wwPDB EM Validation Summary Report (i)

Mar 20, 2024 – 08:17 AM JST

PDB ID	:	7BYN
EMDB ID	:	EMD-30246
Title	:	Cryo-EM structure of human KCNQ4 with linopirdine
Authors	:	Shen, H.; Li, T.; Yue, Z.
Deposited on	:	2020-04-23
Resolution	:	3.30 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

EMDB validation analysis	:	0.0.1.dev70
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.

Metric	Percentile Ranks	Value
Clashscore		24
Ramachandran outliers		0.2%
Sidechain outliers		13.6%

Worse *Better*

▮ Percentile relative to all structures
▯ Percentile relative to all EM structures
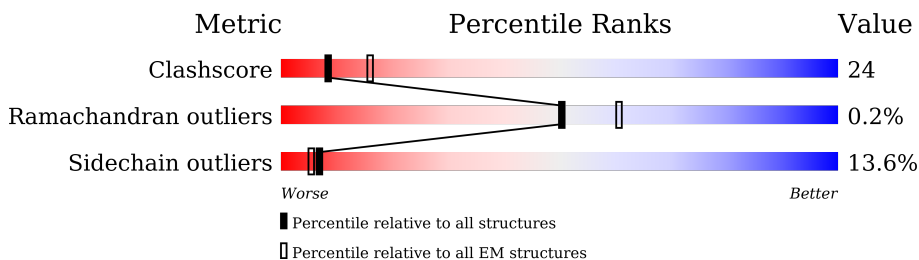
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	979	10% — 21% / 12% / • / 64%
1	C	979	10% — 20% / 13% / • / 64%
1	E	979	10% — 21% / 13% / • / 64%
1	G	979	10% — 20% / 13% / • / 64%
2	B	149	93% — 85% / 13% / •
2	D	149	96% — 83% / 15% / •
2	F	149	93% — 82% / 16% / •
2	H	149	93% — 84% / 14% / •

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	PT5	G	701	-	-	X	-

2   Entry composition ⓘ

There are 5 unique types of molecules in this entry. The entry contains 16349 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Green fluorescent protein,Potassium voltage-gated channel subfamily KQT member 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	354	Total 2872	C 1882	N 501	O 475	S 14	0	0
1	C	354	Total 2872	C 1882	N 501	O 475	S 14	0	0
1	E	354	Total 2872	C 1882	N 501	O 475	S 14	0	0
1	G	354	Total 2872	C 1882	N 501	O 475	S 14	0	0

There are 208 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-283	MET	-	expression tag	UNP P42212
A	-282	HIS	-	expression tag	UNP P42212
A	-281	HIS	-	expression tag	UNP P42212
A	-280	HIS	-	expression tag	UNP P42212
A	-279	HIS	-	expression tag	UNP P42212
A	-278	HIS	-	expression tag	UNP P42212
A	-277	HIS	-	expression tag	UNP P42212
A	-276	HIS	-	expression tag	UNP P42212
A	-275	HIS	-	expression tag	UNP P42212
A	-274	ALA	-	expression tag	UNP P42212
A	-273	ALA	-	expression tag	UNP P42212
A	-272	ASP	-	expression tag	UNP P42212
A	-271	TYR	-	expression tag	UNP P42212
A	-270	LYS	-	expression tag	UNP P42212
A	-269	ASP	-	expression tag	UNP P42212
A	-268	HIS	-	expression tag	UNP P42212
A	-267	ASP	-	expression tag	UNP P42212
A	-266	ILE	-	expression tag	UNP P42212
A	-265	ASP	-	expression tag	UNP P42212
A	-264	TYR	-	expression tag	UNP P42212
A	-263	LYS	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-262	ASP	-	expression tag	UNP P42212
A	-261	ASP	-	expression tag	UNP P42212
A	-260	ASP	-	expression tag	UNP P42212
A	-259	ASP	-	expression tag	UNP P42212
A	-258	LYS	-	expression tag	UNP P42212
A	-257	SER	-	expression tag	UNP P42212
A	-256	ALA	-	expression tag	UNP P42212
A	-255	MET	-	expression tag	UNP P42212
A	-254	VAL	-	expression tag	UNP P42212
A	-191	LEU	PHE	engineered mutation	UNP P42212
A	-190	THR	SER	engineered mutation	UNP P42212
A	-148	THR	LYS	engineered mutation	UNP P42212
A	-49	LYS	ALA	engineered mutation	UNP P42212
A	-24	LEU	HIS	engineered mutation	UNP P42212
A	-16	SER	-	linker	UNP P42212
A	-15	GLY	-	linker	UNP P42212
A	-14	LEU	-	linker	UNP P42212
A	-13	ARG	-	linker	UNP P42212
A	-12	SER	-	linker	UNP P42212
A	-11	GLY	-	linker	UNP P42212
A	-10	LEU	-	linker	UNP P42212
A	-9	GLU	-	linker	UNP P42212
A	-8	VAL	-	linker	UNP P42212
A	-7	LEU	-	linker	UNP P42212
A	-6	PHE	-	linker	UNP P42212
A	-5	GLN	-	linker	UNP P42212
A	-4	GLY	-	linker	UNP P42212
A	-3	PRO	-	linker	UNP P42212
A	-2	GLY	-	linker	UNP P42212
A	-1	GLY	-	linker	UNP P42212
A	0	ARG	-	linker	UNP P42212
C	-283	MET	-	expression tag	UNP P42212
C	-282	HIS	-	expression tag	UNP P42212
C	-281	HIS	-	expression tag	UNP P42212
C	-280	HIS	-	expression tag	UNP P42212
C	-279	HIS	-	expression tag	UNP P42212
C	-278	HIS	-	expression tag	UNP P42212
C	-277	HIS	-	expression tag	UNP P42212
C	-276	HIS	-	expression tag	UNP P42212
C	-275	HIS	-	expression tag	UNP P42212
C	-274	ALA	-	expression tag	UNP P42212
C	-273	ALA	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-272	ASP	-	expression tag	UNP P42212
C	-271	TYR	-	expression tag	UNP P42212
C	-270	LYS	-	expression tag	UNP P42212
C	-269	ASP	-	expression tag	UNP P42212
C	-268	HIS	-	expression tag	UNP P42212
C	-267	ASP	-	expression tag	UNP P42212
C	-266	ILE	-	expression tag	UNP P42212
C	-265	ASP	-	expression tag	UNP P42212
C	-264	TYR	-	expression tag	UNP P42212
C	-263	LYS	-	expression tag	UNP P42212
C	-262	ASP	-	expression tag	UNP P42212
C	-261	ASP	-	expression tag	UNP P42212
C	-260	ASP	-	expression tag	UNP P42212
C	-259	ASP	-	expression tag	UNP P42212
C	-258	LYS	-	expression tag	UNP P42212
C	-257	SER	-	expression tag	UNP P42212
C	-256	ALA	-	expression tag	UNP P42212
C	-255	MET	-	expression tag	UNP P42212
C	-254	VAL	-	expression tag	UNP P42212
C	-191	LEU	PHE	engineered mutation	UNP P42212
C	-190	THR	SER	engineered mutation	UNP P42212
C	-148	THR	LYS	engineered mutation	UNP P42212
C	-49	LYS	ALA	engineered mutation	UNP P42212
C	-24	LEU	HIS	engineered mutation	UNP P42212
C	-16	SER	-	linker	UNP P42212
C	-15	GLY	-	linker	UNP P42212
C	-14	LEU	-	linker	UNP P42212
C	-13	ARG	-	linker	UNP P42212
C	-12	SER	-	linker	UNP P42212
C	-11	GLY	-	linker	UNP P42212
C	-10	LEU	-	linker	UNP P42212
C	-9	GLU	-	linker	UNP P42212
C	-8	VAL	-	linker	UNP P42212
C	-7	LEU	-	linker	UNP P42212
C	-6	PHE	-	linker	UNP P42212
C	-5	GLN	-	linker	UNP P42212
C	-4	GLY	-	linker	UNP P42212
C	-3	PRO	-	linker	UNP P42212
C	-2	GLY	-	linker	UNP P42212
C	-1	GLY	-	linker	UNP P42212
C	0	ARG	-	linker	UNP P42212
E	-283	MET	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-282	HIS	-	expression tag	UNP P42212
E	-281	HIS	-	expression tag	UNP P42212
E	-280	HIS	-	expression tag	UNP P42212
E	-279	HIS	-	expression tag	UNP P42212
E	-278	HIS	-	expression tag	UNP P42212
E	-277	HIS	-	expression tag	UNP P42212
E	-276	HIS	-	expression tag	UNP P42212
E	-275	HIS	-	expression tag	UNP P42212
E	-274	ALA	-	expression tag	UNP P42212
E	-273	ALA	-	expression tag	UNP P42212
E	-272	ASP	-	expression tag	UNP P42212
E	-271	TYR	-	expression tag	UNP P42212
E	-270	LYS	-	expression tag	UNP P42212
E	-269	ASP	-	expression tag	UNP P42212
E	-268	HIS	-	expression tag	UNP P42212
E	-267	ASP	-	expression tag	UNP P42212
E	-266	ILE	-	expression tag	UNP P42212
E	-265	ASP	-	expression tag	UNP P42212
E	-264	TYR	-	expression tag	UNP P42212
E	-263	LYS	-	expression tag	UNP P42212
E	-262	ASP	-	expression tag	UNP P42212
E	-261	ASP	-	expression tag	UNP P42212
E	-260	ASP	-	expression tag	UNP P42212
E	-259	ASP	-	expression tag	UNP P42212
E	-258	LYS	-	expression tag	UNP P42212
E	-257	SER	-	expression tag	UNP P42212
E	-256	ALA	-	expression tag	UNP P42212
E	-255	MET	-	expression tag	UNP P42212
E	-254	VAL	-	expression tag	UNP P42212
E	-191	LEU	PHE	engineered mutation	UNP P42212
E	-190	THR	SER	engineered mutation	UNP P42212
E	-148	THR	LYS	engineered mutation	UNP P42212
E	-49	LYS	ALA	engineered mutation	UNP P42212
E	-24	LEU	HIS	engineered mutation	UNP P42212
E	-16	SER	-	linker	UNP P42212
E	-15	GLY	-	linker	UNP P42212
E	-14	LEU	-	linker	UNP P42212
E	-13	ARG	-	linker	UNP P42212
E	-12	SER	-	linker	UNP P42212
E	-11	GLY	-	linker	UNP P42212
E	-10	LEU	-	linker	UNP P42212
E	-9	GLU	-	linker	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-8	VAL	-	linker	UNP P42212
E	-7	LEU	-	linker	UNP P42212
E	-6	PHE	-	linker	UNP P42212
E	-5	GLN	-	linker	UNP P42212
E	-4	GLY	-	linker	UNP P42212
E	-3	PRO	-	linker	UNP P42212
E	-2	GLY	-	linker	UNP P42212
E	-1	GLY	-	linker	UNP P42212
E	0	ARG	-	linker	UNP P42212
G	-283	MET	-	expression tag	UNP P42212
G	-282	HIS	-	expression tag	UNP P42212
G	-281	HIS	-	expression tag	UNP P42212
G	-280	HIS	-	expression tag	UNP P42212
G	-279	HIS	-	expression tag	UNP P42212
G	-278	HIS	-	expression tag	UNP P42212
G	-277	HIS	-	expression tag	UNP P42212
G	-276	HIS	-	expression tag	UNP P42212
G	-275	HIS	-	expression tag	UNP P42212
G	-274	ALA	-	expression tag	UNP P42212
G	-273	ALA	-	expression tag	UNP P42212
G	-272	ASP	-	expression tag	UNP P42212
G	-271	TYR	-	expression tag	UNP P42212
G	-270	LYS	-	expression tag	UNP P42212
G	-269	ASP	-	expression tag	UNP P42212
G	-268	HIS	-	expression tag	UNP P42212
G	-267	ASP	-	expression tag	UNP P42212
G	-266	ILE	-	expression tag	UNP P42212
G	-265	ASP	-	expression tag	UNP P42212
G	-264	TYR	-	expression tag	UNP P42212
G	-263	LYS	-	expression tag	UNP P42212
G	-262	ASP	-	expression tag	UNP P42212
G	-261	ASP	-	expression tag	UNP P42212
G	-260	ASP	-	expression tag	UNP P42212
G	-259	ASP	-	expression tag	UNP P42212
G	-258	LYS	-	expression tag	UNP P42212
G	-257	SER	-	expression tag	UNP P42212
G	-256	ALA	-	expression tag	UNP P42212
G	-255	MET	-	expression tag	UNP P42212
G	-254	VAL	-	expression tag	UNP P42212
G	-191	LEU	PHE	engineered mutation	UNP P42212
G	-190	THR	SER	engineered mutation	UNP P42212
G	-148	THR	LYS	engineered mutation	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-49	LYS	ALA	engineered mutation	UNP P42212
G	-24	LEU	HIS	engineered mutation	UNP P42212
G	-16	SER	-	linker	UNP P42212
G	-15	GLY	-	linker	UNP P42212
G	-14	LEU	-	linker	UNP P42212
G	-13	ARG	-	linker	UNP P42212
G	-12	SER	-	linker	UNP P42212
G	-11	GLY	-	linker	UNP P42212
G	-10	LEU	-	linker	UNP P42212
G	-9	GLU	-	linker	UNP P42212
G	-8	VAL	-	linker	UNP P42212
G	-7	LEU	-	linker	UNP P42212
G	-6	PHE	-	linker	UNP P42212
G	-5	GLN	-	linker	UNP P42212
G	-4	GLY	-	linker	UNP P42212
G	-3	PRO	-	linker	UNP P42212
G	-2	GLY	-	linker	UNP P42212
G	-1	GLY	-	linker	UNP P42212
G	0	ARG	-	linker	UNP P42212

- Molecule 2 is a protein called Calmodulin-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	146	Total 1151	C 705	N 185	O 252	S 9	0	0
2	D	146	Total 1151	C 705	N 185	O 252	S 9	0	0
2	F	146	Total 1151	C 705	N 185	O 252	S 9	0	0
2	H	146	Total 1151	C 705	N 185	O 252	S 9	0	0

- Molecule 3 is [(2R)-1-octadecanoyloxy-3-[oxidanyl-[(1R,2R,3S,4R,5R,6S)-2,3,6-tris(oxidanyl)-4,5-diphosphonooxy-cyclohexyl]oxy-phospho ryl]oxy-propan-2-yl] (8Z)-icosa-5,8,11,14-tetraenoate (three-letter code: PT5) (formula: $C_{47}H_{85}O_{19}P_3$) (labeled as "Ligand of Interest" by depositor).
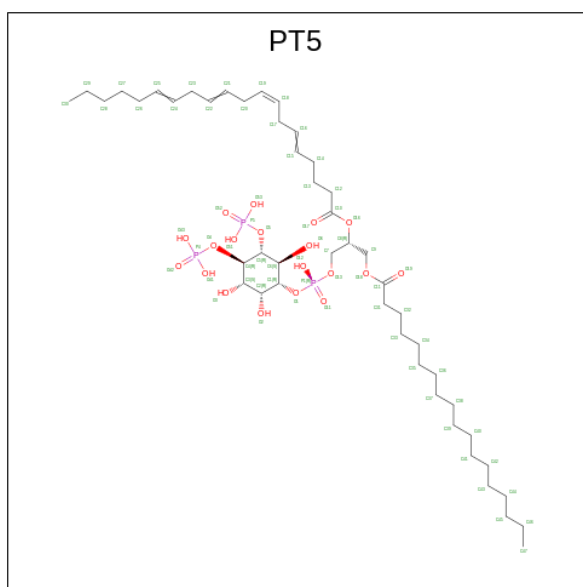
PT5

Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	C	O	P	0
			56	34	19	3	
3	C	1	Total	C	O	P	0
			56	34	19	3	
3	E	1	Total	C	O	P	0
			56	34	19	3	
3	G	1	Total	C	O	P	0
			56	34	19	3	

- Molecule 4 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
4	A	3	Total	K	0
			3	3	

- Molecule 5 is 1-phenyl-3,3-bis(pyridin-4-ylmethyl)indol-2-one (three-letter code: FCC) (formula: $C_{26}H_{21}N_3O$) (labeled as "Ligand of Interest" by depositor).

FCC
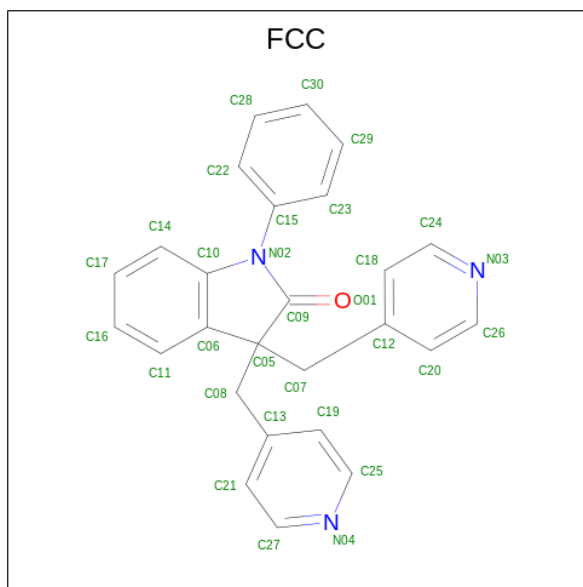
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
5	C	1	30	26	3	1	0

3   Residue-property plots ⓘ

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Green fluorescent protein,Potassium voltage-gated channel subfamily KQT member 4

• Molecule 1: Green fluorescent protein,Potassium voltage-gated channel subfamily KQT member 4

Chain C:

10%

20%   13%   •   64%

• Molecule 1: Green fluorescent protein,Potassium voltage-gated channel subfamily KQT member 4

Chain E:

10%

21%   13%   •   64%

• Molecule 1: Green fluorescent protein,Potassium voltage-gated channel subfamily KQT member 4

Chain G:

• Molecule 2: Calmodulin-3

Chain B:

93%
85% 13%

• Molecule 2: Calmodulin-3

Chain D:

96%
83% 15%

● Molecule 2: Calmodulin-3

93%

Chain F:

82% 16%

● Molecule 2: Calmodulin-3

93%

Chain H:

84% 14%
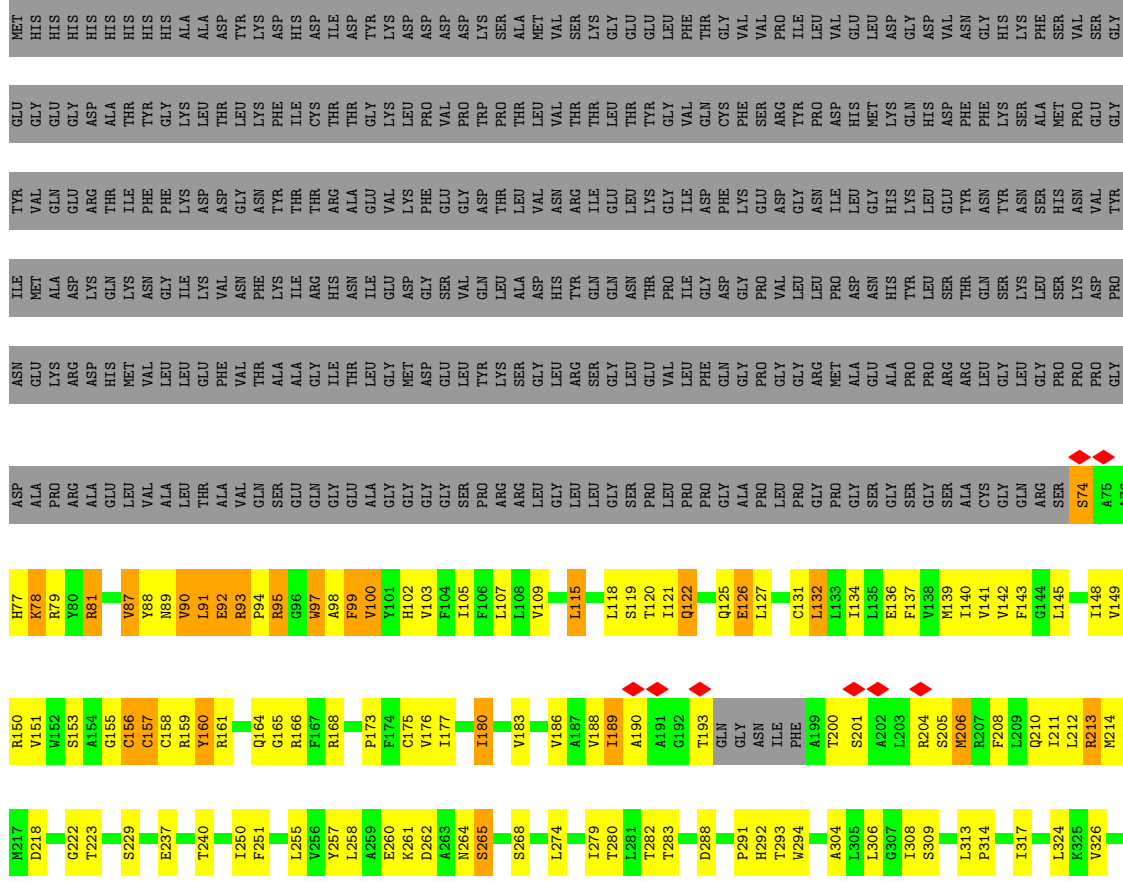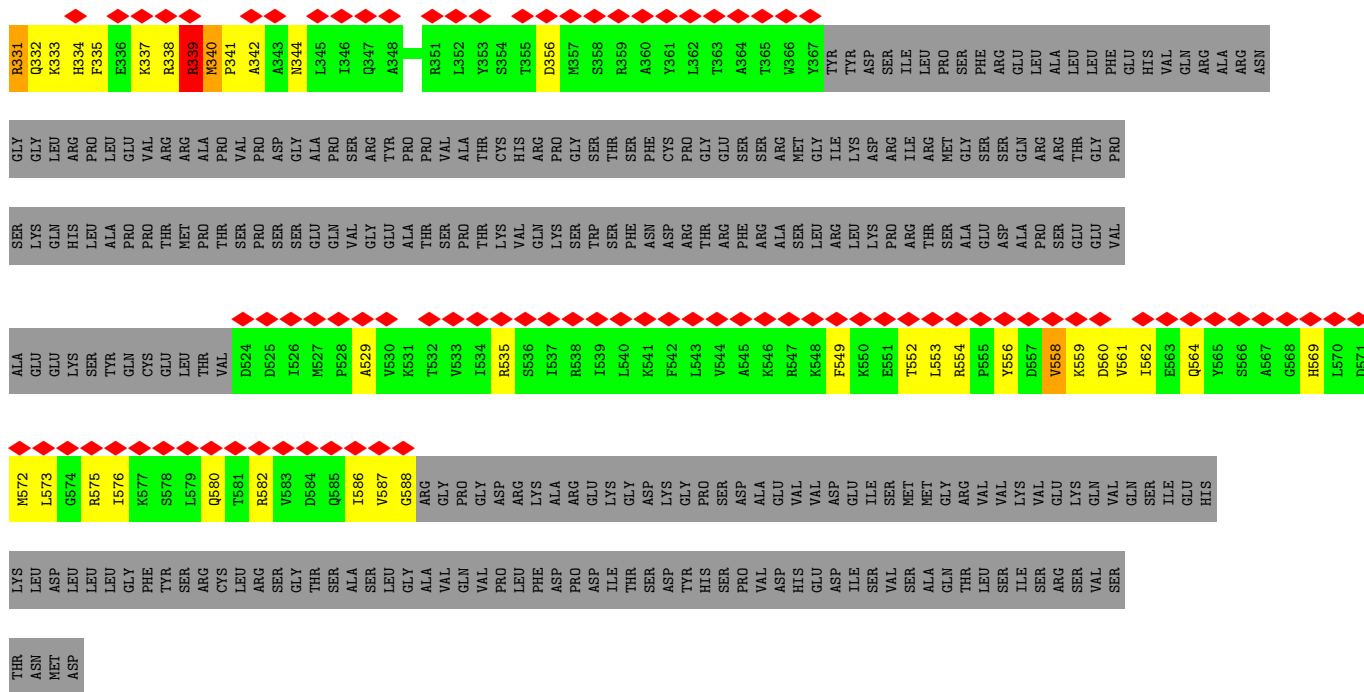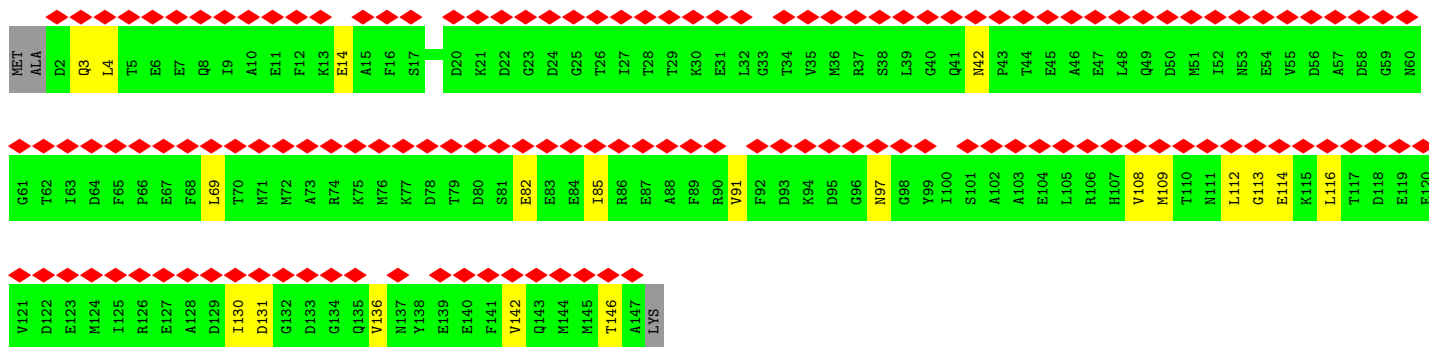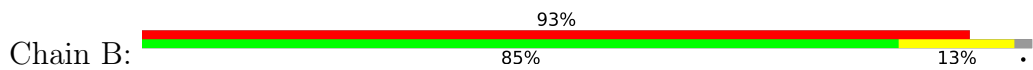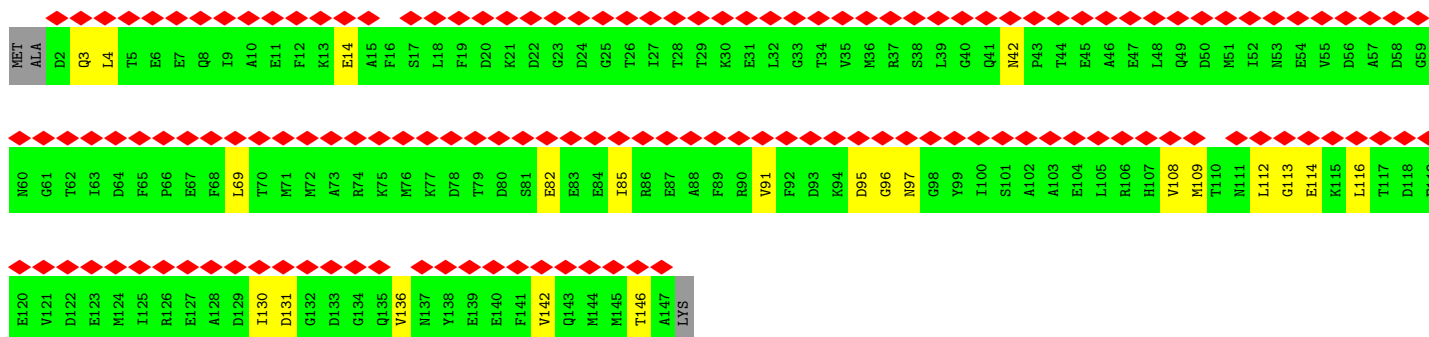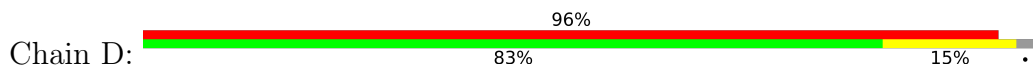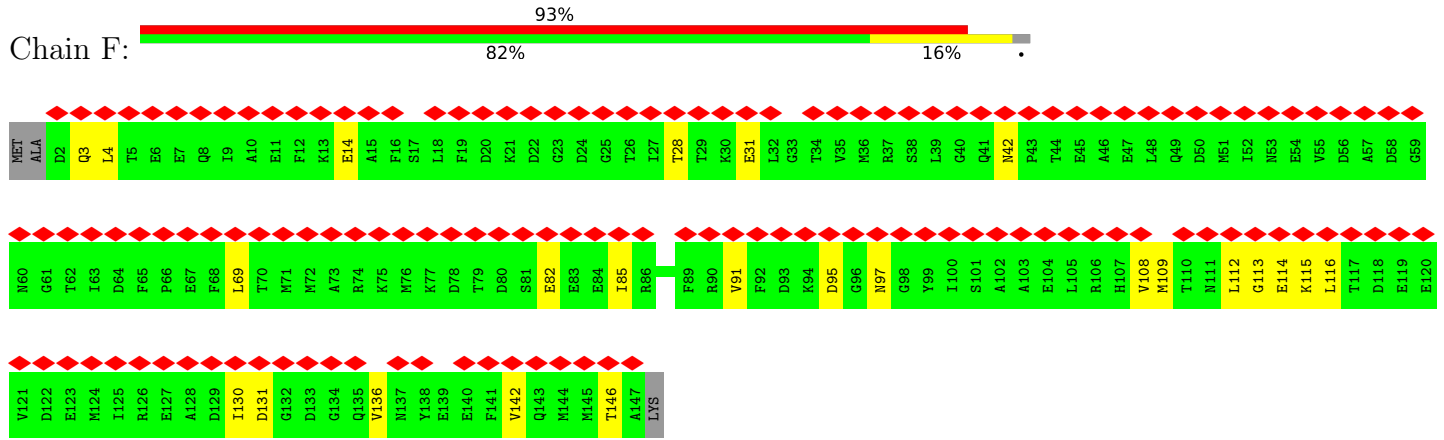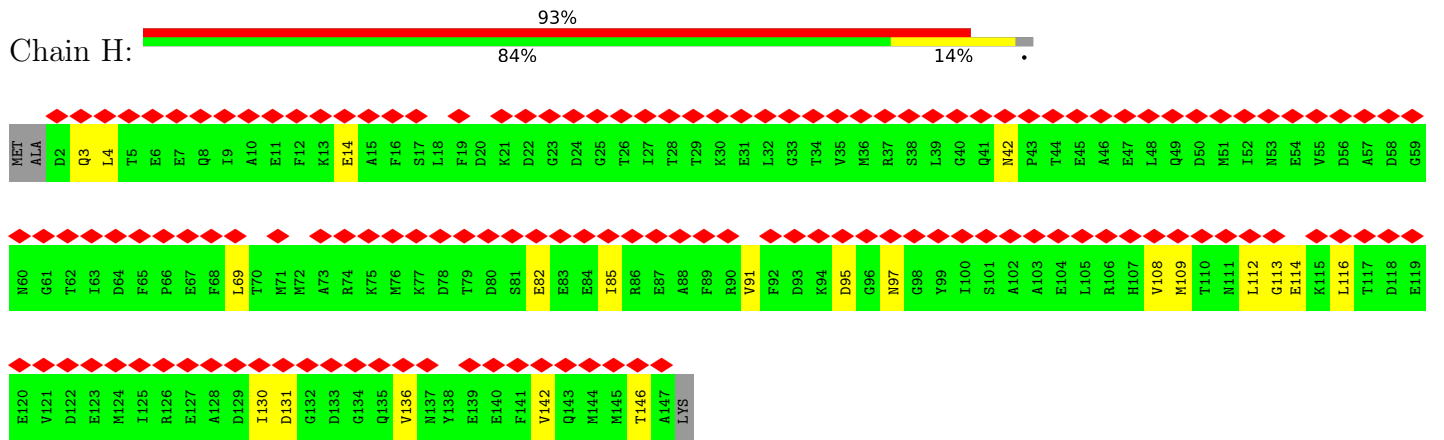
4   Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	229040	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{Å}^2)$	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.142	Depositor
Minimum map value	-0.075	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0185	Depositor
Map size (Å)	347.84, 347.84, 347.84	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.087, 1.087, 1.087	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: PT5, K, FCC

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#|Z|>5$	RMSZ	$\#|Z|>5$
1	A	0.54	0/2944	0.54	0/3983
1	C	0.54	0/2944	0.54	0/3983
1	E	0.54	0/2944	0.54	0/3983
1	G	0.54	0/2944	0.54	0/3983
2	B	0.39	0/1163	0.55	0/1562
2	D	0.39	0/1163	0.55	0/1562
2	F	0.39	0/1163	0.55	0/1562
2	H	0.39	0/1163	0.55	0/1562
All	All	0.50	0/16428	0.54	0/22180

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2872	0	2934	183	0
1	C	2872	0	2934	207	0
1	E	2872	0	2934	207	0
1	G	2872	0	2934	207	0
2	B	1151	0	1075	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	1151	0	1075	36	0
2	F	1151	0	1075	47	0
2	H	1151	0	1075	40	0
3	A	56	0	50	18	0
3	C	56	0	50	13	0
3	E	56	0	50	20	0
3	G	56	0	50	21	0
4	A	3	0	0	0	0
5	C	30	0	0	0	0
All	All	16349	0	16236	785	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 24.

The worst 5 of 785 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:78:LYS:HE3	2:D:131:ASP:CG	1.37	1.46
1:A:341:PRO:HG2	1:A:552:THR:CG2	1.48	1.42
1:G:341:PRO:HG2	1:G:552:THR:CG2	1.50	1.42
1:E:341:PRO:HG2	1:E:552:THR:CG2	1.48	1.40
1:G:78:LYS:HE3	2:H:131:ASP:CG	1.45	1.34

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	348/979 (36%)	337 (97%)	10 (3%)	1 (0%)	41	71
1	C	348/979 (36%)	336 (97%)	11 (3%)	1 (0%)	41	71

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	348/979 (36%)	335 (96%)	12 (3%)	1 (0%)	41	71
1	G	348/979 (36%)	335 (96%)	12 (3%)	1 (0%)	41	71
2	B	144/149 (97%)	141 (98%)	3 (2%)	0	100	100
2	D	144/149 (97%)	141 (98%)	3 (2%)	0	100	100
2	F	144/149 (97%)	141 (98%)	3 (2%)	0	100	100
2	H	144/149 (97%)	141 (98%)	3 (2%)	0	100	100
All	All	1968/4512 (44%)	1907 (97%)	57 (3%)	4 (0%)	50	77

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	339	ARG
1	C	339	ARG
1	E	339	ARG
1	G	339	ARG

5.3.2　Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	299/828 (36%)	246 (82%)	53 (18%)	2	8
1	C	299/828 (36%)	244 (82%)	55 (18%)	1	7
1	E	299/828 (36%)	243 (81%)	56 (19%)	1	7
1	G	299/828 (36%)	241 (81%)	58 (19%)	1	5
2	B	125/127 (98%)	123 (98%)	2 (2%)	62	79
2	D	125/127 (98%)	123 (98%)	2 (2%)	62	79
2	F	125/127 (98%)	123 (98%)	2 (2%)	62	79
2	H	125/127 (98%)	123 (98%)	2 (2%)	62	79
All	All	1696/3820 (44%)	1466 (86%)	230 (14%)	7	16

5 of 230 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	93	ARG
1	G	559	LYS
1	E	204	ARG
1	G	554	ARG
1	G	201	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	580	GLN
1	G	329	GLN
1	E	122	GLN
1	G	580	GLN
1	G	122	GLN

5.3.3   RNA ⓘ

There are no RNA molecules in this entry.

5.4   Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5   Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6   Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 3 are monoatomic - leaving 5 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
3	PT5	A	701	-	56,56,69	0.44	0	69,74,87	0.45	0
5	FCC	C	702	-	34,34,34	2.23	7 (20%)	47,48,48	2.65	19 (40%)
3	PT5	E	701	-	56,56,69	0.44	0	69,74,87	0.45	0
3	PT5	C	701	-	56,56,69	0.44	0	69,74,87	0.44	0
3	PT5	G	701	-	56,56,69	0.44	0	69,74,87	0.44	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PT5	A	701	-	-	30/53/77/90	0/1/1/1
5	FCC	C	702	-	-	6/14/34/34	0/5/5/5
3	PT5	E	701	-	-	26/53/77/90	0/1/1/1
3	PT5	C	701	-	-	26/53/77/90	0/1/1/1
3	PT5	G	701	-	-	21/53/77/90	0/1/1/1

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	702	FCC	C09-N02	6.93	1.45	1.38
5	C	702	FCC	C15-N02	5.39	1.51	1.44
5	C	702	FCC	C05-C09	4.37	1.59	1.53
5	C	702	FCC	C10-C06	4.35	1.44	1.39
5	C	702	FCC	C07-C05	3.96	1.59	1.55

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	C	702	FCC	C05-C07-C12	7.71	126.11	114.86
5	C	702	FCC	C10-N02-C09	-7.58	105.95	110.66
5	C	702	FCC	C15-N02-C10	5.56	133.90	124.26
5	C	702	FCC	C14-C10-C06	-4.53	117.24	121.76
5	C	702	FCC	C22-C15-N02	4.23	124.29	119.74

There are no chirality outliers.

5 of 109 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	701	PT5	C7-O13-P1-O12
3	A	701	PT5	C7-O13-P1-O11
3	A	701	PT5	C7-O13-P1-O1
3	A	701	PT5	C1-O1-P1-O13
3	A	701	PT5	C6-C1-O1-P1

There are no ring outliers.

4 monomers are involved in 72 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	701	PT5	18	0
3	E	701	PT5	20	0
3	C	701	PT5	13	0
3	G	701	PT5	21	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand PT5 A 701

Bond lengths

Bond angles

Torsions

Rings

Ligand FCC C 702

Bond lengths

Bond angles

Torsions

Rings

Ligand PT5 E 701

Bond lengths

Bond angles

Torsions

Rings

Ligand PT5 C 701

Bond lengths

Bond angles

Torsions

Rings

Ligand PT5 G 701

Bond lengths

Bond angles

Torsions

Rings
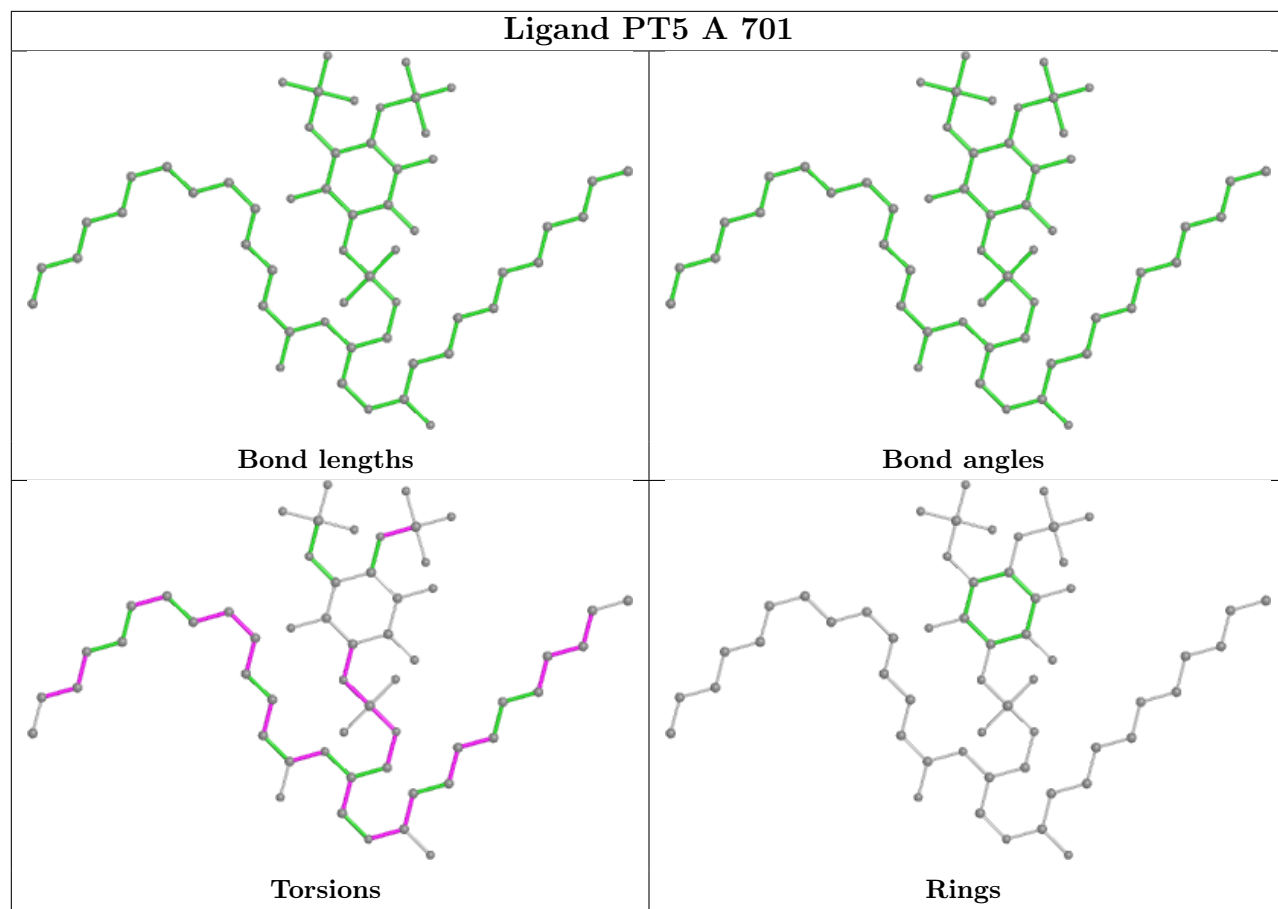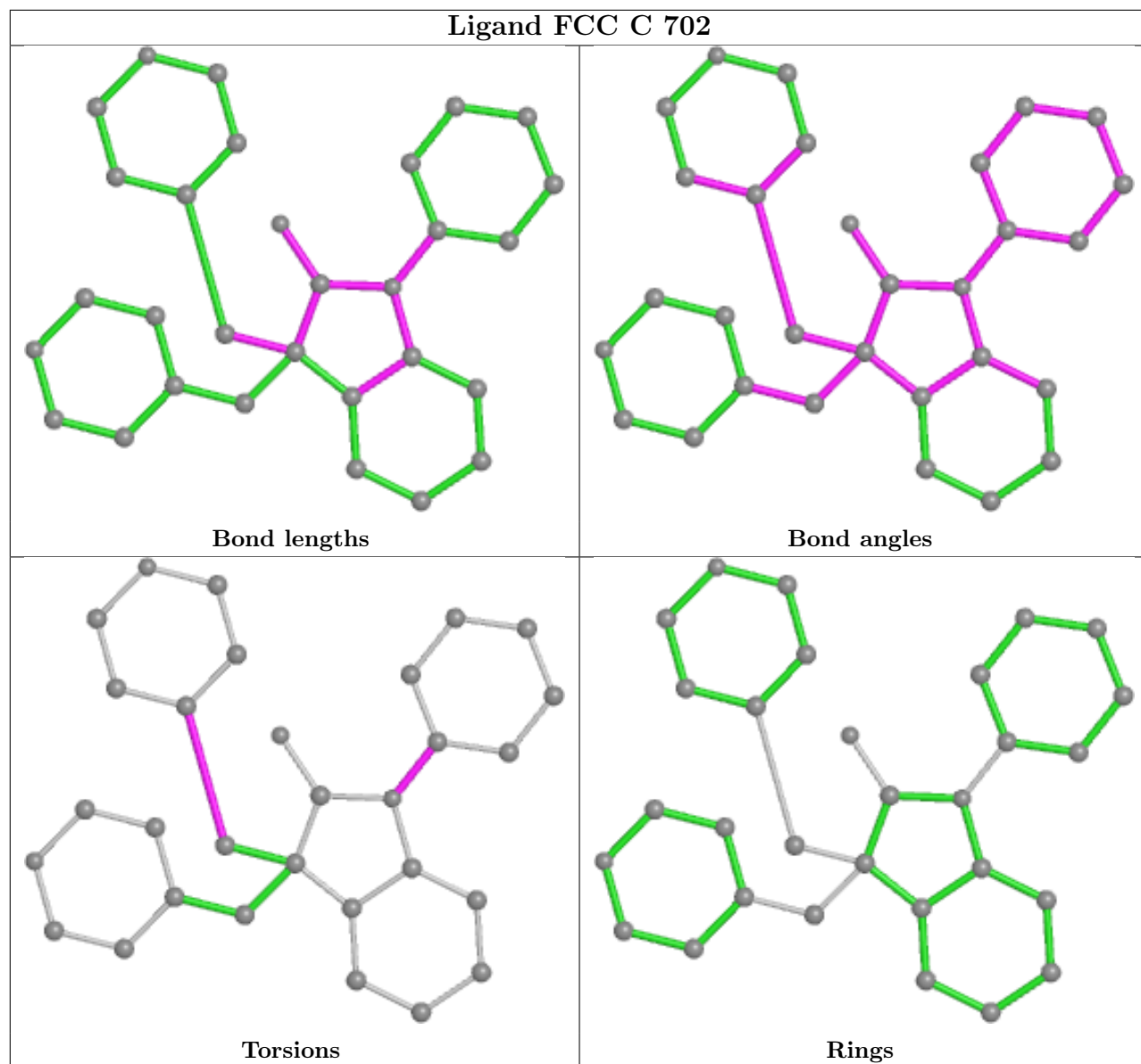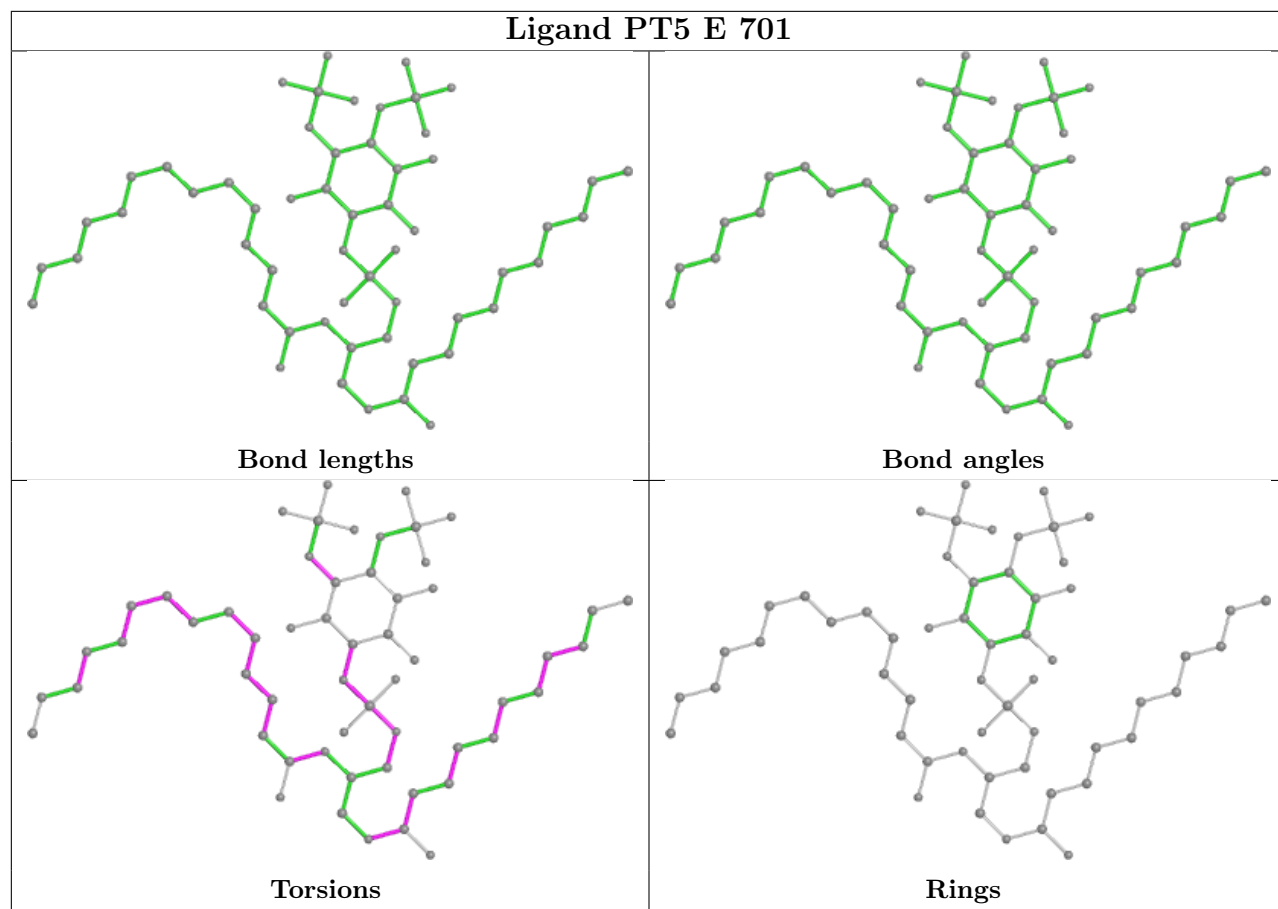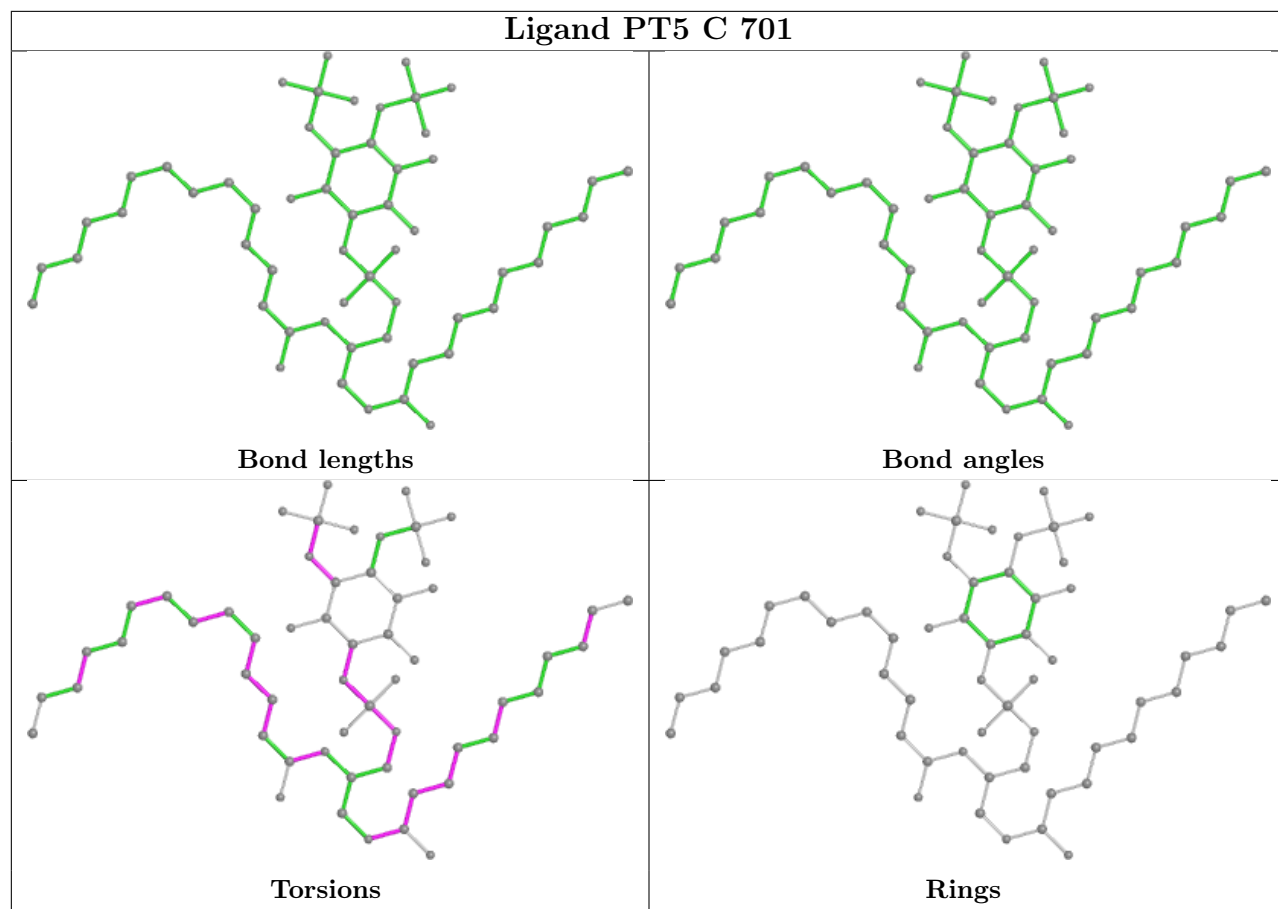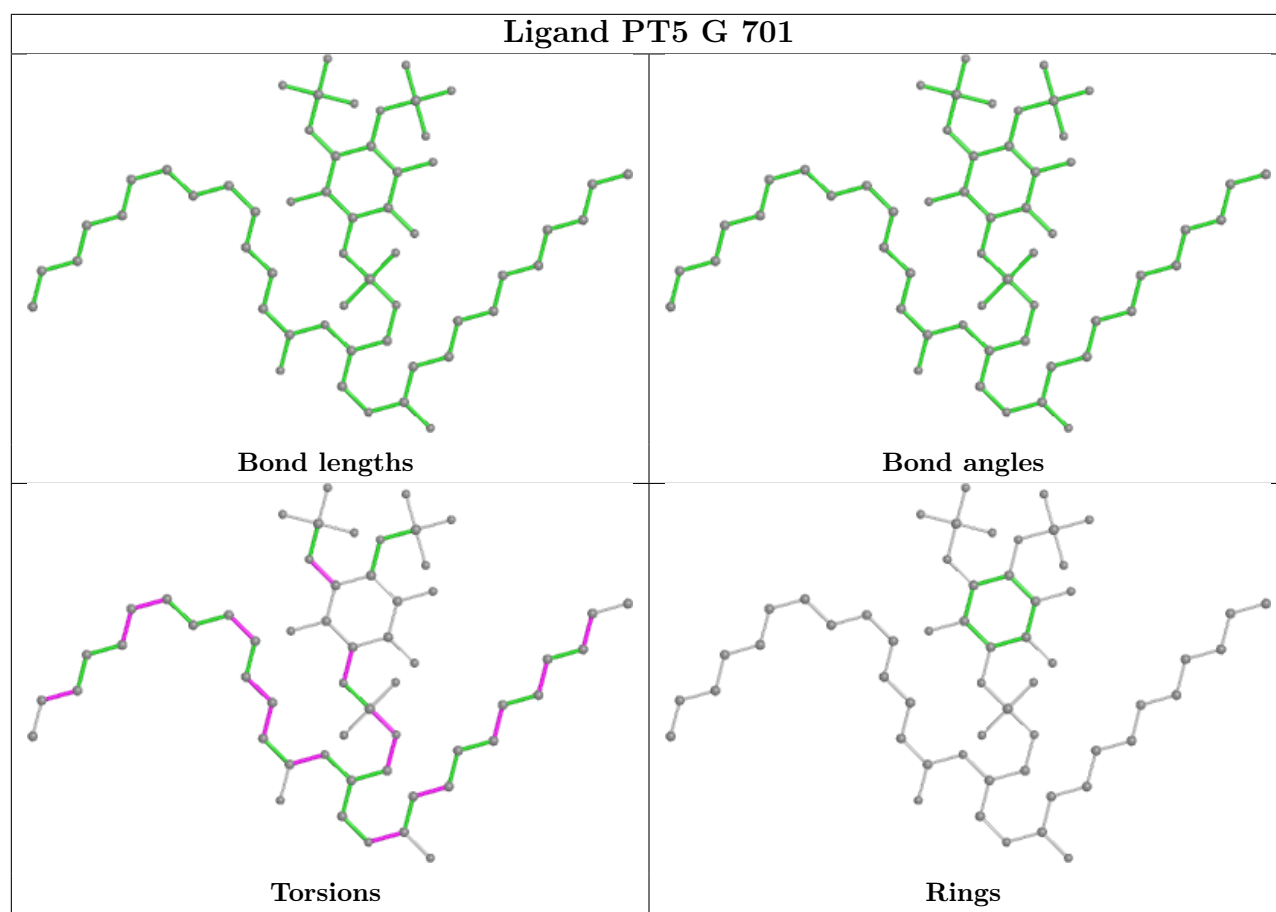
5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6   Map visualisation ⓘ

This section contains visualisations of the EMDB entry EMD-30246. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1   Orthogonal projections ⓘ

6.1.1   Primary map

| X | Y | Z |
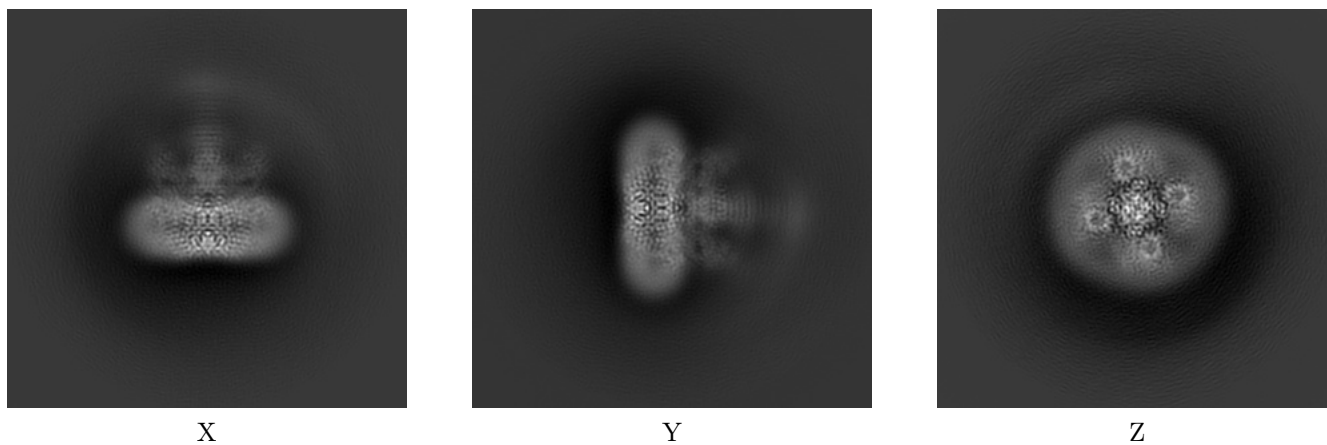
The images above show the map projected in three orthogonal directions.

6.2   Central slices ⓘ

6.2.1   Primary map

| X Index: 160 | Y Index: 160 | Z Index: 160 |
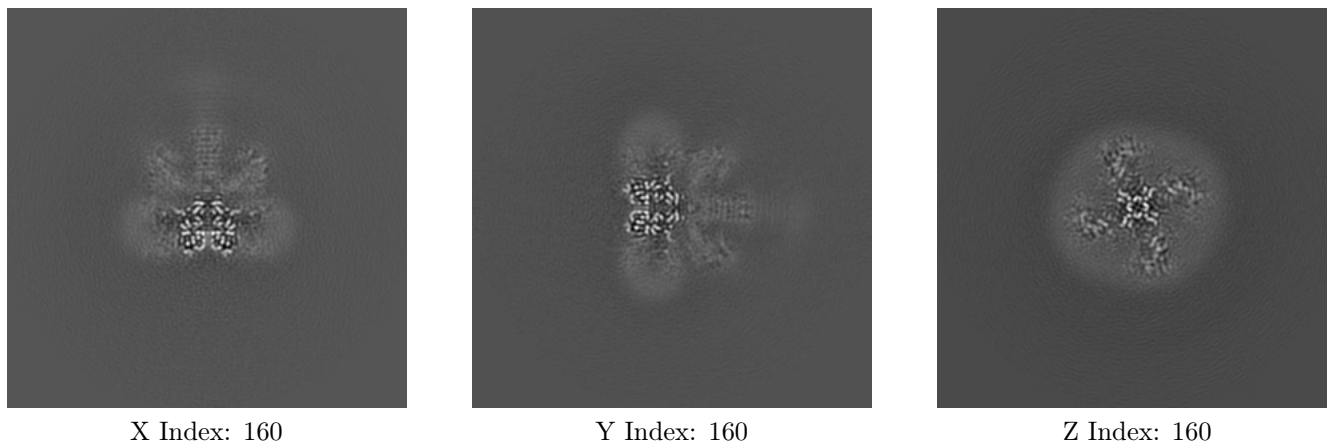
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices ⓘ
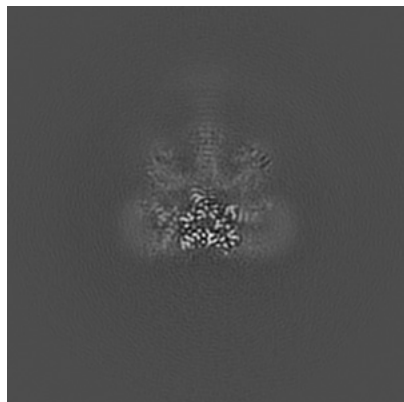
6.3.1 Primary map
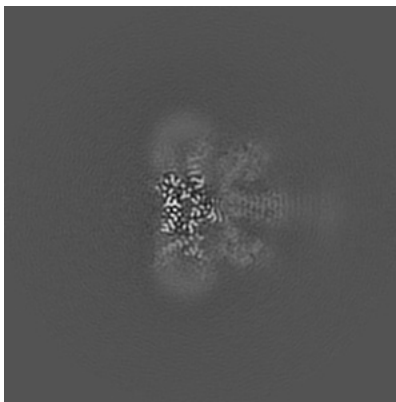
| X Index: 163 | Y Index: 157 | Z Index: 132 |
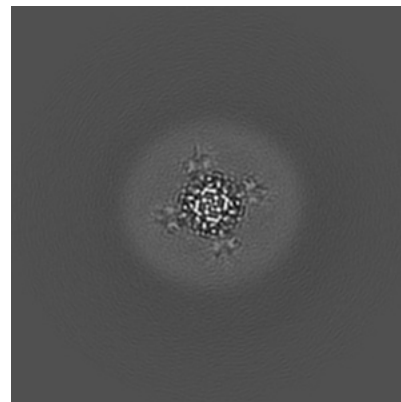
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

6.4.1 Primary map

| X | Y | Z |
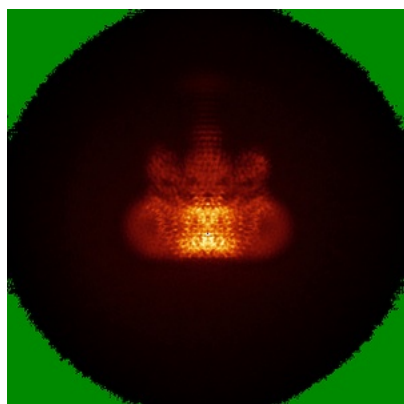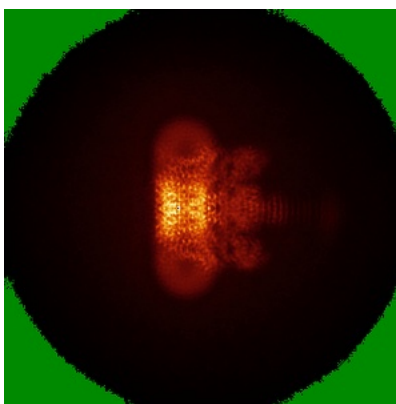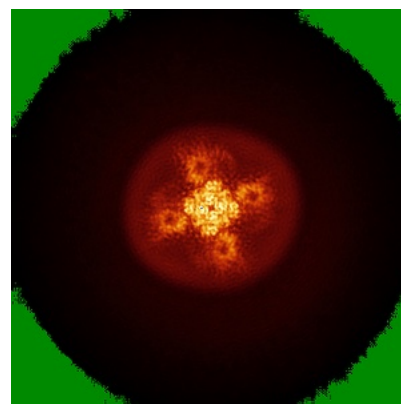
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views ⓘ

6.5.1 Primary map

| X | Y | Z |
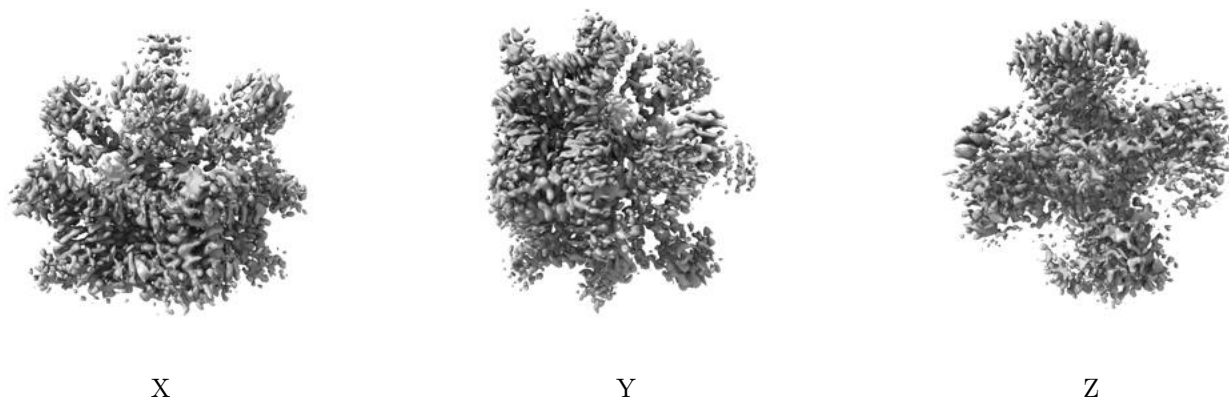
The images above show the 3D surface view of the map at the recommended contour level 0.0185. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.6 Mask visualisation ⓘ

This section was not generated. No masks/segmentation were deposited.

7 Map analysis ⓘ

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ
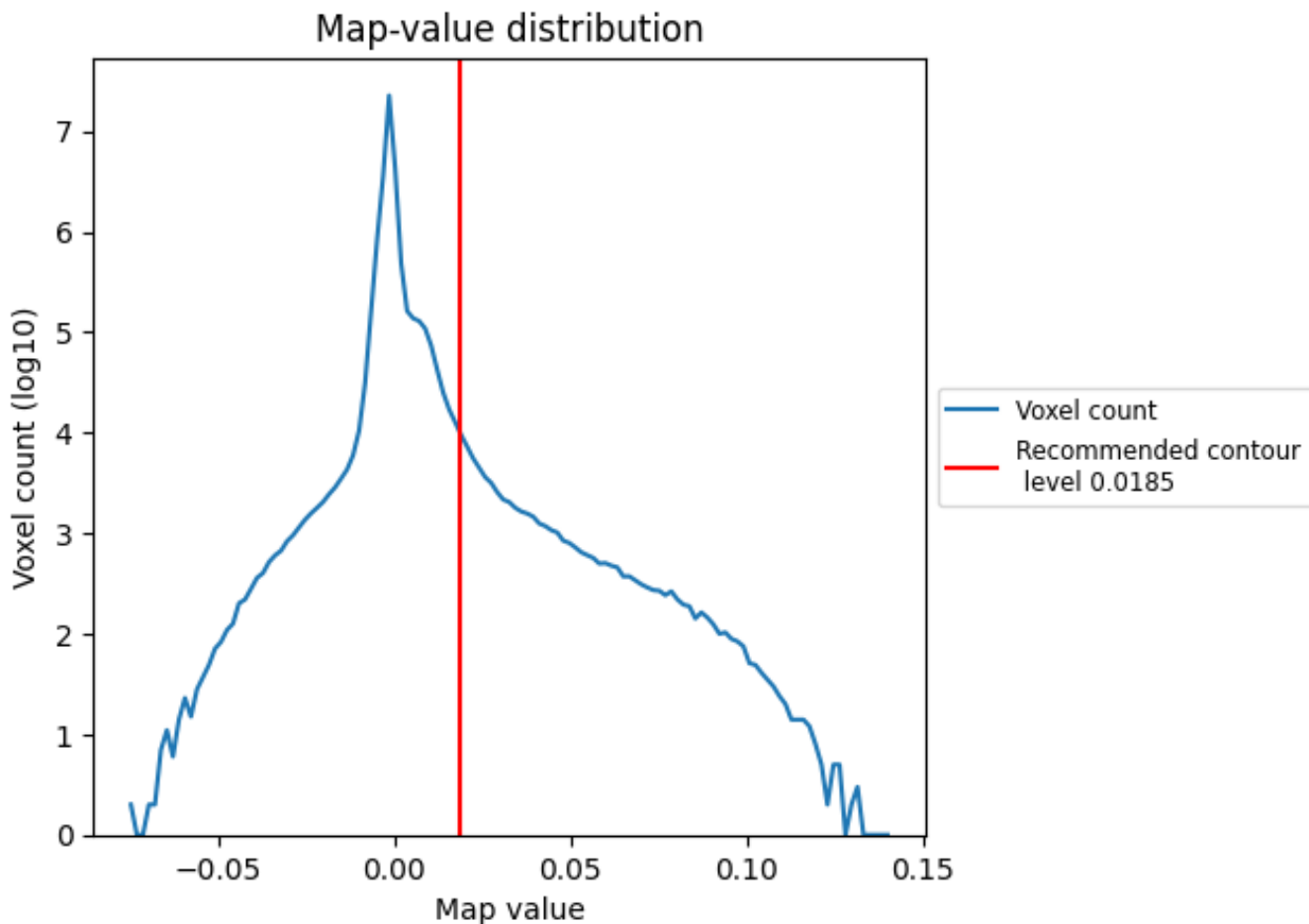
The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

7.2 Volume estimate ⓘ
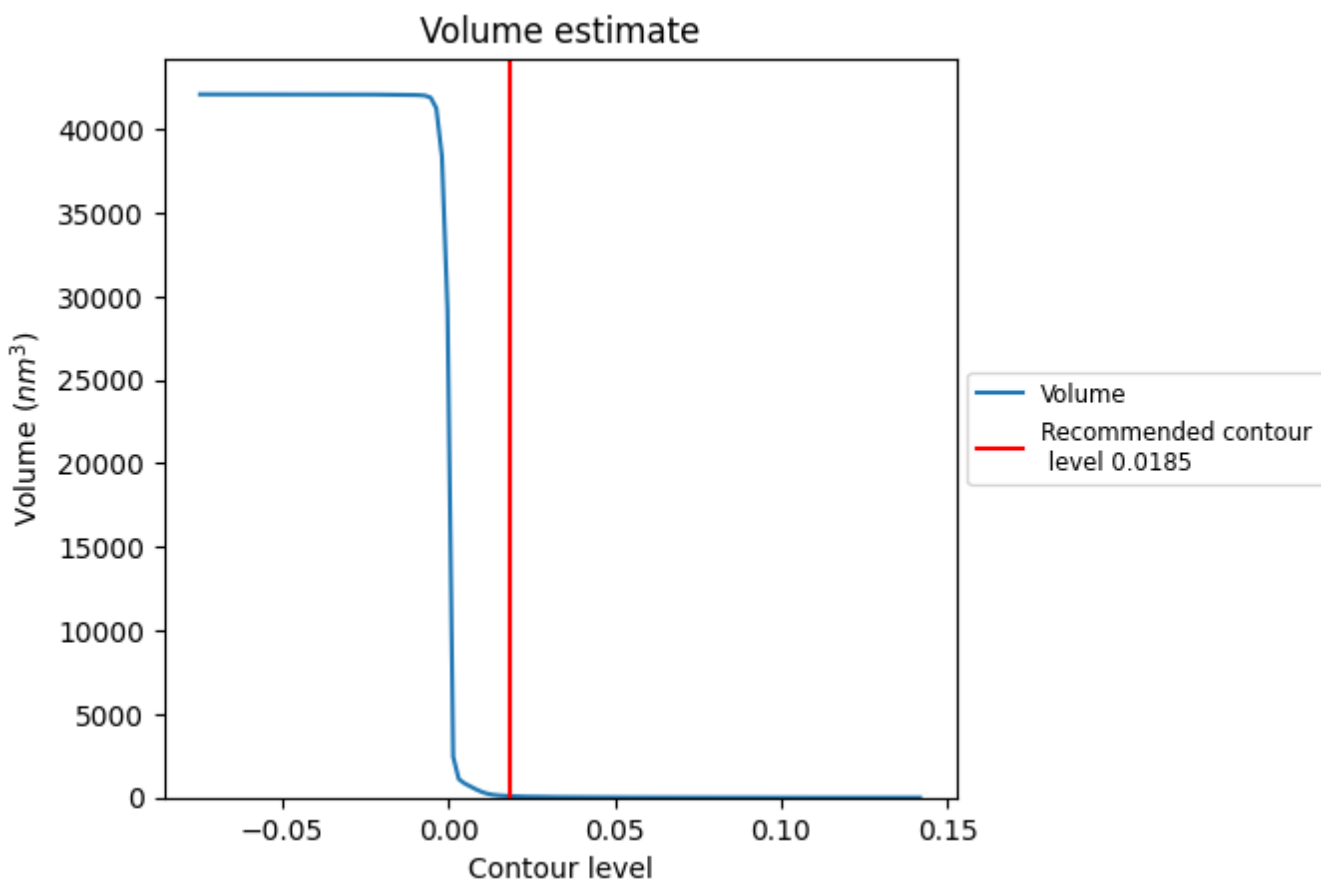
The volume at the recommended contour level is 85 nm^3; this corresponds to an approximate mass of 77 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)
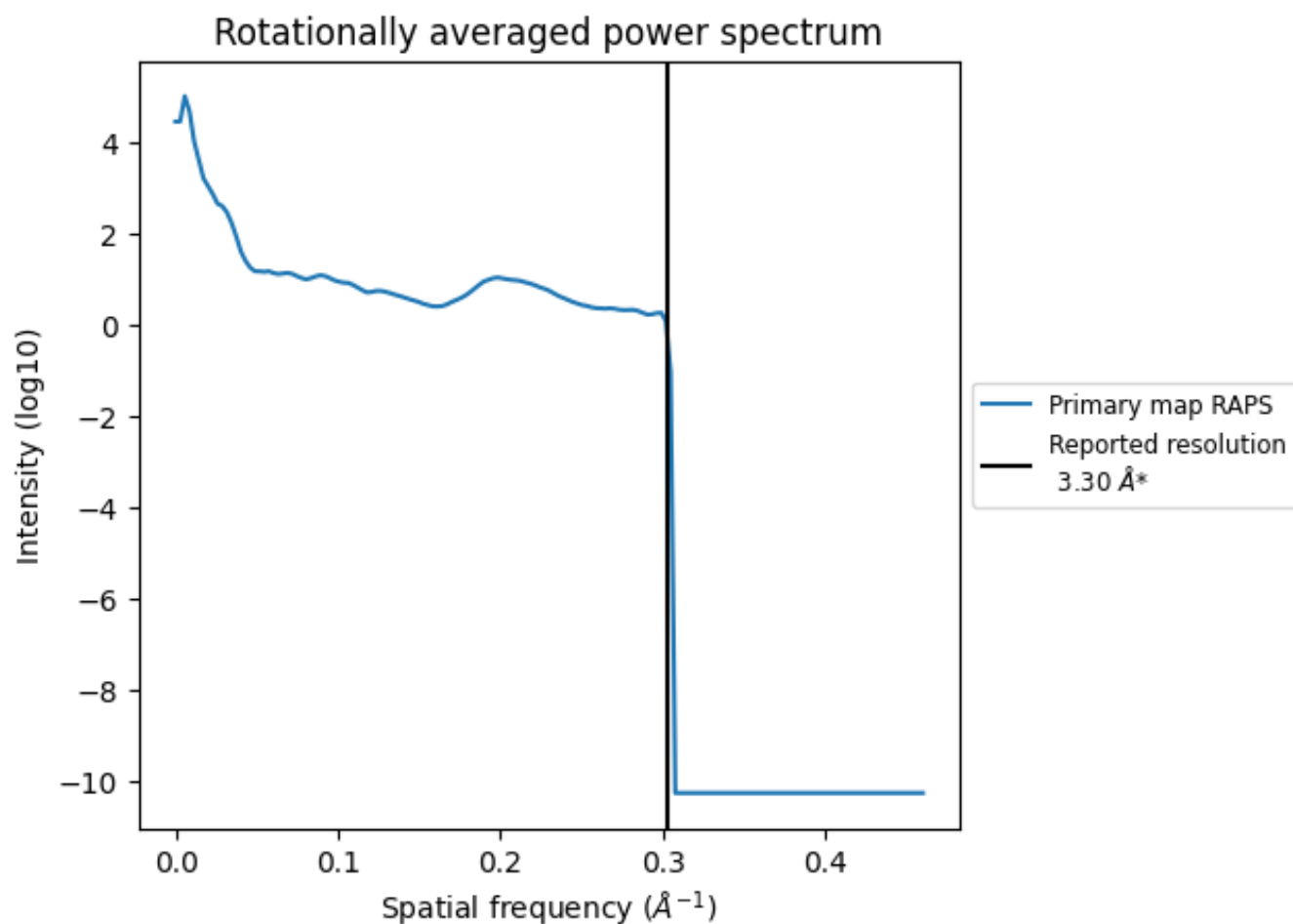
*Reported resolution corresponds to spatial frequency of 0.303 Å^{-1}

8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit ⓘ

This section contains information regarding the fit between EMDB map EMD-30246 and PDB model 7BYN. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay ⓘ
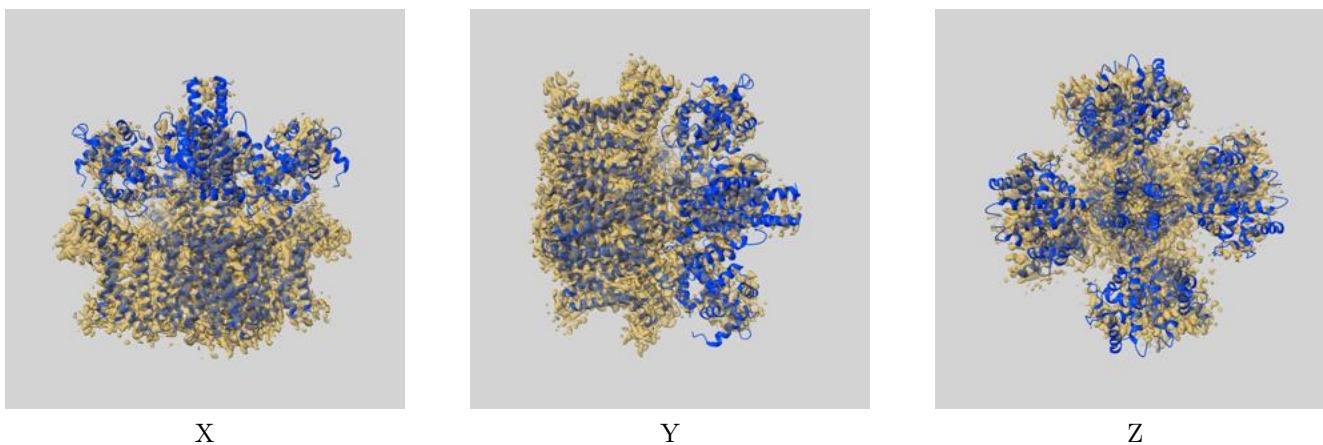
| X | Y | Z |

The images above show the 3D surface view of the map at the recommended contour level 0.0185 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2   Q-score mapped to coordinate model ⓘ

X   Y   Z
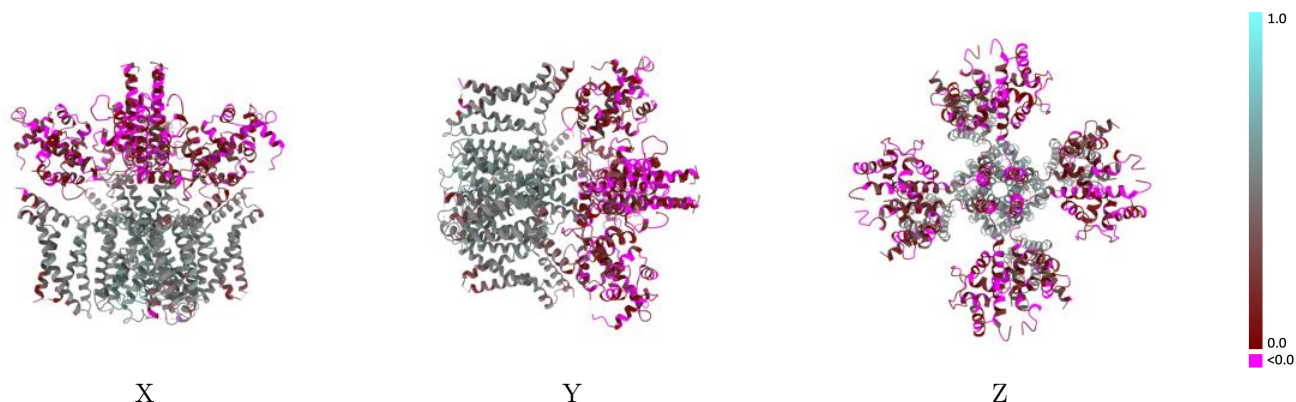
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3   Atom inclusion mapped to coordinate model ⓘ

X   Y   Z
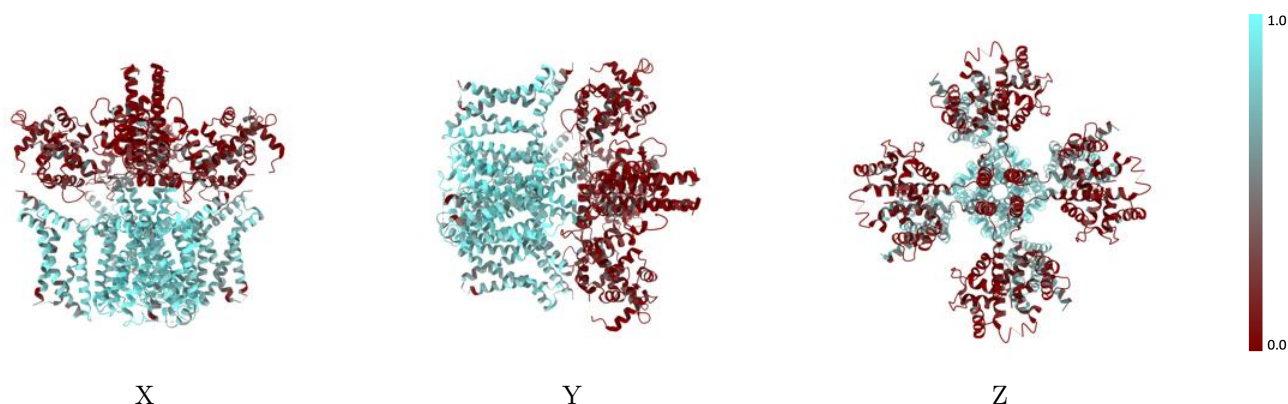
The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0185).

9.4 Atom inclusion ⓘ
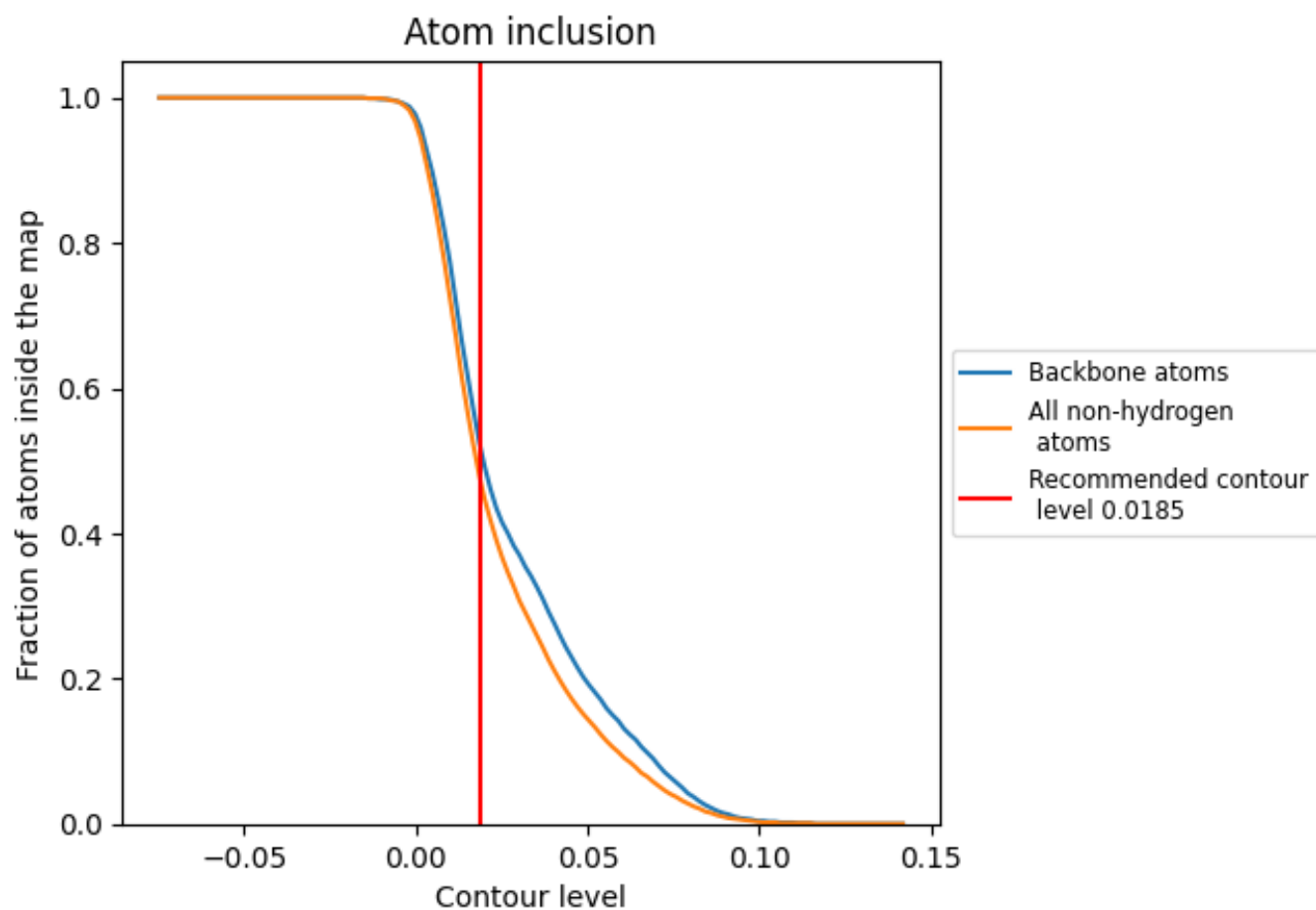
At the recommended contour level, 52% of all backbone atoms, 48% of all non-hydrogen atoms, are inside the map.

9.5   Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.0185) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4790	0.2850
A	0.6420	0.3820
B	0.1200	0.0610
C	0.6260	0.3760
D	0.1010	0.0560
E	0.6220	0.3660
F	0.0820	0.0670
G	0.6230	0.3660
H	0.1150	0.0580

1.0

0.0
<0.0