Algorithm	**RMSD threshold**	**Crystal structures**	**Protein models**		**Distorted structures**		
			High-quality	***Moderate-quality***	***2Å RMSD***	***4Å RMSD***	***6Å RMSD***
SOIPPA	2Å	6.3%	-	-	-	-	-
*e*MatchSite		15.6%	11.5%	6.5%	12.1%	7.3%	4.4%
SOIPPA	5Å	23.6%	-	-	-	-	-
*e*MatchSite		60.7%	56.4%	52.4%	59.5%	50.4%	40.0%