



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 03:37 PM UTC

PDB ID : 6D6Q / pdb_00006d6q
EMDB ID : EMD-7808
Title : Human nuclear exosome-MTR4 RNA complex - overall reconstruction
Authors : Weick, E.-M.; Lima, C.D.
Deposited on : 2018-04-22
Resolution : 3.45 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:

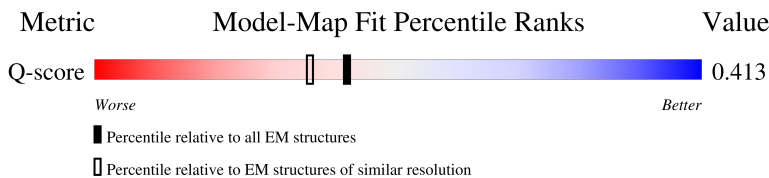
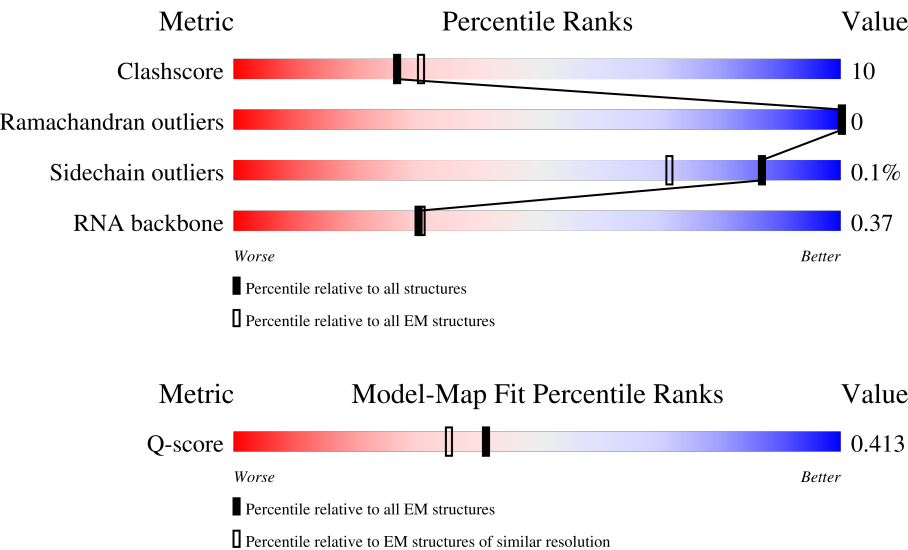
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.45 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.



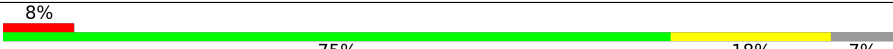
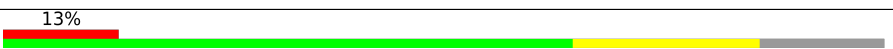
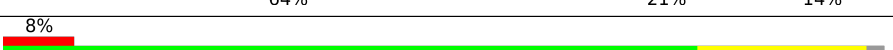
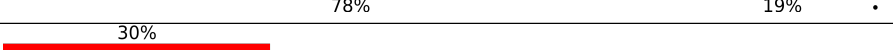
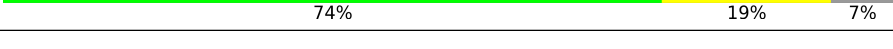
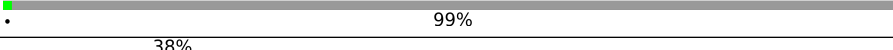
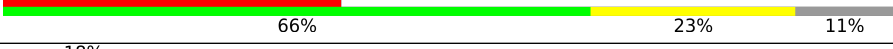
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13836 (2.95 - 3.95)

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	A	473	43% 18% 39%
2	B	249	6% 75% 22%
3	C	278	7% 77% 19% 5%

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Mol	Chain	Length	Quality of chain
4	D	237	
5	E	293	
6	F	272	
7	G	277	
8	H	296	
9	I	197	
10	J	761	
11	K	960	
12	L	162	
13	M	1045	
14	N	16	
15	O	62	

2 Entry composition

There are 18 unique types of molecules in this entry. The entry contains 31639 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 Exosome complex component RRP45.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	287	Total	C	N	O	S	0	0
			2264	1423	404	419	18		

There are 17 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-16	MET	-	expression tag	UNP Q06265
A	-15	GLY	-	expression tag	UNP Q06265
A	-14	SER	-	expression tag	UNP Q06265
A	-13	SER	-	expression tag	UNP Q06265
A	-12	HIS	-	expression tag	UNP Q06265
A	-11	HIS	-	expression tag	UNP Q06265
A	-10	HIS	-	expression tag	UNP Q06265
A	-9	HIS	-	expression tag	UNP Q06265
A	-8	HIS	-	expression tag	UNP Q06265
A	-7	HIS	-	expression tag	UNP Q06265
A	-6	SER	-	expression tag	UNP Q06265
A	-5	GLN	-	expression tag	UNP Q06265
A	-4	ASP	-	expression tag	UNP Q06265
A	-3	PRO	-	expression tag	UNP Q06265
A	-2	ASN	-	expression tag	UNP Q06265
A	-1	SER	-	expression tag	UNP Q06265
A	0	HIS	-	expression tag	UNP Q06265

- Molecule 2 is a protein called Exosome complex component RRP41.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	241	Total	C	N	O	S	0	0
			1824	1126	345	344	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	MET	-	expression tag	UNP Q9NPD3
B	-3	ALA	-	expression tag	UNP Q9NPD3
B	-2	ASP	-	expression tag	UNP Q9NPD3
B	-1	PRO	-	expression tag	UNP Q9NPD3

- Molecule 3 is a protein called Exosome complex component RRP43.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	265	Total	C	N	O	S	0	0
			2020	1272	337	397	14		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	ASP	-	expression tag	UNP Q96B26
C	0	PRO	-	expression tag	UNP Q96B26

- Molecule 4 is a protein called Exosome complex component RRP46.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	208	Total	C	N	O	S	0	0
			1566	979	278	297	12		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-1	SER	-	expression tag	UNP Q9NQT4
D	0	LEU	-	expression tag	UNP Q9NQT4

- Molecule 5 is a protein called Exosome complex component RRP42.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	286	Total	C	N	O	S	0	0
			2194	1373	374	432	15		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	-1	ASP	-	expression tag	UNP Q15024
E	0	PRO	-	expression tag	UNP Q15024

- Molecule 6 is a protein called Exosome complex component MTR3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	252	Total	C	N	O	S	0	0
			1859	1154	353	345	7		

- Molecule 7 is a protein called Exosome complex component RRP40.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	237	Total	C	N	O	S	0	0
			1806	1136	329	329	12		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	-1	ASP	-	expression tag	UNP Q9NQT5
G	0	PRO	-	expression tag	UNP Q9NQT5
G	225	HIS	TYR	variant	UNP Q9NQT5

- Molecule 8 is a protein called Exosome complex component RRP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	289	Total	C	N	O	S	0	0
			2263	1424	405	419	15		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	-2	ASP	-	expression tag	UNP Q13868
H	-1	PRO	-	expression tag	UNP Q13868
H	0	HIS	-	expression tag	UNP Q13868

- Molecule 9 is a protein called Exosome complex component CSL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	183	Total	C	N	O	S	0	0
			1407	884	247	266	10		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	-1	ASP	-	expression tag	UNP Q9Y3B2
I	0	PRO	-	expression tag	UNP Q9Y3B2

- Molecule 10 is a protein called Exosome component 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	J	11	Total	C	N	O	0	0
			86	56	14	16		

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	0	SER	-	expression tag	UNP Q01780
J	313	ASN	ASP	engineered mutation	UNP Q01780
J	649	SER	-	linker	UNP Q01780
J	650	ARG	-	linker	UNP Q01780
J	651	GLY	-	linker	UNP Q01780
J	652	SER	-	linker	UNP Q01780
J	653	GLY	-	linker	UNP Q01780
J	654	SER	-	linker	UNP Q01780
J	655	GLY	-	linker	UNP Q01780
J	656	SER	-	linker	UNP Q01780
J	657	GLY	-	linker	UNP Q01780
J	658	SER	-	linker	UNP Q01780
J	659	GLY	-	linker	UNP Q01780
J	660	SER	-	linker	UNP Q01780

- Molecule 11 is a protein called Exosome complex exonuclease RRP44.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	853	Total	C	N	O	S	0	0
			6856	4329	1233	1260	34		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	-1	GLY	-	expression tag	UNP Q9Y2L1
K	0	SER	-	expression tag	UNP Q9Y2L1
K	146	ASN	ASP	engineered mutation	UNP Q9Y2L1
K	269	SER	ASN	variant	UNP Q9Y2L1
K	487	ASN	ASP	engineered mutation	UNP Q9Y2L1
K	843	ASN	LYS	variant	UNP Q9Y2L1

- Molecule 12 is a protein called M-phase phosphoprotein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	68	Total	C	N	O	S	0	0
			573	371	95	101	6		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	-1	ASP	-	expression tag	UNP Q99547
L	0	PRO	-	expression tag	UNP Q99547

- Molecule 13 is a protein called Exosome RNA helicase MTR4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	709	Total	C	N	O	S	0	0
			5648	3589	963	1052	44		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	-2	SER	-	expression tag	UNP P42285
M	-1	GLY	-	expression tag	UNP P42285
M	0	ASP	-	expression tag	UNP P42285

- Molecule 14 is a RNA chain called RNA (5'-R(*AP*GP*CP*AP*CP*CP*GP*UP*AP*AP*AP*GP*AP*CP*GP*C)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	13	Total	C	N	O	P	0	0
			278	126	56	84	12		

- Molecule 15 is DNA/RNA hybrid called DNA/RNA (62-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	48	Total	C	N	O	P	0	0
			966	443	172	304	47		

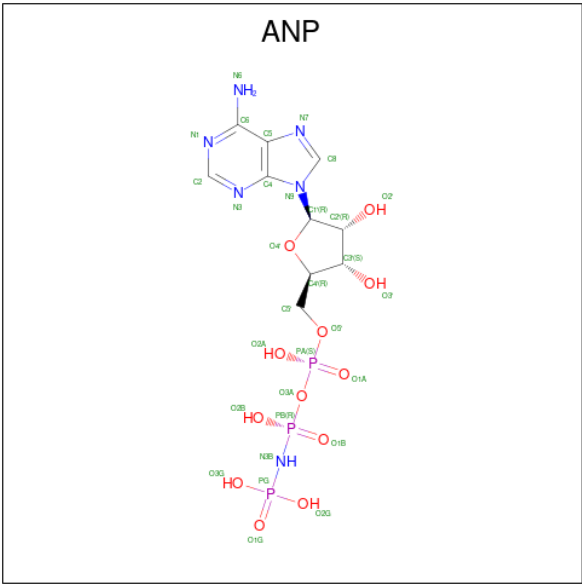
- Molecule 16 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
16	K	1	Total	Mg	0
			1	1	

- Molecule 17 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
17	K	1	Total	Zn	0
			1	1	

- Molecule 18 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃).

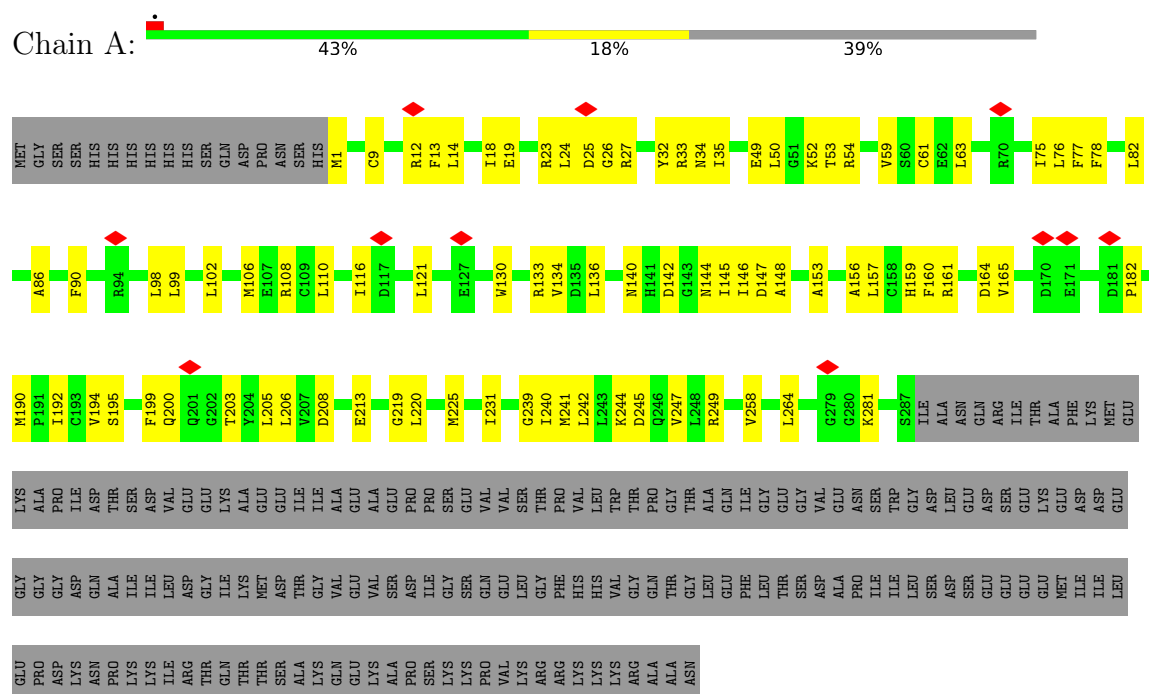


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
18	M	1	27	10	6	9	2	0

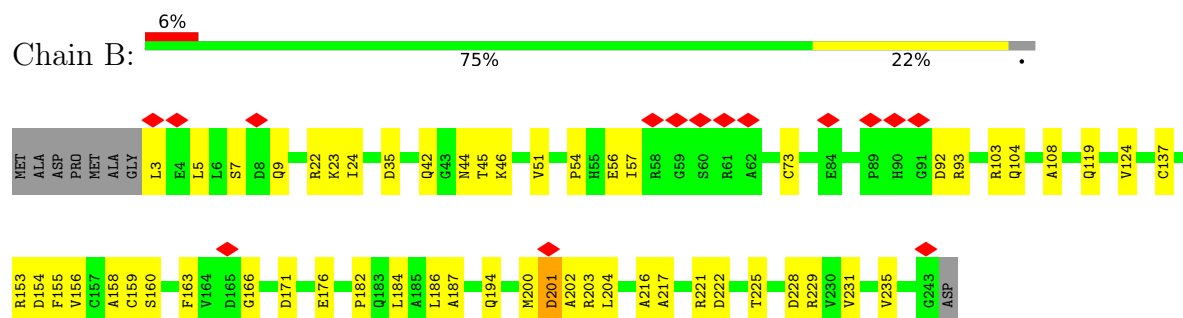
3 Residue-property plots

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.

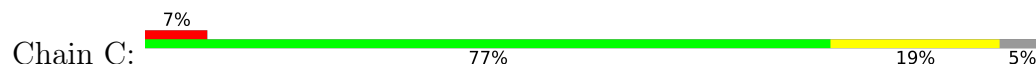
• Molecule 1: Exosome complex component RRP45

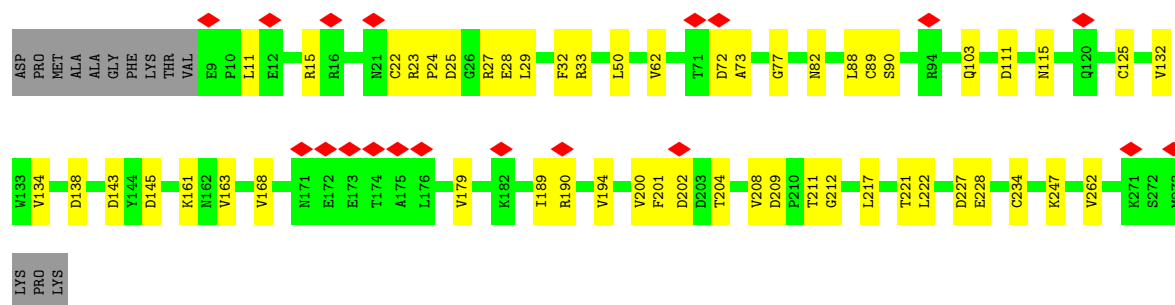


• Molecule 2: Exosome complex component RRP41

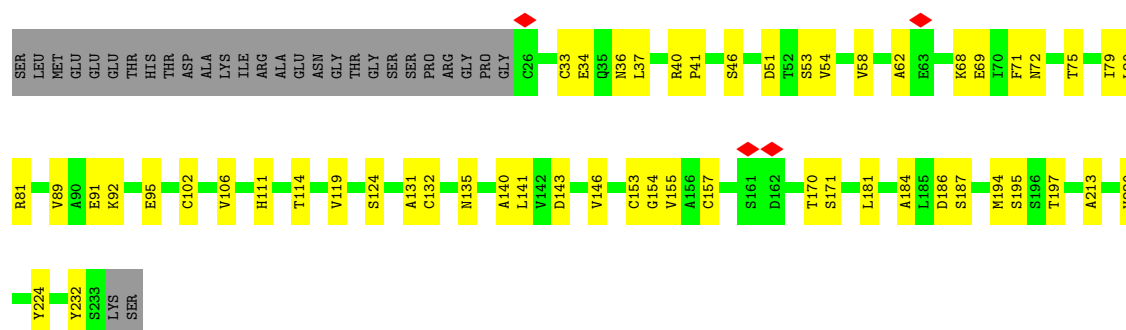


• Molecule 3: Exosome complex component RRP43

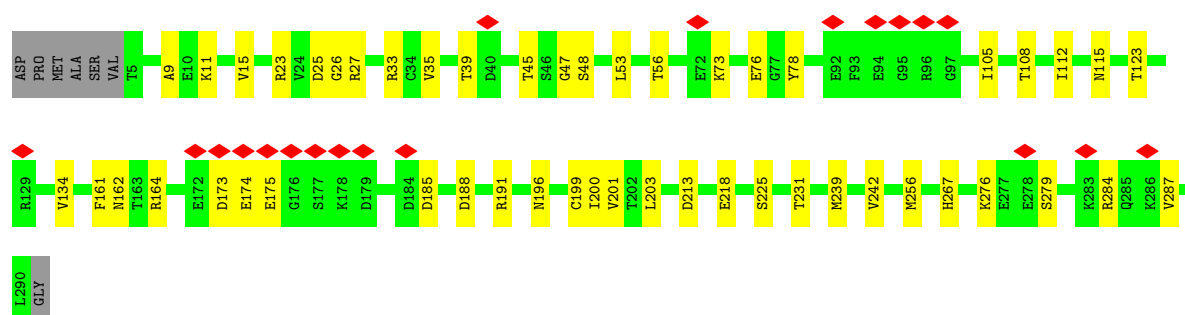
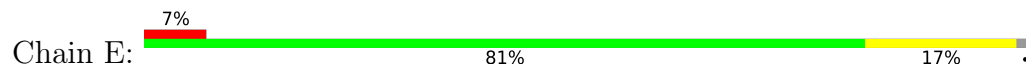




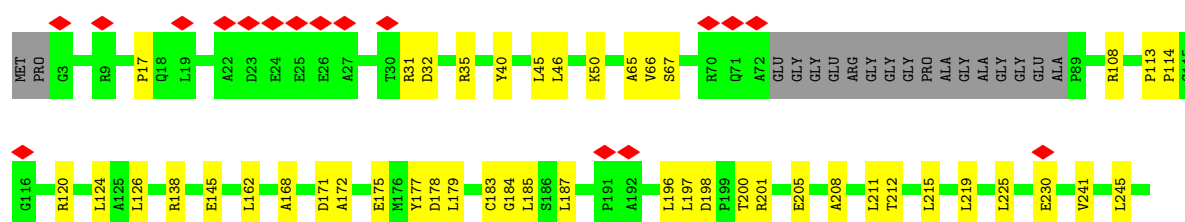
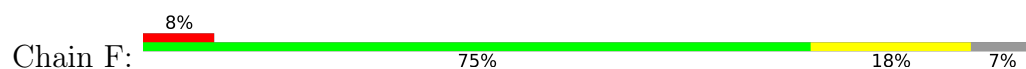
• Molecule 4: Exosome complex component RRP46

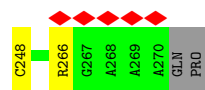


• Molecule 5: Exosome complex component RRP42

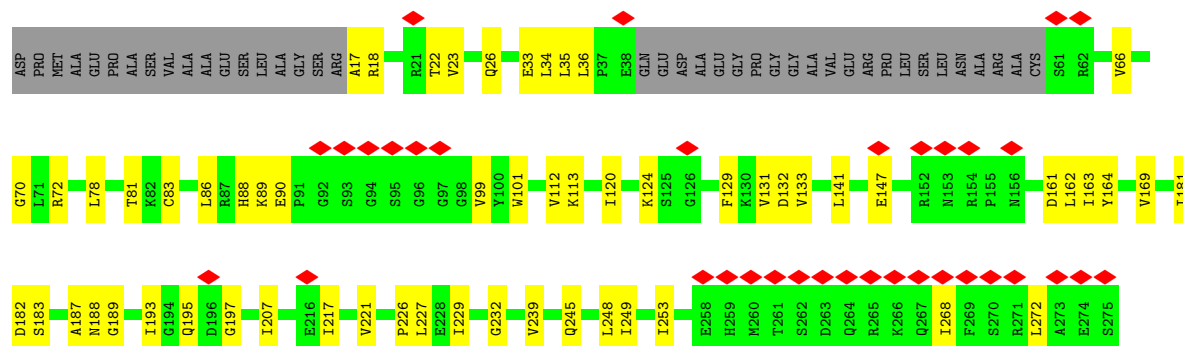


• Molecule 6: Exosome complex component MTR3

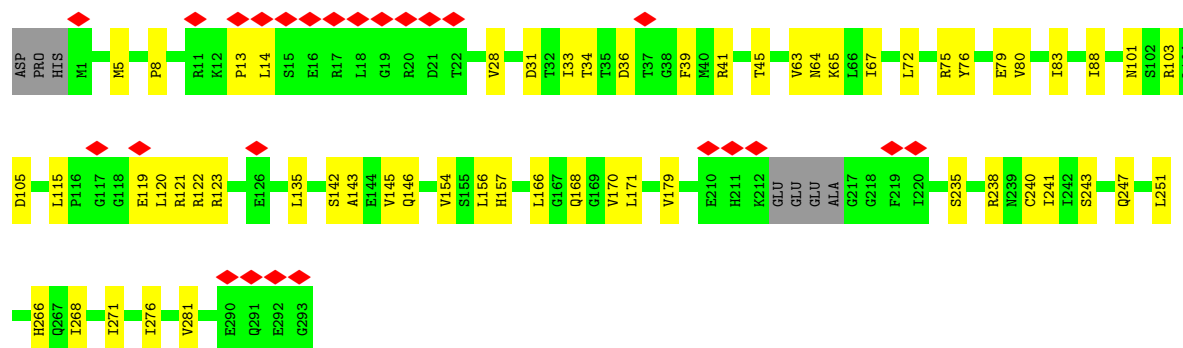
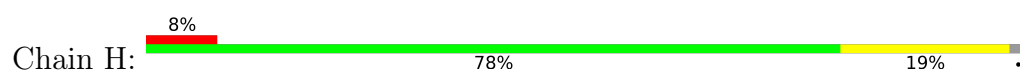




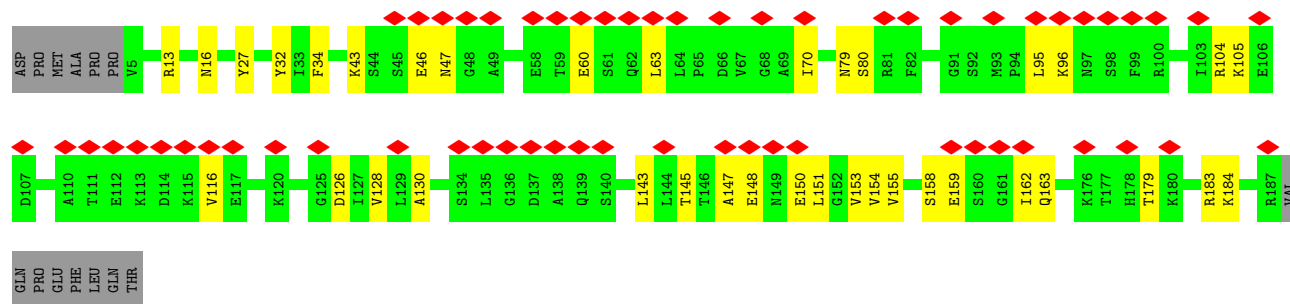
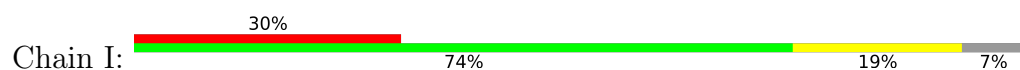
• Molecule 7: Exosome complex component RRP40



• Molecule 8: Exosome complex component RRP4



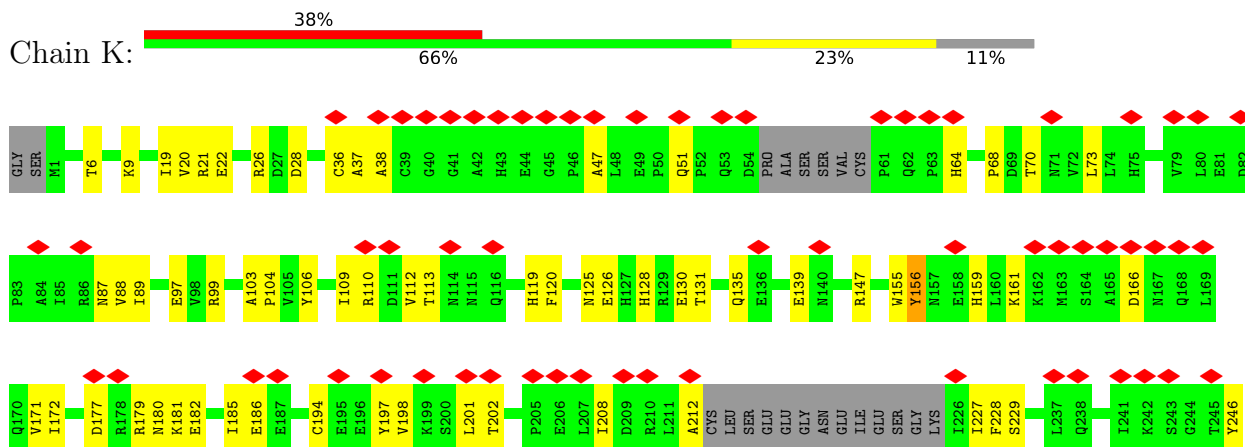
• Molecule 9: Exosome complex component CSL4



• Molecule 10: Exosome component 10

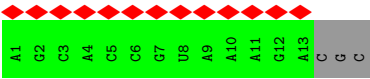
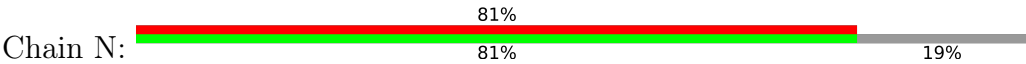


- Molecule 11: Exosome complex exonuclease RRP44

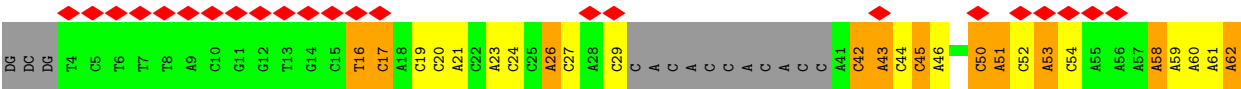




● Molecule 14: RNA (5'-R(*AP*GP*CP*AP*CP*CP*GP*UP*AP*AP*AP*GP*AP*CP*GP*C)-3')



● Molecule 15: DNA/RNA (62-MER)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	122703	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	85.23	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.154	Depositor
Minimum map value	-0.084	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.025	Depositor
Map size ($\text{\AA}$)	410.88, 410.88, 410.88	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.07, 1.07, 1.07	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.32	0/2297	0.41	0/3094
2	B	0.34	0/1849	0.44	0/2500
3	C	0.30	0/2053	0.39	0/2786
4	D	0.31	0/1586	0.41	0/2145
5	E	0.31	0/2225	0.39	0/3007
6	F	0.30	0/1889	0.44	0/2562
7	G	0.24	0/1832	0.39	0/2467
8	H	0.32	0/2296	0.42	0/3092
9	I	0.19	0/1431	0.39	0/1932
10	J	0.21	0/88	0.37	0/118
11	K	0.20	0/6991	0.41	1/9444 (0.0%)
12	L	0.17	0/583	0.42	0/776
13	M	0.21	0/5751	0.40	0/7752
14	N	0.10	0/312	0.20	0/485
15	O	0.43	3/1077 (0.3%)	0.61	3/1668 (0.2%)
All	All	0.27	3/32260 (0.0%)	0.42	4/43828 (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
2	B	0	1
11	K	0	1
All	All	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	O	17	C	P-OP2	9.69	1.68	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	O	16	DT	O3'-P	6.56	1.71	1.61
15	O	17	C	P-OP1	5.32	1.59	1.49

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	O	16	DT	O3'-P-O5'	13.89	124.84	104.00
11	K	648	PRO	CA-N-CD	-9.20	99.13	112.00
15	O	16	DT	P-O3'-C3'	-5.68	111.67	120.20
15	O	16	DT	OP2-P-O3'	-5.55	91.36	108.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	201	ASP	Peptide
11	K	455	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	A	2264	0	2315	72	0
2	B	1824	0	1823	45	0
3	C	2020	0	2035	41	0
4	D	1566	0	1605	37	0
5	E	2194	0	2205	41	0
6	F	1859	0	1889	29	0
7	G	1806	0	1865	46	0
8	H	2263	0	2337	45	0
9	I	1407	0	1432	24	0
10	J	86	0	86	3	0
11	K	6856	0	6907	152	0
12	L	573	0	575	8	0
13	M	5648	0	5681	115	0
14	N	278	0	144	0	0
15	O	966	0	518	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	K	1	0	0	0	0
17	K	1	0	0	0	0
18	M	27	0	12	2	0
All	All	31639	0	31429	627	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 10.

The worst 5 of 627 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)
13:M:237:TYR:OH	13:M:268:GLU:OE2	1.78	0.99
11:K:780:ARG:NH2	15:O:61:A:OP2	1.97	0.97
3:C:111:ASP:OD1	3:C:115:ASN:ND2	1.97	0.96
15:O:42:C:O2'	15:O:43:A:O5'	1.82	0.95
11:K:565:GLU:OE1	11:K:574:LYS:NZ	2.05	0.88

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	285/473 (60%)	263 (92%)	22 (8%)	0	100	100
2	B	239/249 (96%)	215 (90%)	24 (10%)	0	100	100
3	C	263/278 (95%)	237 (90%)	26 (10%)	0	100	100
4	D	206/237 (87%)	197 (96%)	9 (4%)	0	100	100
5	E	284/293 (97%)	249 (88%)	35 (12%)	0	100	100
6	F	248/272 (91%)	230 (93%)	18 (7%)	0	100	100
7	G	233/277 (84%)	211 (91%)	22 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	H	285/296 (96%)	240 (84%)	45 (16%)	0	100	100
9	I	181/197 (92%)	159 (88%)	22 (12%)	0	100	100
10	J	9/761 (1%)	5 (56%)	4 (44%)	0	100	100
11	K	839/960 (87%)	752 (90%)	87 (10%)	0	100	100
12	L	64/162 (40%)	54 (84%)	10 (16%)	0	100	100
13	M	703/1045 (67%)	647 (92%)	56 (8%)	0	100	100
All	All	3839/5500 (70%)	3459 (90%)	380 (10%)	0	100	100

There are no Ramachandran outliers to report.

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	252/411 (61%)	252 (100%)	0	100	100
2	B	184/189 (97%)	184 (100%)	0	100	100
3	C	227/237 (96%)	227 (100%)	0	100	100
4	D	172/195 (88%)	172 (100%)	0	100	100
5	E	249/254 (98%)	249 (100%)	0	100	100
6	F	179/188 (95%)	179 (100%)	0	100	100
7	G	196/223 (88%)	196 (100%)	0	100	100
8	H	251/257 (98%)	251 (100%)	0	100	100
9	I	159/172 (92%)	159 (100%)	0	100	100
10	J	10/672 (2%)	10 (100%)	0	100	100
11	K	758/854 (89%)	756 (100%)	2 (0%)	86	83
12	L	63/148 (43%)	63 (100%)	0	100	100
13	M	618/911 (68%)	618 (100%)	0	100	100
All	All	3318/4711 (70%)	3316 (100%)	2 (0%)	87	87

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	K	156	TYR
11	K	619	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
13	M	153	ASN
13	M	302	GLN
13	M	329	HIS
13	M	300	HIS
9	I	163	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
14	N	12/16 (75%)	0	0
15	O	33/62 (53%)	14 (42%)	2 (6%)
All	All	45/78 (57%)	14 (31%)	2 (4%)

5 of 14 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
15	O	24	C
15	O	26	A
15	O	29	C
15	O	42	C
15	O	43	A

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
15	O	42	C
15	O	53	A

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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	$\# Z > 2$
18	ANP	M	2001	-	28,29,33	1.43	3 (10%)	40,45,52	0.75	1 (2%)

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
18	ANP	M	2001	-	-	5/13/32/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	M	2001	ANP	PB-O1B	6.59	1.56	1.46
18	M	2001	ANP	PB-O2B	-2.64	1.49	1.56
18	M	2001	ANP	PB-O3A	-2.30	1.56	1.59

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	M	2001	ANP	PB-O3A-PA	-4.11	118.94	132.10

There are no chirality outliers.

All (5) torsion outliers are listed below:

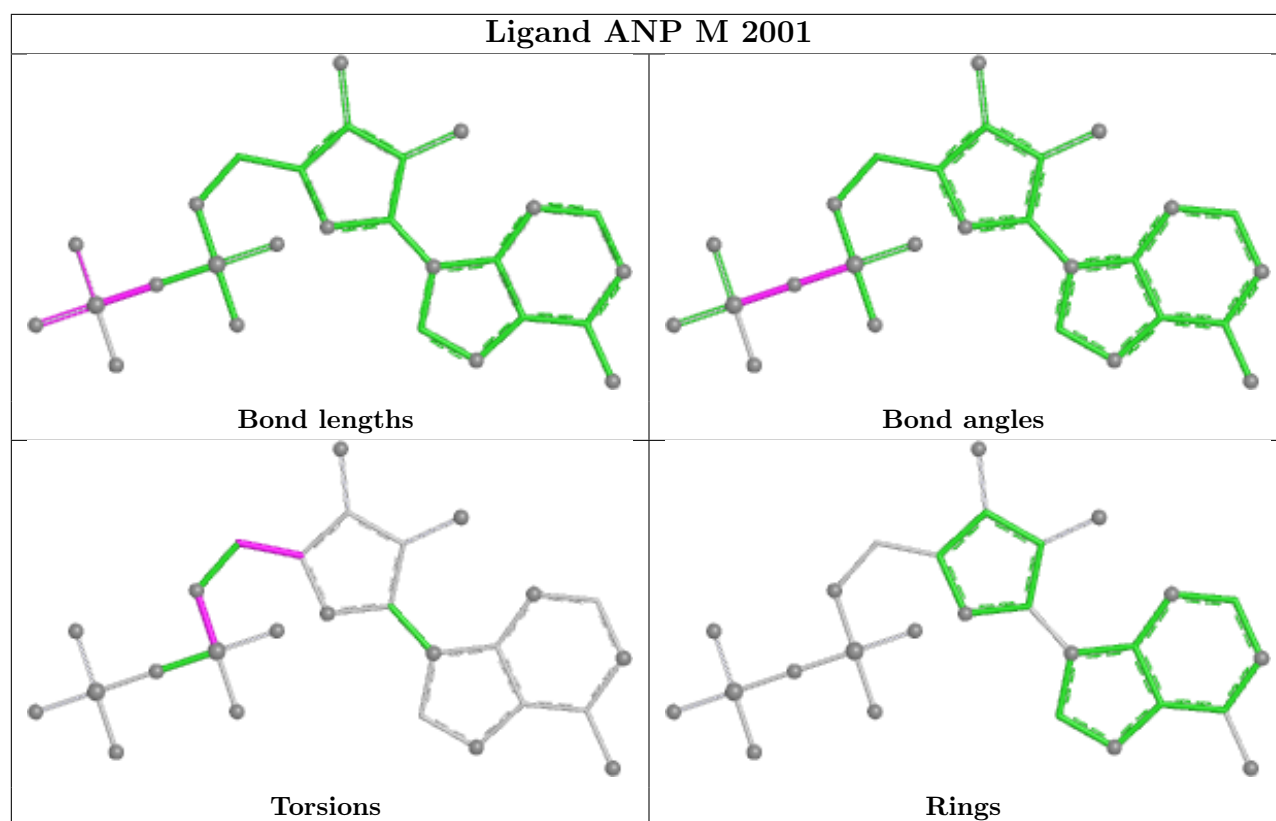
Mol	Chain	Res	Type	Atoms
18	M	2001	ANP	C5'-O5'-PA-O1A
18	M	2001	ANP	C5'-O5'-PA-O2A
18	M	2001	ANP	C5'-O5'-PA-O3A
18	M	2001	ANP	O4'-C4'-C5'-O5'
18	M	2001	ANP	C3'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
18	M	2001	ANP	2	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 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.

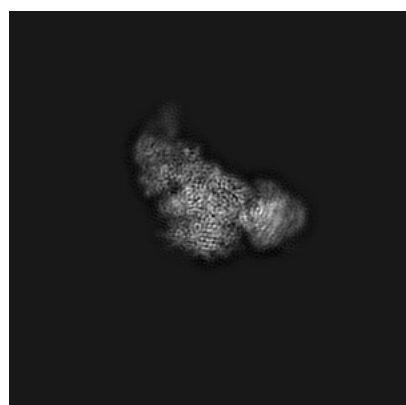
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7808. These allow visual inspection of the internal detail of the map and identification of artifacts.

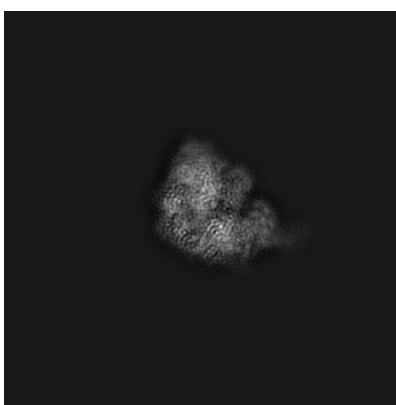
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

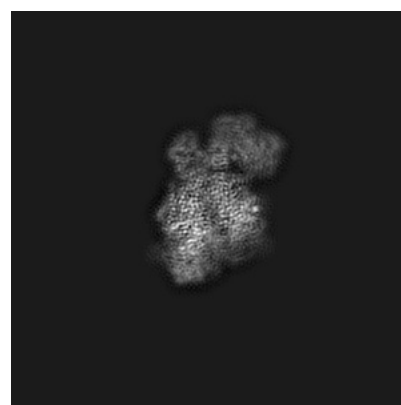
6.1.1 Primary map



X



Y

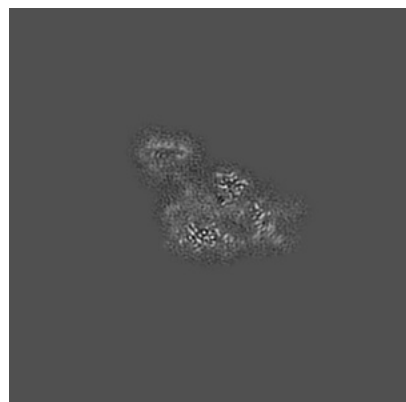


Z

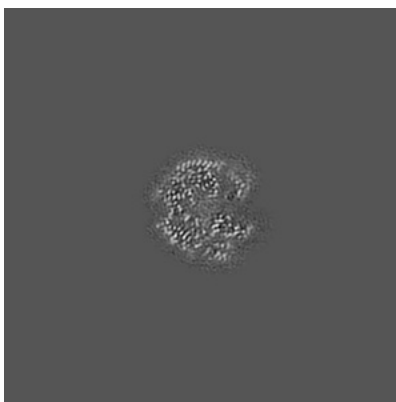
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

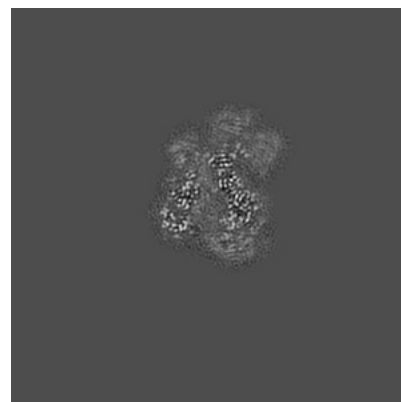
6.2.1 Primary map



X Index: 192



Y Index: 192

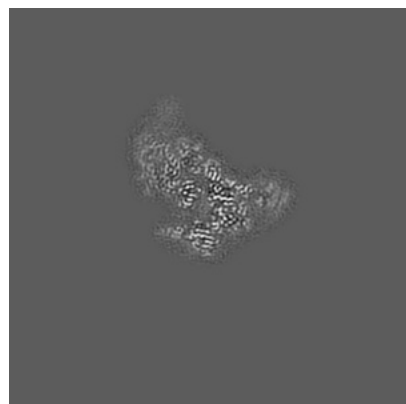


Z Index: 192

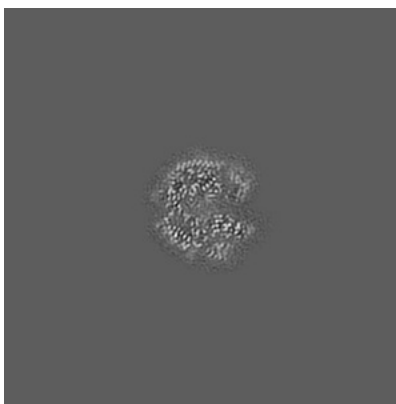
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

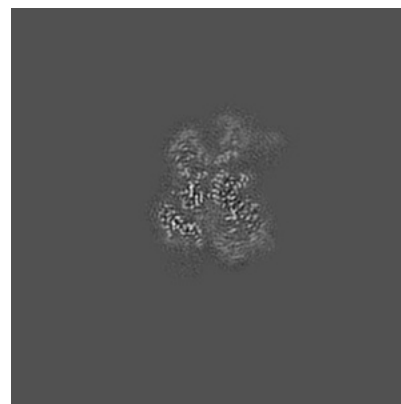
6.3.1 Primary map



X Index: 173



Y Index: 193

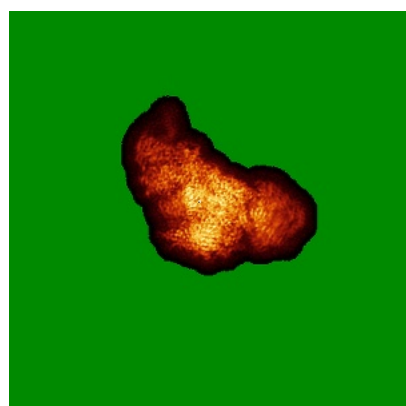


Z Index: 200

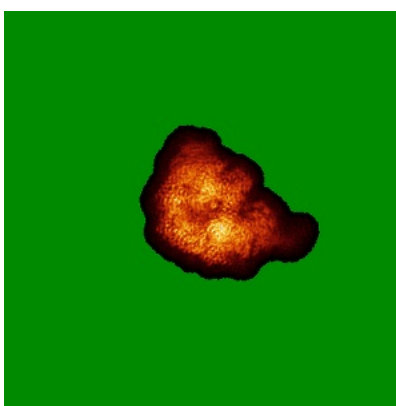
The images above show the largest variance slices of the map in three orthogonal directions.

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

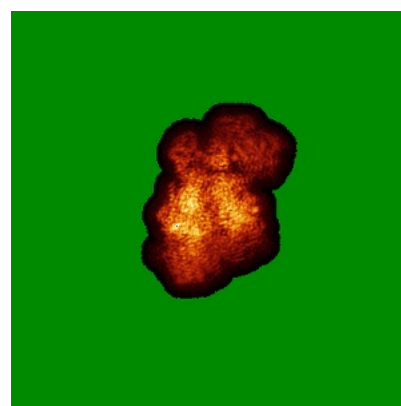
6.4.1 Primary map



X



Y



Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

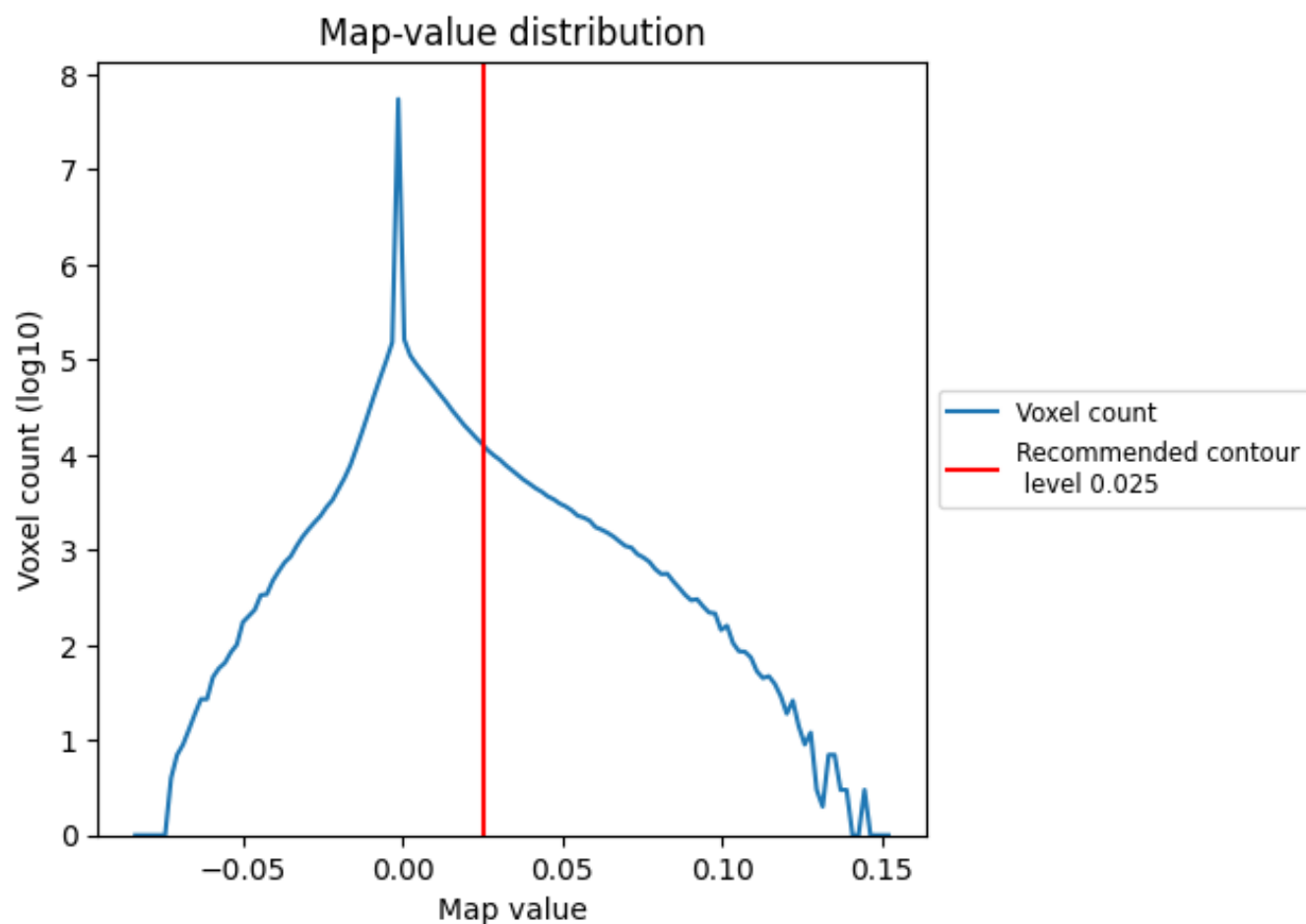
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

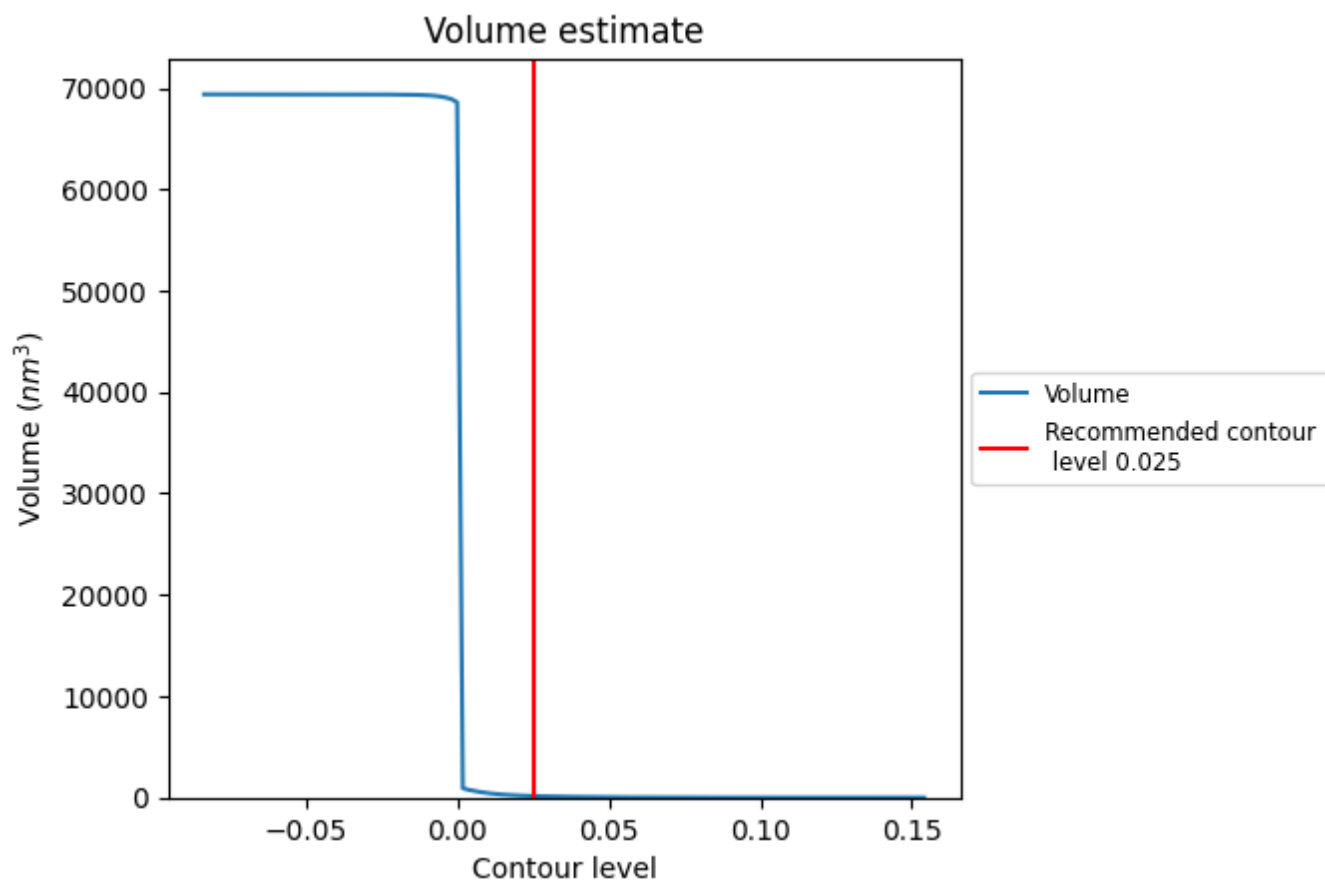
This section contains the results of statistical analysis of the map.

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.

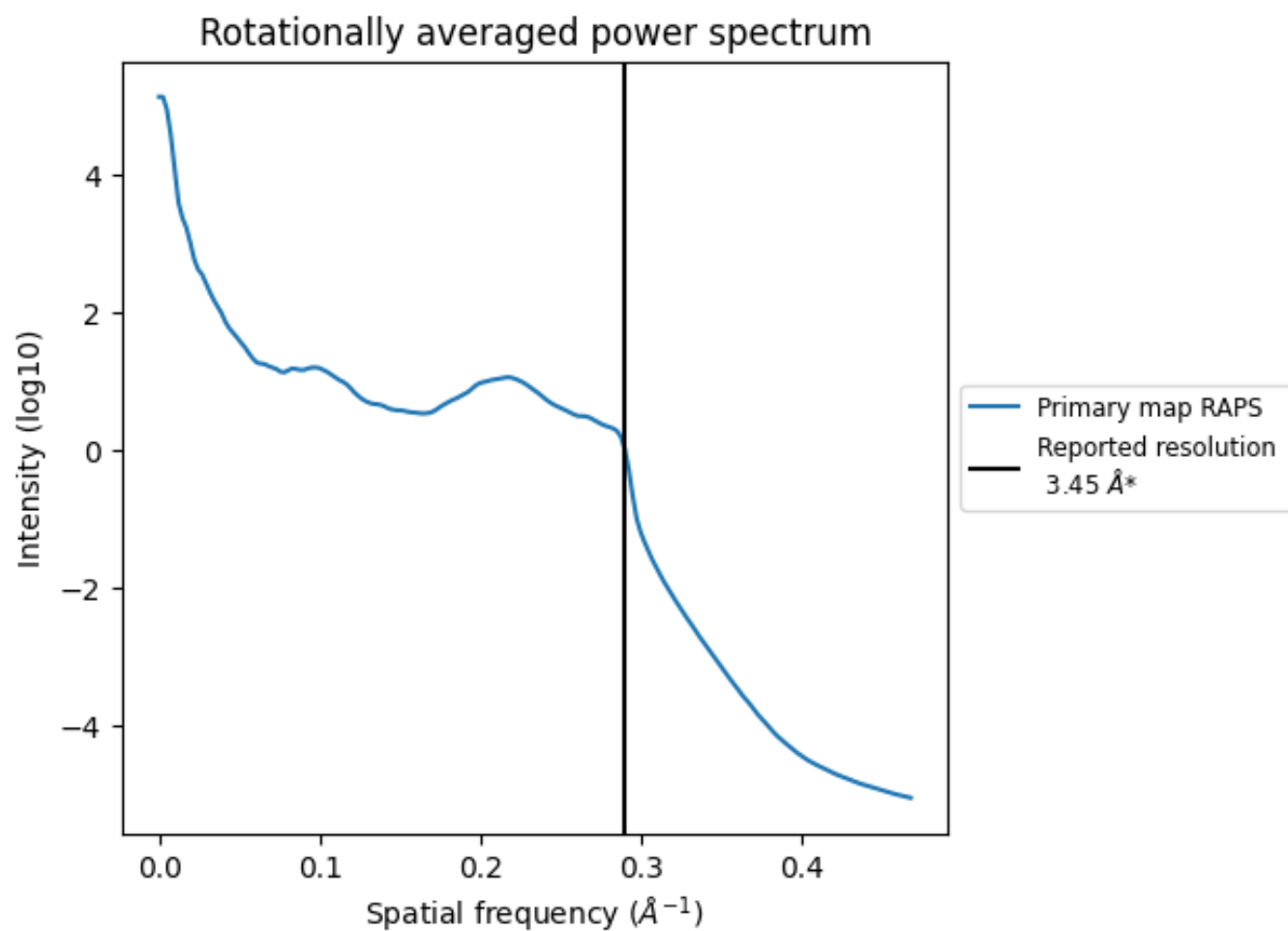
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 149 nm³; this corresponds to an approximate mass of 134 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 ⓘ

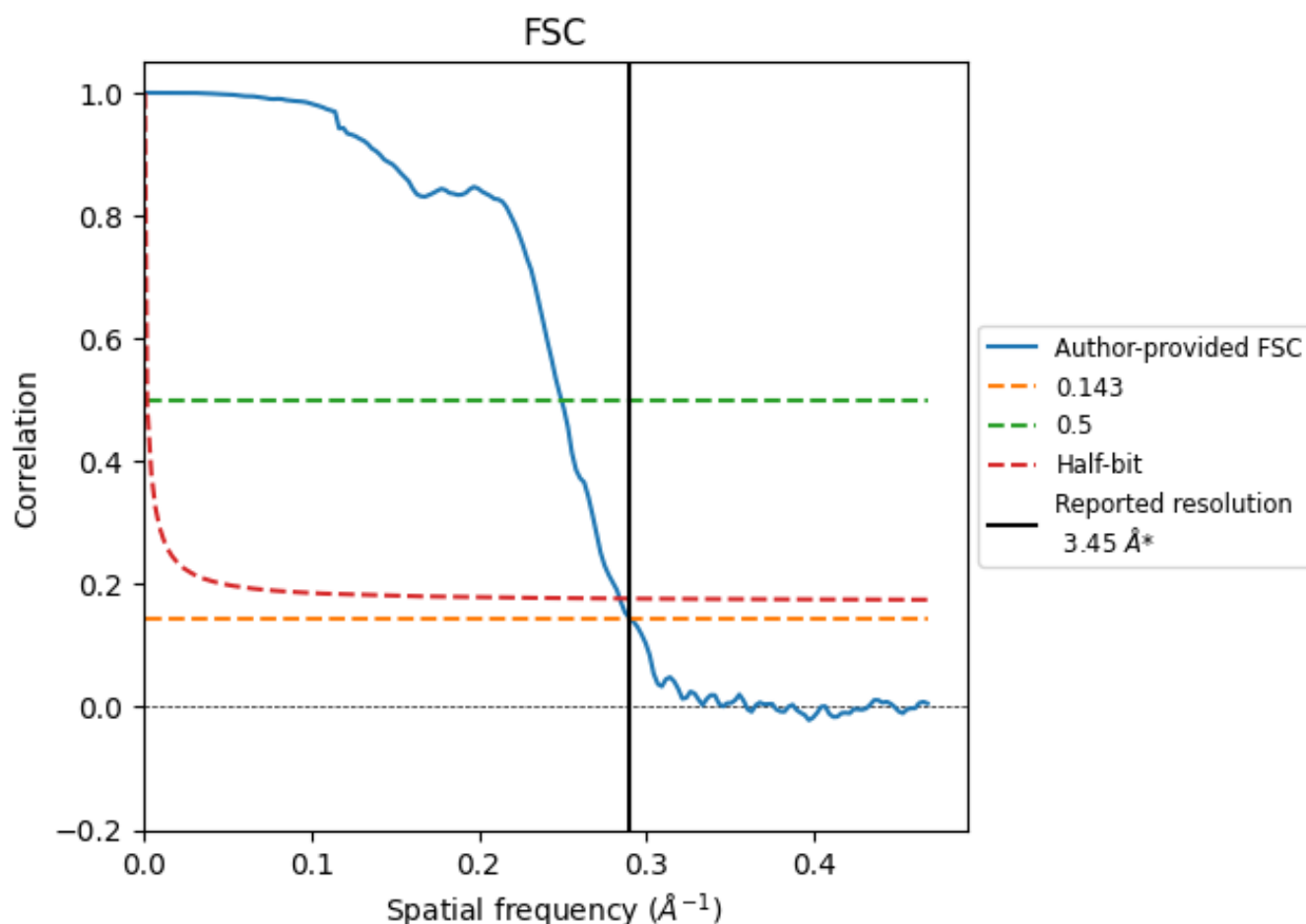


*Reported resolution corresponds to spatial frequency of 0.290 Å⁻¹

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 0.290 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

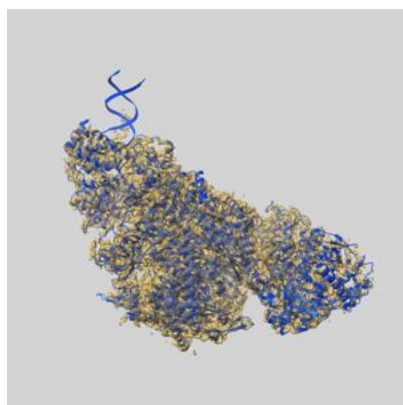
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.45	-	-
Author-provided FSC curve	3.44	4.01	3.52
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

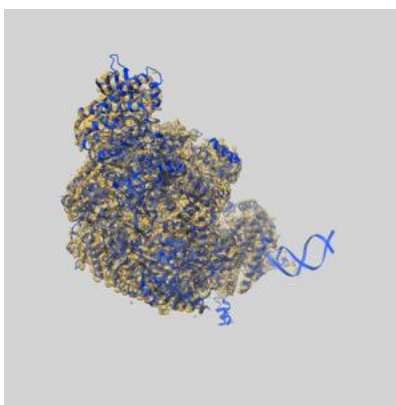
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-7808 and PDB model 6D6Q. Per-residue inclusion information can be found in section 3 on page 10.

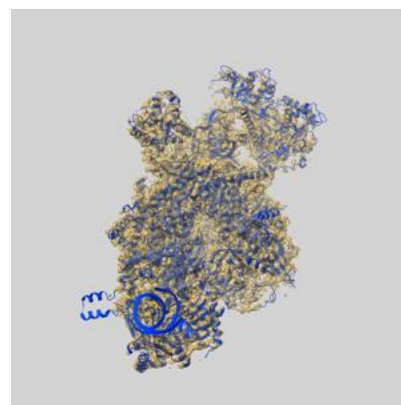
9.1 Map-model overlay [i](#)



X



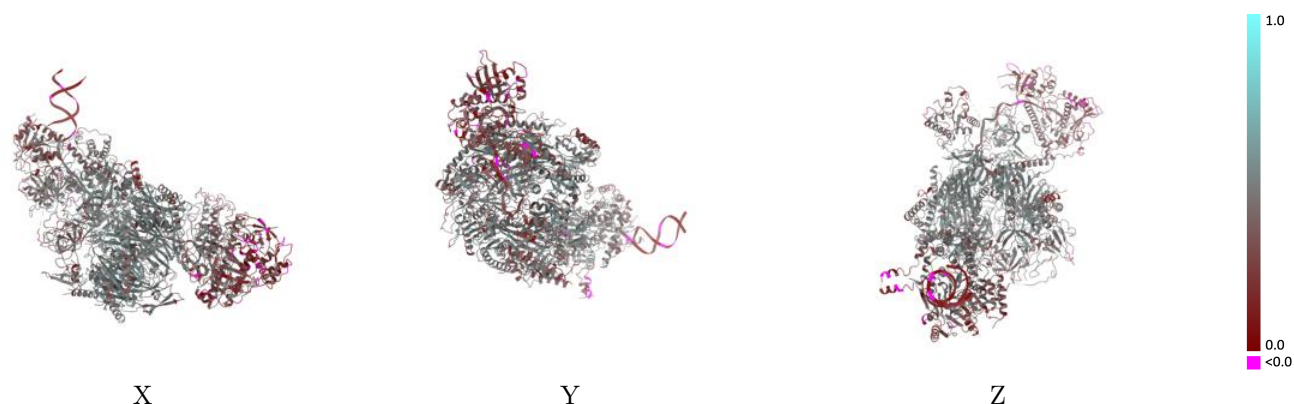
Y



Z

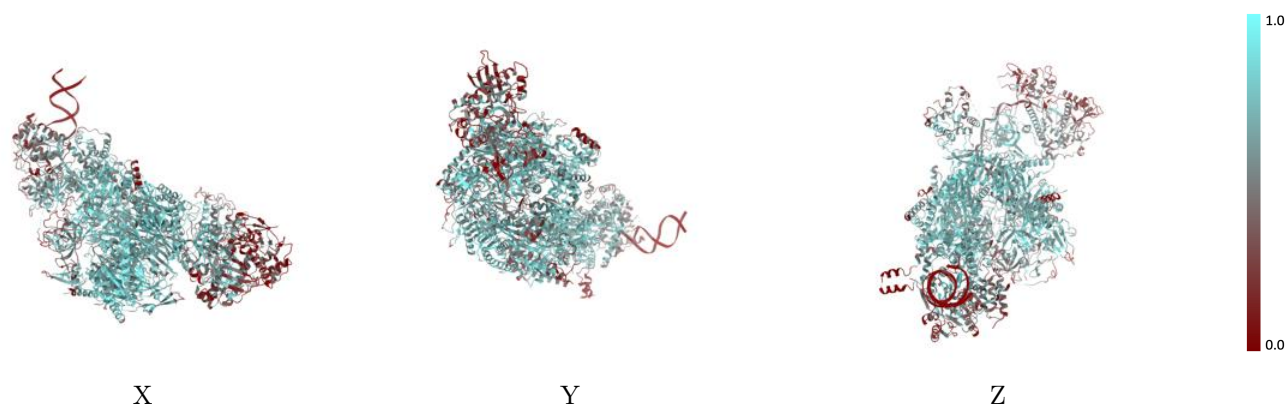
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



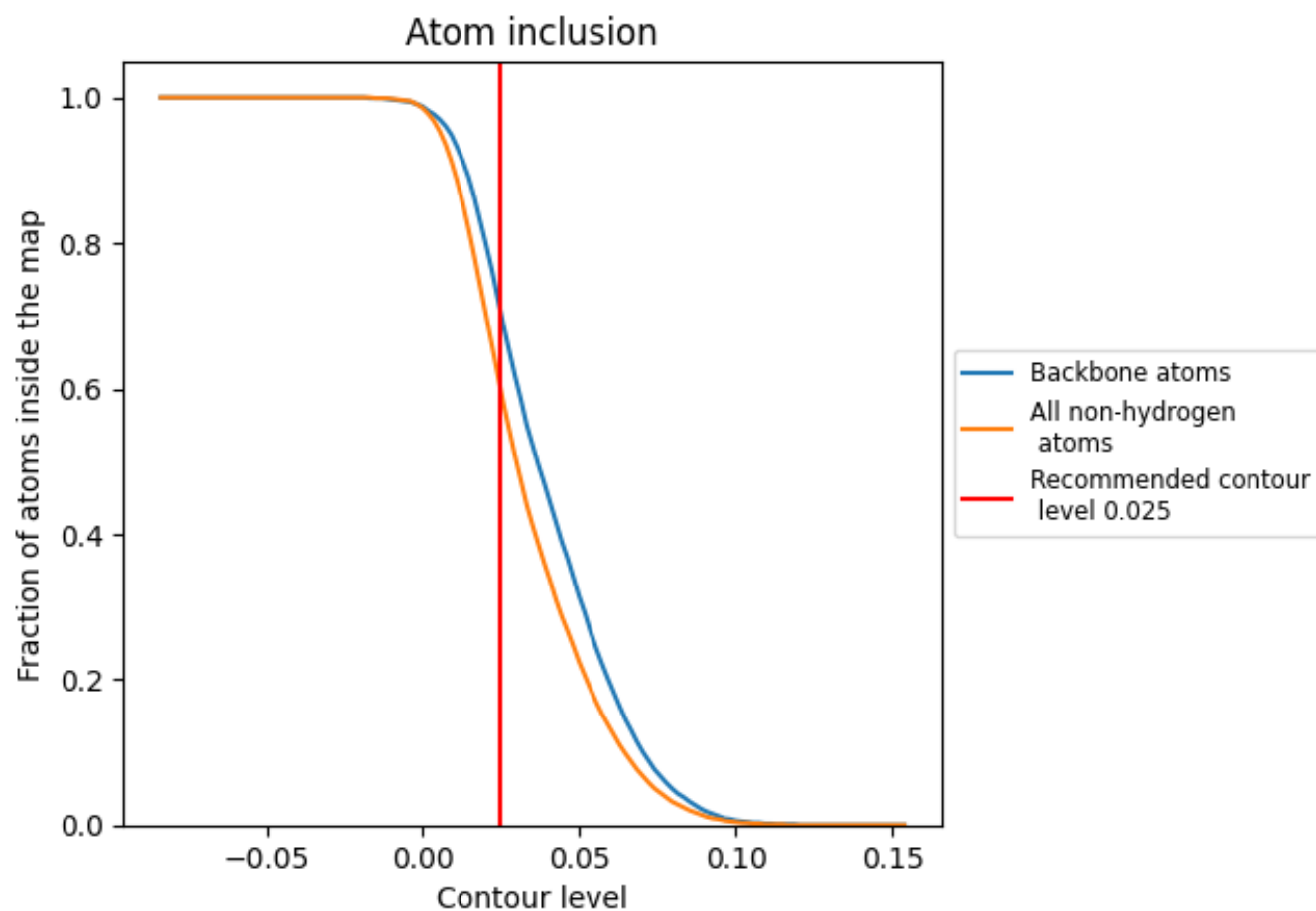
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.025).

9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 60% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5980	 0.4130
A	 0.7300	 0.4860
B	 0.7460	 0.4890
C	 0.7270	 0.4740
D	 0.7620	 0.4930
E	 0.7160	 0.4750
F	 0.7060	 0.4750
G	 0.6380	 0.4350
H	 0.7090	 0.4770
I	 0.5060	 0.4070
J	 0.5120	 0.4210
K	 0.4530	 0.3270
L	 0.4730	 0.3880
M	 0.5370	 0.3850
N	 0.0250	 0.0810
O	 0.4270	 0.2940

