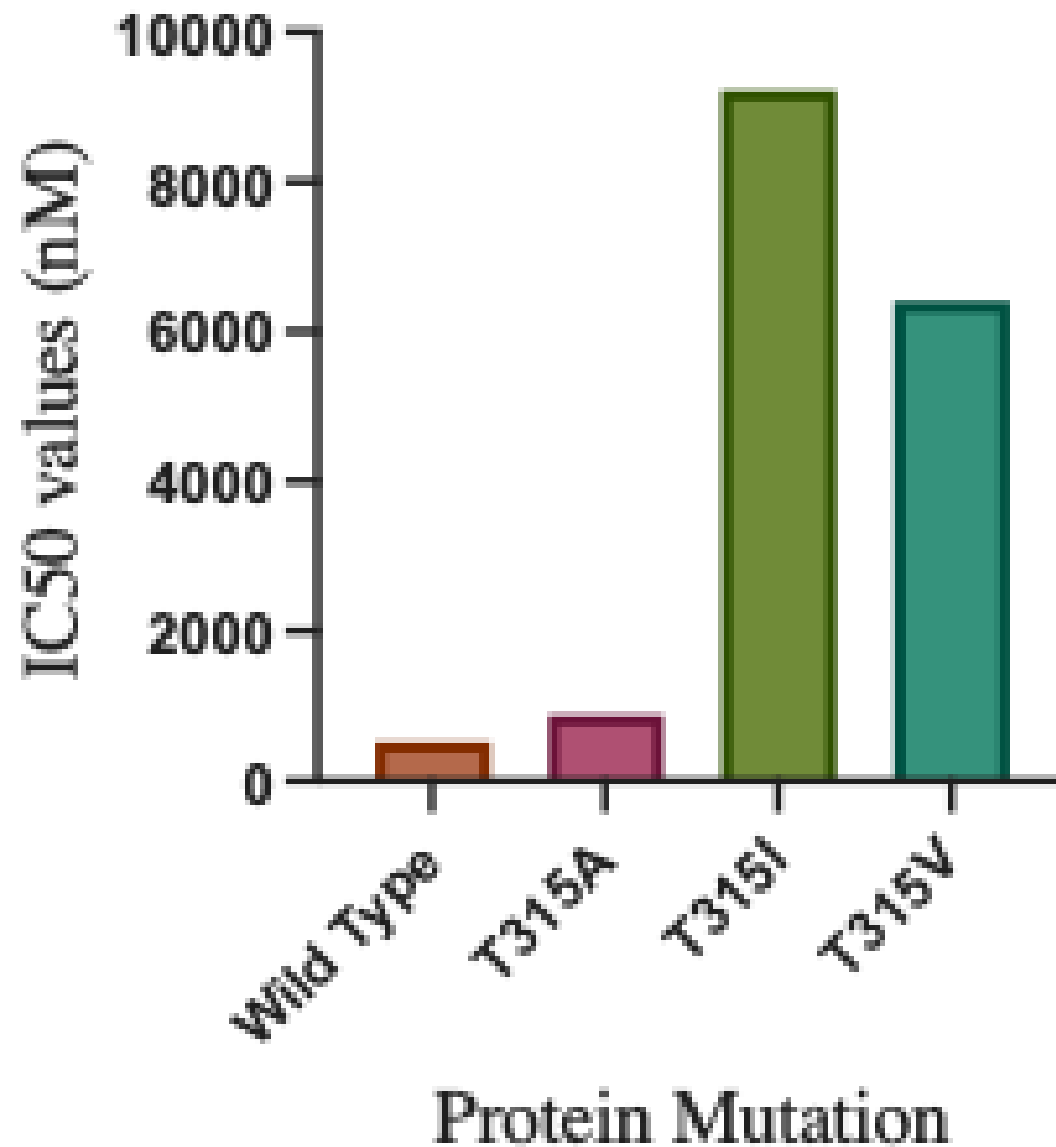


IC50 values (nM) needed to inhibit  
50% of the protein function

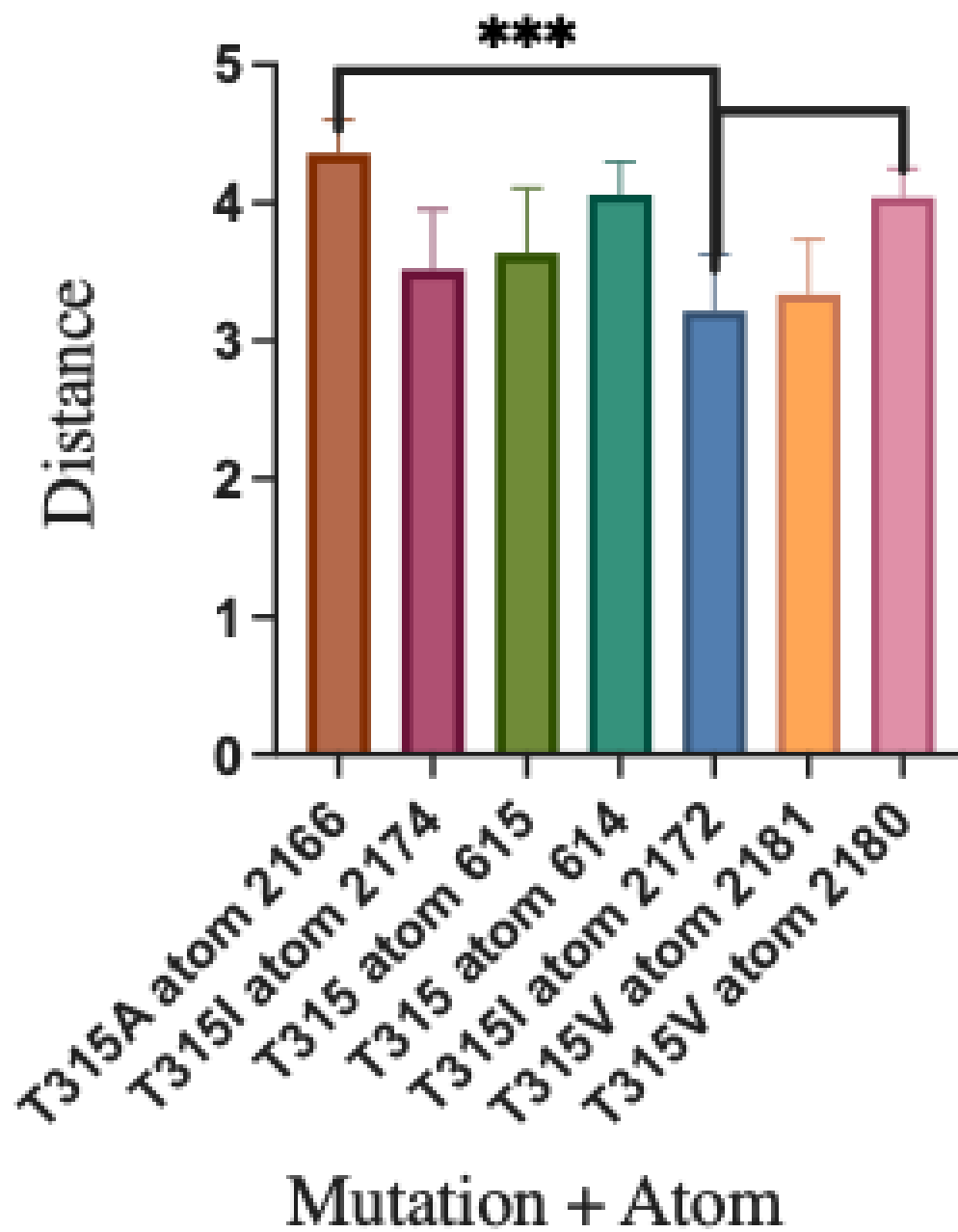


(Redaelli et al.)

Consensus	VSPNYDKWEMERTDITMKHKLGGGQYGEVYEGVWKKYSLTVAVKTLKEDTMEVEEFLKEA	287
Wildtype	.....	287
T315A	.....	287
T315I	.....	287
T315V	.....	287
Consensus	AVMKEIKHPNLVQLLGVCTREPPFYIIXEFMTYGNLLDYLRECNRQEVNAVLLYMATQI	347
Wildtype	.....T.....	347
T315A	.....A.....	347
T315I	.....I.....	347
T315V	.....V.....	347
Consensus	SSAMEYLEKKNFIHRDLAARNCLVGENHLVKVADFGLSRLMTGDTYTAHAGAKFPIKWTA	407
Wildtype	.....	407
T315A	.....	407
T315I	.....	407
T315V	.....	407
Consensus	PESLAYNKFSIKSDVWAFGVLLWEIATYGMSPYPGIDLSQVYELLEKDYRMERPEGCPEK	467
Wildtype	.....	467
T315A	.....	467
T315I	.....	467
T315V	.....	467
Consensus	VYELMRACWQWNPSDRPSFAEIHQAFETMFQES	500
Wildtype	.....	500
T315A	.....	500
T315I	.....	500
T315V	.....	500

Amino acid sequences of wildtype BCR-ABL compared to strings with mutations which are resistance to the TKI imatinib, notably the mutations occur in the T315 location for mutations

# Distance between T315 mutation and imatinib





3D structure of BCR-aBL in green, imatinib in blue,  
T315 amino acid in red