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·	rumoet of structures in samples A,B (isolatea/in situ)	02001,09400/10122,02401

p-value of non-parametric Kolmogorov-Smirnov two-sample test (isolated/in situ)	0.446/0.34
Kolmogorov-Smirnov two-sample test statistic (D) (isolated/in	0.0,1E-16
situ)	
Thoroughness of the structural sampling	
Sampling precision (isolated/in situ)	14.66/12.6 Å
Homogeneity of proportions χ^2 test p-value (Cramers V value)	1.000 (0.000) / 1.000 (0.000) (thresholds: p-value>0.05 OR
(isolated/in situ)	Cramer's V<0.1)
Number of clusters (isolated/in situ)	1/1
Cluster populations (isolated/in situ)	Cluster 1: 99/98 %
Cluster precisions (isolated/in situ)	Cluster 1: 15.42/10.1 Å
Average cross-correlation between localization probability den-	Cluster 1: $0.84/0.92$
sities of samples A and B (isolated/in situ)	
Validation by information used for modeling	
Percent of sequence connectivity restraints satisfied per struc-	99/99 %
ture (isolated/in situ)	
Percent cross-link restraints satisfied by ensemble (isolated/in	89/89 %
situ)	
Percent of transmembrane domain restraints satisfied by en-	98/99 %
semble (isolated/in situ)	
Percent of excluded volume restraints satisfied per structure	99/99 %
$(isolated/in \ situ)$,
6) Software and data availability	
Software	
Modeling programs	IMP PMI module, version develop-548de65454
	Integrative Modeling Platform (IMP), version develop-
	548de65454
Modeling scripts	https://github.com/integrativemodeling/NPC_v3.0
Homology detection and structure prediction	HHPred, version 2.0.16
Visualization and plotting	UCSF Chimera
	Matplotlib, version 3.0.3
Data	
PDB-dev accesion code	TBD