

Summary of integrative structure determination of Modeling of Mouse NPC basket (PDB ID: 9A8L, PDB-Dev ID: PDBDEV_00000385)

1. Model Composition	
	<ul style="list-style-type: none"> - Protein SEC13 homolog: Chain CZ (322 residues) - Nuclear pore complex protein Nup107: Chain EG (926 residues) - Nucleoprotein TPR: Chain J (2431 residues) - Nuclear pore complex protein Nup85: Chain BP (656 residues) - Nucleoporin Nup43: Chain FY (380 residues) - Nucleoprotein TPR: Chain H (2431 residues) - Nucleoporin Nup37: Chain FE (326 residues) - Nucleoporin Nup37: Chain FG (326 residues) - Nucleoporin 153: Chain AH (1462 residues) - Nuclear pore complex protein Nup160: Chain BE (1402 residues) - Nuclear pore complex protein Nup160: Chain BI (1402 residues) - Nucleoporin Nup37: Chain FM (326 residues) - Nuclear pore complex protein Nup98-Nup96: Chain CD (1816 residues) - Nuclear pore complex protein Nup133: Chain FA (1155 residues) - Nuclear pore complex protein Nup50: Chain T (466 residues) - Nuclear pore complex protein Nup133: Chain EP (1155 residues) - Nucleoprotein TPR: Chain M (2431 residues) - Nuclear pore complex protein Nup98-Nup96: Chain CF (1816 residues) - Nucleoporin Nup37: Chain FR (326 residues) - Nucleoporin 153: Chain AU (1462 residues) - Protein SEC13 homolog: Chain CU (322 residues) - Nucleoporin SEH1: Chain DM (360 residues) - Nuclear pore complex protein Nup133: Chain FD (1155 residues) - Nucleoporin Nup43: Chain GD (380 residues) - Nuclear pore complex protein Nup85: Chain CA (656 residues) - Nuclear pore complex protein Nup133: Chain EQ (1155 residues) - Nucleoporin SEH1: Chain DN (360 residues) - Nuclear pore complex protein Nup133: Chain EY (1155 residues) - Nuclear pore complex protein Nup107: Chain EM (926 residues) - Nuclear pore complex protein Nup50: Chain AC (466 residues) - Nucleoporin SEH1: Chain DU (360 residues) - Nuclear pore complex protein Nup98-Nup96: Chain CH (1816 residues) - Nucleoporin 153: Chain AI (1462 residues) - Nucleoporin 153: Chain AV (1462 residues) - Nucleoporin 153: Chain AS (1462 residues) - Nuclear pore complex protein Nup85: Chain BZ (656 residues) - Nuclear pore complex protein Nup85: Chain

CB (656 residues)
- Nucleoporin Nup37: Chain FO (326 residues)
- Nucleoporin 153: Chain AR (1462 residues)
- Nuclear pore complex protein Nup98-Nup96:
Chain CK (1816 residues)
- Nuclear pore complex protein Nup133:
Chain EO (1155 residues)
- Nuclear pore complex protein Nup85: Chain
BT (656 residues)
- Nucleoporin Nup43: Chain FZ (380 residues)
- Protein SEC13 homolog: Chain CY (322
residues)
- Nuclear pore complex protein Nup107:
Chain EN (926 residues)
- Nucleoporin 153: Chain AM (1462 residues)
- Nucleoporin SEH1: Chain DK (360 residues)
- Nucleoprotein TPR: Chain D (2431 residues)
- Nuclear pore complex protein Nup85: Chain
BS (656 residues)
- Nucleoporin Nup37: Chain FK (326 residues)
- Nuclear pore complex protein Nup133:
Chain EU (1155 residues)
- Nuclear pore complex protein Nup98-Nup96:
Chain CQ (1816 residues)
- Nucleoporin SEH1: Chain DJ (360 residues)
- Nucleoporin Nup43: Chain GB (380 residues)
- Nucleoprotein TPR: Chain K (2431 residues)
- Nucleoporin Nup37: Chain FI (326 residues)
- Protein SEC13 homolog: Chain CX (322
residues)
- Nucleoporin Nup43: Chain FW (380 residues)
- Nuclear pore complex protein Nup85: Chain
BO (656 residues)
- Protein SEC13 homolog: Chain DG (322
residues)
- Nuclear pore complex protein Nup133:
Chain ET (1155 residues)
- Nuclear pore complex protein Nup50: Chain
AB (466 residues)
- Nuclear pore complex protein Nup107:
Chain EJ (926 residues)
- Nucleoporin SEH1: Chain DL (360 residues)
- Nuclear pore complex protein Nup107:
Chain EE (926 residues)
- Nuclear pore complex protein Nup160:
Chain AZ (1402 residues)
- Nuclear pore complex protein Nup160:
Chain AY (1402 residues)
- Nucleoporin SEH1: Chain DW (360 residues)
- Nuclear pore complex protein Nup107:
Chain DY (926 residues)
- Nucleoporin 153: Chain AL (1462 residues)
- Nucleoporin 153: Chain AG (1462 residues)
- Nucleoporin Nup43: Chain GH (380 residues)
- Nucleoprotein TPR: Chain C (2431 residues)
- Nucleoprotein TPR: Chain N (2431 residues)
- Nucleoporin Nup43: Chain GF (380 residues)
- Nuclear pore complex protein Nup107:
Chain ED (926 residues)
- Nucleoporin 153: Chain AK (1462 residues)
- Nuclear pore complex protein Nup85: Chain
BM (656 residues)
- Nuclear pore complex protein Nup50: Chain
AD (466 residues)

[Entry composition](#)

- Nuclear pore complex protein Nup98-Nup96: Chain CM (1816 residues)
- Nuclear pore complex protein Nup50: Chain V (466 residues)
- Nuclear pore complex protein Nup98-Nup96: Chain CR (1816 residues)
- Protein SEC13 homolog: Chain CT (322 residues)
- Nucleoporin 153: Chain AN (1462 residues)
- Nucleoporin Nup37: Chain FQ (326 residues)
- Nucleoporin 153: Chain AO (1462 residues)
- Protein SEC13 homolog: Chain DH (322 residues)
- Nucleoporin Nup43: Chain FU (380 residues)
- Nucleoporin SEH1: Chain DX (360 residues)
- Nucleoprotein TPR: Chain I (2431 residues)
- Nucleoporin Nup37: Chain FT (326 residues)
- Nuclear pore complex protein Nup98-Nup96: Chain CE (1816 residues)
- Nuclear pore complex protein Nup107: Chain EI (926 residues)
- Nuclear pore complex protein Nup85: Chain BV (656 residues)
- Nuclear pore complex protein Nup98-Nup96: Chain CI (1816 residues)
- Nucleoporin Nup37: Chain FF (326 residues)
- Nuclear pore complex protein Nup85: Chain BR (656 residues)
- Nuclear pore complex protein Nup50: Chain R (466 residues)
- Protein SEC13 homolog: Chain DC (322 residues)
- Nuclear pore complex protein Nup50: Chain AE (466 residues)
- Nuclear pore complex protein Nup107: Chain EB (926 residues)
- Nuclear pore complex protein Nup133: Chain EV (1155 residues)
- Nuclear pore complex protein Nup50: Chain Q (466 residues)
- Nucleoporin 153: Chain AT (1462 residues)
- Nuclear pore complex protein Nup98-Nup96: Chain CP (1816 residues)
- Nucleoporin Nup43: Chain GE (380 residues)
- Nucleoprotein TPR: Chain G (2431 residues)
- Nuclear pore complex protein Nup85: Chain BX (656 residues)
- Nuclear pore complex protein Nup133: Chain FB (1155 residues)
- Nuclear pore complex protein Nup50: Chain AA (466 residues)
- Nuclear pore complex protein Nup160: Chain AX (1402 residues)
- Nuclear pore complex protein Nup160: Chain BJ (1402 residues)
- Nuclear pore complex protein Nup98-Nup96: Chain CO (1816 residues)
- Nucleoporin Nup43: Chain GI (380 residues)
- Protein SEC13 homolog: Chain CV (322 residues)
- Nucleoporin SEH1: Chain DI (360 residues)
- Nucleoporin SEH1: Chain DT (360 residues)
- Nuclear pore complex protein Nup85: Chain BQ (656 residues)

- Nucleoporin SEH1: Chain DO (360 residues)
- Nucleoporin Nup43: Chain GG (380 residues)
- Protein SEC13 homolog: Chain DA (322 residues)
- Nuclear pore complex protein Nup133: Chain ES (1155 residues)
- Nuclear pore complex protein Nup107: Chain EA (926 residues)
- Nuclear pore complex protein Nup50: Chain Y (466 residues)
- Nuclear pore complex protein Nup133: Chain EW (1155 residues)
- Nuclear pore complex protein Nup133: Chain ER (1155 residues)
- Nuclear pore complex protein Nup160: Chain AW (1402 residues)
- Nucleoporin 153: Chain AQ (1462 residues)
- Nucleoporin 153: Chain AP (1462 residues)
- Nuclear pore complex protein Nup85: Chain BU (656 residues)
- Nuclear pore complex protein Nup50: Chain U (466 residues)
- Nucleoporin SEH1: Chain DP (360 residues)
- Nucleoporin SEH1: Chain DQ (360 residues)
- Nucleoporin SEH1: Chain DV (360 residues)
- Protein SEC13 homolog: Chain DE (322 residues)
- Nucleoporin Nup43: Chain GJ (380 residues)
- Nucleoporin 153: Chain AJ (1462 residues)
- Nuclear pore complex protein Nup50: Chain S (466 residues)
- Nucleoporin Nup37: Chain FP (326 residues)
- Nuclear pore complex protein Nup107: Chain EL (926 residues)
- Nucleoporin Nup43: Chain GA (380 residues)
- Nuclear pore complex protein Nup98-Nup96: Chain CL (1816 residues)
- Nucleoprotein TPR: Chain L (2431 residues)
- Nuclear pore complex protein Nup160: Chain BC (1402 residues)
- Nuclear pore complex protein Nup107: Chain EC (926 residues)
- Nucleoporin Nup37: Chain FH (326 residues)
- Nuclear pore complex protein Nup160: Chain BH (1402 residues)
- Nucleoprotein TPR: Chain E (2431 residues)
- Nuclear pore complex protein Nup160: Chain BB (1402 residues)
- Protein SEC13 homolog: Chain DD (322 residues)
- Nucleoprotein TPR: Chain F (2431 residues)
- Nucleoporin SEH1: Chain DS (360 residues)
- Nuclear pore complex protein Nup107: Chain EF (926 residues)
- Protein SEC13 homolog: Chain DF (322 residues)
- Nucleoporin Nup37: Chain FS (326 residues)
- Nuclear pore complex protein Nup98-Nup96: Chain CG (1816 residues)
- Nuclear pore complex protein Nup50: Chain AF (466 residues)
- Nuclear pore complex protein Nup160: Chain BK (1402 residues)
- Nucleoprotein TPR: Chain A (2431 residues)

- Protein SEC13 homolog: Chain CS (322 residues)
- Nuclear pore complex protein Nup160: Chain BF (1402 residues)
- Nucleoprotein TPR: Chain O (2431 residues)
- Nuclear pore complex protein Nup160: Chain BL (1402 residues)
- Nuclear pore complex protein Nup98-Nup96: Chain CN (1816 residues)
- Nuclear pore complex protein Nup160: Chain BD (1402 residues)
- Nuclear pore complex protein Nup98-Nup96: Chain CC (1816 residues)
- Nucleoporin Nup43: Chain GC (380 residues)
- Nucleoporin SEH1: Chain DR (360 residues)
- Nuclear pore complex protein Nup107: Chain EK (926 residues)
- Nuclear pore complex protein Nup50: Chain X (466 residues)
- Nuclear pore complex protein Nup160: Chain BA (1402 residues)
- Nuclear pore complex protein Nup85: Chain BW (656 residues)
- Nuclear pore complex protein Nup107: Chain EH (926 residues)
- Protein SEC13 homolog: Chain DB (322 residues)
- Nuclear pore complex protein Nup133: Chain EX (1155 residues)
- Nucleoporin Nup43: Chain FX (380 residues)
- Nuclear pore complex protein Nup133: Chain FC (1155 residues)
- Nucleoporin Nup37: Chain FJ (326 residues)
- Nucleoporin Nup43: Chain FV (380 residues)
- Nuclear pore complex protein Nup133: Chain EZ (1155 residues)
- Nuclear pore complex protein Nup98-Nup96: Chain CJ (1816 residues)
- Nuclear pore complex protein Nup85: Chain BY (656 residues)
- Nucleoprotein TPR: Chain B (2431 residues)
- Nucleoprotein TPR: Chain P (2431 residues)
- Nucleoporin Nup37: Chain FN (326 residues)
- Nuclear pore complex protein Nup50: Chain Z (466 residues)
- Nuclear pore complex protein Nup160: Chain BG (1402 residues)
- Nuclear pore complex protein Nup50: Chain W (466 residues)
- Nuclear pore complex protein Nup107: Chain DZ (926 residues)
- Nucleoporin Nup37: Chain FL (326 residues)
- Nuclear pore complex protein Nup85: Chain BN (656 residues)
- Protein SEC13 homolog: Chain CW (322 residues)

<p>Datasets used for modeling</p>	<ul style="list-style-type: none"> - De Novo model, File: 10.5281/zenodo.13131753 - Comparative model, template PDB ID: Not available - 3DEM volume, File: 10.5281/zenodo.13131753 - 3DEM volume, File: 10.5281/zenodo.13131753 - Experimental model, PDB ID: 7r5j - 3DEM volume, EMDB: EMD-44379
<p>2. Representation</p>	
<p>Resolution</p>	<p>Coarse-grained: 1, 2, 3, 5, 13, 15 residue(s) per bead</p>
<p>Number of <i>rigid bodies</i>, <i>flexible units</i></p>	<p>592, 432</p>
	<ul style="list-style-type: none"> - AG: 36-57 - AH: 36-57 - A: 96-120, 124-180, 187-247, 254-285, 289-356, 360-405, 413-451, 511-595, 639-681, 757-883, 901-946, 947-999, 1004-1060, 1064-1106, 1107-1131, 1135-1163, 1170-1201, 1205-1254, 1281-1337, 1343-1420, 1424-1491, 1543-1616, 1627-1690 - B: 96-120, 124-180, 187-247, 254-285, 289-356, 360-405, 413-451, 511-595, 639-681, 757-883, 901-946, 947-999, 1004-1060, 1064-1106, 1107-1131, 1135-1163, 1170-1201, 1205-1254, 1281-1337, 1343-1420, 1424-1491, 1543-1616, 1627-1690 - C: 96-120, 124-180, 187-247, 254-285, 289-356, 360-405, 413-451, 511-595, 639-681, 757-883, 901-946, 947-999, 1004-1060, 1064-1106, 1107-1131, 1135-1163, 1170-1201, 1205-1254, 1281-1337, 1343-1420, 1424-1491, 1543-1616, 1627-1690 - D: 96-120, 124-180, 187-247, 254-285, 289-356, 360-405, 413-451, 511-595, 639-681, 757-883, 901-946, 947-999, 1004-1060, 1064-1106, 1107-1131, 1135-1163, 1170-1201, 1205-1254, 1281-1337, 1343-1420, 1424-1491, 1543-1616, 1627-1690 - E: 96-120, 124-180, 187-247, 254-285, 289-356, 360-405, 413-451, 511-595, 639-681, 757-883, 901-946, 947-999, 1004-1060, 1064-1106, 1107-1131, 1135-1163, 1170-1201, 1205-1254, 1281-1337, 1343-1420, 1424-1491, 1543-1616, 1627-1690 - F: 96-120, 124-180, 187-247, 254-285, 289-356, 360-405, 413-451, 511-595, 639-681, 757-883, 901-946, 947-999, 1004-1060, 1064-1106, 1107-1131, 1135-1163, 1170-1201, 1205-1254, 1281-1337, 1343-1420, 1424-1491, 1543-1616, 1627-1690 - G: 96-120, 124-180, 187-247, 254-285, 289-356, 360-405, 413-451, 511-595, 639-681, 757-883, 901-946, 947-999, 1004-1060, 1064-1106, 1107-1131, 1135-1163, 1170-1201, 1205-1254, 1281-1337, 1343-1420,

1424-1491, 1543-1616, 1627-1690
- H: 96-120, 124-180, 187-247, 254-285, 289-356, 360-405, 413-451, 511-595, 639-681, 757-883, 901-946, 947-999, 1004-1060, 1064-1106, 1107-1131, 1135-1163, 1170-1201, 1205-1254, 1281-1337, 1343-1420, 1424-1491, 1543-1616, 1627-1690
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- J: 96-120, 124-180, 187-247, 254-285, 289-356, 360-405, 413-451, 511-595, 639-681, 757-883, 901-946, 947-999, 1004-1060, 1064-1106, 1107-1131, 1135-1163, 1170-1201, 1205-1254, 1281-1337, 1343-1420, 1424-1491, 1543-1616, 1627-1690
- K: 96-120, 124-180, 187-247, 254-285, 289-356, 360-405, 413-451, 511-595, 639-681, 757-883, 901-946, 947-999, 1004-1060, 1064-1106, 1107-1131, 1135-1163, 1170-1201, 1205-1254, 1281-1337, 1343-1420, 1424-1491, 1543-1616, 1627-1690
- L: 96-120, 124-180, 187-247, 254-285, 289-356, 360-405, 413-451, 511-595, 639-681, 757-883, 901-946, 947-999, 1004-1060, 1064-1106, 1107-1131, 1135-1163, 1170-1201, 1205-1254, 1281-1337, 1343-1420, 1424-1491, 1543-1616, 1627-1690
- M: 96-120, 124-180, 187-247, 254-285, 289-356, 360-405, 413-451, 511-595, 639-681, 757-883, 901-946, 947-999, 1004-1060, 1064-1106, 1107-1131, 1135-1163, 1170-1201, 1205-1254, 1281-1337, 1343-1420, 1424-1491, 1543-1616, 1627-1690
- N: 96-120, 124-180, 187-247, 254-285, 289-356, 360-405, 413-451, 511-595, 639-681, 757-883, 901-946, 947-999, 1004-1060, 1064-1106, 1107-1131, 1135-1163, 1170-1201, 1205-1254, 1281-1337, 1343-1420, 1424-1491, 1543-1616, 1627-1690
- O: 96-120, 124-180, 187-247, 254-285, 289-356, 360-405, 413-451, 511-595, 639-681, 757-883, 901-946, 947-999, 1004-1060, 1064-1106, 1107-1131, 1135-1163, 1170-1201, 1205-1254, 1281-1337, 1343-1420, 1424-1491, 1543-1616, 1627-1690
- P: 96-120, 124-180, 187-247, 254-285, 289-356, 360-405, 413-451, 511-595, 639-681, 757-883, 901-946, 947-999, 1004-1060, 1064-1106, 1107-1131, 1135-1163, 1170-1201, 1205-1254, 1281-1337, 1343-1420, 1424-1491, 1543-1616, 1627-1690
- Q: 151-204, 355-466
- R: 151-204, 355-466
- S: 151-204, 355-466
- T: 151-204, 355-466
- U: 151-204, 355-466
- V: 151-204, 355-466
- W: 151-204, 355-466
- X: 151-204, 355-466
- Y: 151-204, 355-466

Rigid bodies

- Z: 151-204, 355-466
- AA: 151-204, 355-466
- AB: 151-204, 355-466
- AC: 151-204, 355-466
- AD: 151-204, 355-466
- AE: 151-204, 355-466
- AF: 151-204, 355-466
- AI: 36-57
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- CI: 1111-1159, 1194-1816
- CJ: 1111-1159, 1194-1816
- CK: 1111-1159, 1194-1816
- CL: 1111-1159, 1194-1816
- CM: 1111-1159, 1194-1816

- CN: 1111-1159, 1194-1816
- CO: 1111-1159, 1194-1816
- CP: 1111-1159, 1194-1816
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- FB: 70-1155
- FC: 70-1155
- FD: 70-1155
- FE: 1-326
- FF: 1-326
- FG: 1-326
- FH: 1-326
- FI: 1-326
- FJ: 1-326
- FK: 1-326
- FL: 1-326
- FM: 1-326
- FN: 1-326
- FO: 1-326
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- FQ: 1-326
- FR: 1-326
- FS: 1-326
- FT: 1-326
- FU: 1-292, 327-380
- FV: 1-292, 327-380
- FW: 1-292, 327-380
- FX: 1-292, 327-380
- FY: 1-292, 327-380
- FZ: 1-292, 327-380
- GA: 1-292, 327-380
- GB: 1-292, 327-380
- GC: 1-292, 327-380
- GD: 1-292, 327-380
- GE: 1-292, 327-380
- GF: 1-292, 327-380
- GG: 1-292, 327-380
- GH: 1-292, 327-380
- GI: 1-292, 327-380
- GJ: 1-292, 327-380

- AG: 1-35, 58-428, 540-574
- AH: 1-35, 58-428, 540-574
- A: 1-95, 121-123, 181-186, 248-253, 286-288, 357-359, 406-412, 452-510, 596-638, 682-756, 884-900, 1000-1003, 1061-1063, 1132-1134, 1164-1169, 1202-1204, 1255-1280, 1338-1342, 1421-1423, 1492-1542, 1617-1626, 1691-2431
- B: 1-95, 121-123, 181-186, 248-253, 286-288, 357-359, 406-412, 452-510, 596-638, 682-756, 884-900, 1000-1003, 1061-1063, 1132-1134, 1164-1169, 1202-1204, 1255-1280, 1338-1342, 1421-1423, 1492-1542, 1617-1626, 1691-2431
- C: 1-95, 121-123, 181-186, 248-253, 286-288, 357-359, 406-412, 452-510, 596-638, 682-756, 884-900, 1000-1003, 1061-1063, 1132-1134, 1164-1169, 1202-1204, 1255-1280, 1338-1342, 1421-1423, 1492-1542, 1617-1626, 1691-2431
- D: 1-95, 121-123, 181-186, 248-253, 286-288, 357-359, 406-412, 452-510, 596-638, 682-756, 884-900, 1000-1003, 1061-1063, 1132-1134, 1164-1169, 1202-1204, 1255-1280, 1338-1342, 1421-1423, 1492-1542, 1617-1626, 1691-2431

- E: 1-95, 121-123, 181-186, 248-253, 286-288, 357-359, 406-412, 452-510, 596-638, 682-756, 884-900, 1000-1003, 1061-1063, 1132-1134, 1164-1169, 1202-1204, 1255-1280, 1338-1342, 1421-1423, 1492-1542, 1617-1626, 1691-2431

- F: 1-95, 121-123, 181-186, 248-253, 286-288, 357-359, 406-412, 452-510, 596-638, 682-756, 884-900, 1000-1003, 1061-1063, 1132-1134, 1164-1169, 1202-1204, 1255-1280, 1338-1342, 1421-1423, 1492-1542, 1617-1626, 1691-2431

- G: 1-95, 121-123, 181-186, 248-253, 286-288, 357-359, 406-412, 452-510, 596-638, 682-756, 884-900, 1000-1003, 1061-1063, 1132-1134, 1164-1169, 1202-1204, 1255-1280, 1338-1342, 1421-1423, 1492-1542, 1617-1626, 1691-2431

- H: 1-95, 121-123, 181-186, 248-253, 286-288, 357-359, 406-412, 452-510, 596-638, 682-756, 884-900, 1000-1003, 1061-1063, 1132-1134, 1164-1169, 1202-1204, 1255-1280, 1338-1342, 1421-1423, 1492-1542, 1617-1626, 1691-2431

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- J: 1-95, 121-123, 181-186, 248-253, 286-288, 357-359, 406-412, 452-510, 596-638, 682-756, 884-900, 1000-1003, 1061-1063, 1132-1134, 1164-1169, 1202-1204, 1255-1280, 1338-1342, 1421-1423, 1492-1542, 1617-1626, 1691-2431

- K: 1-95, 121-123, 181-186, 248-253, 286-288, 357-359, 406-412, 452-510, 596-638, 682-756, 884-900, 1000-1003, 1061-1063, 1132-1134, 1164-1169, 1202-1204, 1255-1280, 1338-1342, 1421-1423, 1492-1542, 1617-1626, 1691-2431

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- M: 1-95, 121-123, 181-186, 248-253, 286-288, 357-359, 406-412, 452-510, 596-638, 682-756, 884-900, 1000-1003, 1061-1063, 1132-1134, 1164-1169, 1202-1204, 1255-1280, 1338-1342, 1421-1423, 1492-1542, 1617-1626, 1691-2431

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1617-1626, 1691-2431
- Q: 1-150, 205-354
- R: 1-150, 205-354
- S: 1-150, 205-354
- T: 1-150, 205-354
- U: 1-150, 205-354
- V: 1-150, 205-354
- W: 1-150, 205-354
- X: 1-150, 205-354
- Y: 1-150, 205-354
- Z: 1-150, 205-354
- AA: 1-150, 205-354
- AB: 1-150, 205-354
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- AD: 1-150, 205-354
- AE: 1-150, 205-354
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- AI: 1-35, 58-428, 540-574
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- AO: 1-35, 58-428, 540-574
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- AR: 1-35, 58-428, 540-574
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- AX: -
- AY: -
- AZ: -
- BA: -
- BB: -
- BC: -
- BD: -
- BE: -
- BF: -
- BG: -
- BH: -
- BI: -
- BJ: -
- BK: -
- BL: -
- BM: -
- BN: -
- BO: -
- BP: -
- BQ: -
- BR: -
- BS: -
- BT: -
- BU: -
- BV: -

Flexible units

- BW: -
- BX: -
- BY: -
- BZ: -
- CA: -
- CB: -
- CC: -
- CD: -
- CE: -
- CF: -
- CG: -
- CH: -
- CI: -
- CJ: -
- CK: -
- CL: -
- CM: -
- CN: -
- CO: -
- CP: -
- CQ: -
- CR: -
- CS: -
- CT: -
- CU: -
- CV: -
- CW: -
- CX: -
- CY: -
- CZ: -
- DA: -
- DB: -
- DC: -
- DD: -
- DE: -
- DF: -
- DG: -
- DH: -
- DI: -
- DJ: -
- DK: -
- DL: -
- DM: -
- DN: -
- DO: -
- DP: -
- DQ: -
- DR: -
- DS: -
- DT: -
- DU: -
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<i>Structural coverage (rigid bodies)</i>	79%
3. Restraints	
<i>Physical principles</i>	Information about physical principles was not provided

Experimental data	- 1 unique EM3DRestraint: Bayesian EM restraint on Gaussian mixture models
4. Validation	
Number of ensembles	1
Number of models in ensembles	1
Number of deposited models	1
Model precision (uncertainty of models)	41.9, Å
Data quality	Data quality has not been assessed
Model quality: assessment of excluded volume	Satisfaction: 100.00-100.00%
Fit to data used for modeling	Fit of model to information used to compute it has not been determined
Fit to data used for validation	Fit of model to information not used to compute it has not been determined
5. Methodology and Software	
1. Method	Sampling
Name	Replica exchange monte carlo
Number of computed models	500
2. Method	Sampling
Name	Replica exchange monte carlo
Number of computed models	9569309
Software	- IMP PMI module (version 2.19.0) - COCONUT (version 1.0.0) - Integrative Modeling Platform (IMP) (version 2.19.0)