



## wwPDB EM Validation Summary Report ⓘ

Feb 5, 2024 – 09:25 AM EST

PDB ID : 1RY1  
EMDB ID : EMD-1063  
Title : Structure of the signal recognition particle interacting with the elongation-arrested ribosome  
Authors : Halic, M.; Becker, T.; Pool, M.R.; Spahn, C.M.; Grassucci, R.A.; Frank, J.; Beckmann, R.  
Deposited on : 2003-12-19  
Resolution : 12.00 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](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:

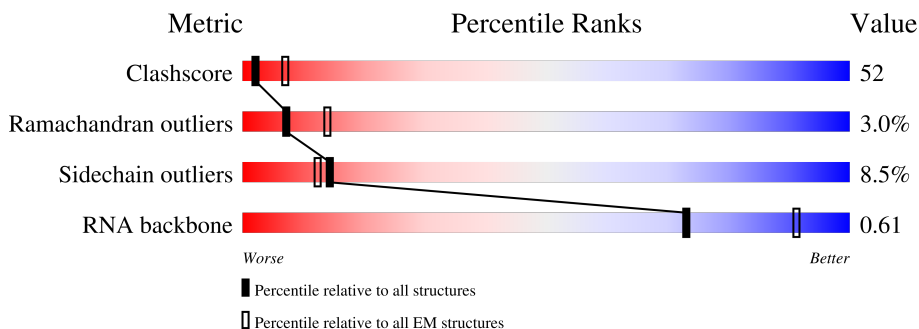
EMDB validation analysis : 0.0.1.dev70  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

# 1 Overall quality at a glance

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

The reported resolution of this entry is 12.00 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	E	50	96% 22% 56% 14% 6% .
2	A	128	100% 36% 52% 12%
3	M	27	100% 15% 48% 15% 22%
4	N	31	100% . 45% 29% 23%
5	O	24	100% 25% 54% 12% 8%
6	P	20	95% 10% 60% 15% 10% 5%
7	Q	12	100% 8% 33% 42% 17%

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Mol	Chain	Length	Quality of chain
8	R	12	<p>100% 25% 58% 17%</p>
9	C	85	<p>73% 29% 46% 7% 16%</p>
10	D	106	<p>66% 42% 25% 28%</p>
11	B	108	<p>99% 41% 50% 7%</p>
12	U	296	<p>99% 52% 41% 6%</p>
13	W	109	<p>100% 52% 40%</p>
14	S	18	<p>100% 33% 67%</p>

## 2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 11794 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 SRP Alu domain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	E	49	1051	466	190	346	49	0	0

- Molecule 2 is a RNA chain called SRP S domain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	A	128	2751	1226	511	886	128	0	0

- Molecule 3 is a RNA chain called SRP RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	M	27	585	260	110	188	27	0	0

- Molecule 4 is a RNA chain called SRP RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	N	31	649	291	109	218	31	0	0

- Molecule 5 is a RNA chain called SRP RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	O	24	511	227	86	174	24	0	0

- Molecule 6 is a RNA chain called SRP RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
6	P	19	401	180	72	130	19	0	0

- Molecule 7 is a RNA chain called SRP RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Q	12	Total	C	N	O	P	0	0
			257	114	45	86	12		

- Molecule 8 is a RNA chain called SRP RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	R	12	Total	C	N	O	P	0	0
			254	113	43	86	12		

- Molecule 9 is a protein called SRP9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	71	Total	C	N	O	S	0	0
			580	369	101	105	5		

- Molecule 10 is a protein called SRP14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	76	Total	C	N	O	S	0	0
			604	382	105	113	4		

- Molecule 11 is a protein called SRP19.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	B	107	Total	C	N	O	S	0	0
			870	549	159	156	6		

- Molecule 12 is a protein called SRP54NG.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	U	294	Total	C	N	O	S	0	0
			2266	1424	413	423	6		

- Molecule 13 is a protein called SRP54M.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	W	109	Total	C	N	O	S	0	0
			865	540	150	164	11		

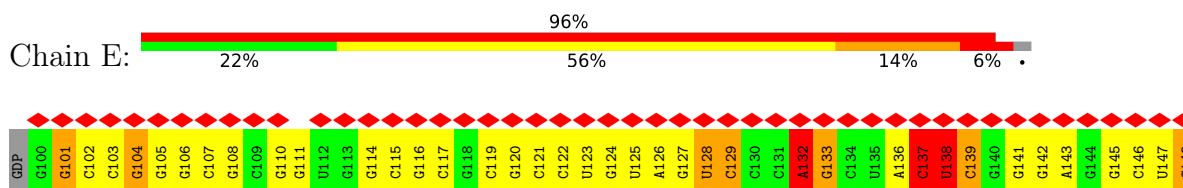
- Molecule 14 is a protein called signal sequence peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
14	S	18	150	103	24	23	0	0

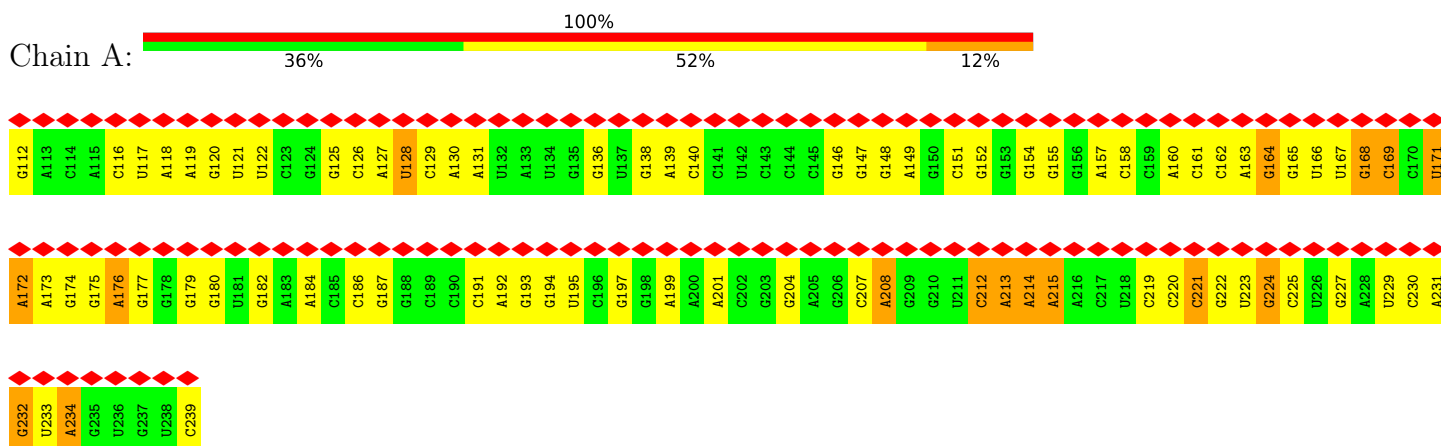
### 3 Residue-property plots [i](#)

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.

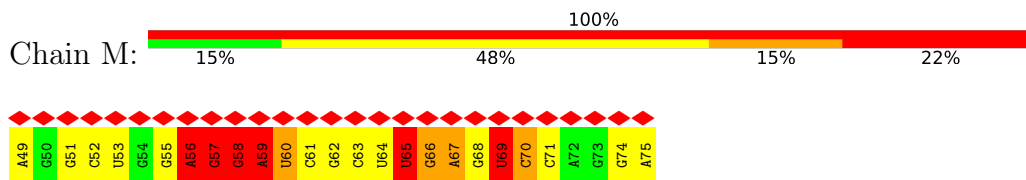
- Molecule 1: SRP Alu domain



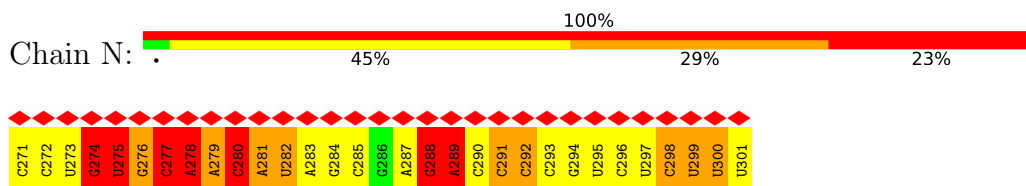
- Molecule 2: SRP S domain



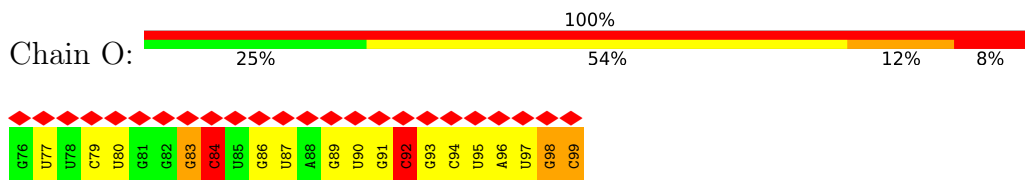
- Molecule 3: SRP RNA



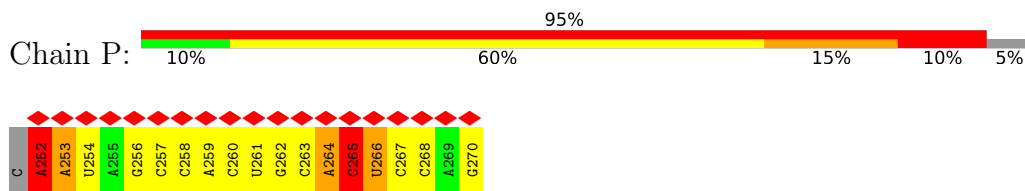
- Molecule 4: SRP RNA



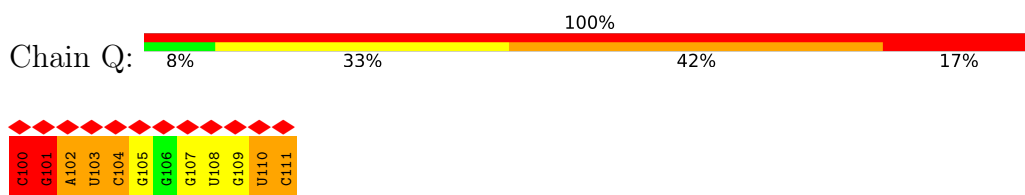
- Molecule 5: SRP RNA



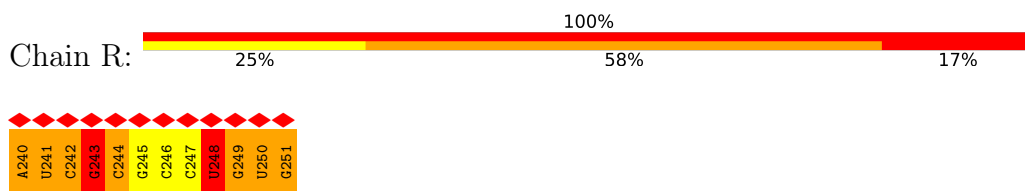
• Molecule 6: SRP RNA



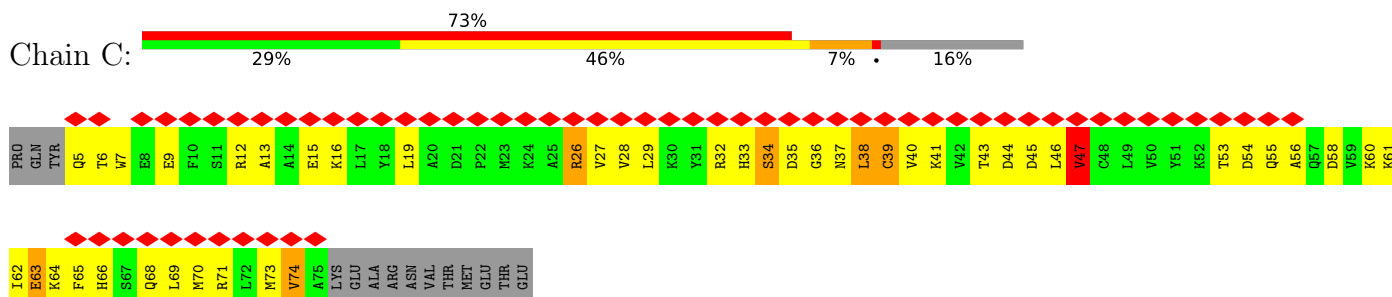
• Molecule 7: SRP RNA



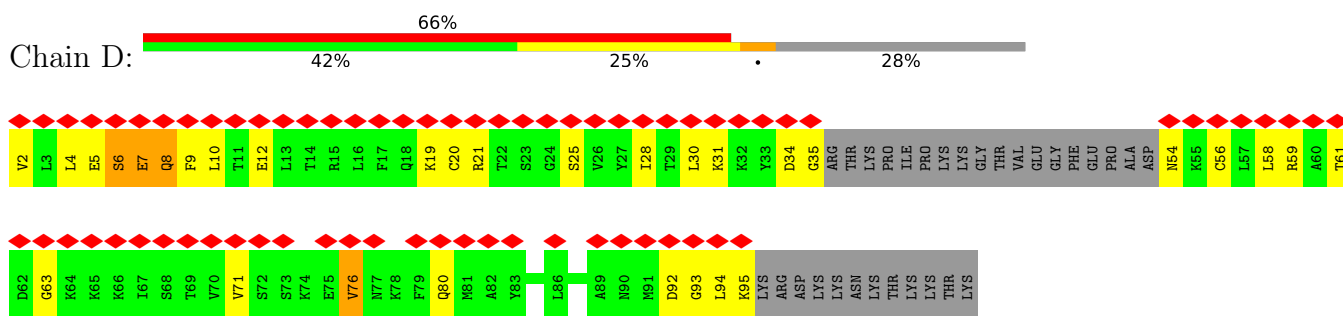
• Molecule 8: SRP RNA



• Molecule 9: SRP9

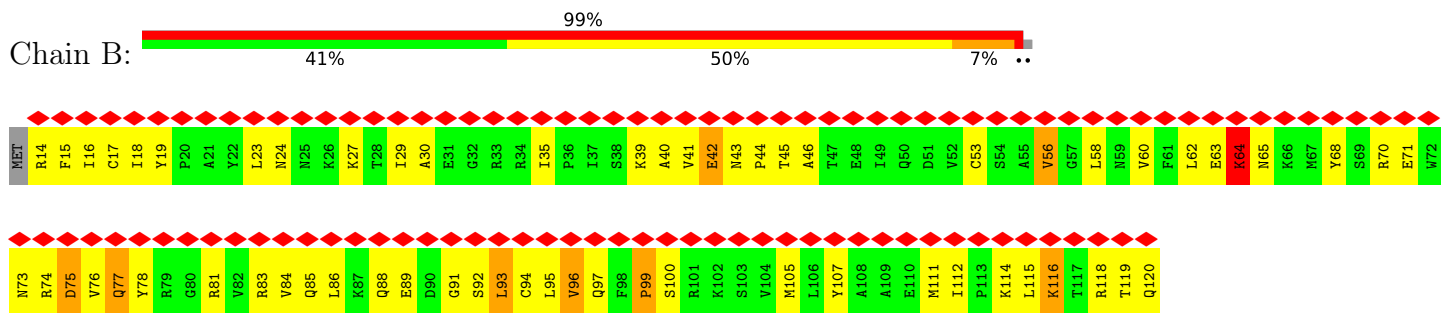


• Molecule 10: SRP14

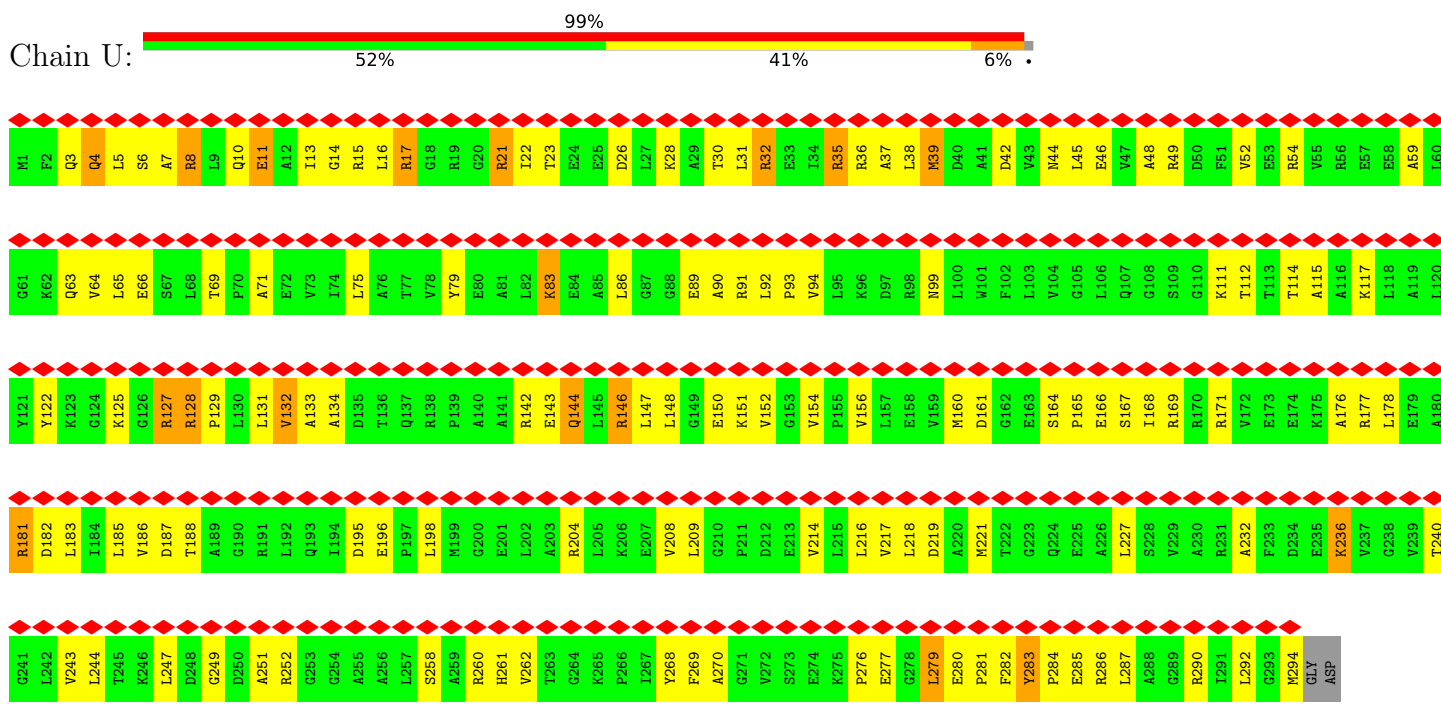


• Molecule 11: SRP19

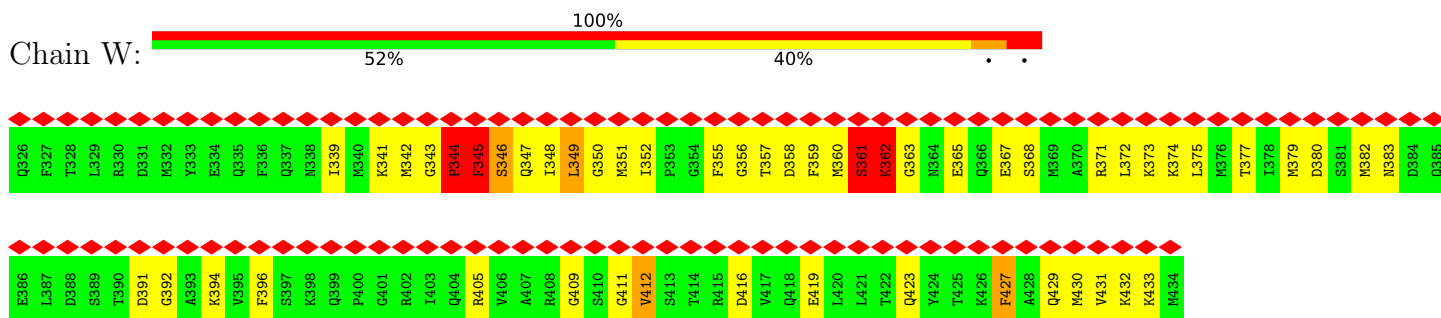




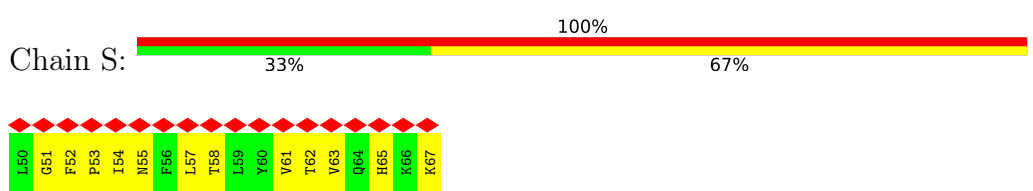
• Molecule 12: SRP54NG



• Molecule 13: SRP54M



• Molecule 14: signal sequence peptide



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	Not provided	
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	160	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	10	Depositor
Minimum defocus (nm)	10000	Depositor
Maximum defocus (nm)	45000	Depositor
Magnification	52000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	0.002	Depositor
Minimum map value	-0.001	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.000	Depositor
Recommended contour level	0.00055	Depositor
Map size ( $\text{\AA}$ )	423.8, 423.8, 423.8	wwPDB
Map dimensions	130, 130, 130	wwPDB
Map angles ( $^\circ$ )	90, 90, 90	wwPDB
Pixel spacing ( $\text{\AA}$ )	3.26, 3.26, 3.26	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: CCC

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	E	0.57	0/1173	0.81	3/1829 (0.2%)
2	A	0.45	0/3055	0.70	0/4766
3	M	1.23	2/651 (0.3%)	2.01	12/1005 (1.2%)
4	N	2.23	4/721 (0.6%)	2.65	18/1116 (1.6%)
5	O	0.85	0/567	2.75	6/877 (0.7%)
6	P	0.91	0/446	2.33	5/689 (0.7%)
7	Q	2.50	2/284 (0.7%)	3.20	10/436 (2.3%)
8	R	1.31	1/282 (0.4%)	2.53	9/437 (2.1%)
9	C	0.42	0/589	0.66	0/791
10	D	0.39	0/608	0.66	0/809
11	B	0.46	0/884	0.69	0/1188
12	U	0.27	0/2291	0.50	0/3086
13	W	0.95	2/876 (0.2%)	1.26	8/1165 (0.7%)
14	S	0.55	0/154	0.72	0/208
All	All	0.89	11/12581 (0.1%)	1.42	71/18402 (0.4%)

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	A	0	3
13	W	0	5
All	All	0	8

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	N	288	G	O3'-P	40.60	2.09	1.61
7	Q	110	U	O3'-P	38.67	2.07	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	N	292	C	O3'-P	34.73	2.02	1.61
3	M	74	G	O3'-P	19.79	1.84	1.61
13	W	345	PHE	C-N	-18.39	0.91	1.34

The worst 5 of 71 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	O	92	C	P-O3'-C3'	-65.35	41.28	119.70
4	N	280	C	P-O3'-C3'	-57.26	50.99	119.70
6	P	252	A	P-O3'-C3'	-45.34	65.29	119.70
7	Q	101	G	P-O3'-C3'	-40.29	71.36	119.70
3	M	69	U	O3'-P-O5'	-36.27	35.09	104.00

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	197	G	Sidechain
2	A	201	A	Sidechain
2	A	208	A	Sidechain
13	W	344	PRO	Peptide,Mainchain
13	W	361	SER	Mainchain

## 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	E	1051	0	528	84	0
2	A	2751	0	1387	96	0
3	M	585	0	289	99	0
4	N	649	0	330	150	0
5	O	511	0	258	25	0
6	P	401	0	208	108	0
7	Q	257	0	129	83	0
8	R	254	0	128	75	0
9	C	580	0	594	85	0
10	D	604	0	638	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	B	870	0	901	80	0
12	U	2266	0	2367	226	0
13	W	865	0	865	233	0
14	S	150	0	158	64	0
All	All	11794	0	8780	1071	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 52.

The worst 5 of 1071 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)
6:P:252:A:C2	8:R:250:U:H2'	1.25	1.63
12:U:281:PRO:CB	13:W:347:GLN:HG3	1.15	1.61
4:N:274:G:H2'	4:N:275:U:C5	1.11	1.59
12:U:283:TYR:CZ	13:W:360:MET:HE2	1.34	1.58
12:U:283:TYR:CE1	13:W:360:MET:HB2	1.05	1.56

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	
9	C	69/85 (81%)	57 (83%)	9 (13%)	3 (4%)	2	22
10	D	72/106 (68%)	63 (88%)	5 (7%)	4 (6%)	2	19
11	B	105/108 (97%)	87 (83%)	11 (10%)	7 (7%)	1	15
12	U	292/296 (99%)	273 (94%)	18 (6%)	1 (0%)	41	77
13	W	107/109 (98%)	100 (94%)	2 (2%)	5 (5%)	2	21
14	S	16/18 (89%)	14 (88%)	2 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	661/722 (92%)	594 (90%)	47 (7%)	20 (3%)	7	28

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	C	34	SER
9	C	47	VAL
10	D	6	SER
11	B	42	GLU
11	B	75	ASP

### 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	
9	C	64/77 (83%)	58 (91%)	6 (9%)	8	28
10	D	69/96 (72%)	66 (96%)	3 (4%)	29	53
11	B	96/97 (99%)	92 (96%)	4 (4%)	30	54
12	U	233/234 (100%)	202 (87%)	31 (13%)	4	18
13	W	96/96 (100%)	91 (95%)	5 (5%)	23	48
14	S	17/17 (100%)	17 (100%)	0	100	100
All	All	575/617 (93%)	526 (92%)	49 (8%)	14	33

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	U	127	ARG
12	U	161	ASP
12	U	128	ARG
12	U	146	ARG
12	U	182	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
13	W	383	ASN
13	W	385	GLN
13	W	429	GLN
13	W	423	GLN
11	B	73	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	E	48/50 (96%)	11 (22%)	2 (4%)
2	A	127/128 (99%)	22 (17%)	1 (0%)
3	M	24/27 (88%)	8 (33%)	3 (12%)
4	N	28/31 (90%)	12 (42%)	9 (32%)
5	O	22/24 (91%)	4 (18%)	1 (4%)
6	P	18/20 (90%)	2 (11%)	2 (11%)
7	Q	10/12 (83%)	4 (40%)	2 (20%)
8	R	11/12 (91%)	6 (54%)	3 (27%)
All	All	288/304 (94%)	69 (23%)	23 (7%)

5 of 69 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	E	101	G
1	E	104	G
1	E	128	U
1	E	129	C
1	E	132	A

5 of 23 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	N	299	U
6	P	265	C
6	P	252	A
7	Q	100	C
4	N	274	G

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

1 non-standard protein/DNA/RNA residue is 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
2	CCC	A	239	8,2	20,25,26	0.69	0	28,38,41	2.90	5 (17%)

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
2	CCC	A	239	8,2	-	0/7/35/36	0/3/3/3

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
2	A	239	CCC	O2C-PC-O1C	11.05	145.57	109.89
2	A	239	CCC	O3'-PC-O1C	-7.07	97.11	115.76
2	A	239	CCC	O2'-PC-O1C	-5.43	101.44	115.76
2	A	239	CCC	O2'-C2'-C3'	4.21	112.79	105.08
2	A	239	CCC	O3'-C3'-C2'	3.36	111.24	105.08

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides 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
3	M	5
7	Q	3
4	N	3
5	O	2
13	W	2
6	P	1
8	R	1

The worst 5 of 17 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	O	77:U	O3'	78:U	P	3.09
1	M	64:U	O3'	65:U	P	2.87
1	M	55:G	O3'	56:A	P	2.73
1	P	257:C	O3'	258:C	P	2.65
1	M	70:C	O3'	71:C	P	2.57

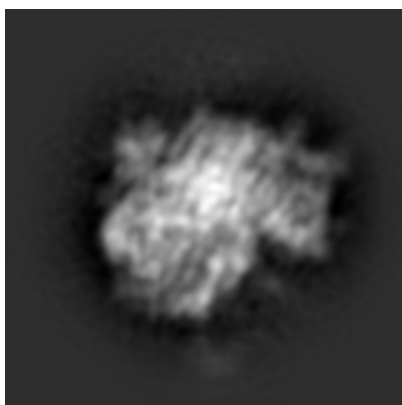
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1063. These allow visual inspection of the internal detail of the map and identification of artifacts.

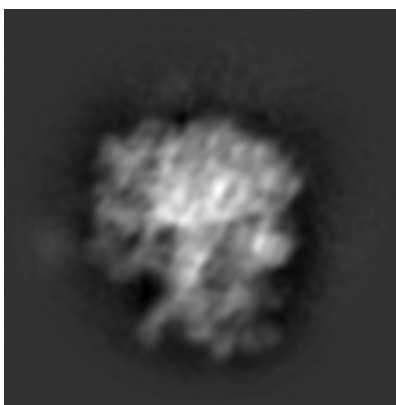
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

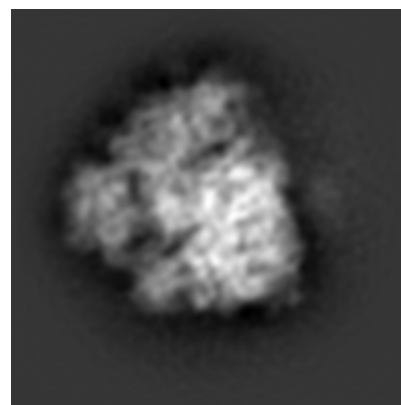
#### 6.1.1 Primary map



X



Y

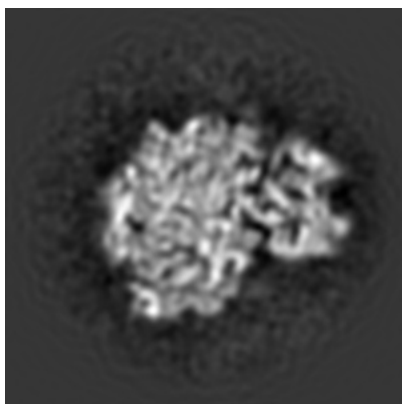


Z

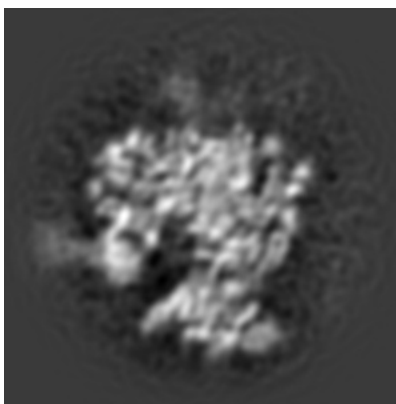
The images above show the map projected in three orthogonal directions.

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

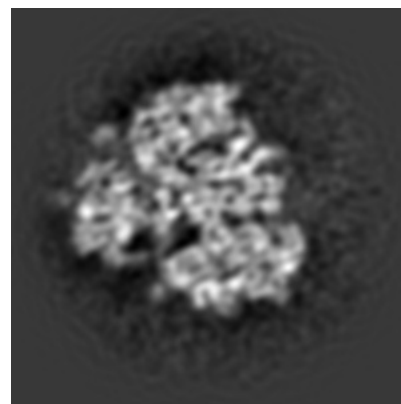
#### 6.2.1 Primary map



X Index: 65



Y Index: 65

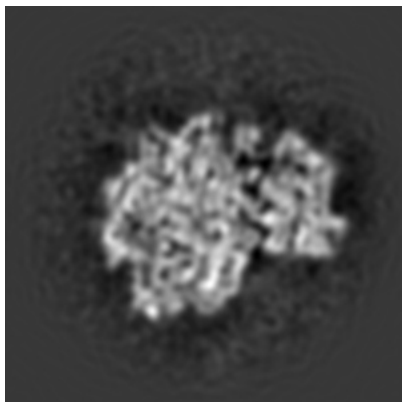


Z Index: 65

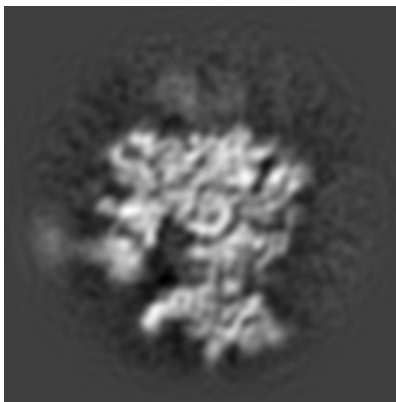
The images above show central slices of the map in three orthogonal directions.

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

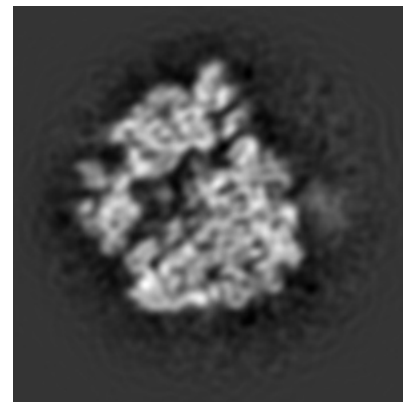
### 6.3.1 Primary map



X Index: 63



Y Index: 67

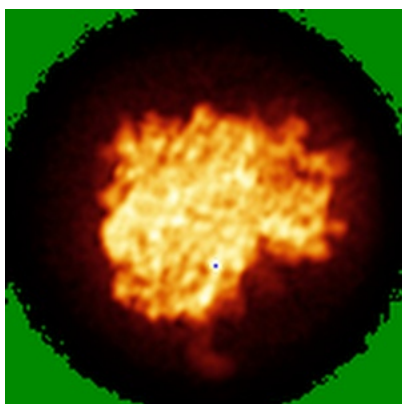


Z Index: 59

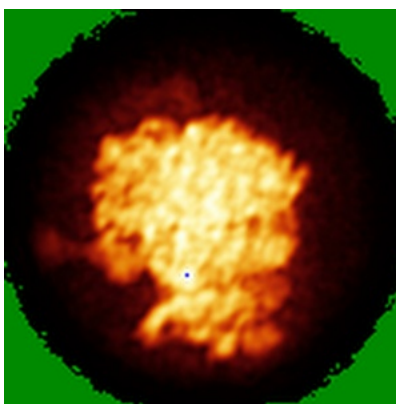
The images above show the largest variance slices of the map in three orthogonal directions.

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

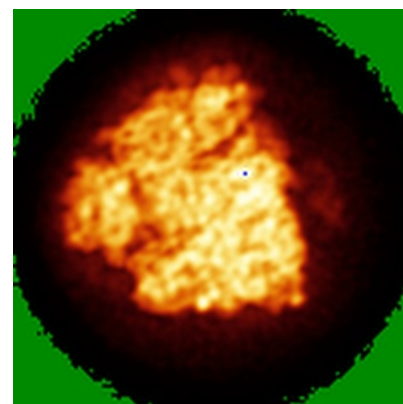
### 6.4.1 Primary map



X



Y

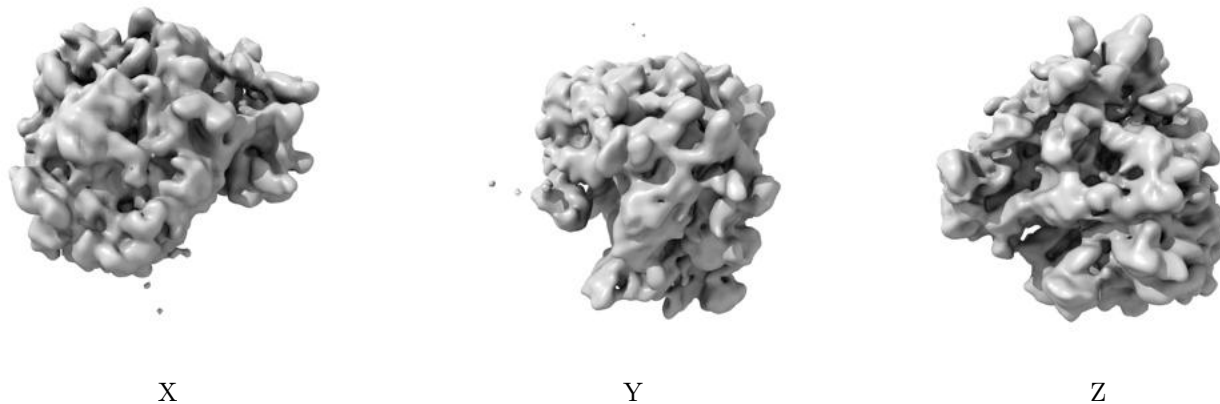


Z

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 0.00055. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

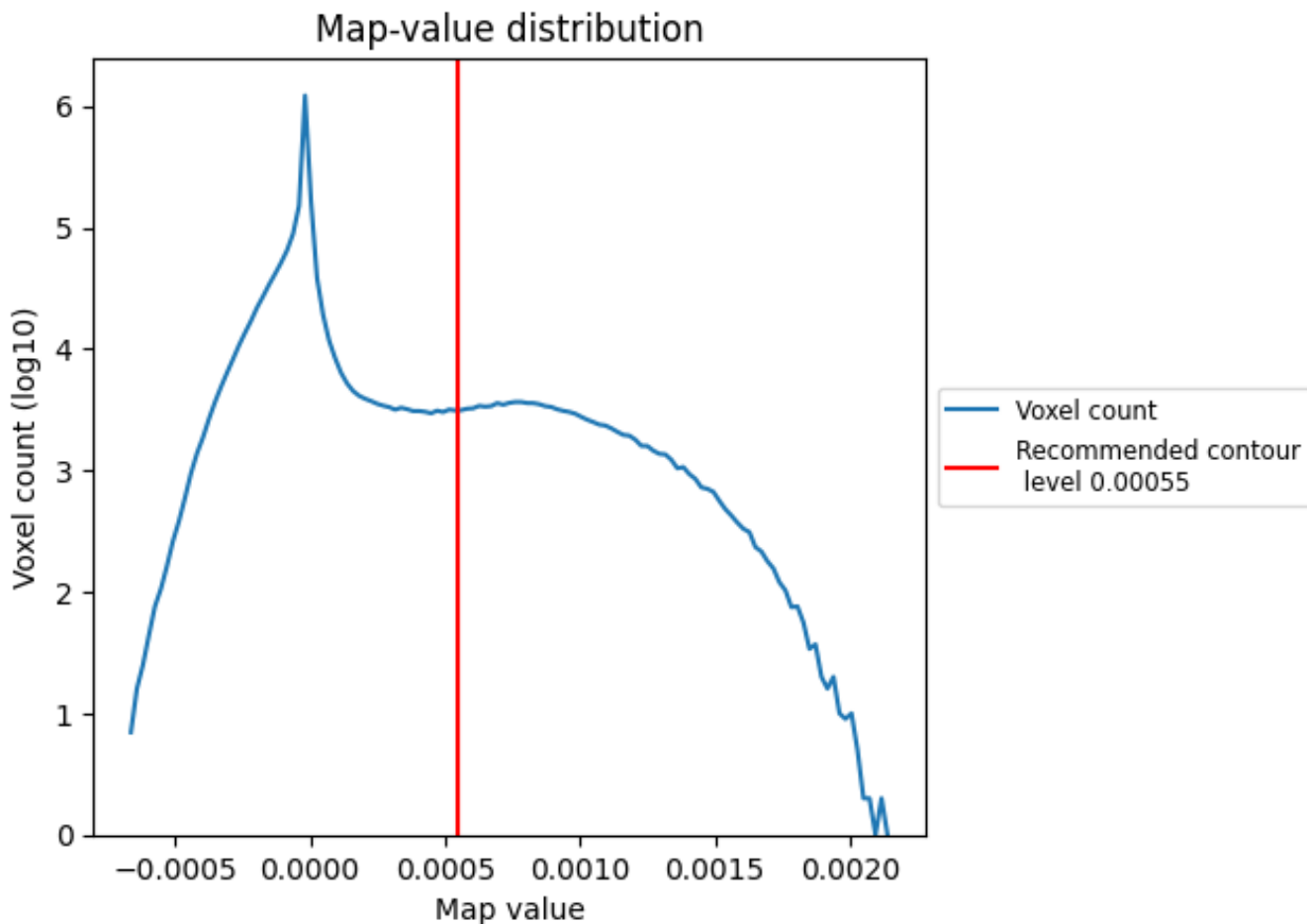
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

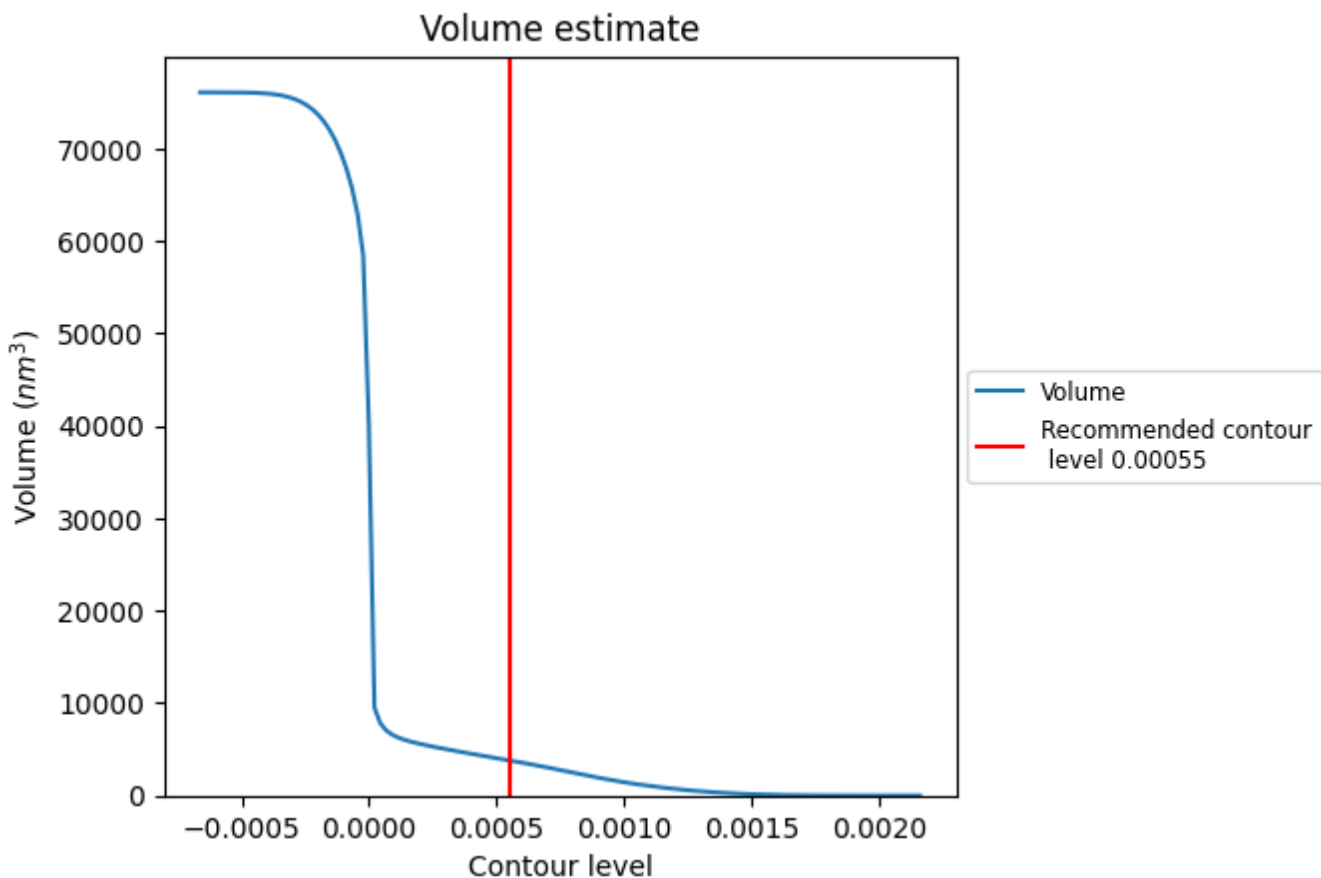
This section contains the results of statistical analysis of the map.

### 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.

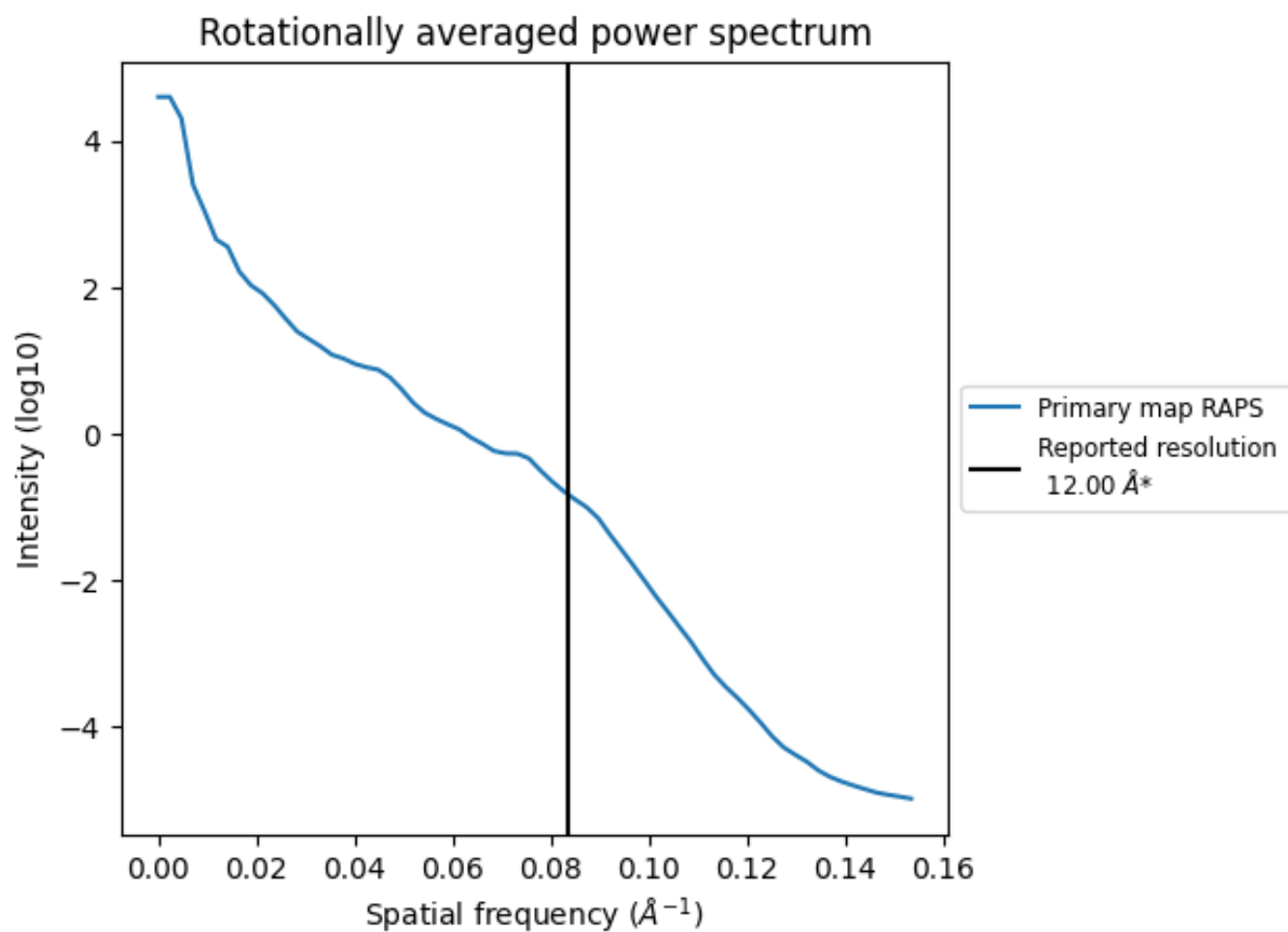
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 3809 nm<sup>3</sup>; this corresponds to an approximate mass of 3440 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 0.083 Å<sup>-1</sup>

## 8 Fourier-Shell correlation

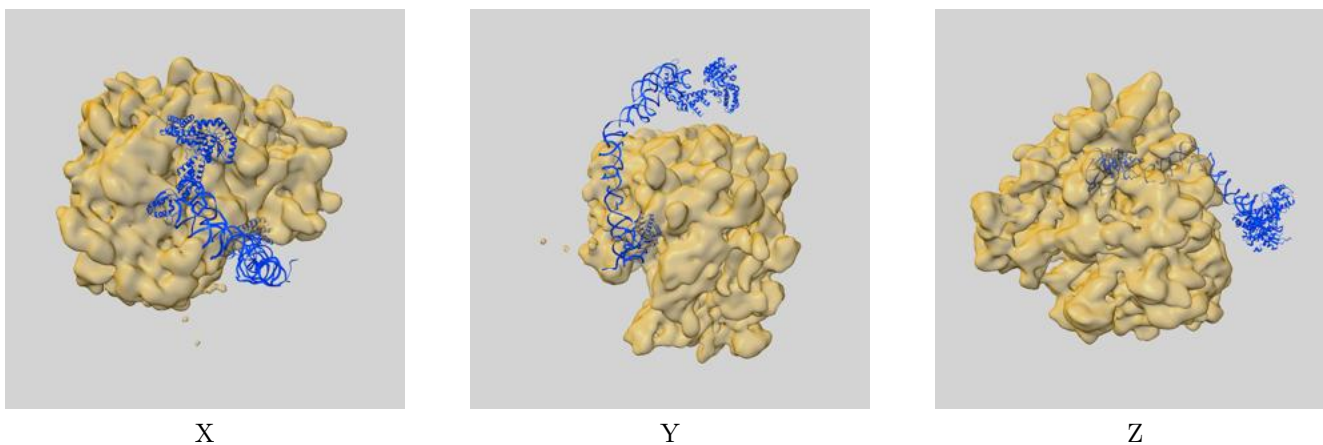
This section was not generated. No FSC curve or half-maps provided.



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

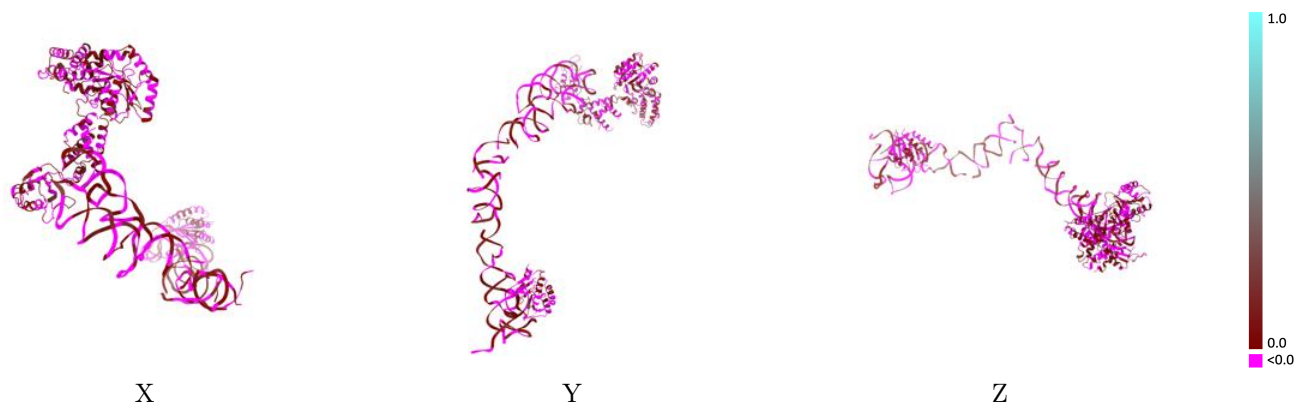
This section contains information regarding the fit between EMDB map EMD-1063 and PDB model 1RY1. Per-residue inclusion information can be found in section 3 on page 7.

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



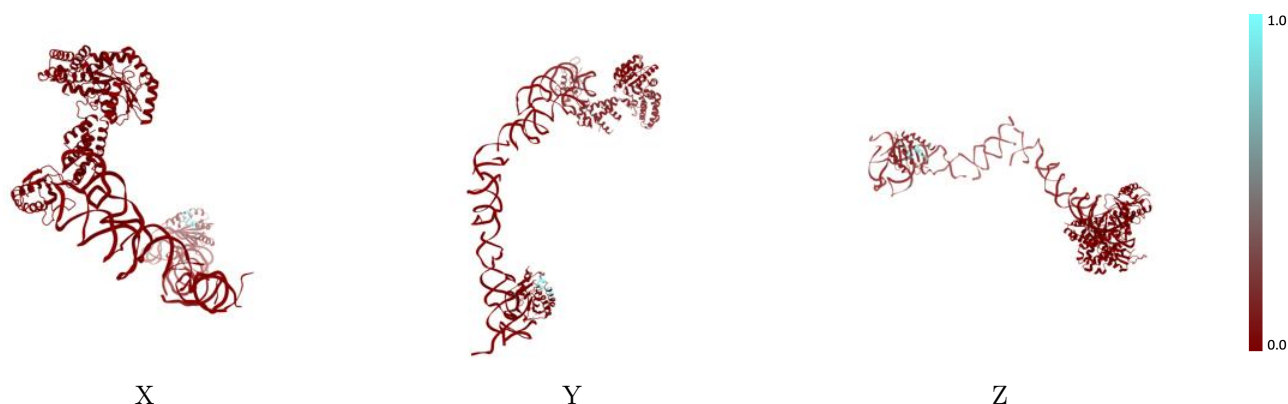
The images above show the 3D surface view of the map at the recommended contour level 0.00055 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



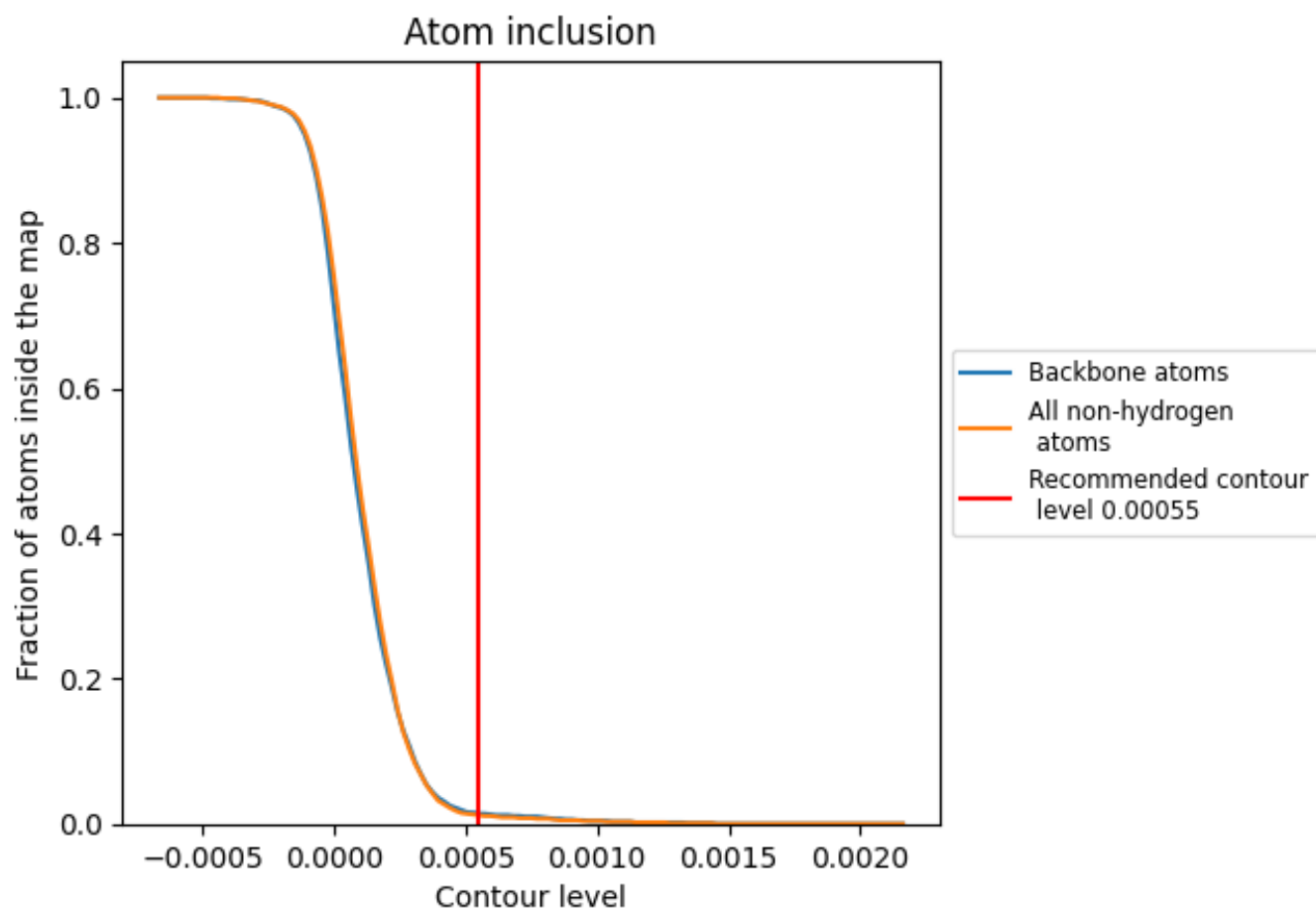
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00055).































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 2% of all backbone atoms, 1% 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 (0.00055) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.0120	 0.0080
A	 0.0000	 0.0050
B	 0.0000	 0.0140
C	 0.1360	 -0.0390
D	 0.0690	 -0.0040
E	 0.0230	 -0.0010
M	 0.0000	 0.0300
N	 0.0000	 0.0490
O	 0.0000	 0.0520
P	 0.0000	 0.0240
Q	 0.0000	 0.0130
R	 0.0000	 0.0060
S	 0.0000	 -0.1010
U	 0.0000	 -0.0010
W	 0.0000	 0.0310

