic simulation: Binding site 1 (black), Binding site two (red) and allosteric binding site (green).
(F) RMSF of MMP-9 calculated by molecular dynamic simulation: Binding site 1 (black), Binding site two (red) and allosteric binding site (green).

Table S1.- Pocket properties calculated by Protein Plus server/

POCKET PROPERTIES	BINDING SITE 1	BINDING SITE 2
ACCEPTOR	11	7
DEPTH (Å)	12.92	6.30
DONORS	5	1
HYDROPHOBICITY	0.64	0.70
SURFACE ($Å^2$)	324.85	203.11
SURFACE VOLUME RATIO	1.59	2.31
VOLUME ($Å^3$)	204.80	88.06