



wwPDB EM Validation Summary Report ⓘ

Sep 29, 2025 – 11:36 AM EDT

PDB ID : 9NNB / pdb_00009nnb
EMDB ID : EMD-49570
Title : Cryo-EM structure of the Retron Ec78 complex, PtuA:PtuB:RT (4:2:1)
Authors : Wang, B.; Li, H.
Deposited on : 2025-03-05
Resolution : 2.75 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev129
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.46

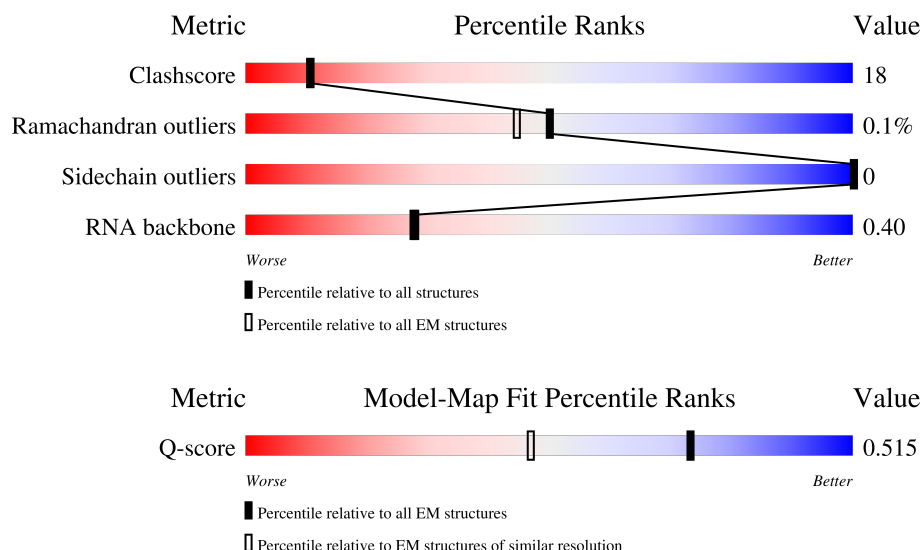
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.75 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	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
RNA backbone	6643	2191	-
Q-score	-	25397	10570 (2.25 - 3.25)

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 $\leq 5\%$. 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	C	550	
1	D	550	
1	E	550	

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Mol	Chain	Length	Quality of chain
1	F	550	<div><div></div><div>11%</div><div>67%</div><div>28%</div><div></div><div></div></div>
2	J	232	<div><div></div><div>17%</div><div>58%</div><div>33%</div><div>9%</div><div></div></div>
2	K	232	<div><div></div><div>16%</div><div>47%</div><div>41%</div><div></div><div>9%</div></div>
3	N	78	<div><div></div><div></div><div>51%</div><div>42%</div><div>6%</div><div></div></div>
4	B	311	<div><div></div><div></div><div>71%</div><div>29%</div><div></div><div></div></div>
5	L	67	<div><div></div><div></div><div>28%</div><div>25%</div><div>7%</div><div>39%</div><div></div></div>

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 25392 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 Retron I-A effector PtuA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	550	Total	C	N	O	S	0	0
			4390	2762	771	842	15		
1	D	503	Total	C	N	O	S	0	0
			4027	2540	708	766	13		
1	E	550	Total	C	N	O	S	0	0
			4390	2762	771	842	15		
1	F	527	Total	C	N	O	S	0	0
			4207	2647	740	806	14		

There are 152 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	25	SER	THR	conflict	UNP P0DV91
C	27	LYS	ASN	conflict	UNP P0DV91
C	28	ALA	MET	conflict	UNP P0DV91
C	37	GLY	ASP	conflict	UNP P0DV91
C	42	MET	THR	conflict	UNP P0DV91
C	57	ILE	THR	conflict	UNP P0DV91
C	84	LEU	PHE	conflict	UNP P0DV91
C	130	MET	LEU	conflict	UNP P0DV91
C	139	ASP	ASN	conflict	UNP P0DV91
C	142	SER	ALA	conflict	UNP P0DV91
C	180	LYS	ARG	conflict	UNP P0DV91
C	192	VAL	ALA	conflict	UNP P0DV91
C	193	ASN	LYS	conflict	UNP P0DV91
C	215	ILE	THR	conflict	UNP P0DV91
C	219	THR	ALA	conflict	UNP P0DV91
C	232	THR	ALA	conflict	UNP P0DV91
C	254	VAL	ILE	conflict	UNP P0DV91
C	274	THR	SER	conflict	UNP P0DV91
C	291	PHE	LEU	conflict	UNP P0DV91
C	297	ILE	SER	conflict	UNP P0DV91
C	307	ARG	LYS	conflict	UNP P0DV91
C	308	VAL	MET	conflict	UNP P0DV91

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Chain	Residue	Modelled	Actual	Comment	Reference
C	309	LEU	VAL	conflict	UNP P0DV91
C	321	ALA	SER	conflict	UNP P0DV91
C	331	ASN	LYS	conflict	UNP P0DV91
C	337	ILE	THR	conflict	UNP P0DV91
C	396	GLN	GLU	conflict	UNP P0DV91
C	416	ALA	VAL	conflict	UNP P0DV91
C	444	GLU	ASP	conflict	UNP P0DV91
C	450	ASP	ASN	conflict	UNP P0DV91
C	478	SER	PRO	conflict	UNP P0DV91
C	491	ASN	ASP	conflict	UNP P0DV91
C	506	HIS	GLN	conflict	UNP P0DV91
C	509	VAL	GLU	conflict	UNP P0DV91
C	513	GLN	LYS	conflict	UNP P0DV91
C	516	ALA	THR	conflict	UNP P0DV91
C	523	ILE	ALA	conflict	UNP P0DV91
C	541	LEU	ILE	conflict	UNP P0DV91
D	25	SER	THR	conflict	UNP P0DV91
D	27	LYS	ASN	conflict	UNP P0DV91
D	28	ALA	MET	conflict	UNP P0DV91
D	37	GLY	ASP	conflict	UNP P0DV91
D	42	MET	THR	conflict	UNP P0DV91
D	57	ILE	THR	conflict	UNP P0DV91
D	84	LEU	PHE	conflict	UNP P0DV91
D	130	MET	LEU	conflict	UNP P0DV91
D	139	ASP	ASN	conflict	UNP P0DV91
D	142	SER	ALA	conflict	UNP P0DV91
D	180	LYS	ARG	conflict	UNP P0DV91
D	192	VAL	ALA	conflict	UNP P0DV91
D	193	ASN	LYS	conflict	UNP P0DV91
D	215	ILE	THR	conflict	UNP P0DV91
D	219	THR	ALA	conflict	UNP P0DV91
D	232	THR	ALA	conflict	UNP P0DV91
D	254	VAL	ILE	conflict	UNP P0DV91
D	274	THR	SER	conflict	UNP P0DV91
D	291	PHE	LEU	conflict	UNP P0DV91
D	297	ILE	SER	conflict	UNP P0DV91
D	307	ARG	LYS	conflict	UNP P0DV91
D	308	VAL	MET	conflict	UNP P0DV91
D	309	LEU	VAL	conflict	UNP P0DV91
D	321	ALA	SER	conflict	UNP P0DV91
D	331	ASN	LYS	conflict	UNP P0DV91
D	337	ILE	THR	conflict	UNP P0DV91

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Chain	Residue	Modelled	Actual	Comment	Reference
D	396	GLN	GLU	conflict	UNP P0DV91
D	416	ALA	VAL	conflict	UNP P0DV91
D	444	GLU	ASP	conflict	UNP P0DV91
D	450	ASP	ASN	conflict	UNP P0DV91
D	478	SER	PRO	conflict	UNP P0DV91
D	491	ASN	ASP	conflict	UNP P0DV91
D	506	HIS	GLN	conflict	UNP P0DV91
D	509	VAL	GLU	conflict	UNP P0DV91
D	513	GLN	LYS	conflict	UNP P0DV91
D	516	ALA	THR	conflict	UNP P0DV91
D	523	ILE	ALA	conflict	UNP P0DV91
D	541	LEU	ILE	conflict	UNP P0DV91
E	25	SER	THR	conflict	UNP P0DV91
E	27	LYS	ASN	conflict	UNP P0DV91
E	28	ALA	MET	conflict	UNP P0DV91
E	37	GLY	ASP	conflict	UNP P0DV91
E	42	MET	THR	conflict	UNP P0DV91
E	57	ILE	THR	conflict	UNP P0DV91
E	84	LEU	PHE	conflict	UNP P0DV91
E	130	MET	LEU	conflict	UNP P0DV91
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E	180	LYS	ARG	conflict	UNP P0DV91
E	192	VAL	ALA	conflict	UNP P0DV91
E	193	ASN	LYS	conflict	UNP P0DV91
E	215	ILE	THR	conflict	UNP P0DV91
E	219	THR	ALA	conflict	UNP P0DV91
E	232	THR	ALA	conflict	UNP P0DV91
E	254	VAL	ILE	conflict	UNP P0DV91
E	274	THR	SER	conflict	UNP P0DV91
E	291	PHE	LEU	conflict	UNP P0DV91
E	297	ILE	SER	conflict	UNP P0DV91
E	307	ARG	LYS	conflict	UNP P0DV91
E	308	VAL	MET	conflict	UNP P0DV91
E	309	LEU	VAL	conflict	UNP P0DV91
E	321	ALA	SER	conflict	UNP P0DV91
E	331	ASN	LYS	conflict	UNP P0DV91
E	337	ILE	THR	conflict	UNP P0DV91
E	396	GLN	GLU	conflict	UNP P0DV91
E	416	ALA	VAL	conflict	UNP P0DV91
E	444	GLU	ASP	conflict	UNP P0DV91
E	450	ASP	ASN	conflict	UNP P0DV91

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Chain	Residue	Modelled	Actual	Comment	Reference
E	478	SER	PRO	conflict	UNP P0DV91
E	491	ASN	ASP	conflict	UNP P0DV91
E	506	HIS	GLN	conflict	UNP P0DV91
E	509	VAL	GLU	conflict	UNP P0DV91
E	513	GLN	LYS	conflict	UNP P0DV91
E	516	ALA	THR	conflict	UNP P0DV91
E	523	ILE	ALA	conflict	UNP P0DV91
E	541	LEU	ILE	conflict	UNP P0DV91
F	25	SER	THR	conflict	UNP P0DV91
F	27	LYS	ASN	conflict	UNP P0DV91
F	28	ALA	MET	conflict	UNP P0DV91
F	37	GLY	ASP	conflict	UNP P0DV91
F	42	MET	THR	conflict	UNP P0DV91
F	57	ILE	THR	conflict	UNP P0DV91
F	84	LEU	PHE	conflict	UNP P0DV91
F	130	MET	LEU	conflict	UNP P0DV91
F	139	ASP	ASN	conflict	UNP P0DV91
F	142	SER	ALA	conflict	UNP P0DV91
F	180	LYS	ARG	conflict	UNP P0DV91
F	192	VAL	ALA	conflict	UNP P0DV91
F	193	ASN	LYS	conflict	UNP P0DV91
F	215	ILE	THR	conflict	UNP P0DV91
F	219	THR	ALA	conflict	UNP P0DV91
F	232	THR	ALA	conflict	UNP P0DV91
F	254	VAL	ILE	conflict	UNP P0DV91
F	274	THR	SER	conflict	UNP P0DV91
F	291	PHE	LEU	conflict	UNP P0DV91
F	297	ILE	SER	conflict	UNP P0DV91
F	307	ARG	LYS	conflict	UNP P0DV91
F	308	VAL	MET	conflict	UNP P0DV91
F	309	LEU	VAL	conflict	UNP P0DV91
F	321	ALA	SER	conflict	UNP P0DV91
F	331	ASN	LYS	conflict	UNP P0DV91
F	337	ILE	THR	conflict	UNP P0DV91
F	396	GLN	GLU	conflict	UNP P0DV91
F	416	ALA	VAL	conflict	UNP P0DV91
F	444	GLU	ASP	conflict	UNP P0DV91
F	450	ASP	ASN	conflict	UNP P0DV91
F	478	SER	PRO	conflict	UNP P0DV91
F	491	ASN	ASP	conflict	UNP P0DV91
F	506	HIS	GLN	conflict	UNP P0DV91
F	509	VAL	GLU	conflict	UNP P0DV91

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Chain	Residue	Modelled	Actual	Comment	Reference
F	513	GLN	LYS	conflict	UNP P0DV91
F	516	ALA	THR	conflict	UNP P0DV91
F	523	ILE	ALA	conflict	UNP P0DV91
F	541	LEU	ILE	conflict	UNP P0DV91

- Molecule 2 is a protein called Retron I-A effector PtuB.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	J	211	Total	C	N	O	S	0	0
			1712	1083	293	325	11		
2	K	211	Total	C	N	O	S	0	0
			1712	1083	293	325	11		

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	2	ARG	LYS	conflict	UNP P0DV92
J	9	ARG	SER	conflict	UNP P0DV92
J	17	ILE	THR	conflict	UNP P0DV92
J	41	GLY	GLU	conflict	UNP P0DV92
J	53	CYS	ARG	conflict	UNP P0DV92
J	72	ASN	SER	conflict	UNP P0DV92
J	82	ARG	LYS	conflict	UNP P0DV92
J	156	PHE	LEU	conflict	UNP P0DV92
J	175	THR	SER	conflict	UNP P0DV92
J	181	ASP	GLU	conflict	UNP P0DV92
J	201	TYR	PHE	conflict	UNP P0DV92
J	211	PHE	SER	conflict	UNP P0DV92
J	217	LEU	-	expression tag	UNP P0DV92
J	218	GLU	-	expression tag	UNP P0DV92
J	219	VAL	-	expression tag	UNP P0DV92
J	220	LEU	-	expression tag	UNP P0DV92
J	221	PHE	-	expression tag	UNP P0DV92
J	222	GLN	-	expression tag	UNP P0DV92
J	223	GLY	-	expression tag	UNP P0DV92
J	224	PRO	-	expression tag	UNP P0DV92
J	225	GLU	-	expression tag	UNP P0DV92
J	226	ALA	-	expression tag	UNP P0DV92
J	227	HIS	-	expression tag	UNP P0DV92
J	228	HIS	-	expression tag	UNP P0DV92
J	229	HIS	-	expression tag	UNP P0DV92
J	230	HIS	-	expression tag	UNP P0DV92

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Chain	Residue	Modelled	Actual	Comment	Reference
J	231	HIS	-	expression tag	UNP P0DV92
J	232	HIS	-	expression tag	UNP P0DV92
K	2	ARG	LYS	conflict	UNP P0DV92
K	9	ARG	SER	conflict	UNP P0DV92
K	17	ILE	THR	conflict	UNP P0DV92
K	41	GLY	GLU	conflict	UNP P0DV92
K	53	CYS	ARG	conflict	UNP P0DV92
K	72	ASN	SER	conflict	UNP P0DV92
K	82	ARG	LYS	conflict	UNP P0DV92
K	156	PHE	LEU	conflict	UNP P0DV92
K	175	THR	SER	conflict	UNP P0DV92
K	181	ASP	GLU	conflict	UNP P0DV92
K	201	TYR	PHE	conflict	UNP P0DV92
K	211	PHE	SER	conflict	UNP P0DV92
K	217	LEU	-	expression tag	UNP P0DV92
K	218	GLU	-	expression tag	UNP P0DV92
K	219	VAL	-	expression tag	UNP P0DV92
K	220	LEU	-	expression tag	UNP P0DV92
K	221	PHE	-	expression tag	UNP P0DV92
K	222	GLN	-	expression tag	UNP P0DV92
K	223	GLY	-	expression tag	UNP P0DV92
K	224	PRO	-	expression tag	UNP P0DV92
K	225	GLU	-	expression tag	UNP P0DV92
K	226	ALA	-	expression tag	UNP P0DV92
K	227	HIS	-	expression tag	UNP P0DV92
K	228	HIS	-	expression tag	UNP P0DV92
K	229	HIS	-	expression tag	UNP P0DV92
K	230	HIS	-	expression tag	UNP P0DV92
K	231	HIS	-	expression tag	UNP P0DV92
K	232	HIS	-	expression tag	UNP P0DV92

- Molecule 3 is a DNA chain called DNA (73-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	N	73	Total	C	N	O	P	0	0
			1501	711	285	432	73		

- Molecule 4 is a protein called Retron I-A Ec78 reverse transcriptase.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	311	Total	C	N	O	S	0	0
			2501	1604	441	446	10		

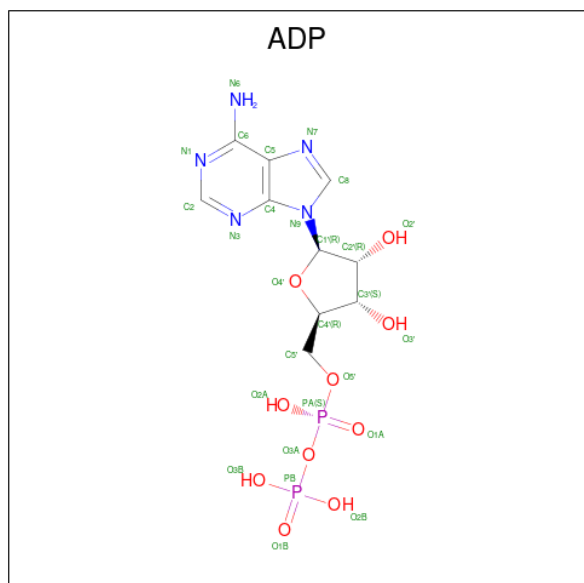
There are 17 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	6	GLY	ARG	conflict	UNP A0AB38GW94
B	17	ASP	GLY	conflict	UNP A0AB38GW94
B	63	SER	ASN	conflict	UNP A0AB38GW94
B	64	LEU	PHE	conflict	UNP A0AB38GW94
B	119	GLN	LEU	conflict	UNP A0AB38GW94
B	129	LEU	PHE	conflict	UNP A0AB38GW94
B	142	ARG	HIS	conflict	UNP A0AB38GW94
B	176	LYS	ASN	conflict	UNP A0AB38GW94
B	178	VAL	LEU	conflict	UNP A0AB38GW94
B	193	SER	CYS	conflict	UNP A0AB38GW94
B	197	ASP	ASN	conflict	UNP A0AB38GW94
B	206	LEU	ILE	conflict	UNP A0AB38GW94
B	208	VAL	ALA	conflict	UNP A0AB38GW94
B	217	ALA	GLU	conflict	UNP A0AB38GW94
B	239	ILE	VAL	conflict	UNP A0AB38GW94
B	278	ILE	THR	conflict	UNP A0AB38GW94
B	290	SER	GLY	conflict	UNP A0AB38GW94

- Molecule 5 is a RNA chain called RNA (41-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L	41	Total	C	N	O	P	0	0
			869	389	149	290	41		

- Molecule 6 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
6	C	1	Total	C	N	O	P	0
			27	10	5	10	2	
6	D	1	Total	C	N	O	P	0
			27	10	5	10	2	
6	F	1	Total	C	N	O	P	0
			27	10	5	10	2	

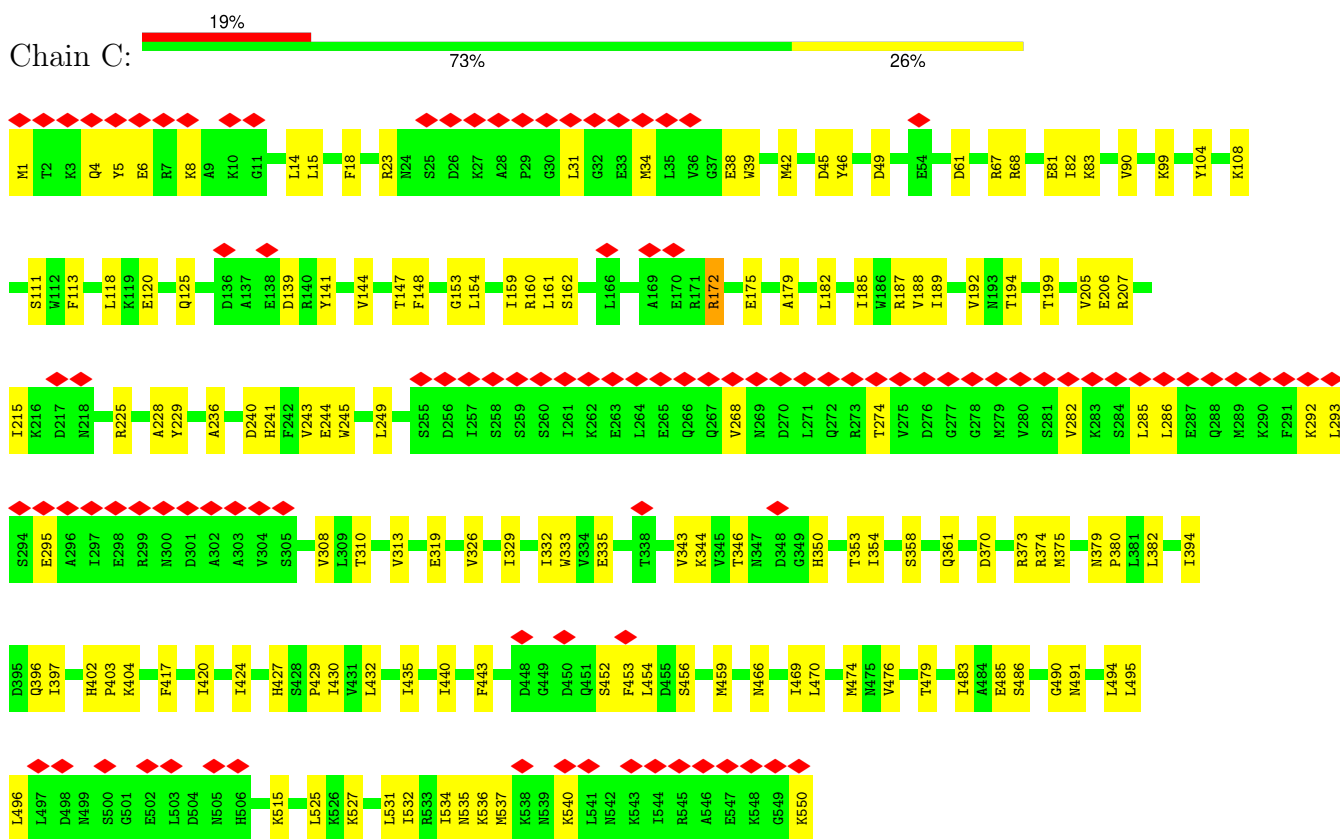
- Molecule 7 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
7	J	1	Total	Zn	0
			1	1	
7	K	1	Total	Zn	0
			1	1	

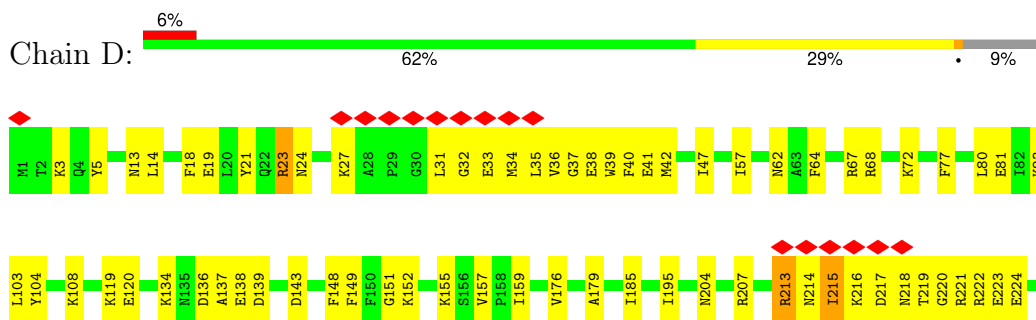
3 Residue-property plots

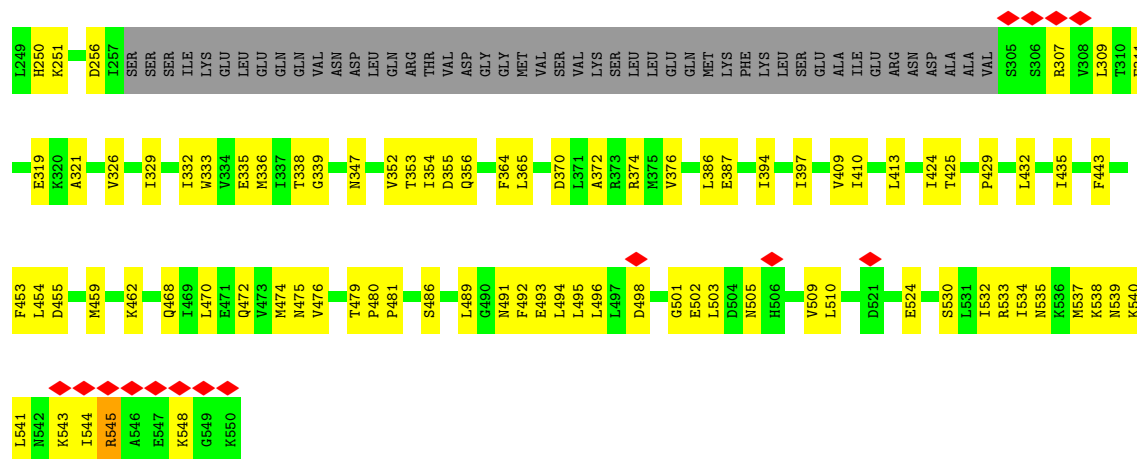
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Retron I-A effector PtuaA

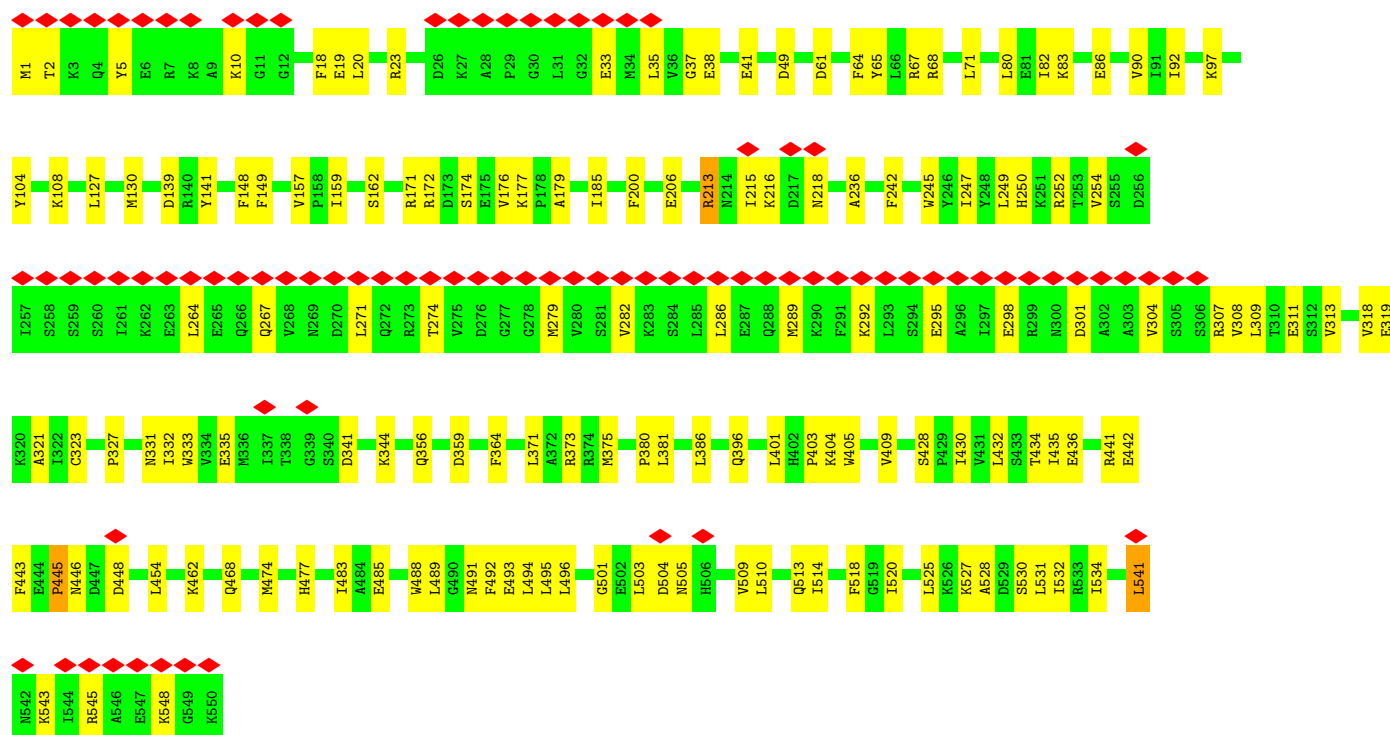


- Molecule 1: Retron I-A effector PtuaA

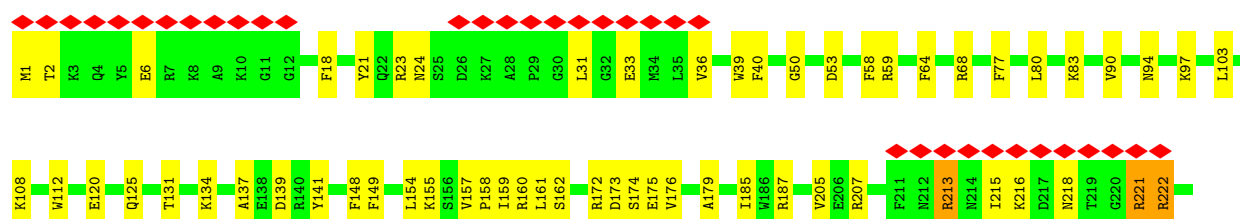


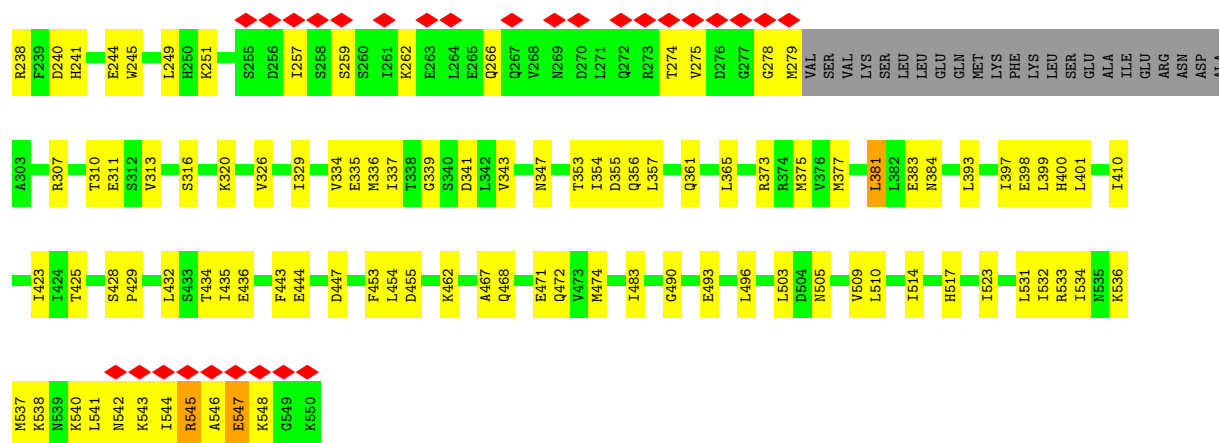


• Molecule 1: Retron I-A effector Ptua

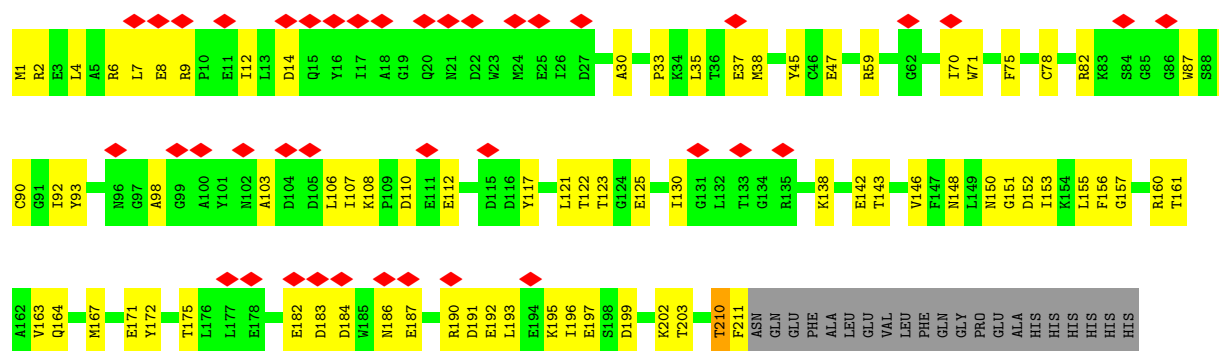


• Molecule 1: Retron I-A effector Ptua

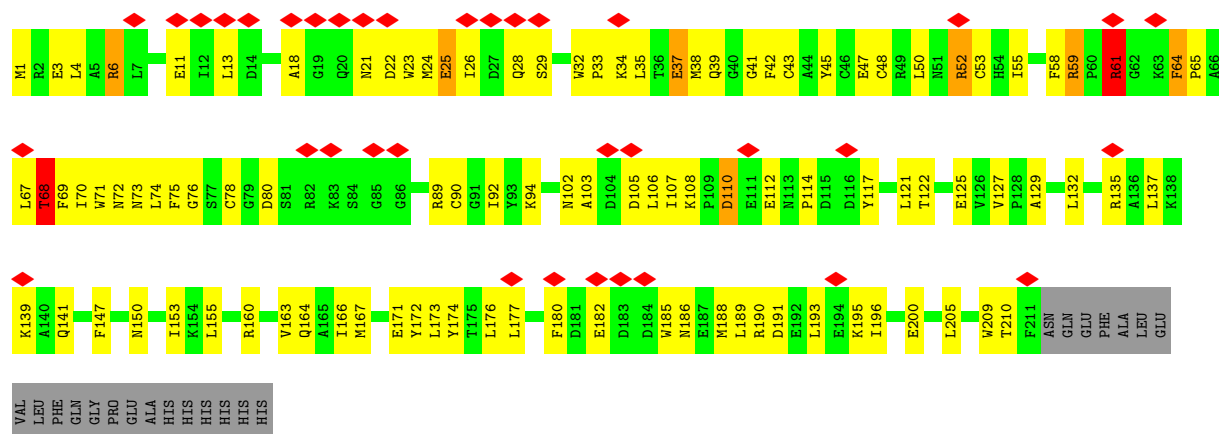




• Molecule 2: Retron I-A effector PtuB



• Molecule 2: Retron I-A effector PtuB

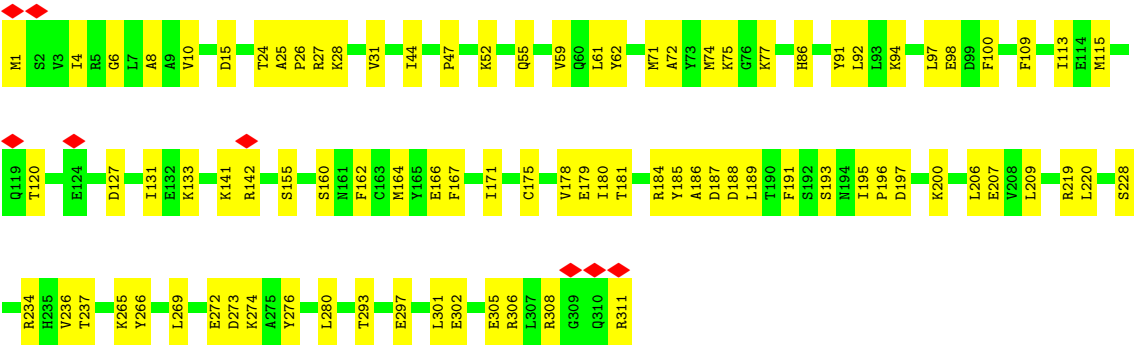


• Molecule 3: DNA (73-MER)

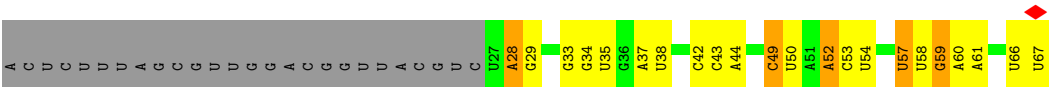
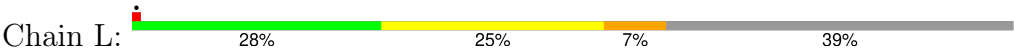




• Molecule 4: Retron I-A Ec78 reverse transcriptase



• Molecule 5: RNA (41-MER)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	140378	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOCONTINUUM (6k x 4k)	Depositor
Maximum map value	2.495	Depositor
Minimum map value	-1.368	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.055	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	294.768, 294.768, 294.768	wwPDB
Map dimensions	356, 356, 356	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.828, 0.828, 0.828	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ADP, ZN

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	C	0.24	0/4464	0.40	0/6020
1	D	0.33	1/4099 (0.0%)	0.48	0/5530
1	E	0.24	0/4464	0.43	1/6020 (0.0%)
1	F	0.36	2/4279 (0.0%)	0.54	3/5772 (0.1%)
2	J	0.33	0/1752	0.46	0/2368
2	K	0.64	4/1752 (0.2%)	0.71	6/2368 (0.3%)
3	N	0.25	0/1686	0.46	0/2600
4	B	0.21	0/2554	0.37	0/3444
5	L	0.22	0/970	0.43	0/1508
All	All	0.32	7/26020 (0.0%)	0.47	10/35630 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1
1	D	0	5
1	E	0	1
1	F	0	4
2	J	0	1
2	K	0	4
4	B	0	3
All	All	0	19

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	158	PRO	C-O	12.09	1.33	1.24
1	F	158	PRO	CA-C	-8.37	1.44	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	K	25	GLU	CD-OE1	-7.40	1.11	1.25
2	K	37	GLU	CD-OE1	-7.40	1.11	1.25
1	D	215	ILE	CB-CG2	-6.00	1.32	1.52

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	158	PRO	O-C-N	-8.89	116.42	122.73
2	K	68	THR	OG1-CB-CG2	6.56	122.42	109.30
1	F	381	LEU	CD1-CG-CD2	6.26	124.58	110.80
2	K	37	GLU	CG-CD-OE1	-6.14	104.28	118.40
1	E	541	LEU	CD1-CG-CD2	-5.76	98.14	110.80

There are no chirality outliers.

5 of 19 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	172	ARG	Sidechain
1	D	213	ARG	Sidechain
1	D	23	ARG	Sidechain
1	D	338	THR	Peptide
1	D	34	MET	Peptide

5.2 Too-close contacts [i](#)

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	C	4390	0	4400	132	0
1	D	4027	0	4028	177	0
1	E	4390	0	4400	144	0
1	F	4207	0	4206	178	0
2	J	1712	0	1640	76	0
2	K	1712	0	1640	187	0
3	N	1501	0	818	33	0
4	B	2501	0	2565	65	0
5	L	869	0	438	21	0
6	C	27	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	D	27	0	12	0	0
6	F	27	0	12	0	0
7	J	1	0	0	0	0
7	K	1	0	0	0	0
All	All	25392	0	24171	910	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 18.

The worst 5 of 910 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)
2:K:39:GLN:NE2	2:K:50:LEU:HD11	1.58	1.16
1:F:544:ILE:HA	1:F:547:GLU:OE1	1.48	1.12
2:K:61:ARG:HD3	2:K:68:THR:CG2	1.78	1.12
1:E:541:LEU:HD13	2:K:185:TRP:CH2	1.87	1.08
1:D:453:PHE:HE2	5:L:50:U:C2	1.72	1.07

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	C	548/550 (100%)	527 (96%)	21 (4%)	0	100	100
1	D	499/550 (91%)	469 (94%)	30 (6%)	0	100	100
1	E	548/550 (100%)	524 (96%)	23 (4%)	1 (0%)	44	63
1	F	523/550 (95%)	490 (94%)	33 (6%)	0	100	100
2	J	209/232 (90%)	196 (94%)	13 (6%)	0	100	100
2	K	209/232 (90%)	187 (90%)	21 (10%)	1 (0%)	25	41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	B	309/311 (99%)	297 (96%)	12 (4%)	0	100	100
All	All	2845/2975 (96%)	2690 (95%)	153 (5%)	2 (0%)	50	70

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	445	PRO
2	K	68	THR

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	C	489/489 (100%)	489 (100%)	0	100	100
1	D	447/489 (91%)	447 (100%)	0	100	100
1	E	489/489 (100%)	489 (100%)	0	100	100
1	F	468/489 (96%)	468 (100%)	0	100	100
2	J	180/198 (91%)	180 (100%)	0	100	100
2	K	180/198 (91%)	180 (100%)	0	100	100
4	B	272/272 (100%)	272 (100%)	0	100	100
All	All	2525/2624 (96%)	2525 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
4	B	89	ASN
4	B	102	ASN
2	K	28	GLN
1	D	468	GLN
1	D	406	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	L	40/67 (59%)	12 (30%)	0

5 of 12 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	L	28	A
5	L	33	G
5	L	37	A
5	L	38	U
5	L	42	C

There are no RNA pucker outliers to report.

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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	$\# Z > 2$
6	ADP	C	701	-	24,29,29	0.71	0	29,45,45	0.72	1 (3%)
6	ADP	F	601	-	24,29,29	0.72	0	29,45,45	0.73	1 (3%)
6	ADP	D	601	-	24,29,29	0.73	0	29,45,45	0.71	1 (3%)

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
6	ADP	C	701	-	-	5/12/32/32	0/3/3/3
6	ADP	F	601	-	-	6/12/32/32	0/3/3/3
6	ADP	D	601	-	-	7/12/32/32	0/3/3/3

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	F	601	ADP	C5-C6-N6	2.37	123.92	120.31
6	C	701	ADP	C5-C6-N6	2.24	123.72	120.31
6	D	601	ADP	C5-C6-N6	2.17	123.61	120.31

There are no chirality outliers.

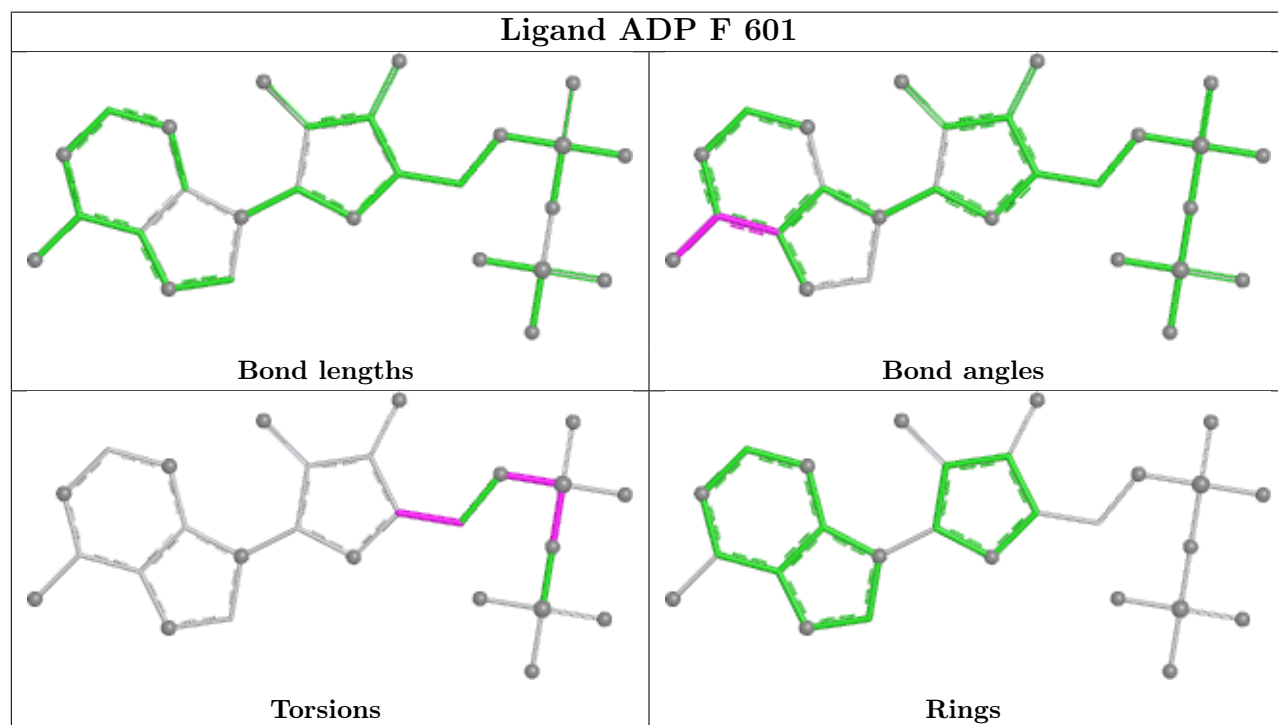
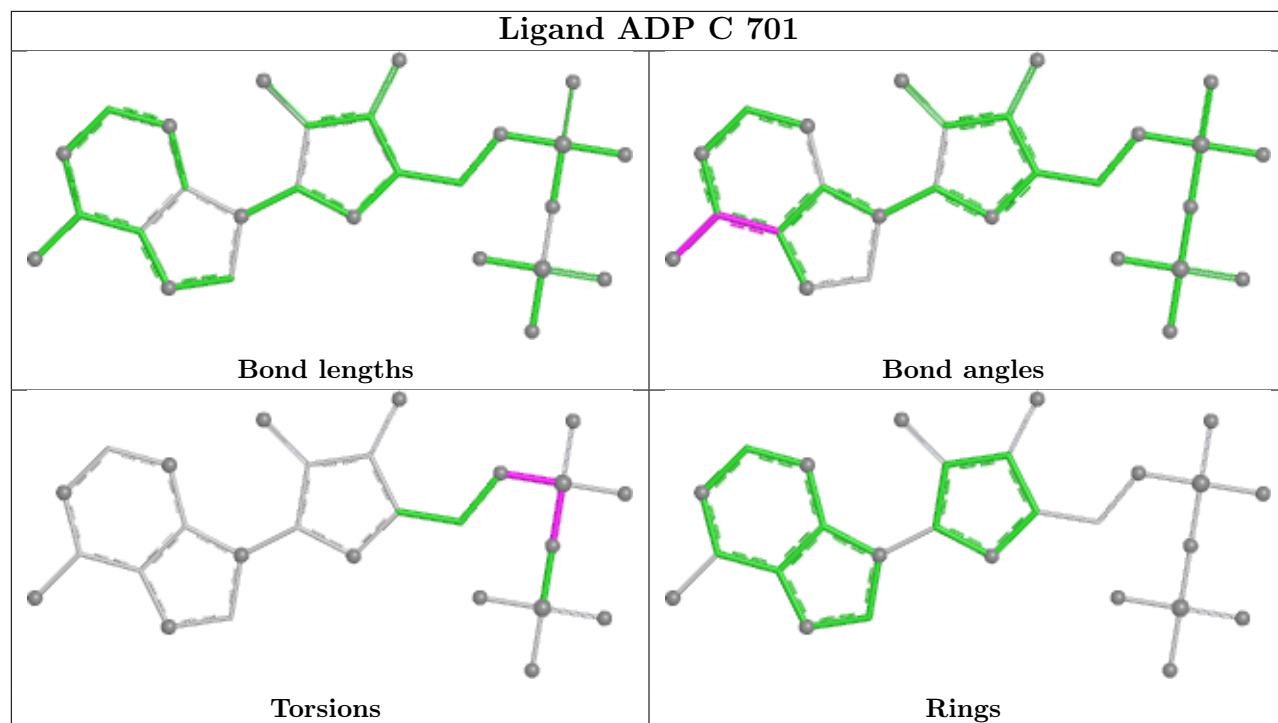
5 of 18 torsion outliers are listed below:

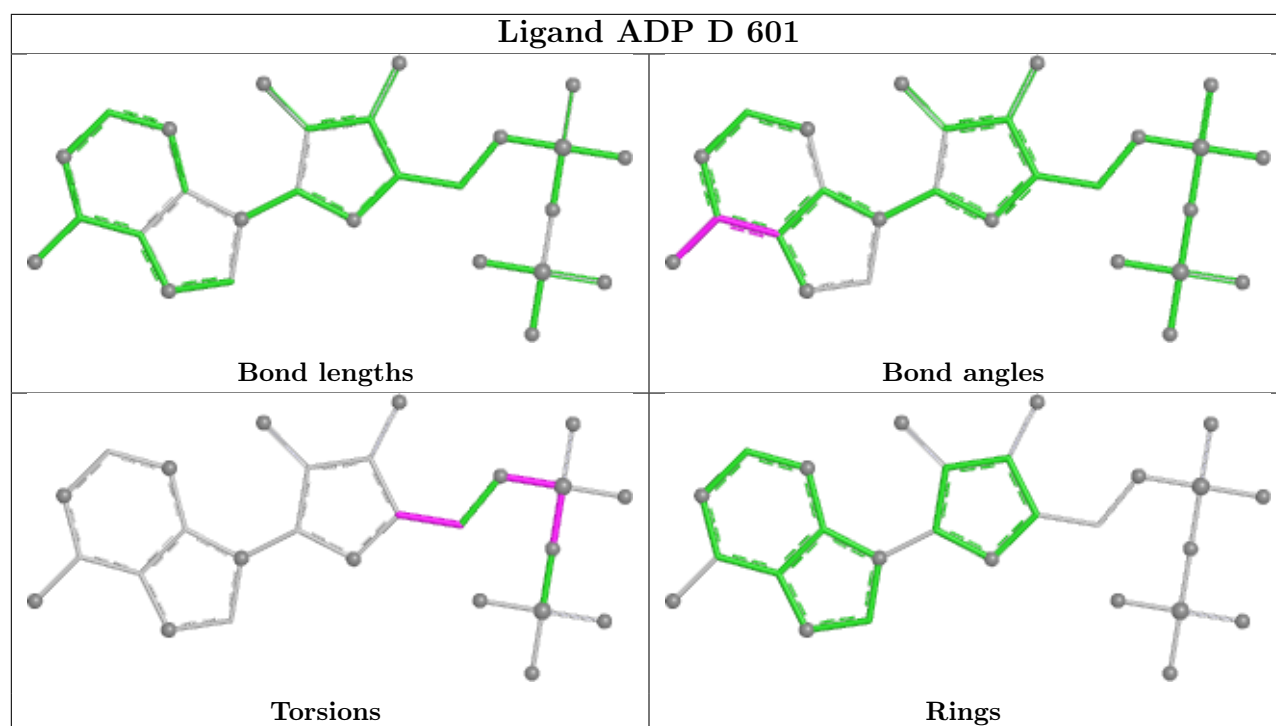
Mol	Chain	Res	Type	Atoms
6	C	701	ADP	C5'-O5'-PA-O1A
6	C	701	ADP	C5'-O5'-PA-O2A
6	C	701	ADP	C5'-O5'-PA-O3A
6	D	601	ADP	C5'-O5'-PA-O1A
6	D	601	ADP	C5'-O5'-PA-O2A

There are no ring outliers.

No monomer is involved in short contacts.

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 than 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.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

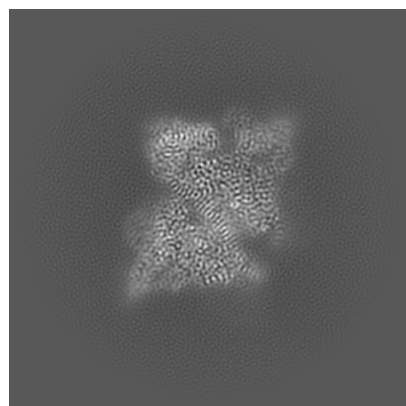
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-49570. These allow visual inspection of the internal detail of the map and identification of artifacts.

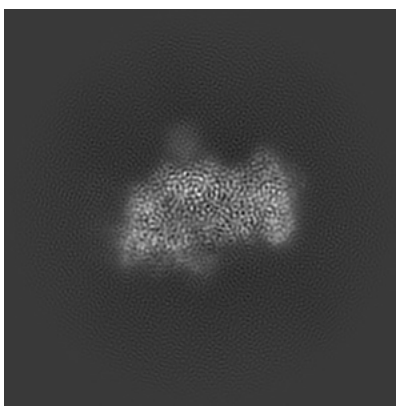
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

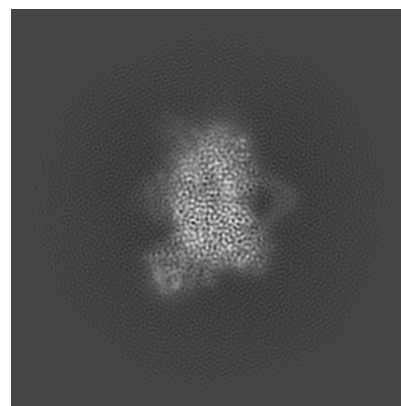
6.1.1 Primary map



X

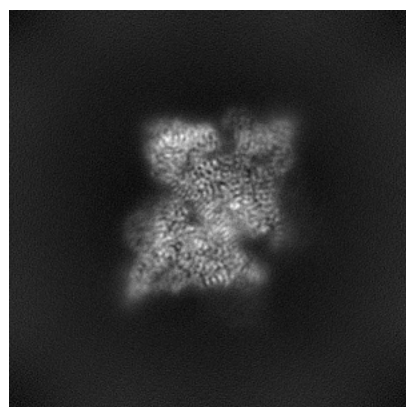


Y

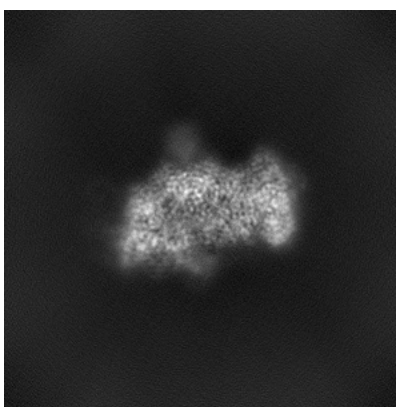


Z

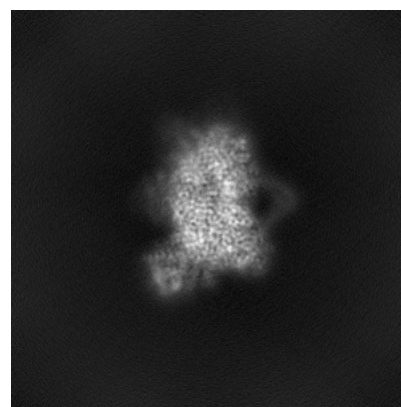
6.1.2 Raw map



X



Y

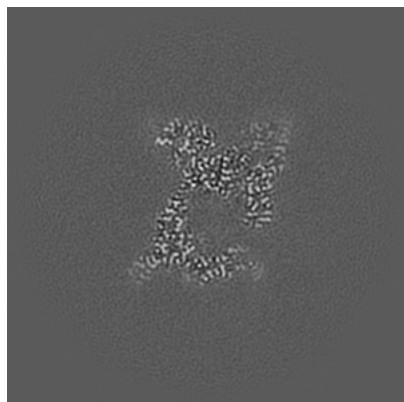


Z

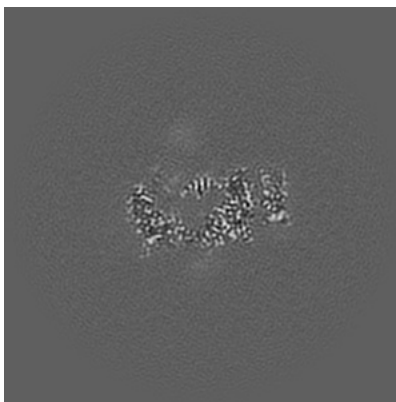
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

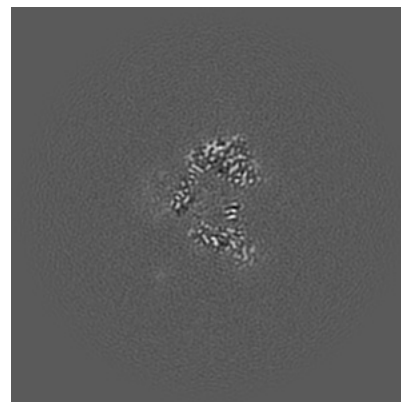
6.2.1 Primary map



X Index: 178

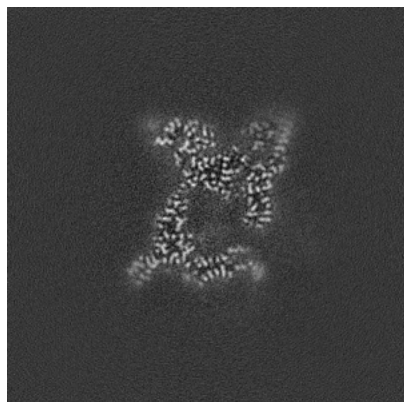


Y Index: 178

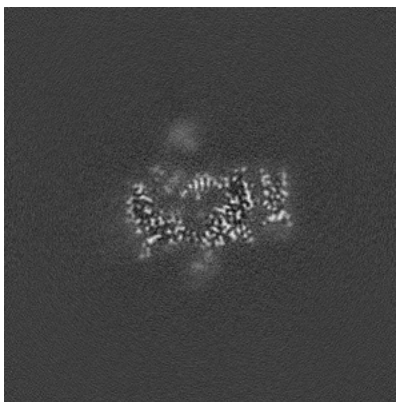


Z Index: 178

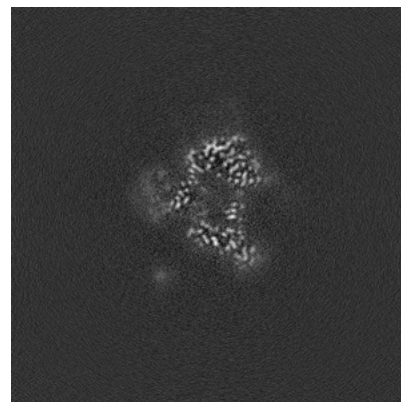
6.2.2 Raw map



X Index: 178



Y Index: 178

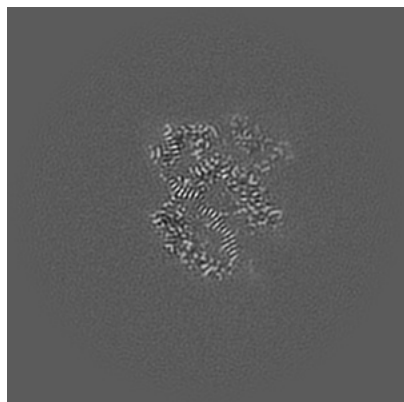


Z Index: 178

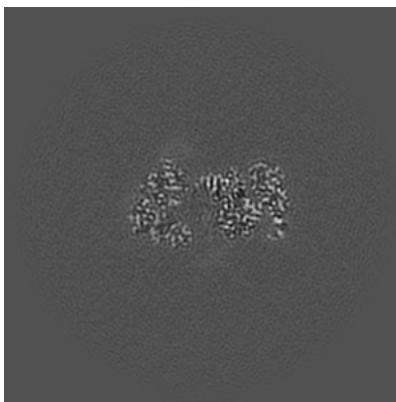
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

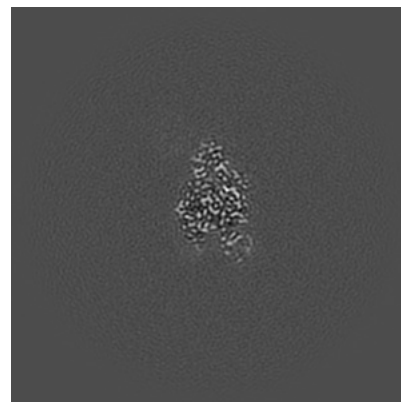
6.3.1 Primary map



X Index: 191

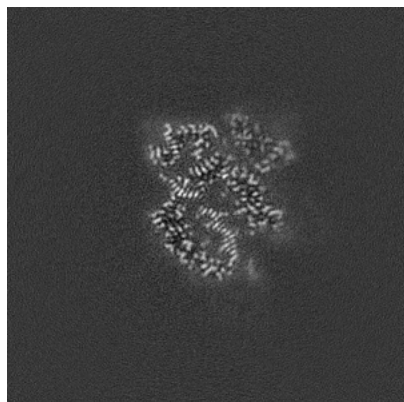


Y Index: 166

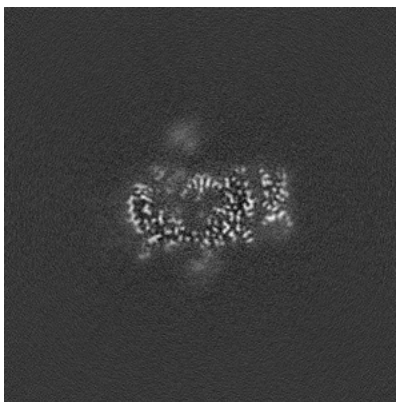


Z Index: 205

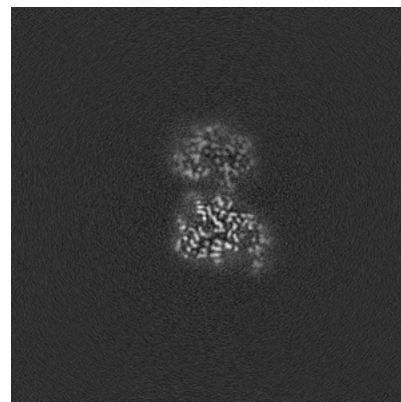
6.3.2 Raw map



X Index: 191



Y Index: 177

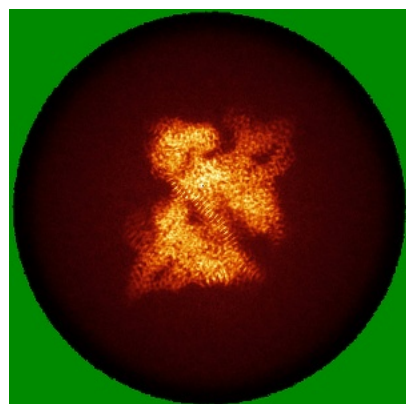


Z Index: 239

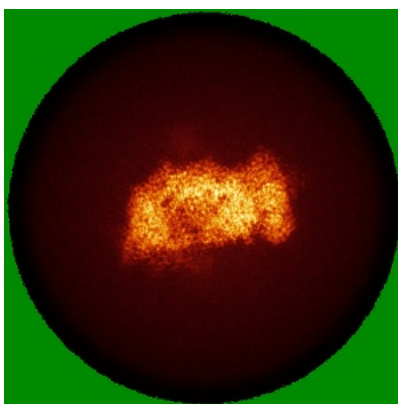
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

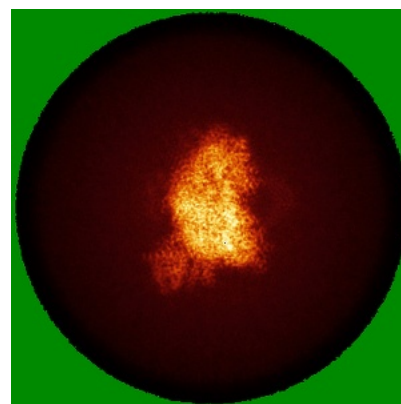
6.4.1 Primary map



X

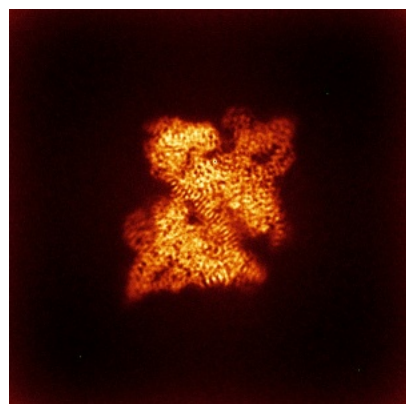


Y

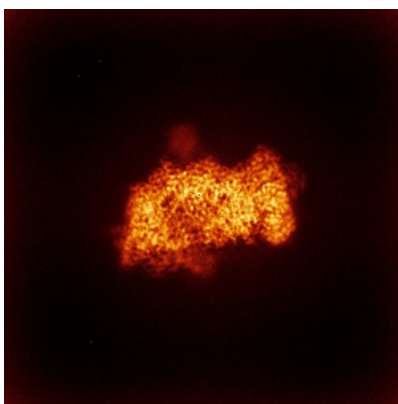


Z

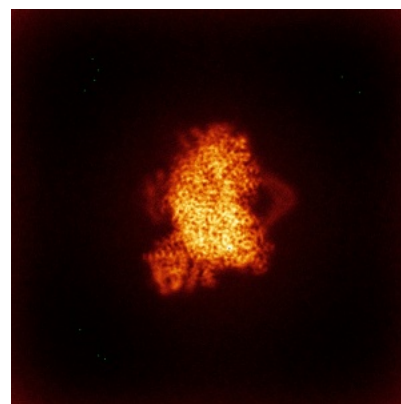
6.4.2 Raw map



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 [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

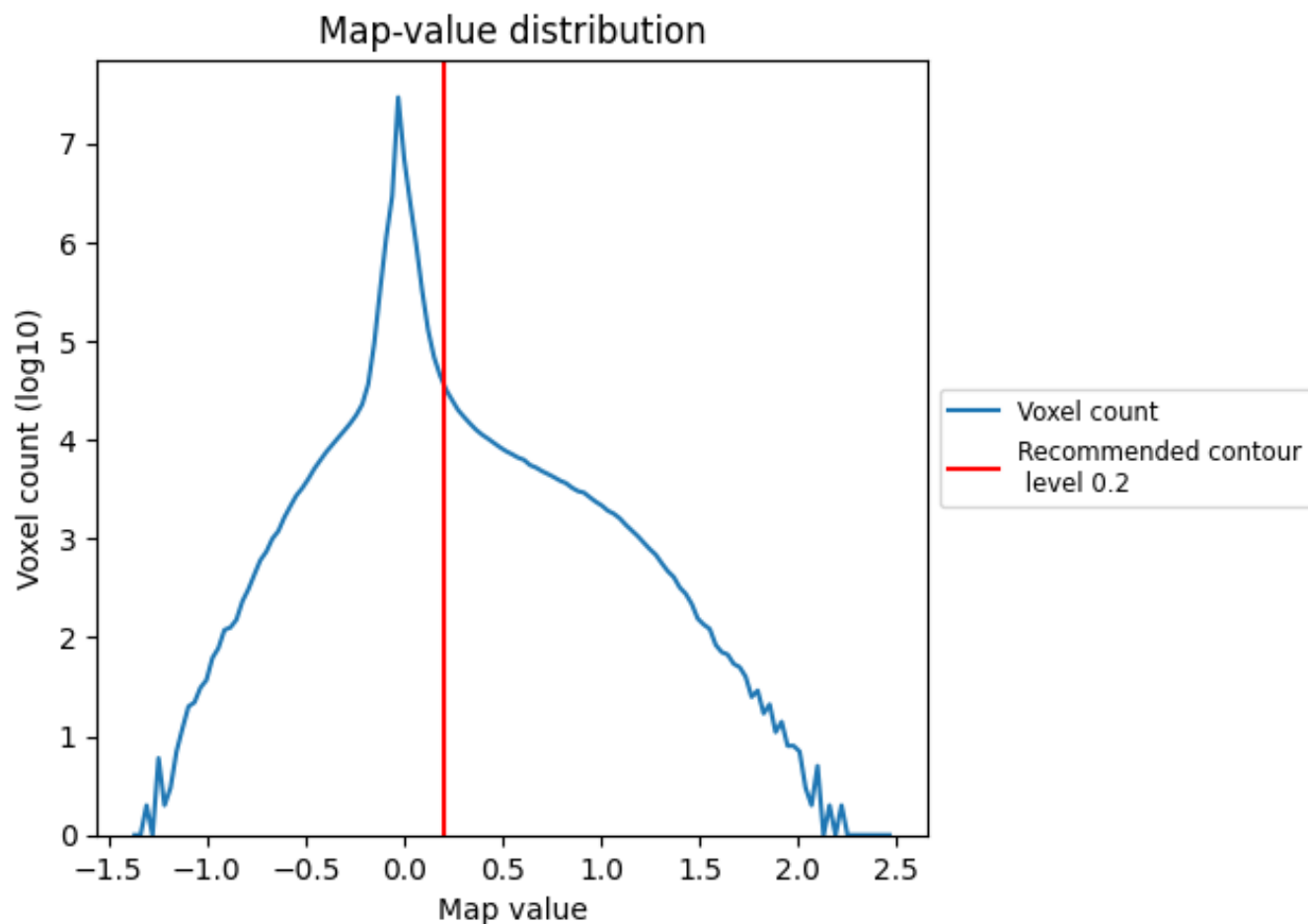
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

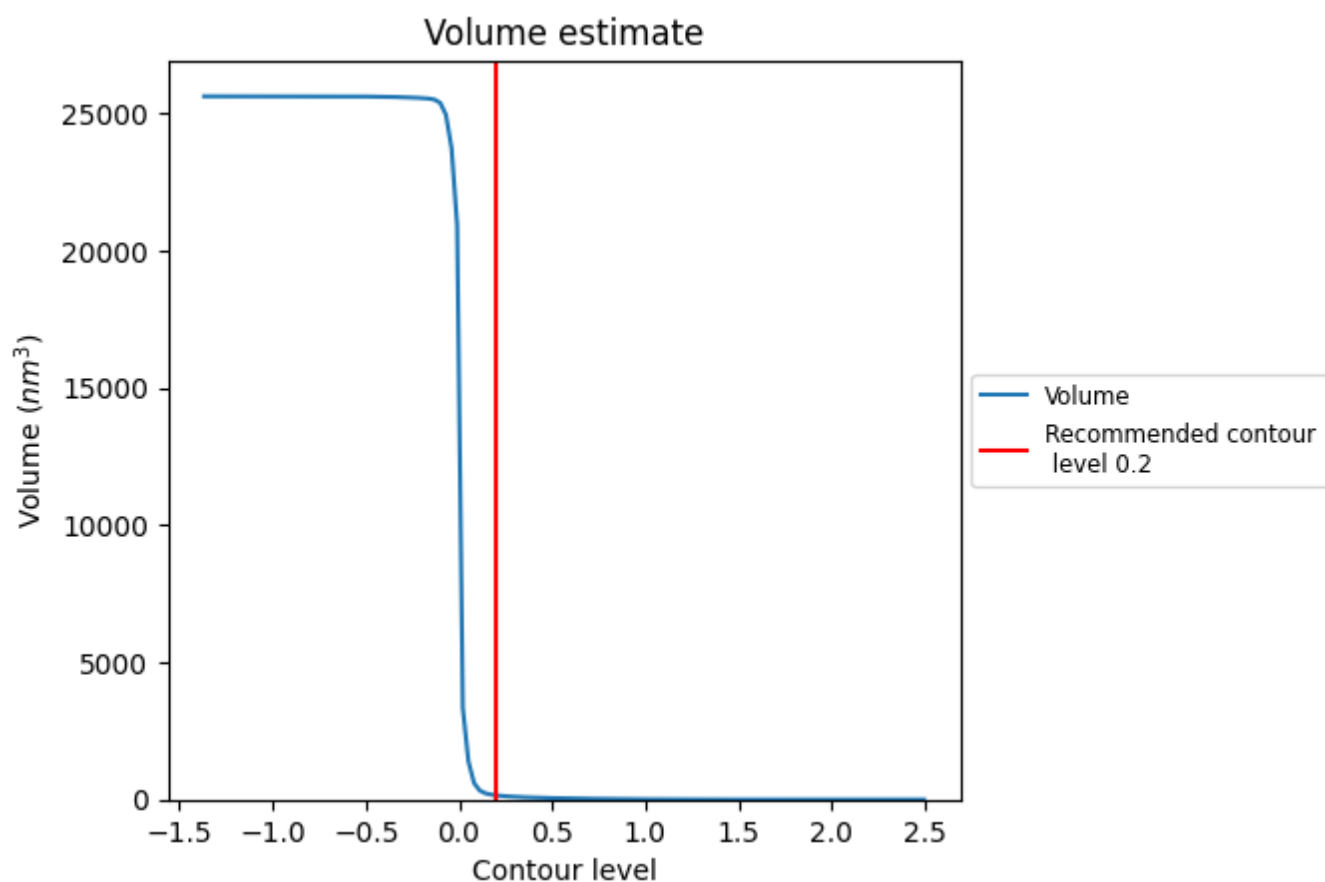
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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.

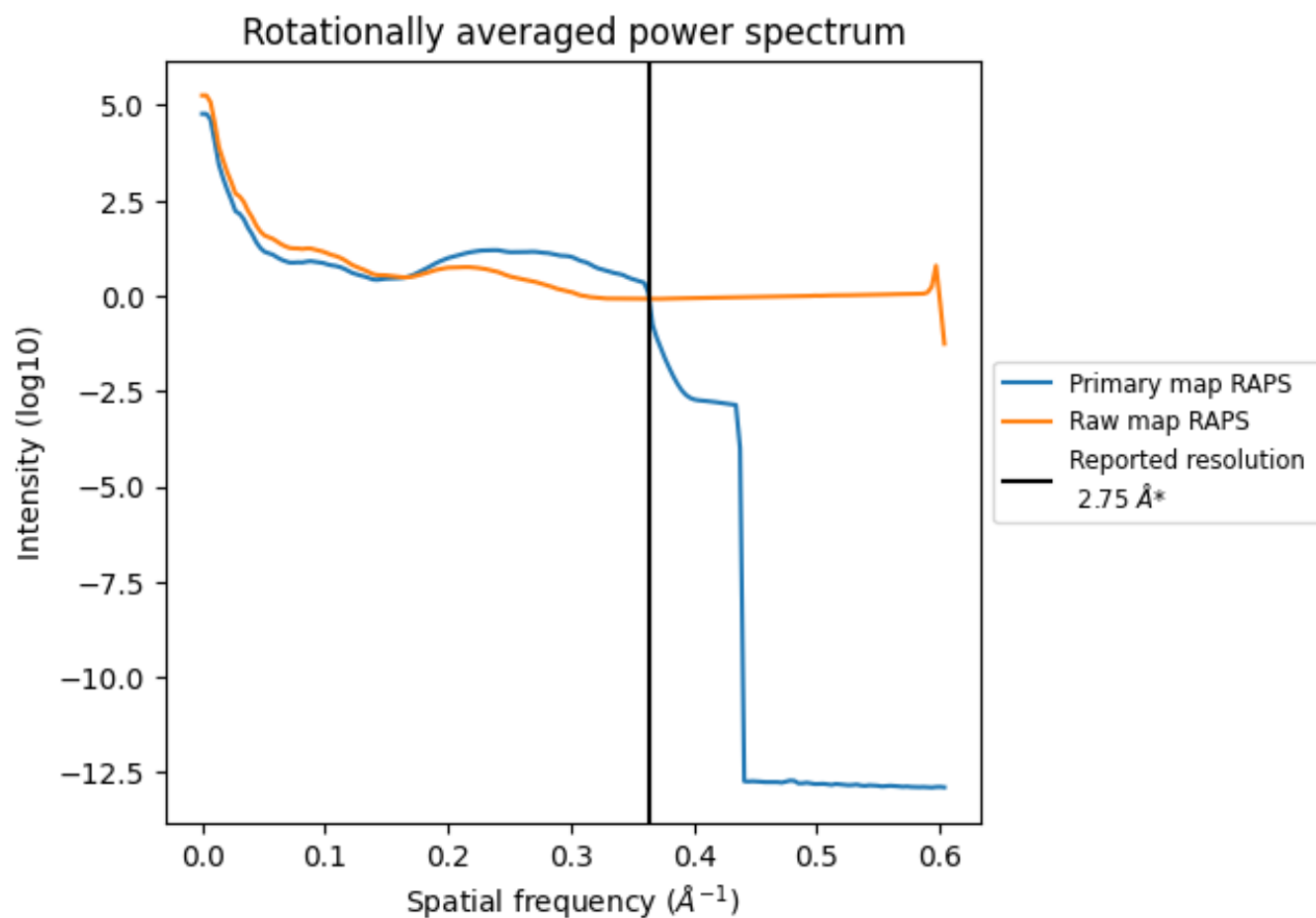
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 153 nm³; this corresponds to an approximate mass of 138 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 ⓘ

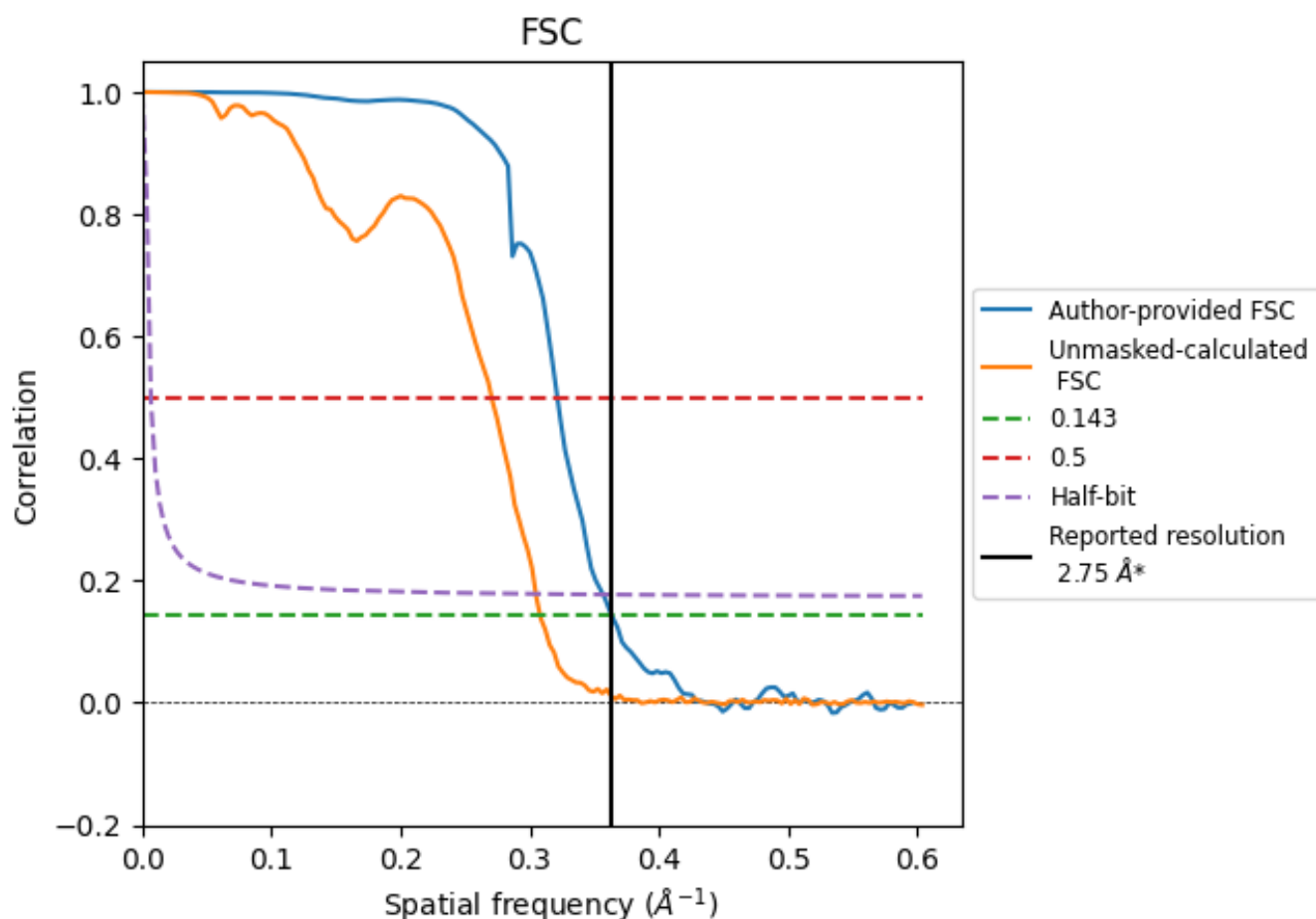


*Reported resolution corresponds to spatial frequency of 0.364 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.364 \AA^{-1}

8.2 Resolution estimates [i](#)

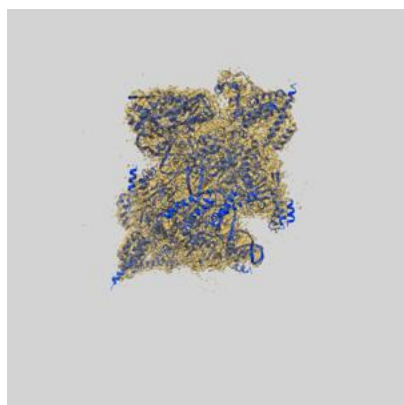
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.75	-	-
Author-provided FSC curve	2.75	3.11	2.80
Unmasked-calculated*	3.24	3.70	3.28

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.24 differs from the reported value 2.75 by more than 10 %

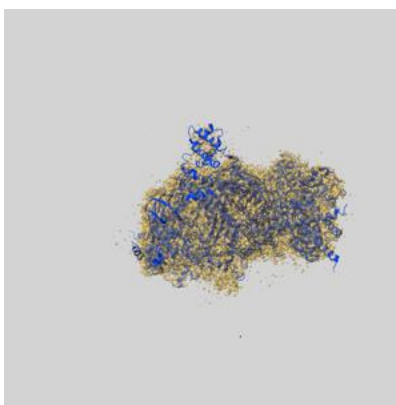
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-49570 and PDB model 9NNB. Per-residue inclusion information can be found in section [3](#) on page [12](#).

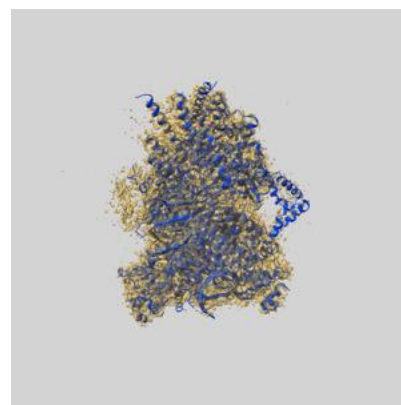
9.1 Map-model overlay [i](#)



X



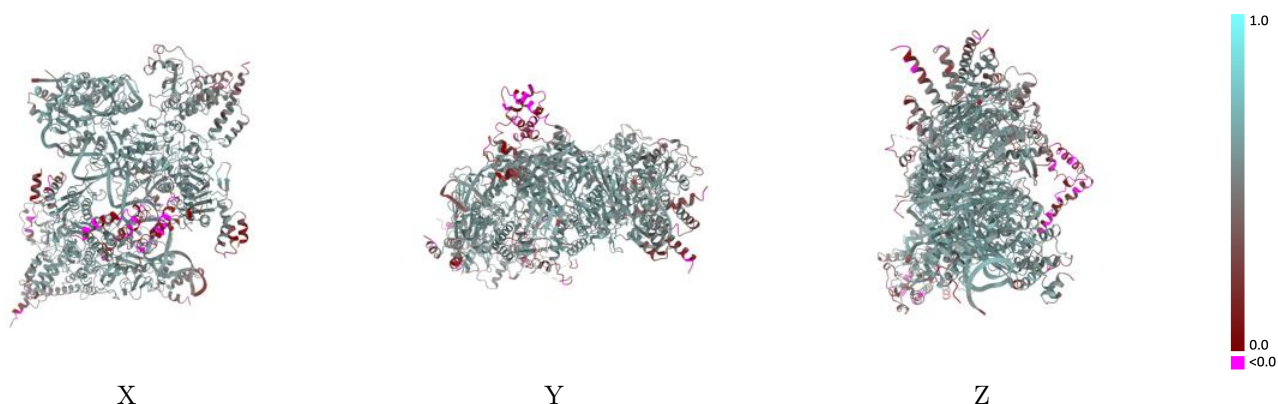
Y



Z

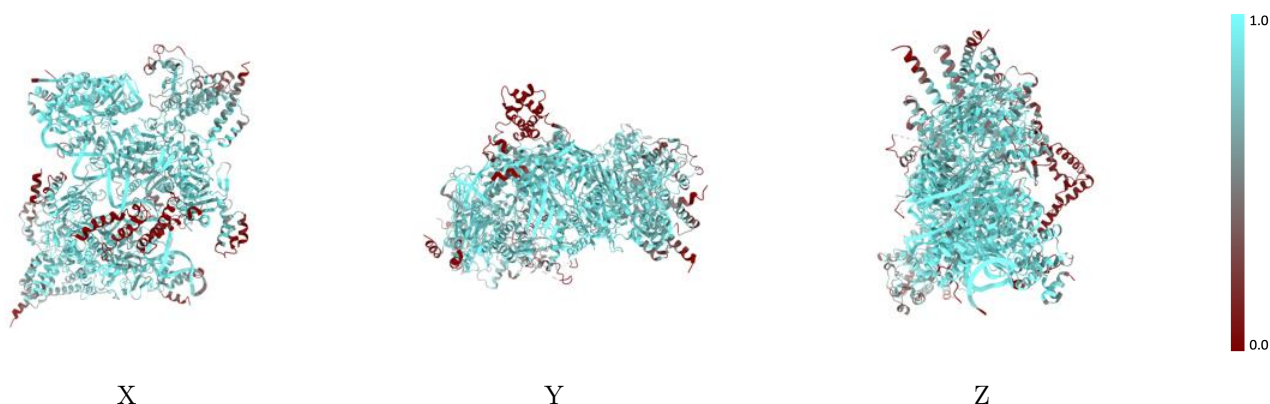
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



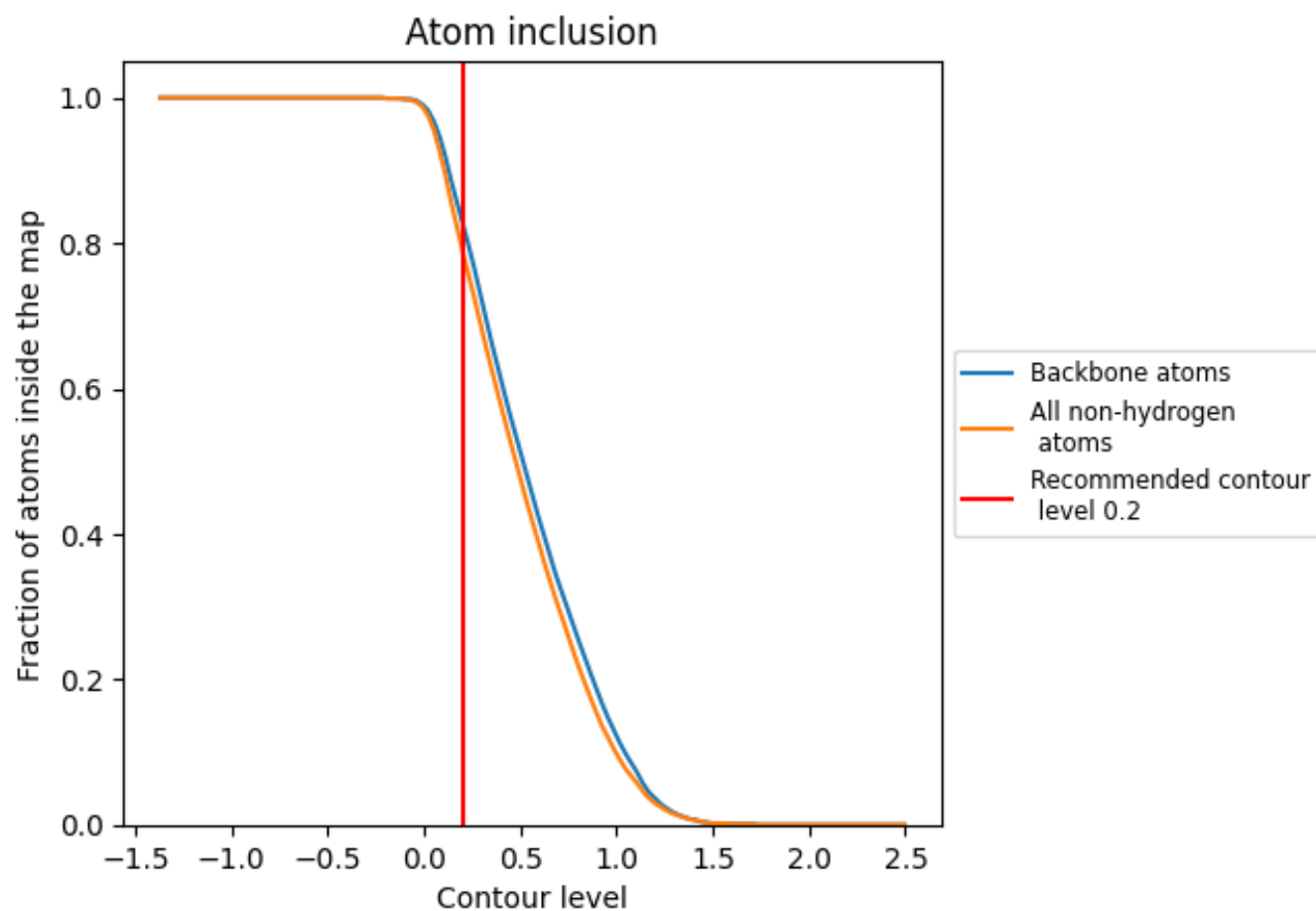
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 [i](#)



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 (0.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 79% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7890	<div></div> 0.5150
B	<div></div> 0.8820	<div></div> 0.5660
C	<div></div> 0.7320	<div></div> 0.4780
D	<div></div> 0.8540	<div></div> 0.5590
E	<div></div> 0.7530	<div></div> 0.4950
F	<div></div> 0.7850	<div></div> 0.5160
J	<div></div> 0.6610	<div></div> 0.4730
K	<div></div> 0.6700	<div></div> 0.4260
L	<div></div> 0.9440	<div></div> 0.5930
N	<div></div> 0.9350	<div></div> 0.5770

1.0

0.0

<0.0