



# wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 03:34 AM UTC

PDB ID : 2OM7 / pdb\_00002om7  
EMDB ID : EMD-1315  
Title : Structural Basis for Interaction of the Ribosome with the Switch Regions of GTP-bound Elongation Factors  
Authors : Connell, S.R.; Wilson, D.N.; Rost, M.; Schueler, M.; Giesebrecht, J.; Dabrowski, M.; Mielke, T.; Fucini, P.; Spahn, C.M.T.  
Deposited on : 2007-01-21  
Resolution : 7.30 Å (reported)  
Based on initial models : 1GIX, 1YL3, 1FNM, 2J00, 2J01

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

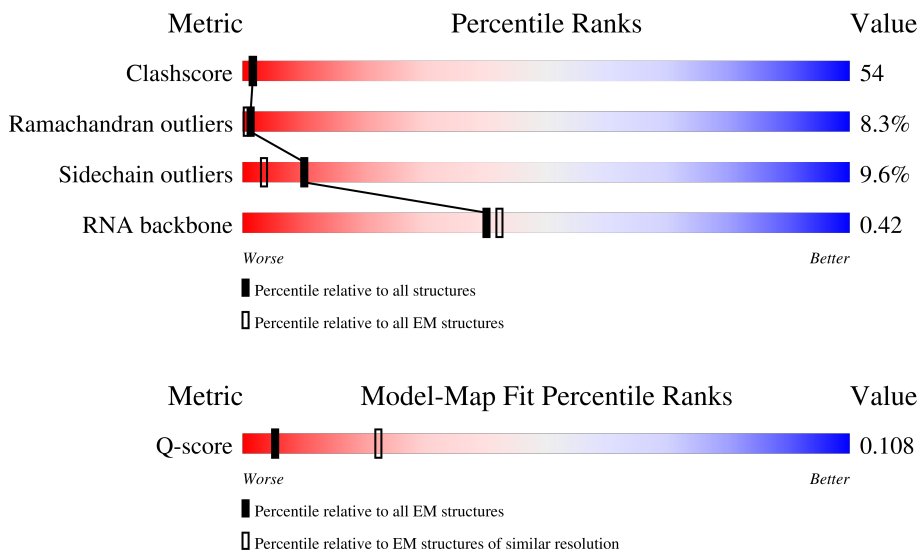
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 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 7.30 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.



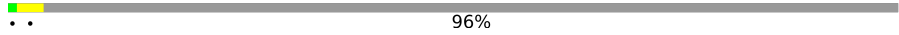
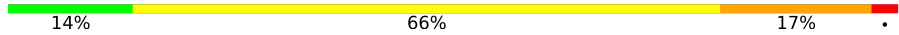

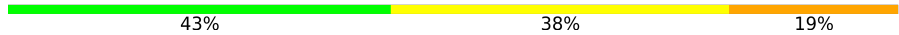



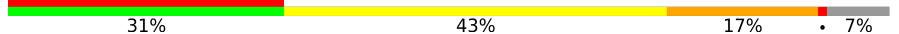
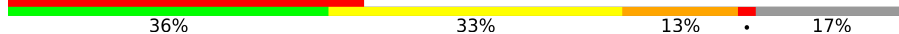
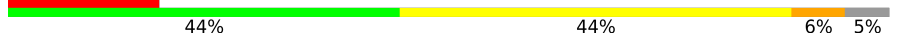
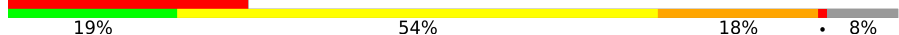
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	436 ( 6.80 - 7.80 )

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  $\geq 3$ , 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	12	
2	B	28	
3	C	96	

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Mol	Chain	Length	Quality of chain
4	D	303	 96%
5	F	29	 14% 66% 17%
6	G	54	 35% 43% 22%
7	H	42	 43% 38% 19%
8	I	58	 34% 45% 19%
9	J	102	 16% 29% 25% 28%
10	M	74	 11% 36% 32% 20%
11	E	135	 31% 43% 17% 7%
12	K	229	 40% 36% 33% 13% 17%
13	L	691	 17% 44% 44% 6% 5%
14	N	256	 27% 19% 54% 18% 8%

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
10	4SU	M	8	-	-	X	-

## 2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 19031 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 RNA chain called Fragment of 16S rRNA (h14).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	12	256	114	46	84	12	0	0

- Molecule 2 is a RNA chain called Fragment of 16S rRNA (h15).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	B	10	214	95	38	71	10	0	0

- Molecule 3 is a RNA chain called Fragment of 16S rRNA (h44).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	C	96	2069	919	387	667	96	0	0

- Molecule 4 is a RNA chain called 16S ribosomal RNA (H5).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	D	13	278	124	50	91	13	0	0

- Molecule 5 is a RNA chain called Fragment of 23S rRNA (H95).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	F	29	624	278	116	201	29	0	0

- Molecule 6 is a RNA chain called Fragment of 23S rRNA (H68).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
6	G	54	1172	521	228	369	54	0	0

- Molecule 7 is a RNA chain called Fragment of23S rRNA (H89).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
7	H	42	898	399	161	296	42	0	0

- Molecule 8 is a RNA chain called Fragment of23S rRNA (H42-44).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
8	I	58	1241	554	224	405	58	0	0

- Molecule 9 is a RNA chain called Fragment of23S rRNA (H76).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
9	J	73	1569	696	284	516	73	0	0

- Molecule 10 is a RNA chain called p/E-tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	N	O	P	S		
10	M	74	1570	702	269	524	74	1	0	0

- Molecule 11 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	E	125	971	611	196	163	1	0	1

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	2	VAL	-	insertion	UNP P17293
E	3	ALA	-	insertion	UNP P17293
E	4	LEU	-	insertion	UNP P17293

- Molecule 12 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms			AltConf	Trace	
			Total	C	N			O
12	K	191	1142	691	221	230	0	1

- Molecule 13 is a protein called Elongation factor G.

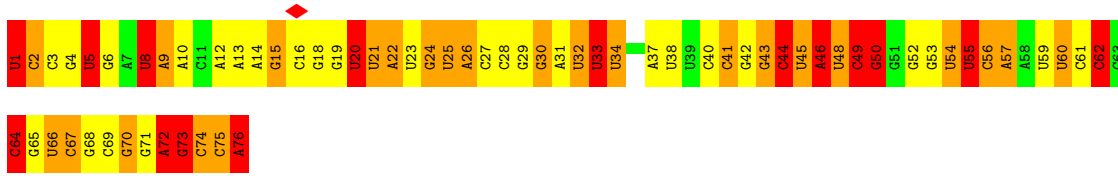
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	L	655	5126	3259	874	975	18	0	0

- Molecule 14 is a protein called 30S ribosomal protein S2.

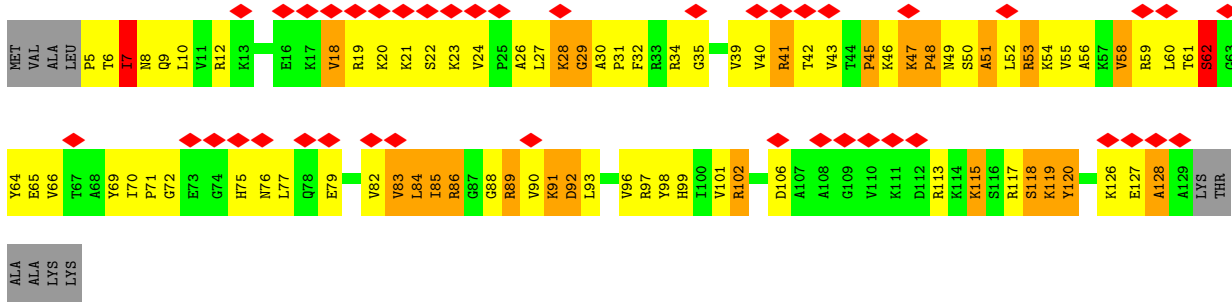
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	N	235	1901	1213	342	341	5	0	1



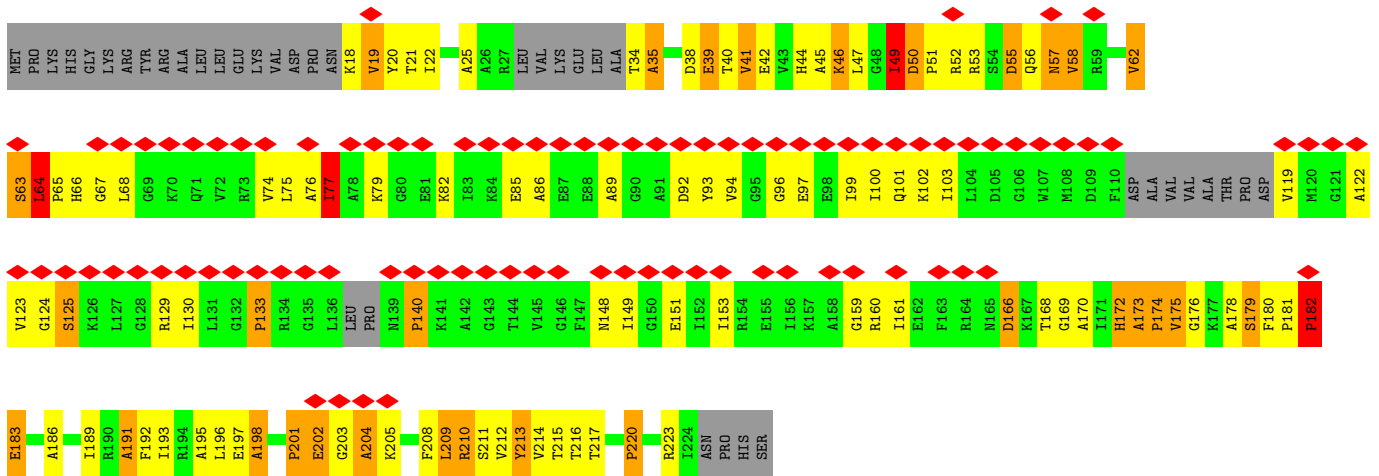




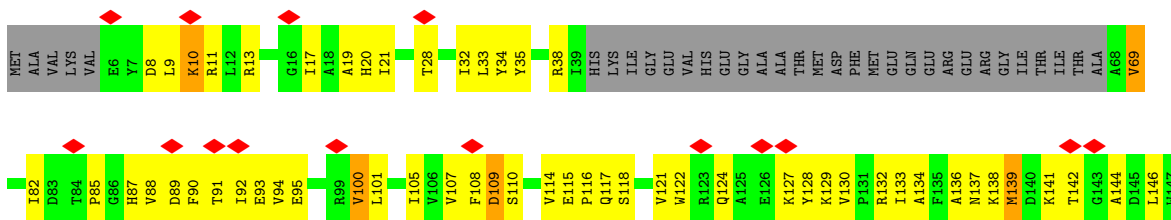
• Molecule 11: 30S ribosomal protein S12

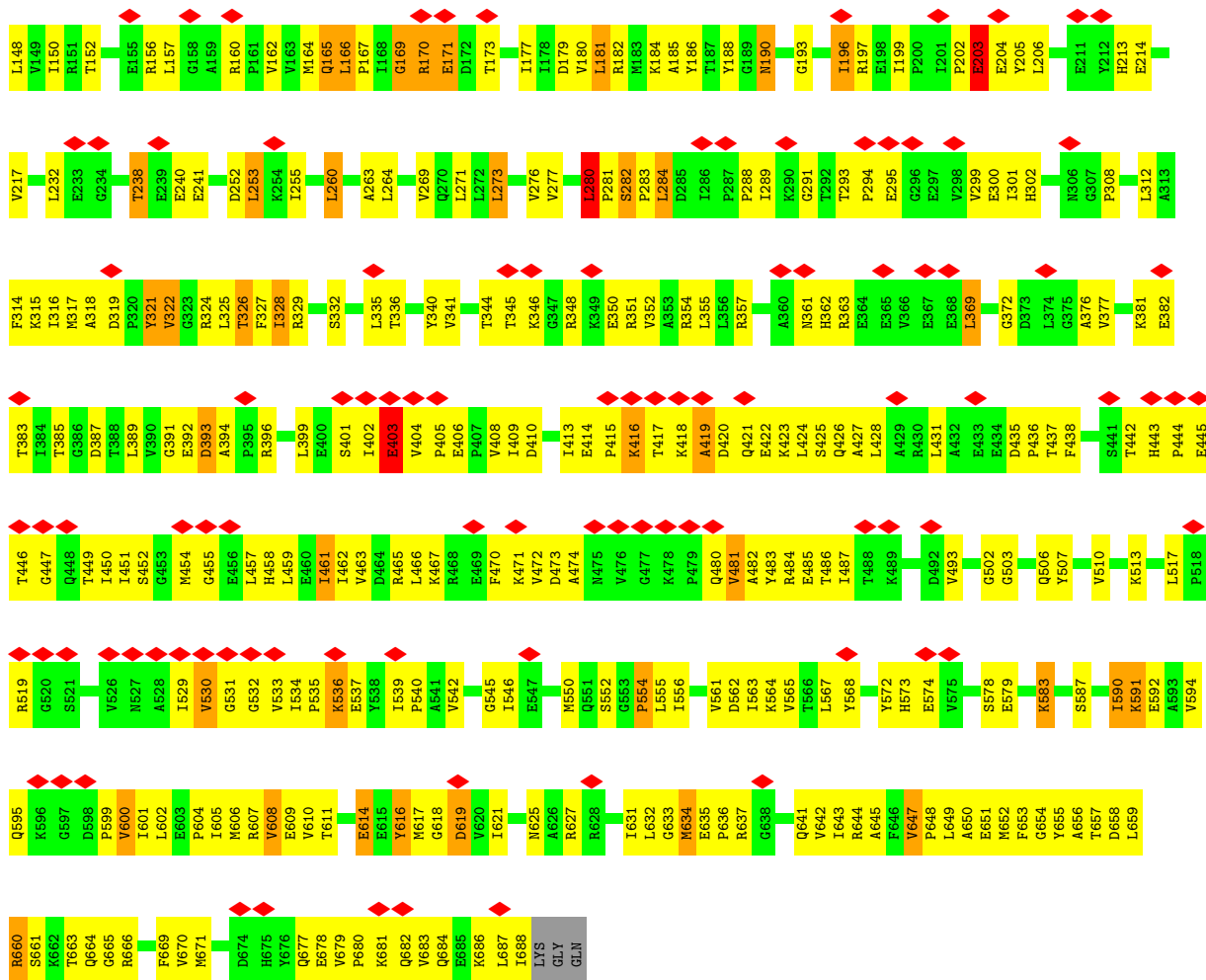


• Molecule 12: 50S ribosomal protein L1

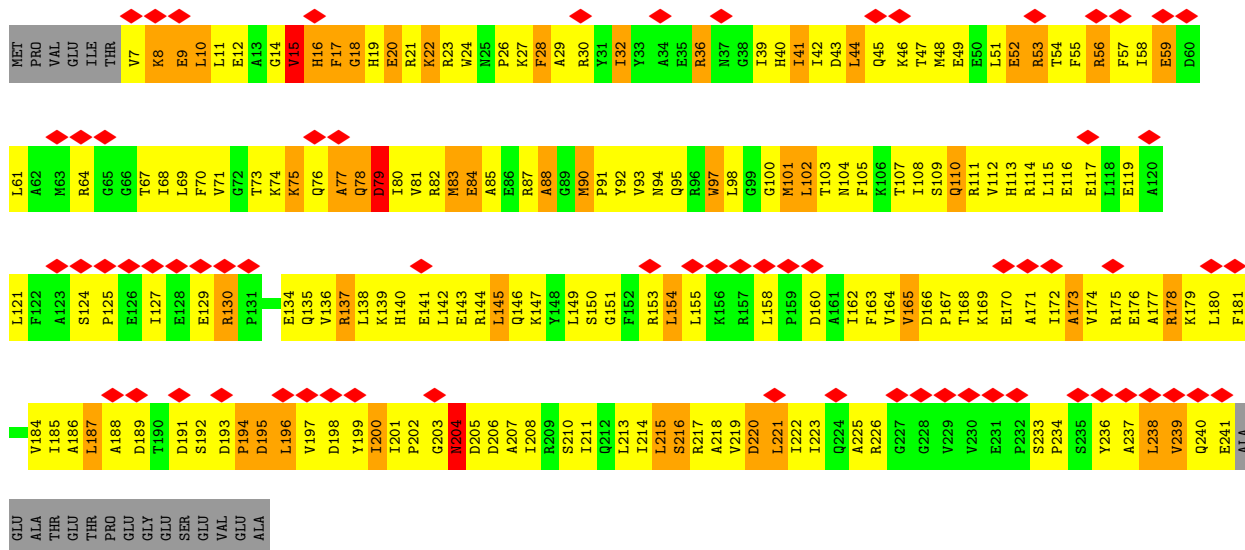
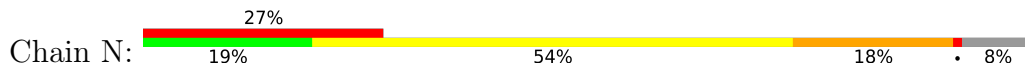


• Molecule 13: Elongation factor G





• Molecule 14: 30S ribosomal protein S2



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	77038	Depositor
Resolution determination method	Not provided	
CTF correction method	defocus groups	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	19	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	39000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	11069.200	Depositor
Minimum map value	-4968.550	Depositor
Average map value	-29.848	Depositor
Map value standard deviation	976.693	Depositor
Recommended contour level	1820	Depositor
Map size ( $\text{\AA}$ )	378, 378, 378	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ( $^\circ$ )	90, 90, 90	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.26, 1.26, 1.26	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: 4SU, PSU, 5MC, 5MU, H2U

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	0.55	0/285	0.63	0/442
2	B	0.56	0/237	0.65	0/365
3	C	0.60	0/2315	0.71	3/3613 (0.1%)
4	D	0.61	0/309	0.65	0/477
5	F	0.56	0/698	0.74	1/1087 (0.1%)
6	G	0.61	0/1314	0.74	1/2051 (0.0%)
7	H	0.57	0/1002	0.70	1/1561 (0.1%)
8	I	0.76	2/1388 (0.1%)	1.12	10/2162 (0.5%)
9	J	0.50	0/1753	0.70	2/2735 (0.1%)
10	M	1.55	15/1616 (0.9%)	2.26	64/2512 (2.5%)
11	E	0.68	1/987 (0.1%)	1.09	5/1322 (0.4%)
12	K	0.65	1/1145 (0.1%)	1.07	12/1556 (0.8%)
13	L	0.70	1/5219 (0.0%)	1.18	33/7063 (0.5%)
14	N	0.60	1/1936 (0.1%)	0.93	5/2611 (0.2%)
All	All	0.75	21/20204 (0.1%)	1.12	137/29557 (0.5%)

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
3	C	0	7
5	F	1	0
7	H	0	1
8	I	0	5
9	J	1	0
All	All	2	14

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	M	33	U	O3'-P	24.81	1.98	1.61
10	M	15	G	O3'-P	18.83	1.89	1.61
10	M	26	A	O3'-P	-18.60	1.33	1.61
10	M	24	G	O3'-P	15.21	1.83	1.61
10	M	56	C	O3'-P	14.12	1.82	1.61

The worst 5 of 137 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	L	600	VAL	O-C-N	-27.72	92.28	123.05
10	M	15	G	O3'-P-O5'	27.12	144.68	104.00
10	M	8	4SU	O3'-P-O5'	-27.02	52.65	104.00
10	M	25	U	P-O3'-C3'	24.67	157.21	120.20
10	M	31	A	O3'-P-O5'	-24.23	67.66	104.00

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	F	2662	A	C1'
9	J	2191	G	C3'

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	371	G	Sidechain
3	C	1407	C	Sidechain
3	C	1417	G	Sidechain
3	C	1418	A	Sidechain
3	C	1434	A	Sidechain

## 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	256	0	131	5	0
2	B	214	0	110	24	0
3	C	2069	0	1046	86	0
4	D	278	0	141	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	F	624	0	314	86	0
6	G	1172	0	591	47	0
7	H	898	0	456	20	0
8	I	1241	0	625	316	0
9	J	1569	0	790	79	0
10	M	1570	0	800	109	0
11	E	971	0	1057	113	0
12	K	1142	0	865	117	0
13	L	5126	0	5164	647	0
14	N	1901	0	1951	261	0
All	All	19031	0	14041	1771	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 54.

The worst 5 of 1771 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)
4:D:55:A:C2	13:L:322:VAL:HG12	1.22	1.75
13:L:556:ILE:CD1	13:L:601:ILE:HD13	1.28	1.64
13:L:408:VAL:CG1	13:L:669:PHE:HE1	1.12	1.57
5:F:2661:G:N1	13:L:20:HIS:CE1	1.72	1.54
2:B:368:U:C5	13:L:354:ARG:CD	1.92	1.52

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
11	E	123/135 (91%)	83 (68%)	24 (20%)	16 (13%)	<b>0</b> <b>4</b>
12	K	183/229 (80%)	90 (49%)	50 (27%)	43 (24%)	<b>0</b> <b>1</b>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	L	645/691 (93%)	583 (90%)	55 (8%)	7 (1%)	11	46
14	N	233/256 (91%)	150 (64%)	51 (22%)	32 (14%)	0	3
All	All	1184/1311 (90%)	906 (76%)	180 (15%)	98 (8%)	1	9

5 of 98 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	E	28	LYS
11	E	47	LYS
11	E	91	LYS
11	E	92	ASP
12	K	19	VAL

### 5.3.2 Protein sidechains [i](#)

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	
11	E	104/111 (94%)	93 (89%)	11 (11%)	6	21
12	K	61/181 (34%)	55 (90%)	6 (10%)	7	24
13	L	553/582 (95%)	504 (91%)	49 (9%)	9	28
14	N	202/220 (92%)	180 (89%)	22 (11%)	6	20
All	All	920/1094 (84%)	832 (90%)	88 (10%)	10	25

5 of 88 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	L	583	LYS
14	N	36	ARG
13	L	614	GLU
13	L	660	ARG
14	N	75	LYS

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

Mol	Chain	Res	Type
13	L	458	HIS
14	N	94	ASN
13	L	500	GLN
14	N	204	ASN
14	N	37	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	11/12 (91%)	1 (9%)	0
10	M	74/74 (100%)	26 (35%)	2 (2%)
2	B	8/28 (28%)	0	0
3	C	95/96 (98%)	11 (11%)	2 (2%)
4	D	11/303 (3%)	0	0
5	F	28/29 (96%)	7 (25%)	1 (3%)
6	G	53/54 (98%)	12 (22%)	1 (1%)
7	H	41/42 (97%)	8 (19%)	1 (2%)
8	I	57/58 (98%)	35 (61%)	5 (8%)
9	J	72/102 (70%)	29 (40%)	2 (2%)
All	All	450/798 (56%)	129 (28%)	14 (3%)

5 of 129 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	345	C
3	C	1419	G
3	C	1442	G
3	C	1442(A)	G
3	C	1442(B)	A

5 of 14 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	I	1085	A
8	I	1097	U
10	M	33	U
9	J	2191	G
10	M	1	U

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

6 non-standard protein/DNA/RNA residues are modelled in this entry.

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
10	H2U	M	21	10	18,21,22	0.58	0	19,30,33	0.92	1 (5%)
10	H2U	M	20	10	18,21,22	0.50	0	19,30,33	0.70	1 (5%)
10	PSU	M	55	10	18,21,22	0.68	0	21,30,33	0.83	1 (4%)
10	5MC	M	49	10	19,22,23	0.67	0	26,32,35	0.99	1 (3%)
10	4SU	M	8	10	18,21,22	0.66	0	25,30,33	0.54	0
10	5MU	M	54	10	19,22,23	0.74	0	27,32,35	1.39	3 (11%)

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
10	H2U	M	21	10	-	2/7/38/39	0/2/2/2
10	H2U	M	20	10	-	0/7/38/39	0/2/2/2
10	PSU	M	55	10	-	4/7/25/26	0/2/2/2
10	5MC	M	49	10	-	2/7/25/26	0/2/2/2
10	4SU	M	8	10	-	0/7/25/26	0/2/2/2
10	5MU	M	54	10	-	2/7/25/26	0/2/2/2

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	M	54	5MU	C5-C4-N3	3.94	118.75	115.32
10	M	54	5MU	C4-N3-C2	-3.09	123.28	127.34
10	M	49	5MC	C5-C4-N3	-2.57	119.12	121.75
10	M	21	H2U	N3-C2-N1	-2.27	114.36	116.65
10	M	20	H2U	N3-C2-N1	-2.19	114.44	116.65

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	M	49	5MC	O4'-C4'-C5'-O5'
10	M	55	PSU	C3'-C4'-C5'-O5'
10	M	55	PSU	O4'-C4'-C5'-O5'
10	M	49	5MC	C3'-C4'-C5'-O5'
10	M	21	H2U	O4'-C4'-C5'-O5'

There are no ring outliers.

5 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	M	20	H2U	2	0
10	M	55	PSU	3	0
10	M	49	5MC	5	0
10	M	8	4SU	7	0
10	M	54	5MU	2	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
10	M	10
13	L	3

The worst 5 of 13 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	L	485:GLU	C	486:THR	N	15.61
1	L	400:GLU	C	401:SER	N	15.51
1	L	598:ASP	C	599:PRO	N	2.97
1	M	37:A	O3'	38:U	P	2.27
1	M	48:U	O3'	49:5MC	P	1.99

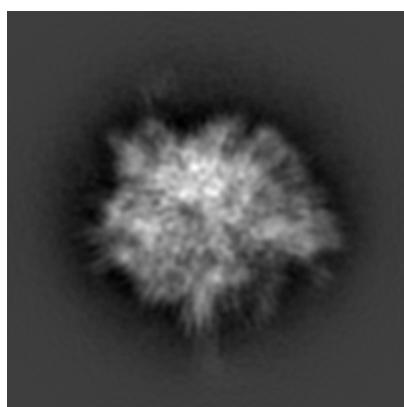
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1315. These allow visual inspection of the internal detail of the map and identification of artifacts.

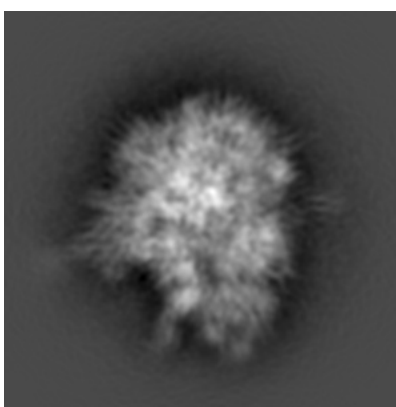
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

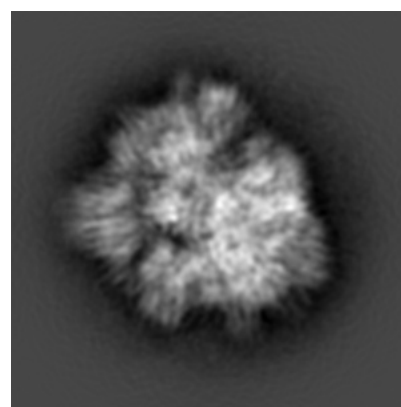
#### 6.1.1 Primary map



X



Y

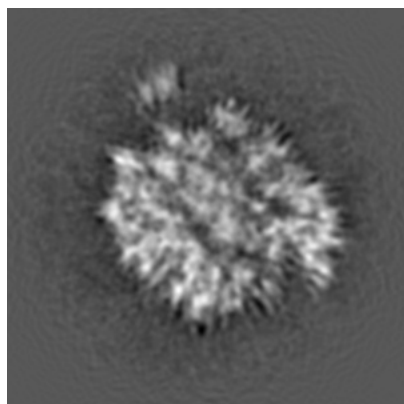


Z

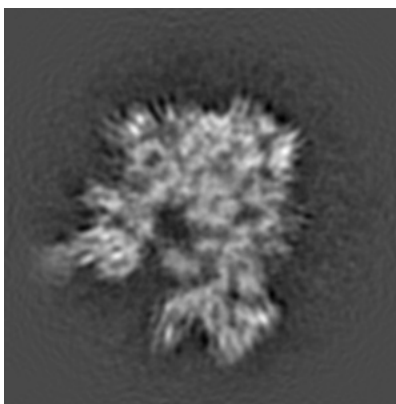
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

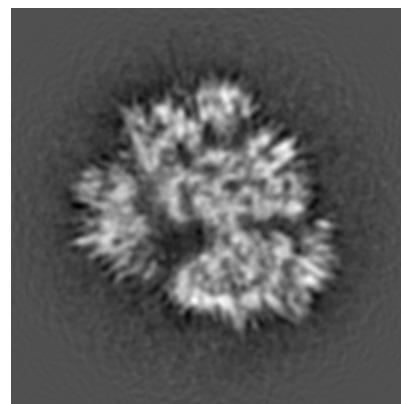
#### 6.2.1 Primary map



X Index: 150



Y Index: 150

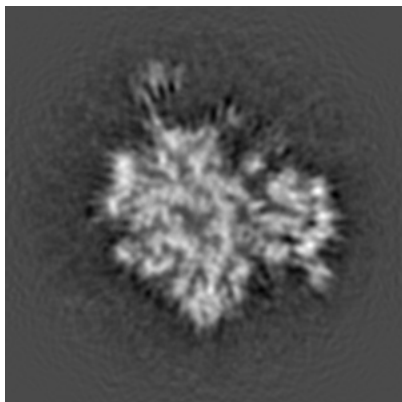


Z Index: 150

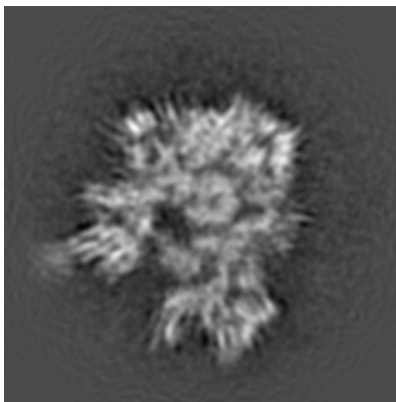
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

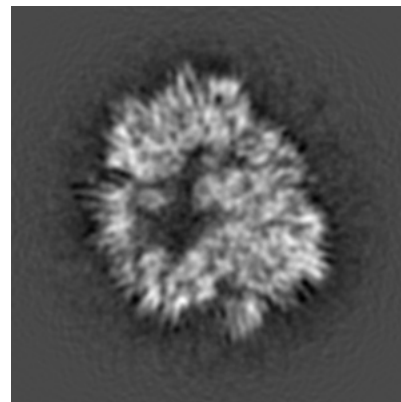
### 6.3.1 Primary map



X Index: 155



Y Index: 152

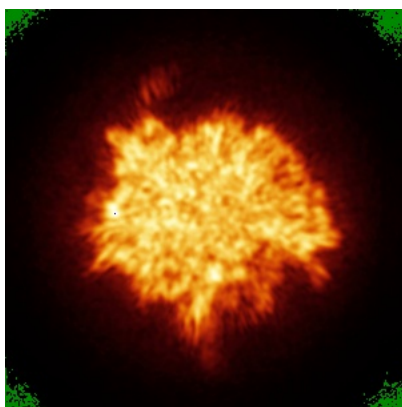


Z Index: 137

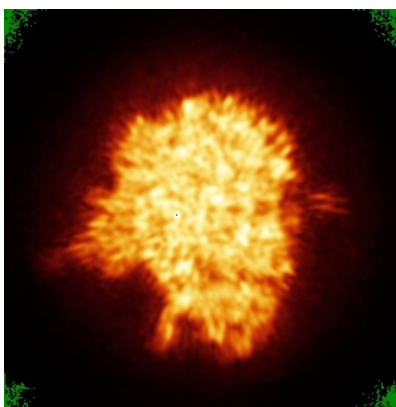
The images above show the largest variance slices of the map in three orthogonal directions.

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

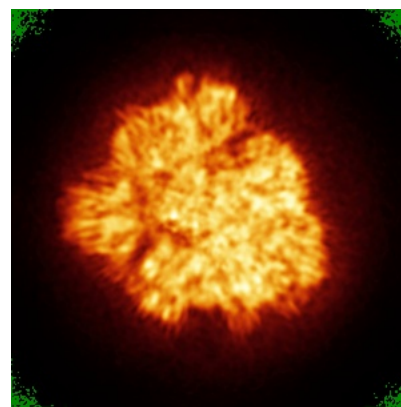
### 6.4.1 Primary map



X



Y

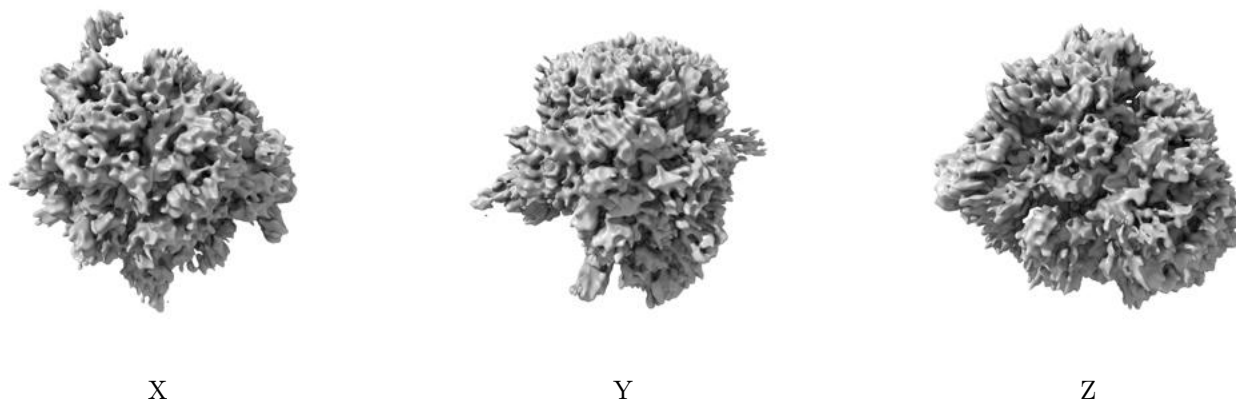


Z

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 1820.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

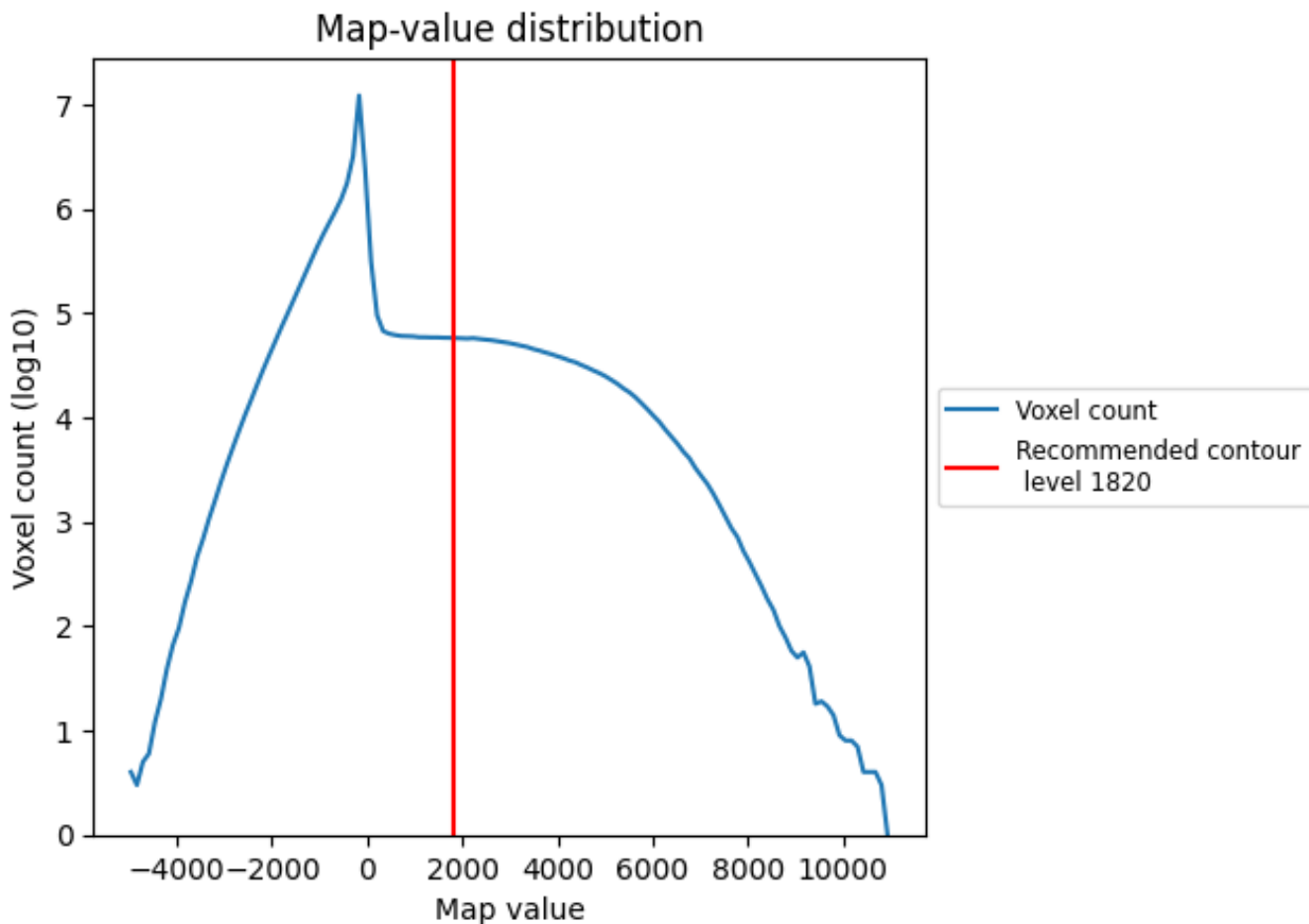
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

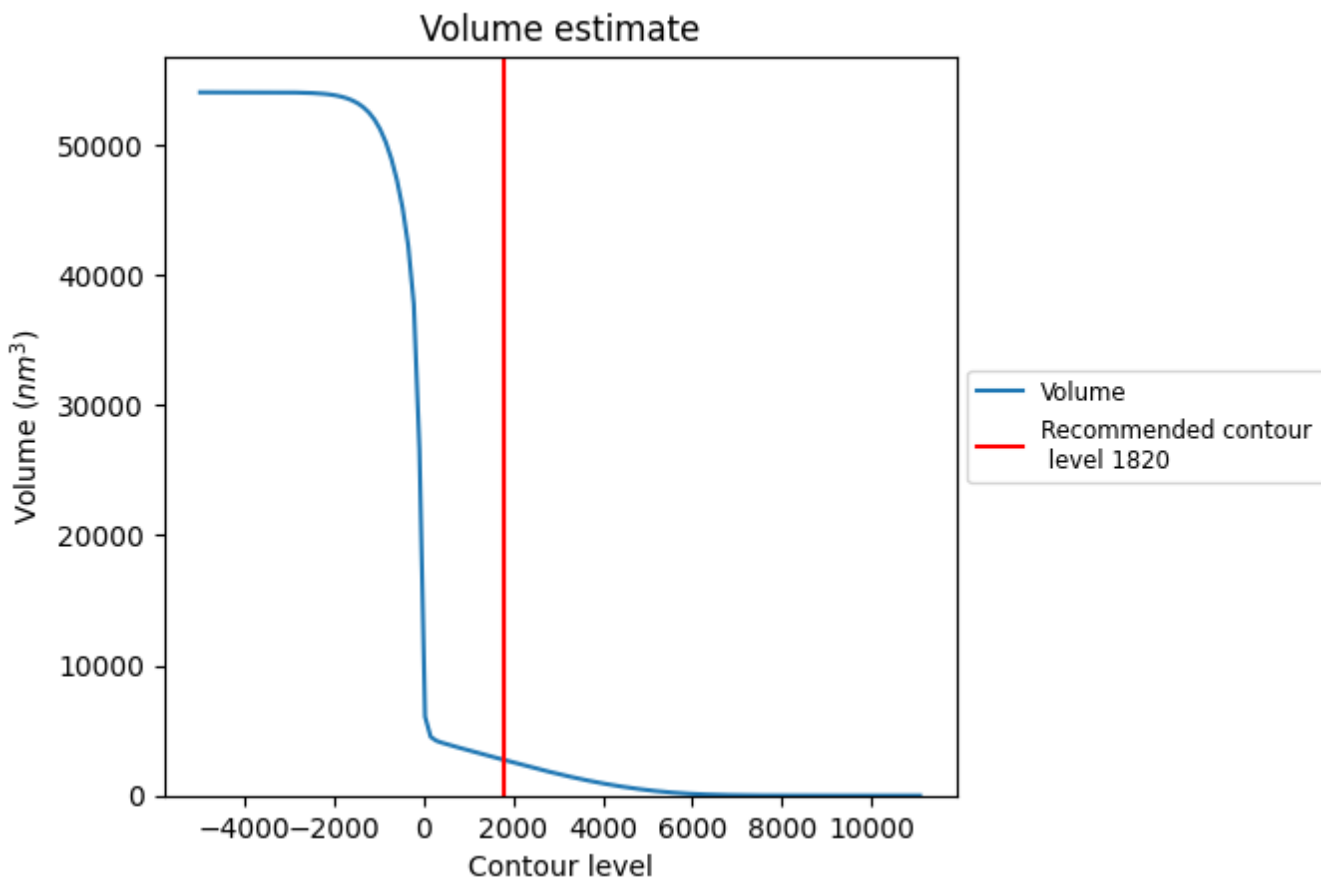
This section contains the results of statistical analysis of the map.

### 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.

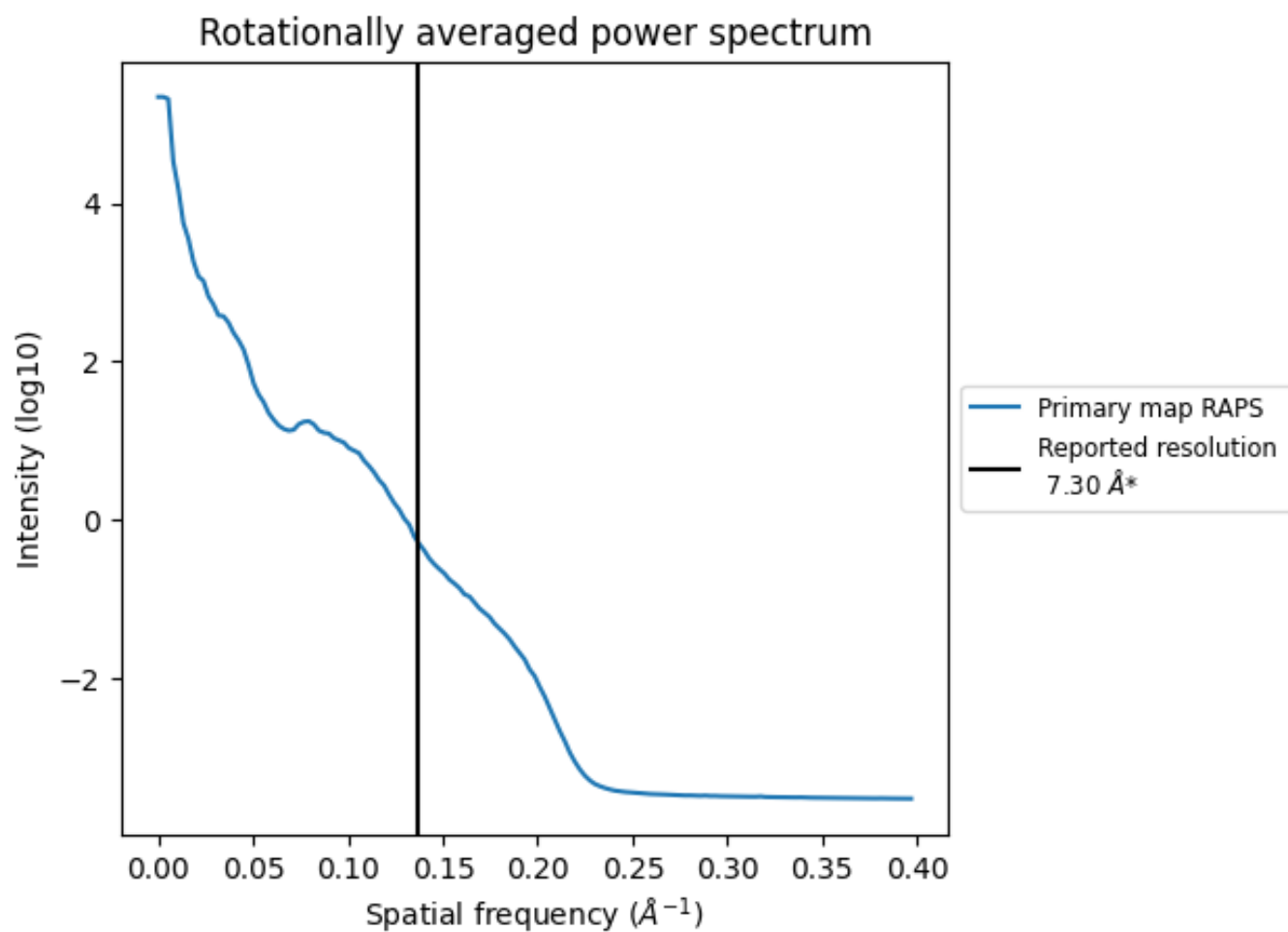
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2722  $\text{nm}^3$ ; this corresponds to an approximate mass of 2458 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 0.137 Å<sup>-1</sup>

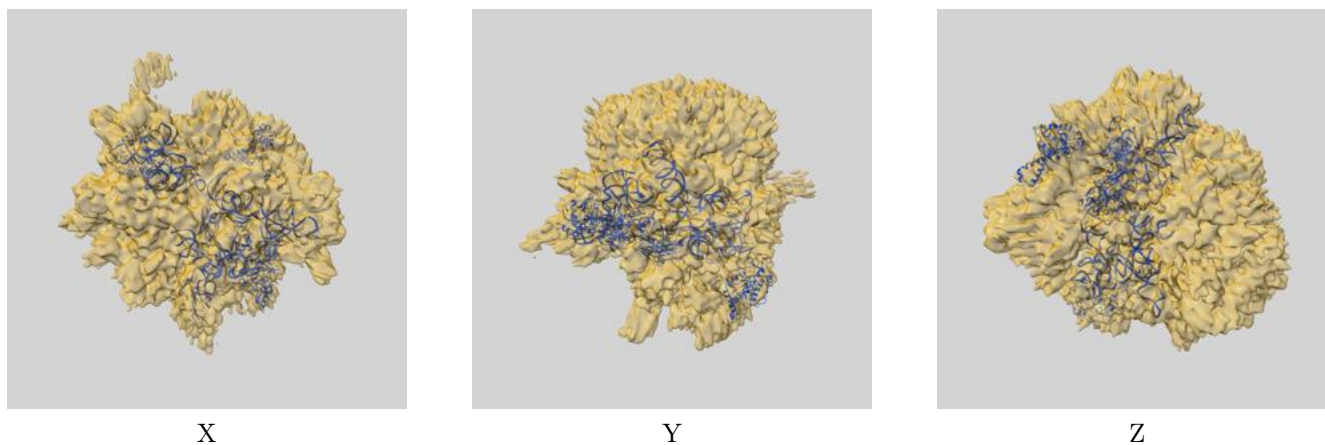
## 8 Fourier-Shell correlation

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

## 9 Map-model fit [i](#)

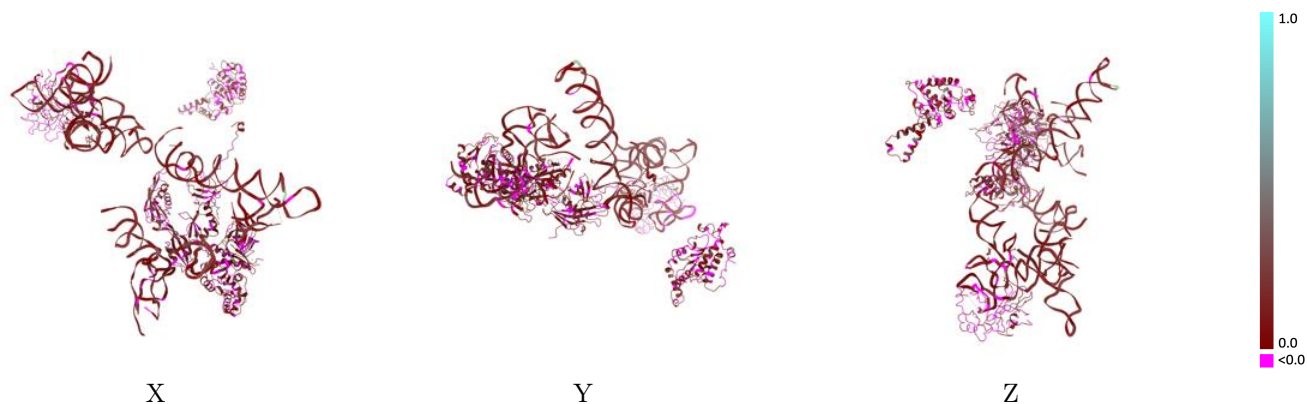
This section contains information regarding the fit between EMDB map EMD-1315 and PDB model 2OM7. Per-residue inclusion information can be found in section 3 on page 7.

### 9.1 Map-model overlay [i](#)



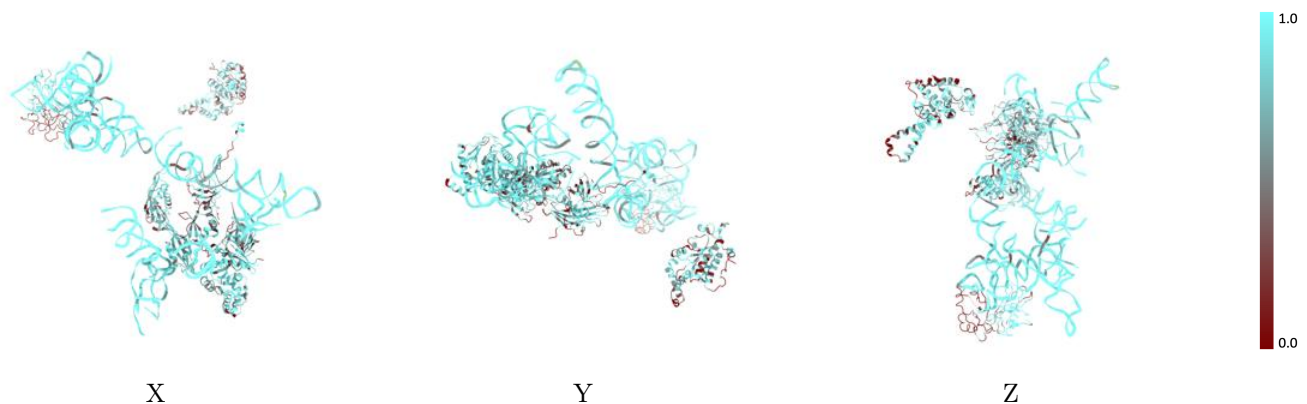
The images above show the 3D surface view of the map at the recommended contour level 1820.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



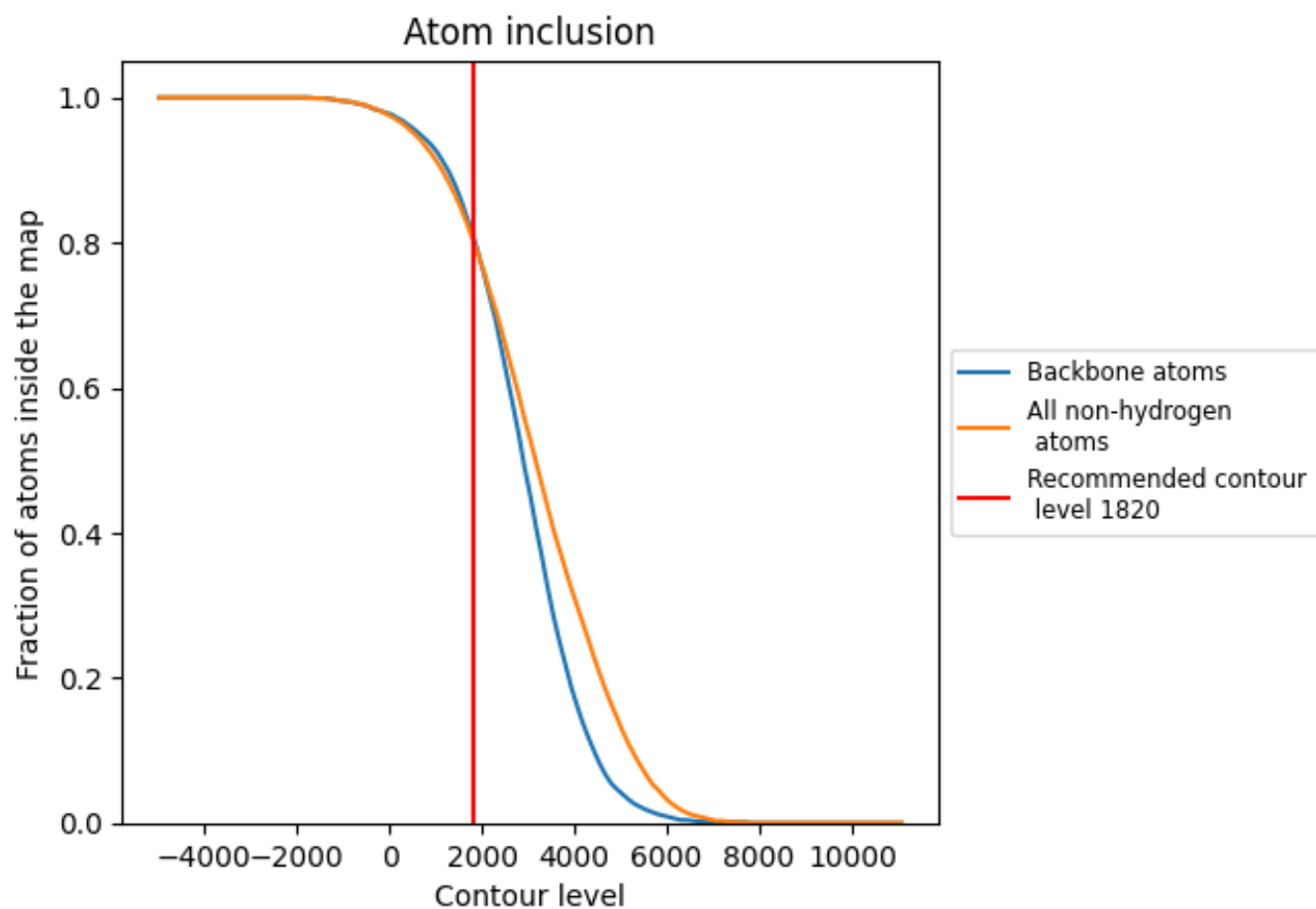
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1820).































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 80% 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 (1820) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8020	 0.1080
A	 0.7580	 0.1270
B	 0.9530	 0.1210
C	 0.8840	 0.1420
D	 0.9570	 0.1070
E	 0.5810	 0.0790
F	 0.9620	 0.1450
G	 0.9510	 0.1700
H	 0.9640	 0.1480
I	 0.9500	 0.1170
J	 0.9110	 0.0980
K	 0.5030	 0.0150
L	 0.7330	 0.1000
M	 0.9340	 0.1240
N	 0.6220	 0.0820

