A   Appendix

Table 2. Attributes of the structure used for for the project. PDB id: 4O3M

PDB ID	Experimental Method	Year of Deposition	Chain(s) covering BLM	Sequence Length	Resolution, R-value free, R-value work
4O3M	X-RAY DIFFRACTION	18/12/2013	A	659	2.3, 0.2153, 0.181

Side chain [1]	Side chain [2]	Distance (Å)
1036	1066	4.3
1063	1066	4.5
1066	1055	4.5
1063	1055	4.4
1063	1036	4.4
1055	1036	4.3

Table 3. Side chain distances for the binding side of Zn

Side chain [1]	Side chain [2]	Distance (Å)
982	1242	15.8
669	1242	8.3
672	1242	11.2
696	1242	10.7
668	1242	14.8
669	982	14.6
672	982	16.4
696	982	12.2
668	982	22.3

Table 4. Side chain distances for the binding side of ADP

Table 5. Variant Classification Based on $\Delta\Delta G$

Classification	$\Delta\Delta G$ Range (kcal/mol)
Stabilizing	$\Delta\Delta G \leq -3$
Neutral	$-2 < \Delta\Delta G < 2$
Uncertain	$2 \leq \Delta\Delta G < 3$ or $-3 \leq \Delta\Delta G < 3$
Destabilizing	$\Delta\Delta G \geq 3$

Percentage(%)	4O3M	Models
over 60	**693**, 699, 729, 753, 762, 764, 783, 853, **908**, 967, 973, 1004, **1023**, 1029, 1049, 1145, 1189, 1253, 1260, 1282, 1285	**693**, **908**,**1023**
over 70	**693**, 699, 753, 762, 764, 783, 853, 908, 1023, 1049, 1145, 1189, 1253	**693**
over 80	**693**, 699, 753, 1049	**693**

Table 6. Residues related to bloom syndrome where 60, 70, 80 % of mutations were destabilizing($\Delta\Delta G \geq 3$). Common residues are shown in **bold**.