39c22a602	1) Gathering information	
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Resolution of unstructured components 20 [R20] residues per bead 92.49 % RB1: rpobs_1342 RB2: rpocs_831, rpoc135-1374 REcluded volume; applied to the R1 representation pE-MAP MIC pair-restraints; applied to the R1 representation pE-MAP mic pair restraints; applied to the R1 representation pE-MAP mic pair restraints; applied to the R1 representation pE-MAP mic pair restraints; applied to the R1 representation pE-MAP mic pair restraints; applied to the R1 representation pE-MAP mic pair restraints; applied to the R1 representation pE-MAP mic pair restraints; applied to the R1 representation pE-MAP mic pair restraints; applied to the R1 representation pE-MAP mic pair restraints; applied to the R1 representation pE-MAP mic pair restraints; applied to the R1 representation pE-MAP mic pair restraints; applied to the R1 representation pE-MAP mic pair restraints; applied to the R1 representation pE-MAP mic pair restraints; applied to the R1 representation pE-MAP mic pair restraints; applied to the R1 representation pE-MAP mic pair restraints; applied to the R1 representation pE-MAP mic pair restraints; applied to the R1 representation pE-MAP mic pair restraints; applied to the R1 representation pE-MAP mic pair restraints; applied to the R1 representation pE-MAP mic pair restraints; applied to t		rpoc: 932-1134
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RB2: rpocs_saj.rpocs_list=137-12	Structural coverage	92.49 %
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$39\mathrm{c}22\mathrm{a}602$	Percent of sequence connectivity restraints satisfied per structure Percent pE-MAP restraints satisfied per structure Percent of excluded volume restraints satisfied per structure 5) Benchmark Structural accuracy (95 % CI) PDB used for benchmark 6) Software and data availability	94 % 99 % 15.0 (12.1-18.2) Å 4YG2
	Percent of sequence connectivity restraints satisfied per structure Percent pE-MAP restraints satisfied per structure Percent of excluded volume restraints satisfied per structure 5) Benchmark Structural accuracy (95 % CI) PDB used for benchmark 6) Software and data availability	94 % 99 % 15.0 (12.1-18.2) Å 4YG2 IMP PMI module, version develop-39c22a602
	Percent of sequence connectivity restraints satisfied per structure Percent pE-MAP restraints satisfied per structure Percent of excluded volume restraints satisfied per structure 5) Benchmark Structural accuracy (95 % CI) PDB used for benchmark 6) Software and data availability	94 % 99 % 15.0 (12.1-18.2) Å 4YG2 IMP PMI module, version develop-39c22a602 Integrative Modeling Platform (IMP), version develop-
Modeling scripts and data https://integrativemodeling.org/systems/pemap Homology detection and structure prediction HHPred, version 2.0.16	Percent of sequence connectivity restraints satisfied per structure Percent pE-MAP restraints satisfied per structure Percent of excluded volume restraints satisfied per structure 5) Benchmark Structural accuracy (95 % CI) PDB used for benchmark 6) Software and data availability Modeling programs	94 % 99 % 15.0 (12.1-18.2) Å 4YG2 IMP PMI module, version develop-39c22a602 Integrative Modeling Platform (IMP), version develop-39c22a602