



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 10:33 AM UTC

PDB ID : 7EGQ / pdb_00007egq
EMDB ID : EMD-31138
Title : Co-transcriptional capping machineries in SARS-CoV-2 RTC: Coupling of N7-methyltransferase and 3'-5' exoribonuclease with polymerase reveals mechanisms for capping and proofreading
Authors : Yan, L.M.; Yang, Y.X.; Li, M.Y.; Zhang, Y.; Zheng, L.T.; Ge, J.; Huang, Y.C.; Liu, Z.Y.; Wang, T.; Gao, S.; Zhang, R.; Huang, Y.Y.; Guddat, L.W.; Gao, Y.; Rao, Z.H.; Lou, Z.Y.
Deposited on : 2021-03-25
Resolution : 3.35 Å(reported)

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

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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:

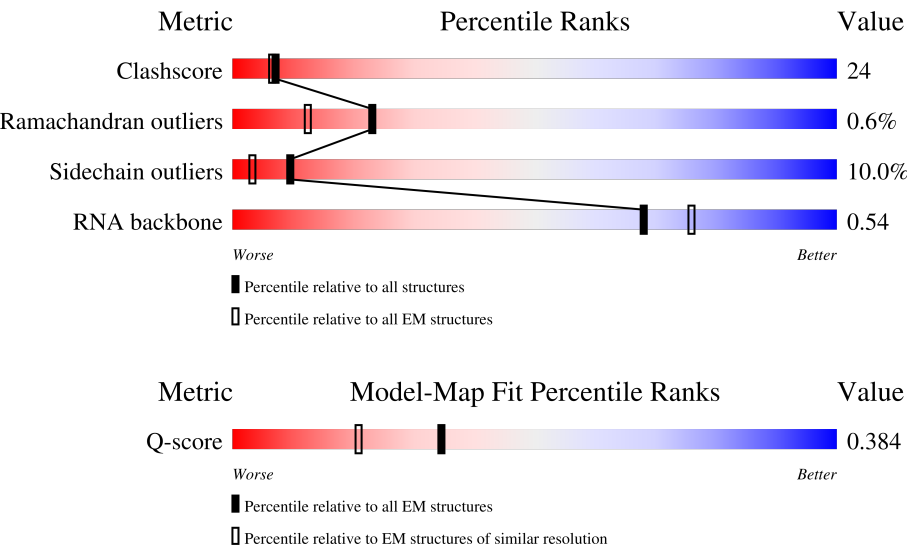
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.35 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	14390 (2.85 - 3.85)

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	932	62%28%8% ..
1	N	932	61%29%8% ..
2	B	198	10% 55%35% . . 6%

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Mol	Chain	Length	Quality of chain
2	D	198	
2	O	198	
2	Q	198	
3	C	83	
3	P	83	
4	E	601	
4	F	601	
4	R	601	
4	S	601	
5	G	117	
5	T	117	
6	H	139	
6	U	139	
7	K	527	
7	X	527	
8	I	25	
8	L	25	
9	J	33	
9	M	33	

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	ZN	X	600	-	-	X	-

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 54547 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 RNA-directed RNA polymerase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	926	Total	C	N	O	S	0	0
			7462	4766	1252	1390	54		
1	N	926	Total	C	N	O	S	0	0
			7462	4766	1252	1390	54		

- Molecule 2 is a protein called Non-structural protein 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	187	Total	C	N	O	S	0	0
			1400	873	241	275	11		
2	D	186	Total	C	N	O	S	0	0
			1418	892	243	272	11		
2	O	187	Total	C	N	O	S	0	0
			1400	873	241	275	11		
2	Q	186	Total	C	N	O	S	0	0
			1418	892	243	272	11		

- Molecule 3 is a protein called Non-structural protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	72	Total	C	N	O	S	0	0
			553	349	91	107	6		
3	P	72	Total	C	N	O	S	0	0
			553	349	91	107	6		

- Molecule 4 is a protein called Helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	588	Total	C	N	O	S	1	0
			4567	2908	767	857	35		
4	R	588	Total	C	N	O	S	1	0
			4567	2908	767	857	35		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	596	Total	C	N	O	S	0	0
			4630	2940	787	869	34		
4	S	596	Total	C	N	O	S	0	0
			4630	2940	787	869	34		

- Molecule 5 is a protein called Non-structural protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	113	Total	C	N	O	S	0	0
			868	549	150	164	5		
5	T	113	Total	C	N	O	S	0	0
			868	549	150	164	5		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	-3	SER	-	expression tag	UNP P0DTD1
G	-2	ASN	-	expression tag	UNP P0DTD1
G	-1	ALA	-	expression tag	UNP P0DTD1
G	0	MET	-	expression tag	UNP P0DTD1
T	-3	SER	-	expression tag	UNP P0DTD1
T	-2	ASN	-	expression tag	UNP P0DTD1
T	-1	ALA	-	expression tag	UNP P0DTD1
T	0	MET	-	expression tag	UNP P0DTD1

- Molecule 6 is a protein called Non-structural protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	H	131	Total	C	N	O	S	0	0
			955	593	160	186	16		
6	U	130	Total	C	N	O	S	0	0
			947	589	159	183	16		

- Molecule 7 is a protein called Proofreading exoribonuclease.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	K	523	Total	C	N	O	S	0	0
			4169	2674	710	749	36		
7	X	524	Total	C	N	O	S	0	0
			4177	2679	710	752	36		

- Molecule 8 is a RNA chain called primer RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	25	Total	C	N	O	P	0	0
			545	242	105	173	25		
8	L	25	Total	C	N	O	P	0	0
			545	242	105	173	25		

- Molecule 9 is a RNA chain called Template RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	33	Total	C	N	O	P	0	0
			692	310	116	233	33		
9	M	33	Total	C	N	O	P	0	0
			692	310	116	233	33		

- Molecule 10 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
10	A	2	Total	Zn	0
			2	2	
10	E	3	Total	Zn	0
			3	3	
10	H	2	Total	Zn	0
			2	2	
10	K	3	Total	Zn	0
			3	3	
10	N	2	Total	Zn	0
			2	2	
10	R	3	Total	Zn	0
			3	3	
10	U	2	Total	Zn	0
			2	2	
10	X	3	Total	Zn	0
			3	3	
10	F	3	Total	Zn	0
			3	3	
10	S	3	Total	Zn	0
			3	3	

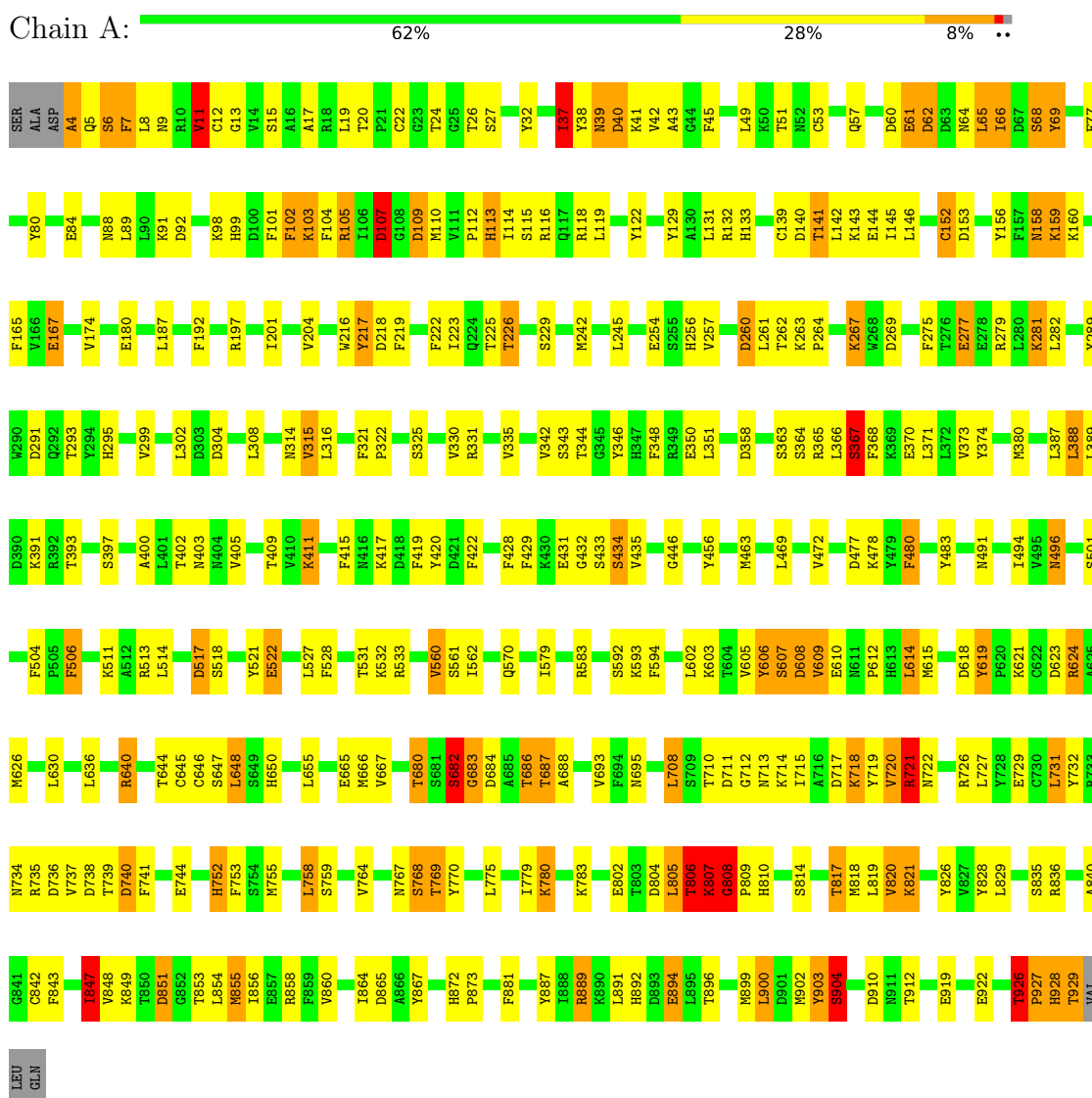
- Molecule 11 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
11	K	2	Total 2	Mg 2	0
11	X	1	Total 1	Mg 1	0

3 Residue-property plots

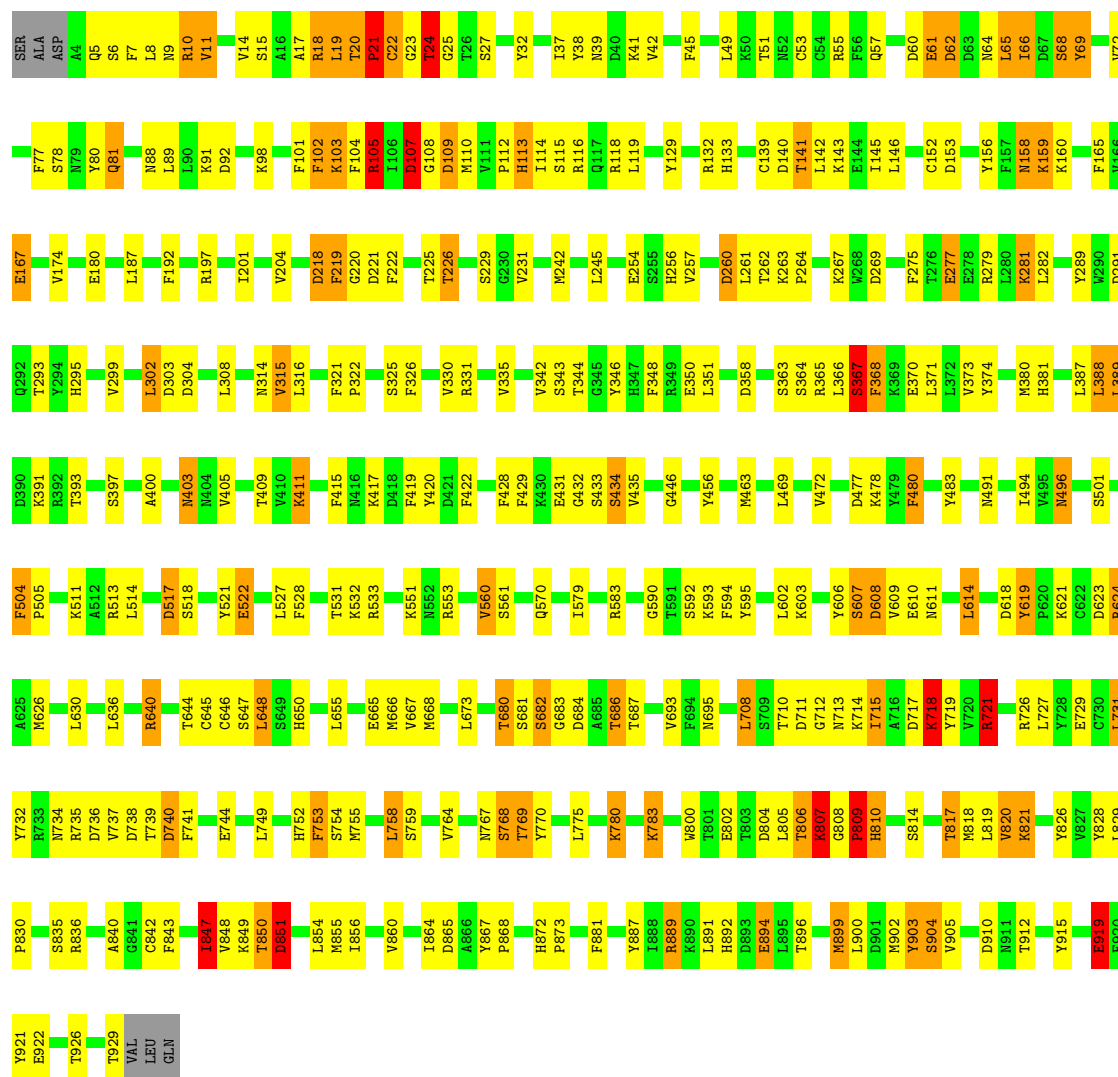
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: RNA-directed RNA polymerase

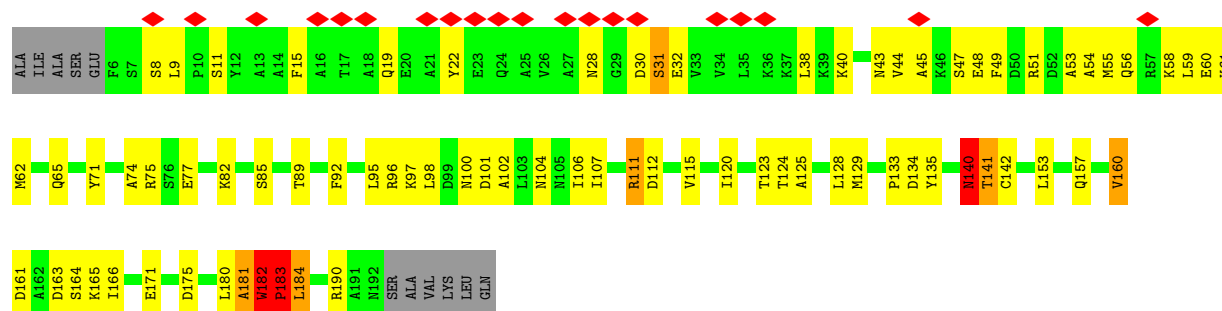


• Molecule 1: RNA-directed RNA polymerase



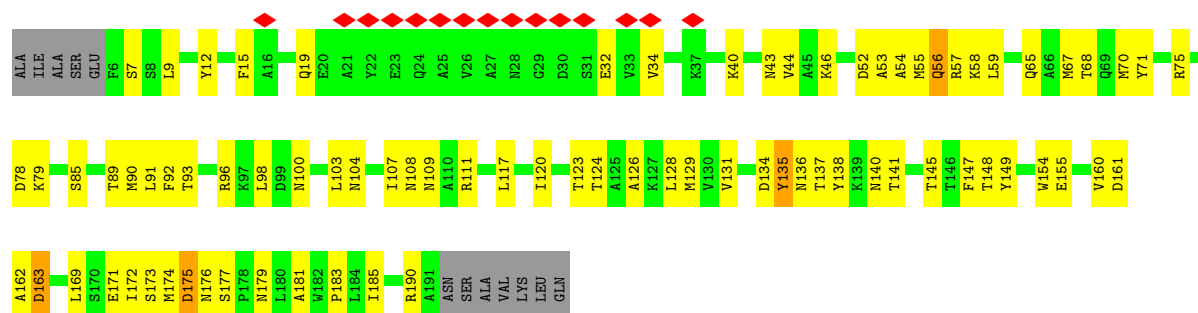


• Molecule 2: Non-structural protein 8

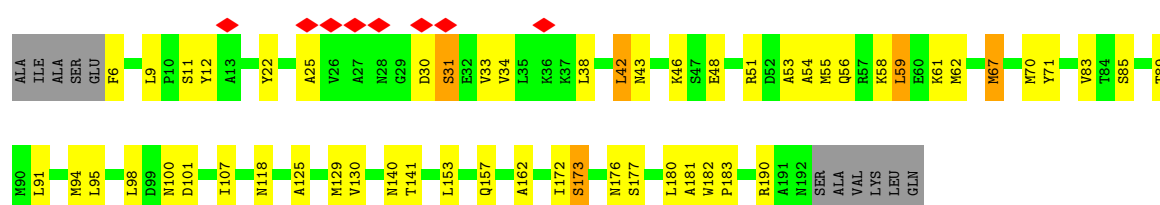


• Molecule 2: Non-structural protein 8

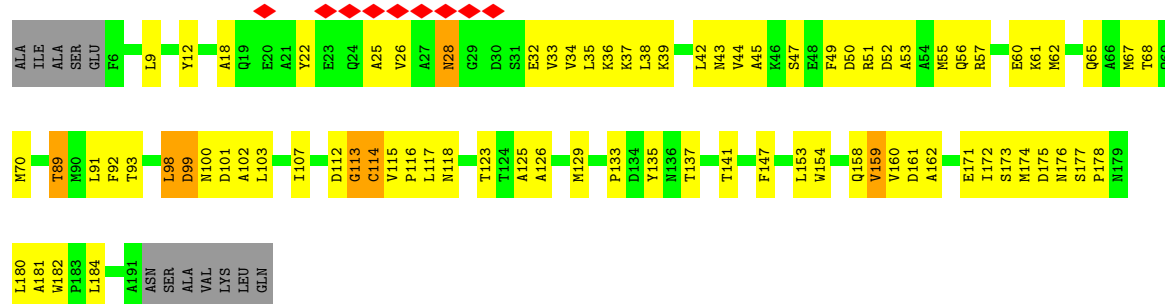




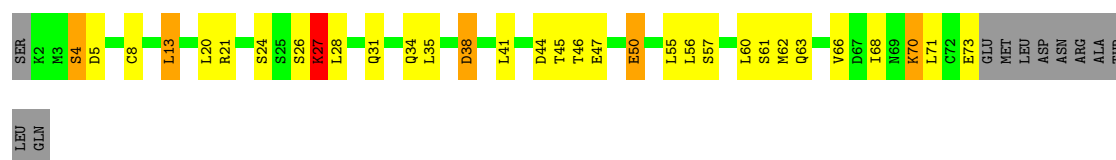
- Molecule 2: Non-structural protein 8



- Molecule 2: Non-structural protein 8



- Molecule 3: Non-structural protein 7



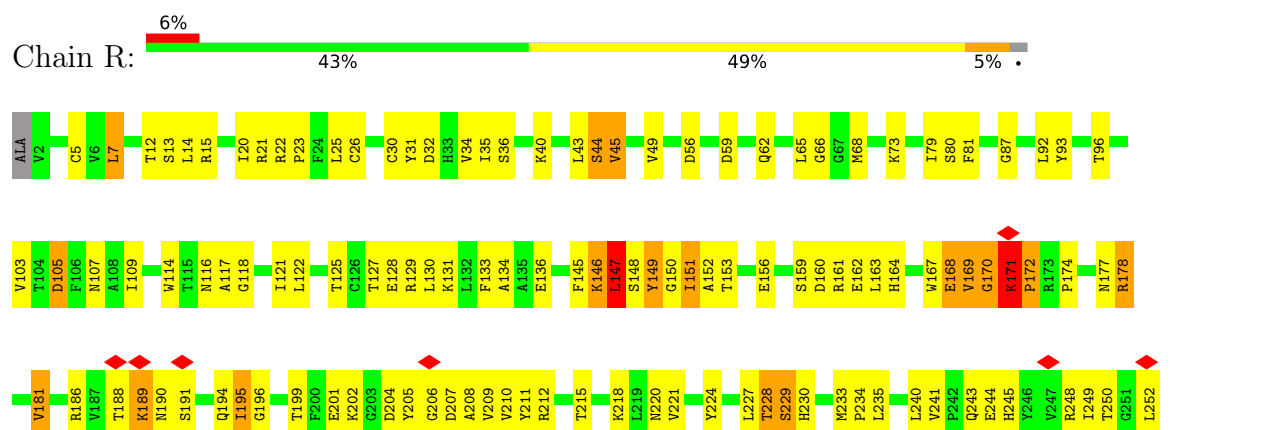
- Molecule 3: Non-structural protein 7

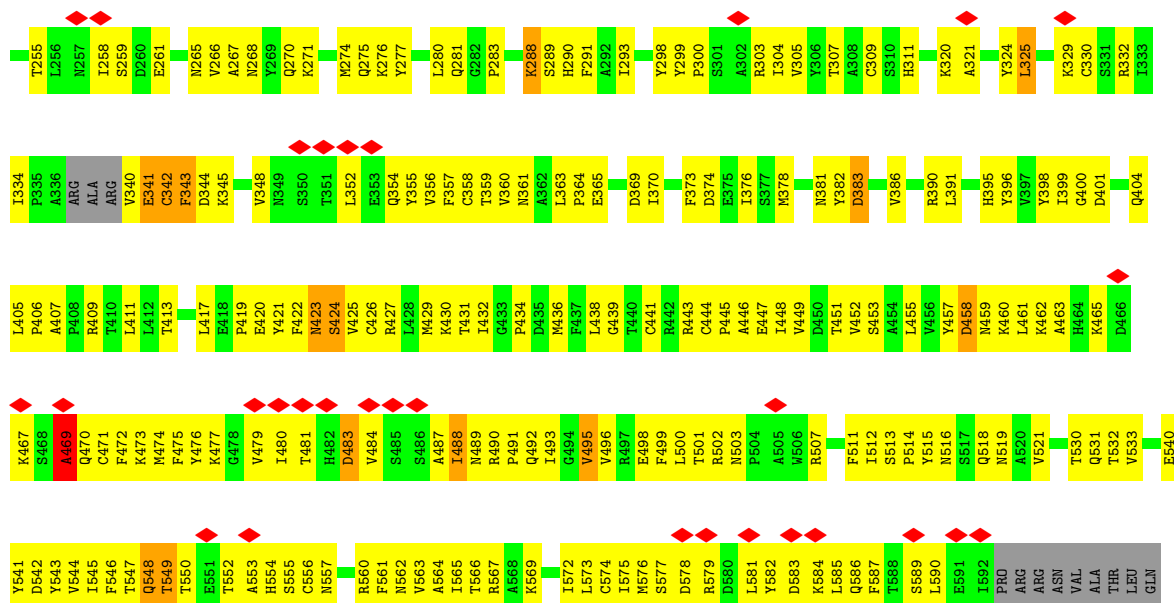


● Molecule 4: Helicase

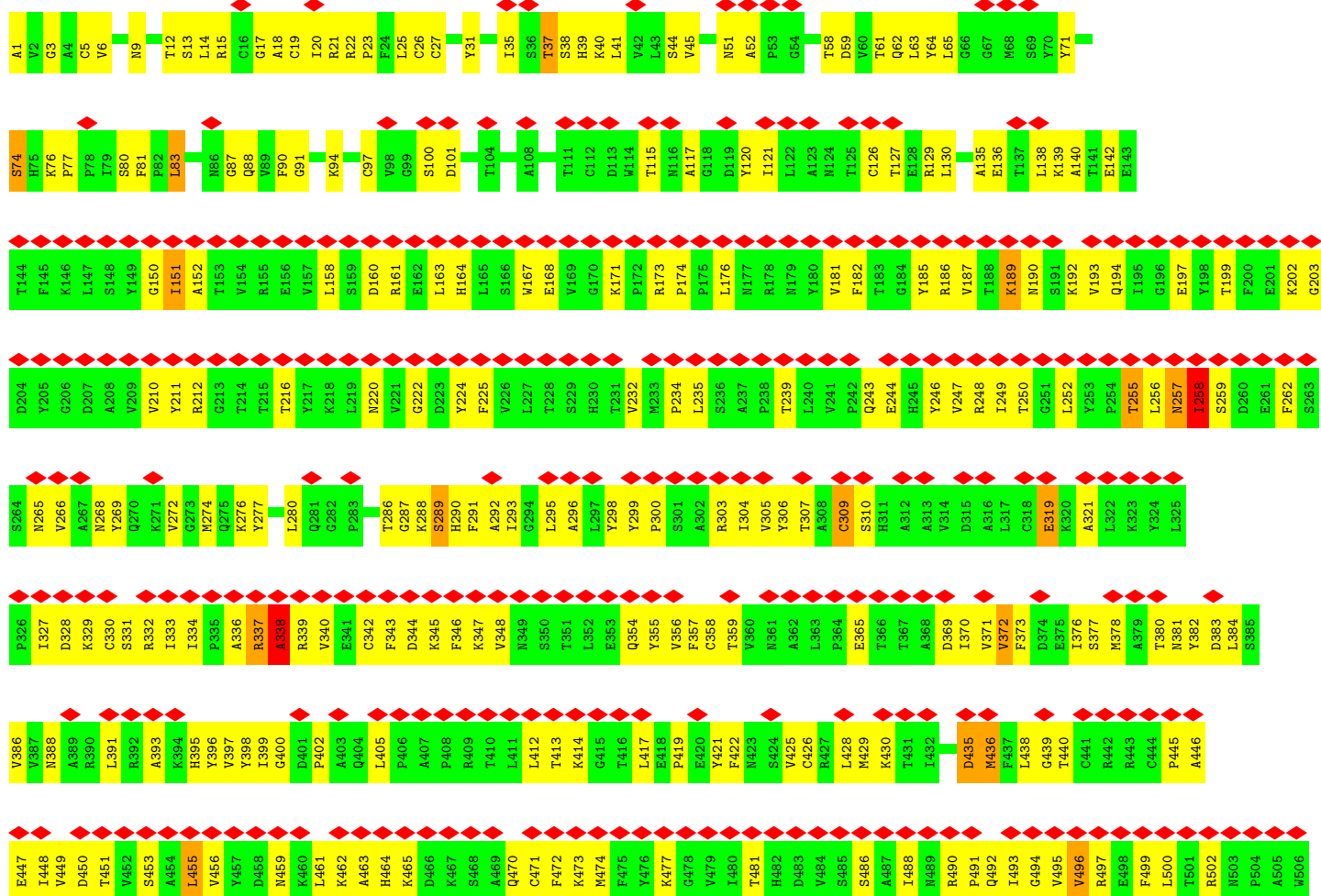


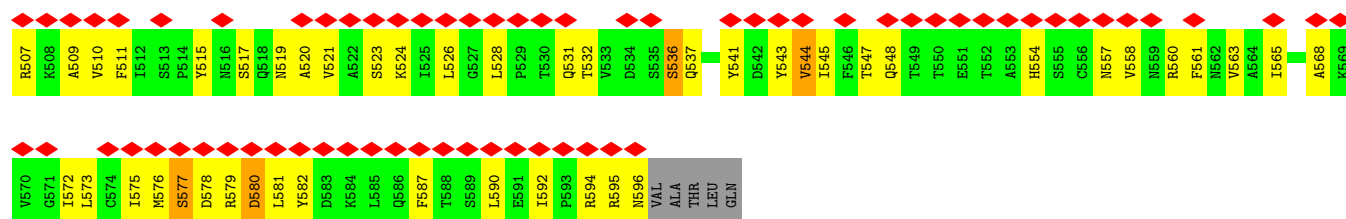
● Molecule 4: Helicase



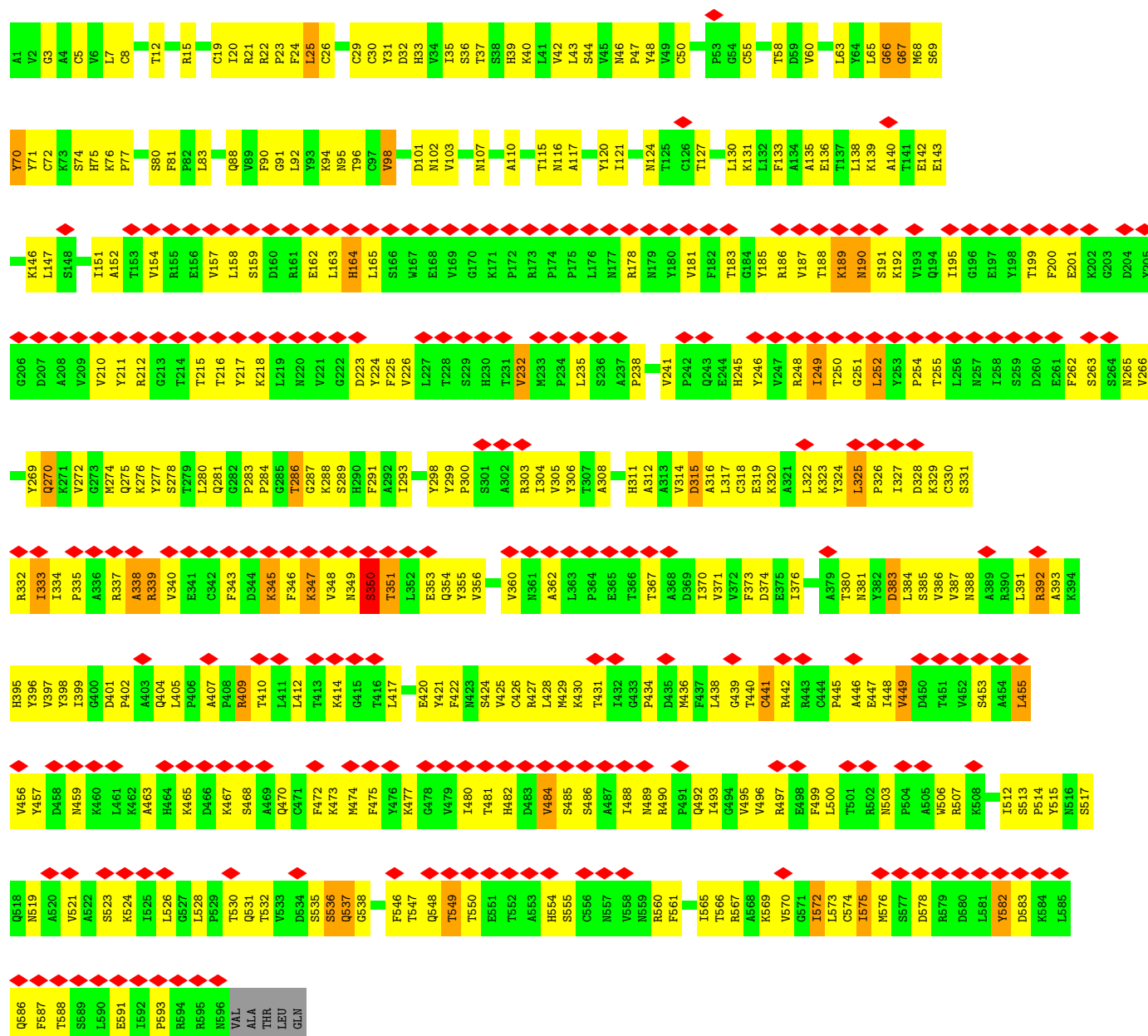
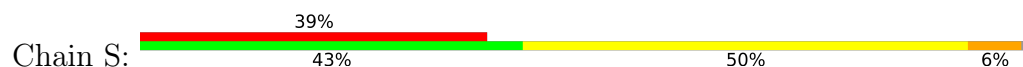


• Molecule 4: Helicase



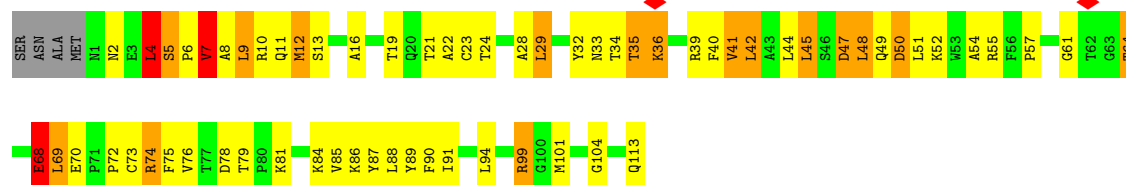


• Molecule 4: Helicase



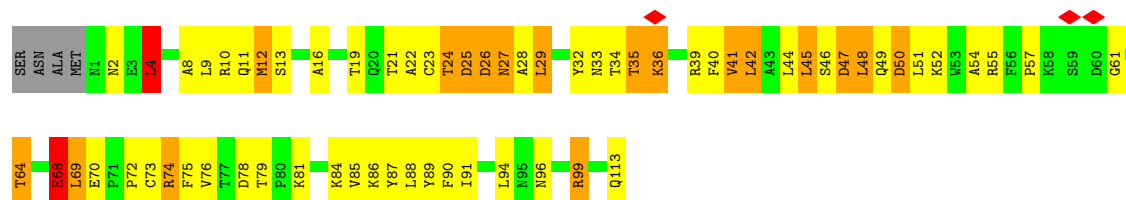
• Molecule 5: Non-structural protein 9

Chain G: 



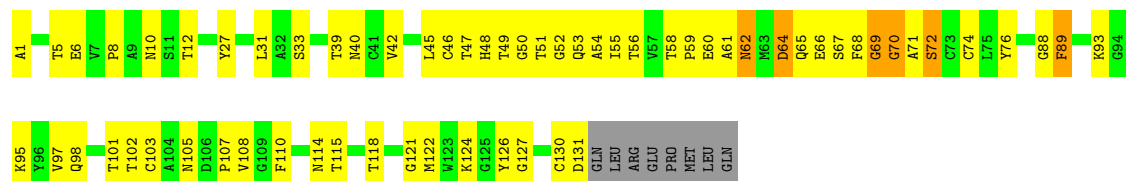
- Molecule 5: Non-structural protein 9

Chain T: 



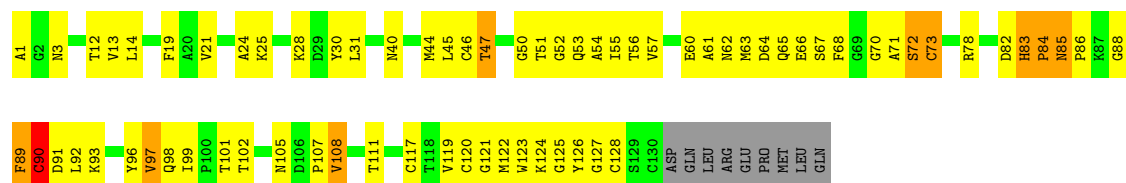
- Molecule 6: Non-structural protein 10

Chain H: 



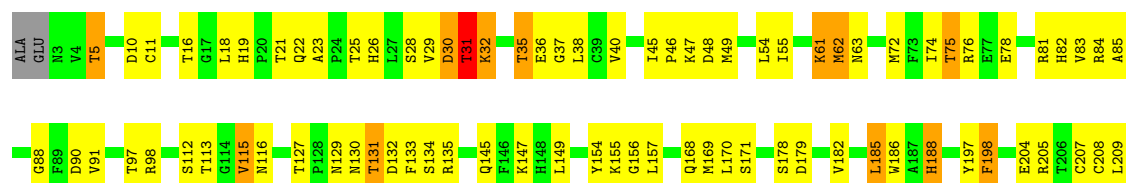
- Molecule 6: Non-structural protein 10

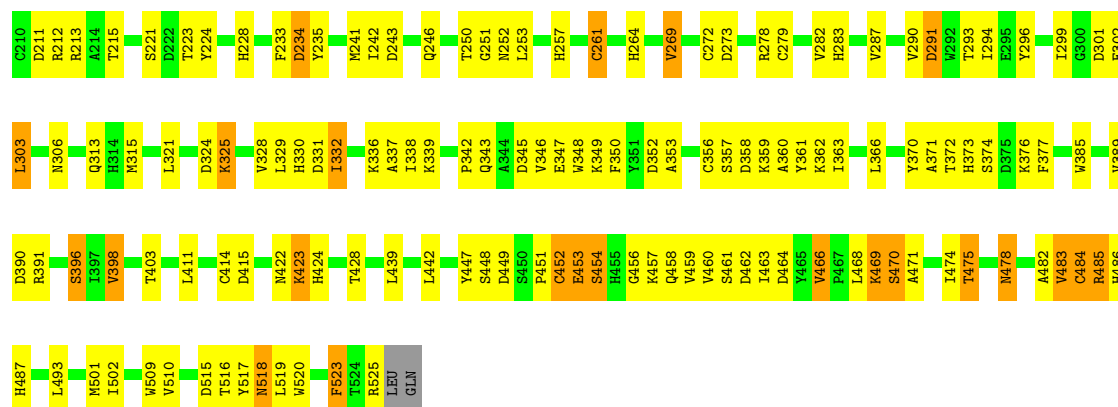
Chain U: 



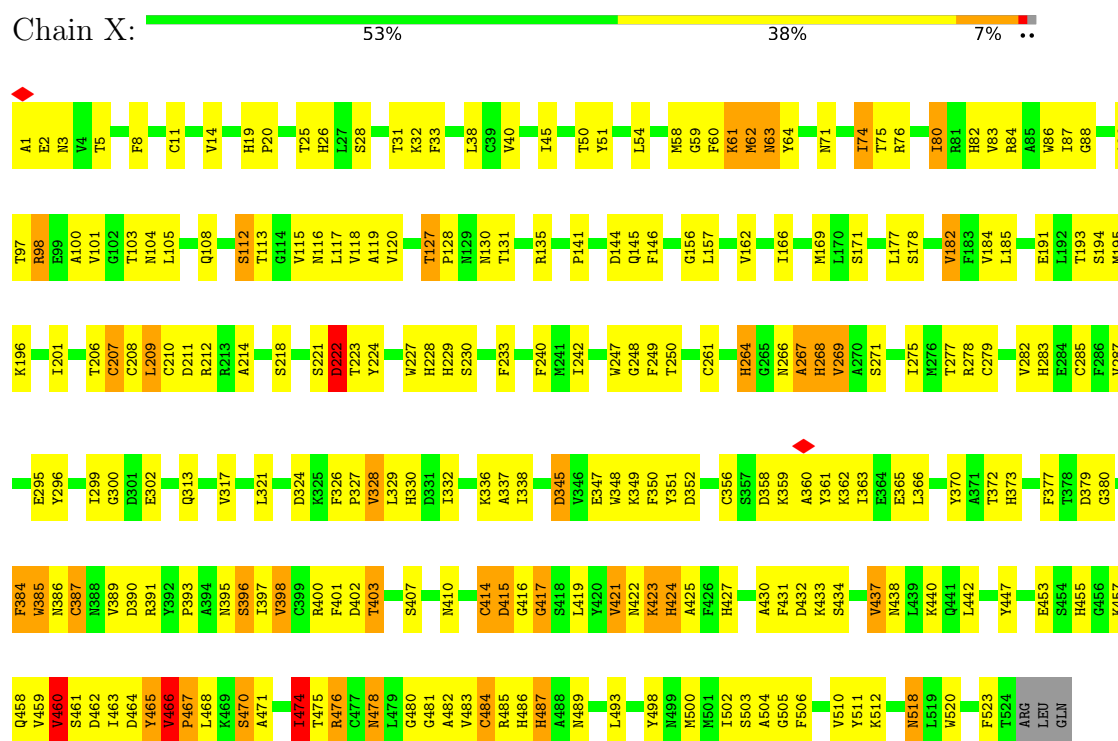
- Molecule 7: Proofreading exoribonuclease

Chain K: 





• Molecule 7: Proofreading exoribonuclease



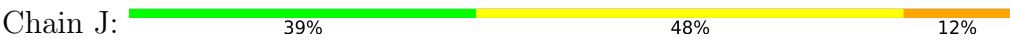
• Molecule 8: primer RNA



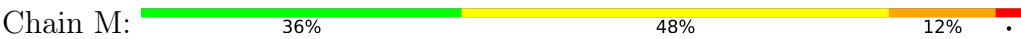
• Molecule 8: primer RNA



● Molecule 9: Template RNA



● Molecule 9: Template RNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	135801	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	2.438	Depositor
Minimum map value	-0.945	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.058	Depositor
Recommended contour level	0.25	Depositor
Map size (Å)	474.87997, 474.87997, 474.87997	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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

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	0.61	14/7651 (0.2%)	1.19	79/10383 (0.8%)
1	N	0.51	2/7651 (0.0%)	1.00	56/10383 (0.5%)
2	B	0.43	1/1418 (0.1%)	1.16	18/1927 (0.9%)
2	D	0.23	0/1437	0.72	5/1948 (0.3%)
2	O	0.36	0/1418	0.82	10/1927 (0.5%)
2	Q	0.26	0/1437	1.15	14/1948 (0.7%)
3	C	0.35	0/556	0.73	3/749 (0.4%)
3	P	0.35	0/556	0.92	3/749 (0.4%)
4	E	0.21	0/4670	0.66	15/6358 (0.2%)
4	F	0.19	0/4734	0.97	35/6443 (0.5%)
4	R	0.21	0/4670	0.97	32/6358 (0.5%)
4	S	0.19	0/4734	0.95	29/6443 (0.5%)
5	G	0.41	0/884	0.84	6/1200 (0.5%)
5	T	0.35	0/884	1.58	9/1200 (0.8%)
6	H	0.32	0/976	1.11	5/1327 (0.4%)
6	U	0.48	1/968 (0.1%)	1.18	15/1316 (1.1%)
7	K	0.39	1/4288 (0.0%)	0.96	38/5831 (0.7%)
7	X	0.39	1/4297 (0.0%)	1.16	54/5844 (0.9%)
8	I	0.42	0/611	0.34	0/953
8	L	0.42	0/611	0.34	0/953
9	J	0.56	1/770 (0.1%)	0.55	1/1195 (0.1%)
9	M	0.71	5/770 (0.6%)	0.59	2/1195 (0.2%)
All	All	0.40	26/55991 (0.0%)	0.99	429/76630 (0.6%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	O	0	1
4	E	0	1
4	R	0	2
All	All	0	5

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	810	HIS	CA-C	-8.60	1.41	1.53
1	A	810	HIS	N-CA	-7.69	1.36	1.46
1	A	607	SER	CA-C	-7.60	1.42	1.53
9	M	21	G	C1'-N9	-6.95	1.37	1.48
1	A	810	HIS	C-O	-6.94	1.15	1.23

The worst 5 of 429 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	T	25	ASP	N-CA-C	42.65	157.46	110.97
4	R	170	GLY	N-CA-C	38.00	158.62	112.64
7	X	208	CYS	N-CA-C	34.16	152.10	111.11
1	A	217	TYR	N-CA-C	32.75	154.65	114.04
4	S	536	SER	N-CA-C	28.41	148.46	113.23

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	926	THR	Peptide
4	E	230	HIS	Peptide
2	O	182	TRP	Peptide
4	R	147	LEU	Peptide
4	R	171	LYS	Peptide

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	7462	0	7201	278	0
1	N	7462	0	7202	287	0
2	B	1400	0	1372	67	0
2	D	1418	0	1427	52	0
2	O	1400	0	1372	31	0
2	Q	1418	0	1427	63	0
3	C	553	0	585	28	0
3	P	553	0	585	21	0
4	E	4567	0	4508	314	0
4	F	4630	0	4584	258	0
4	R	4567	0	4508	297	0
4	S	4630	0	4584	257	0
5	G	868	0	880	64	0
5	T	868	0	880	60	0
6	H	955	0	910	41	0
6	U	947	0	906	59	0
7	K	4169	0	4051	144	0
7	X	4177	0	4058	186	0
8	I	545	0	272	22	0
8	L	545	0	272	19	0
9	J	692	0	355	37	0
9	M	692	0	355	57	0
10	A	2	0	0	0	0
10	E	3	0	0	0	0
10	F	3	0	0	0	0
10	H	2	0	0	0	0
10	K	3	0	0	0	0
10	N	2	0	0	0	0
10	R	3	0	0	0	0
10	S	3	0	0	0	0
10	U	2	0	0	0	0
10	X	3	0	0	2	0
11	K	2	0	0	0	0
11	X	1	0	0	0	0
All	All	54547	0	52294	2528	0

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

The worst 5 of 2528 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:PHE:HZ	1:A:113:HIS:CD2	1.45	1.32
9:M:22:U:H2'	9:M:23:C:N3	1.46	1.28
4:F:337:ARG:O	4:F:337:ARG:HD3	1.24	1.28
6:U:70:GLY:HA3	6:U:92:LEU:O	1.28	1.28
9:M:22:U:H2'	9:M:23:C:C2	1.68	1.26

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	924/932 (99%)	825 (89%)	97 (10%)	2 (0%)	43	70
1	N	924/932 (99%)	831 (90%)	88 (10%)	5 (0%)	24	52
2	B	185/198 (93%)	175 (95%)	7 (4%)	3 (2%)	7	28
2	D	184/198 (93%)	172 (94%)	11 (6%)	1 (0%)	24	52
2	O	185/198 (93%)	172 (93%)	10 (5%)	3 (2%)	7	28
2	Q	184/198 (93%)	171 (93%)	13 (7%)	0	100	100
3	C	70/83 (84%)	69 (99%)	1 (1%)	0	100	100
3	P	70/83 (84%)	69 (99%)	1 (1%)	0	100	100
4	E	585/601 (97%)	530 (91%)	55 (9%)	0	100	100
4	F	594/601 (99%)	515 (87%)	77 (13%)	2 (0%)	36	63
4	R	585/601 (97%)	530 (91%)	52 (9%)	3 (0%)	24	52
4	S	594/601 (99%)	516 (87%)	73 (12%)	5 (1%)	16	44
5	G	111/117 (95%)	97 (87%)	12 (11%)	2 (2%)	6	26
5	T	111/117 (95%)	100 (90%)	11 (10%)	0	100	100
6	H	129/139 (93%)	113 (88%)	15 (12%)	1 (1%)	16	44
6	U	128/139 (92%)	111 (87%)	17 (13%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	K	521/527 (99%)	445 (85%)	70 (13%)	6 (1%)	10	33
7	X	522/527 (99%)	434 (83%)	83 (16%)	5 (1%)	12	38
All	All	6606/6792 (97%)	5875 (89%)	693 (10%)	38 (1%)	23	49

5 of 38 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	181	ALA
7	K	454	SER
7	K	485	ARG
1	N	850	THR
2	O	183	PRO

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	818/823 (99%)	696 (85%)	122 (15%)	3	12
1	N	818/823 (99%)	690 (84%)	128 (16%)	2	10
2	B	146/167 (87%)	138 (94%)	8 (6%)	19	47
2	D	150/167 (90%)	142 (95%)	8 (5%)	20	48
2	O	146/167 (87%)	134 (92%)	12 (8%)	10	35
2	Q	150/167 (90%)	141 (94%)	9 (6%)	17	44
3	C	67/77 (87%)	51 (76%)	16 (24%)	1	2
3	P	67/77 (87%)	51 (76%)	16 (24%)	1	2
4	E	507/523 (97%)	496 (98%)	11 (2%)	45	63
4	F	514/523 (98%)	494 (96%)	20 (4%)	28	54
4	R	507/523 (97%)	490 (97%)	17 (3%)	32	58
4	S	514/523 (98%)	474 (92%)	40 (8%)	11	37
5	G	94/97 (97%)	68 (72%)	26 (28%)	0	1
5	T	94/97 (97%)	72 (77%)	22 (23%)	1	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	H	105/113 (93%)	95 (90%)	10 (10%)	8	29
6	U	104/113 (92%)	92 (88%)	12 (12%)	5	20
7	K	458/462 (99%)	410 (90%)	48 (10%)	6	24
7	X	459/462 (99%)	413 (90%)	46 (10%)	7	26
All	All	5718/5904 (97%)	5147 (90%)	571 (10%)	9	26

5 of 571 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	U	108	VAL
7	X	127	THR
6	U	102	THR
4	F	255	THR
6	H	72	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 68 such sidechains are listed below:

Mol	Chain	Res	Type
4	F	33	HIS
4	F	220	ASN
4	S	107	ASN
7	K	65	GLN
6	H	80	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
8	I	24/25 (96%)	2 (8%)	1 (4%)
8	L	24/25 (96%)	2 (8%)	1 (4%)
9	J	32/33 (96%)	7 (21%)	0
9	M	32/33 (96%)	4 (12%)	2 (6%)
All	All	112/116 (96%)	15 (13%)	4 (3%)

5 of 15 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	I	15	G
8	I	23	C

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Mol	Chain	Res	Type
9	J	19	A
9	J	20	U
9	J	21	G

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	I	22	G
8	L	22	G
9	M	22	U
9	M	23	C

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

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 29 ligands modelled in this entry, 29 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

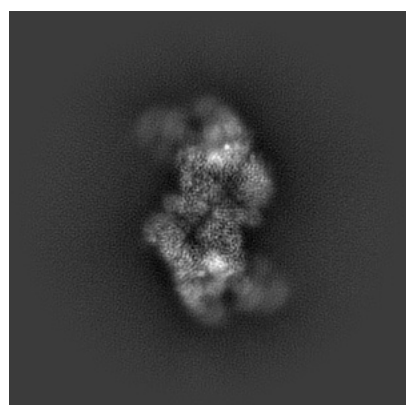
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31138. These allow visual inspection of the internal detail of the map and identification of artifacts.

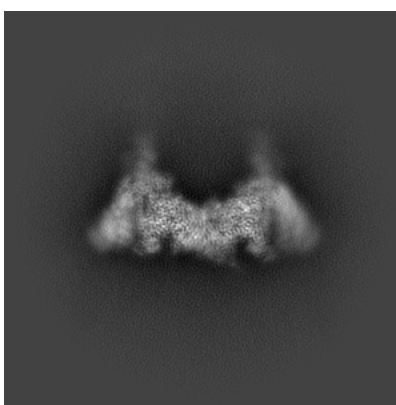
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

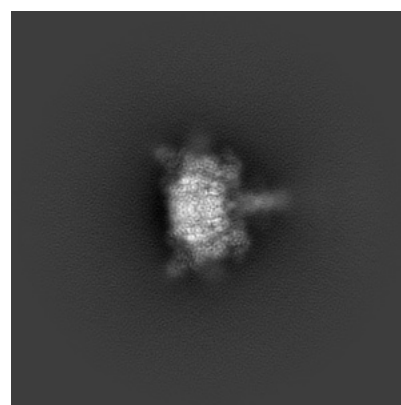
6.1.1 Primary map



X



Y

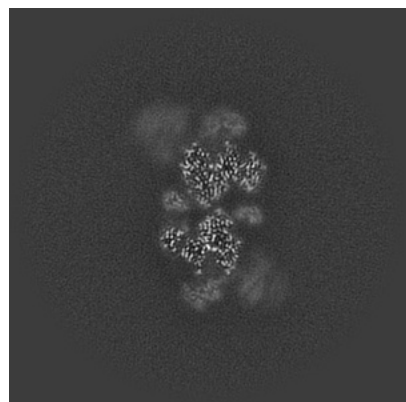


Z

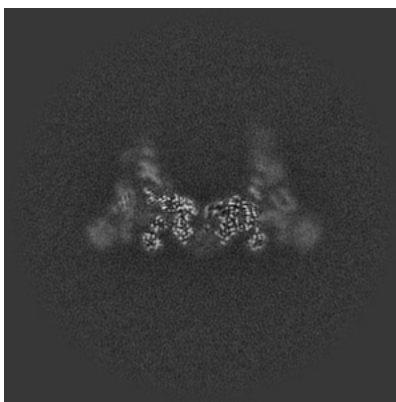
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

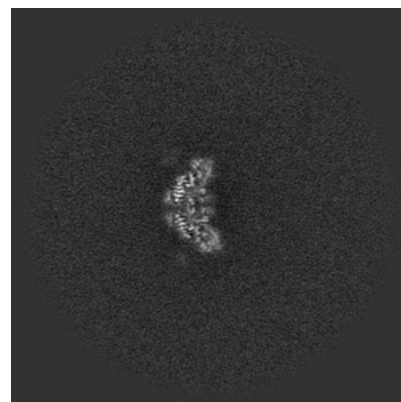
6.2.1 Primary map



X Index: 224



Y Index: 224

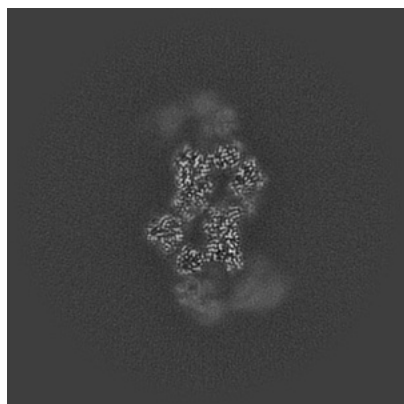


Z Index: 224

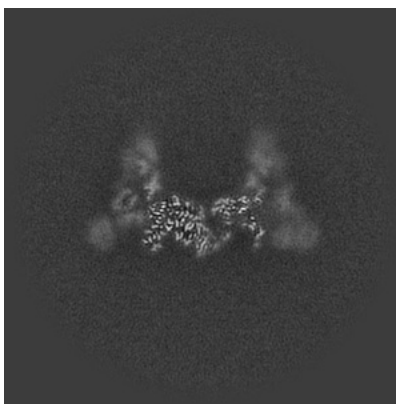
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

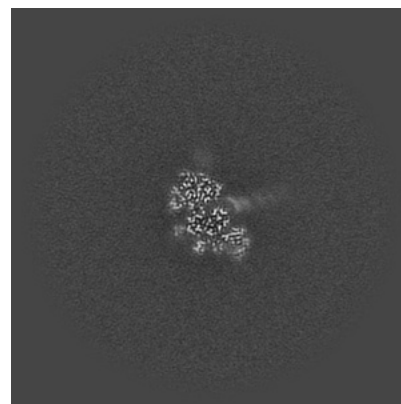
6.3.1 Primary map



X Index: 203



Y Index: 232

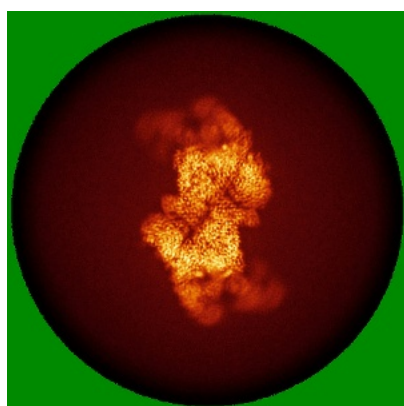


Z Index: 172

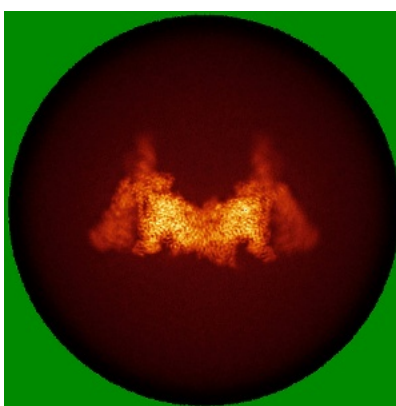
The images above show the largest variance slices of the map in three orthogonal directions.

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

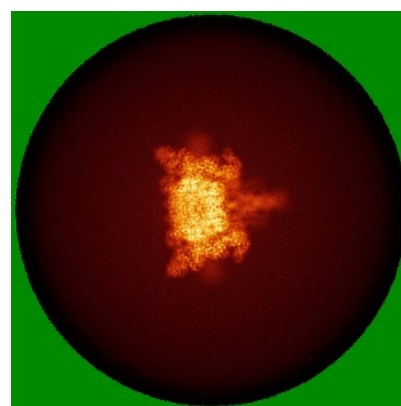
6.4.1 Primary map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.25. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

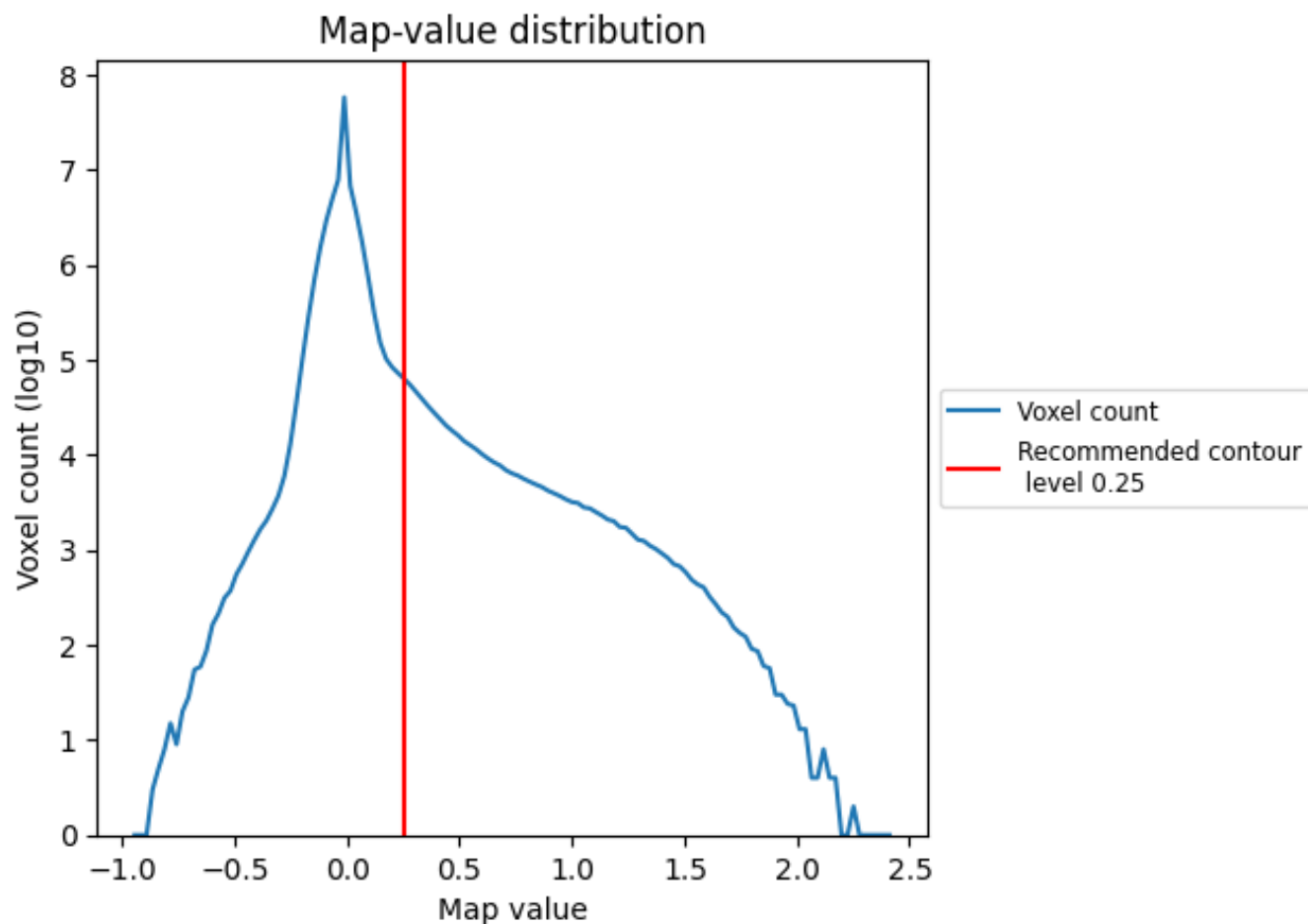
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

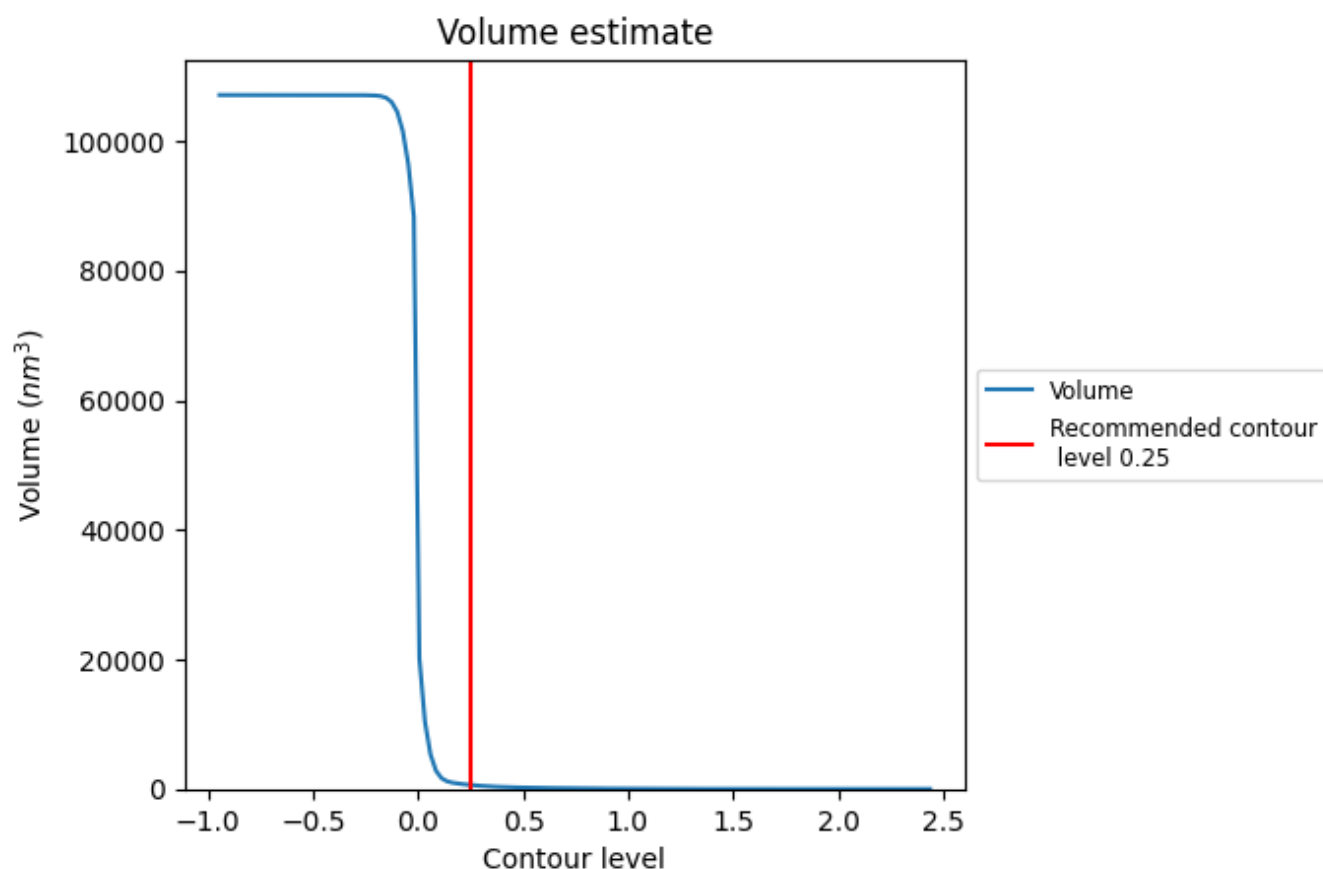
This section contains the results of statistical analysis of the map.

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.

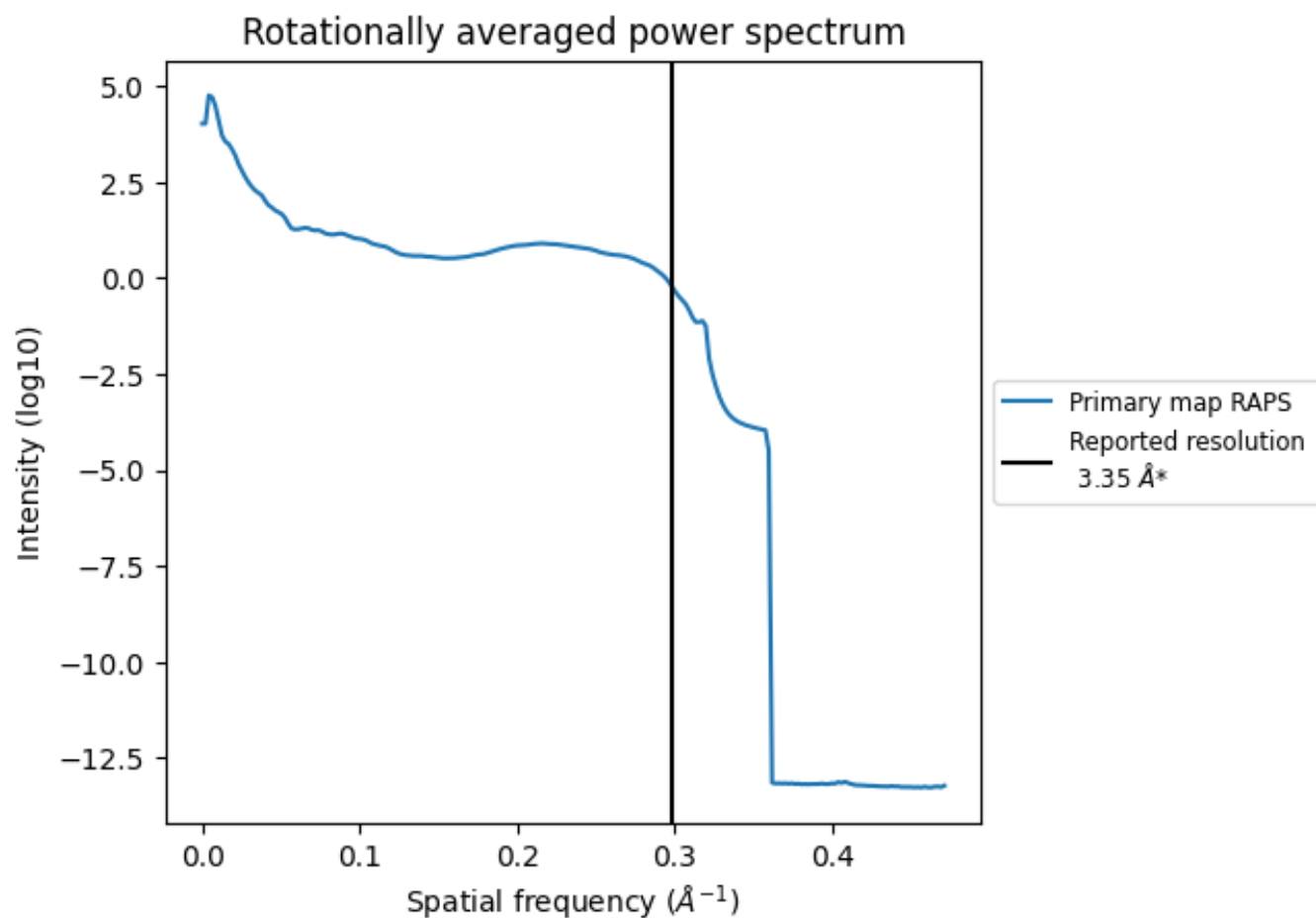
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 614 nm³; this corresponds to an approximate mass of 555 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 0.299 Å⁻¹

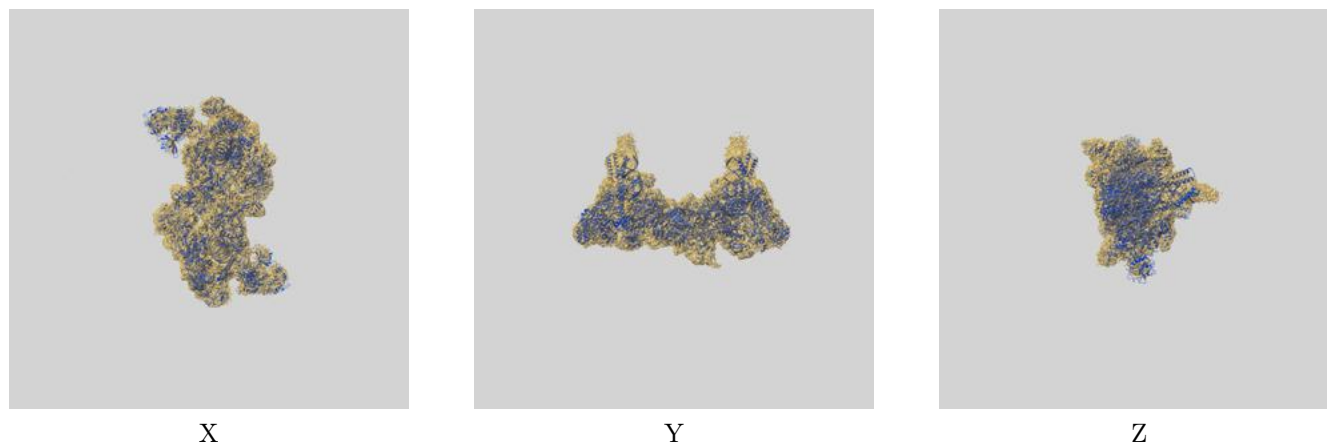
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

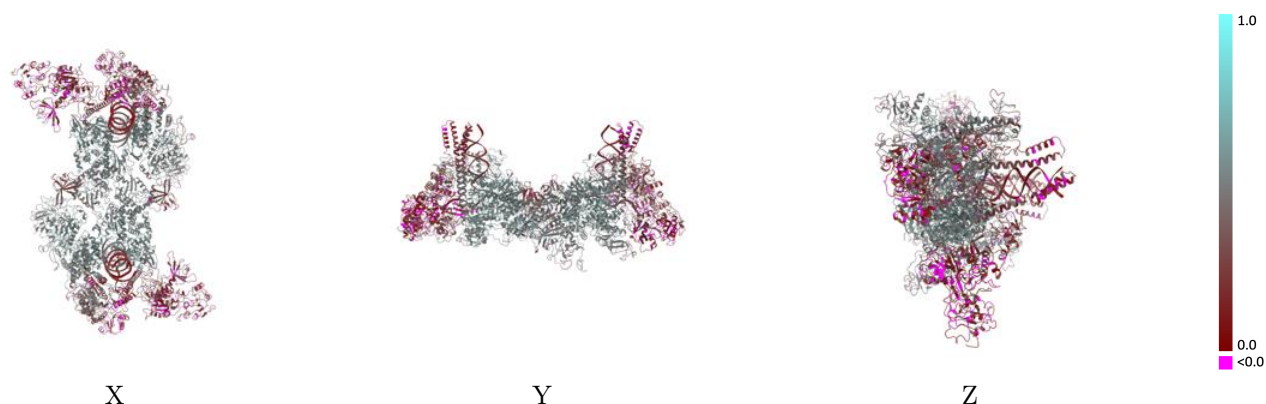
This section contains information regarding the fit between EMDB map EMD-31138 and PDB model 7EGQ. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

9.1 Map-model overlay [i](#)



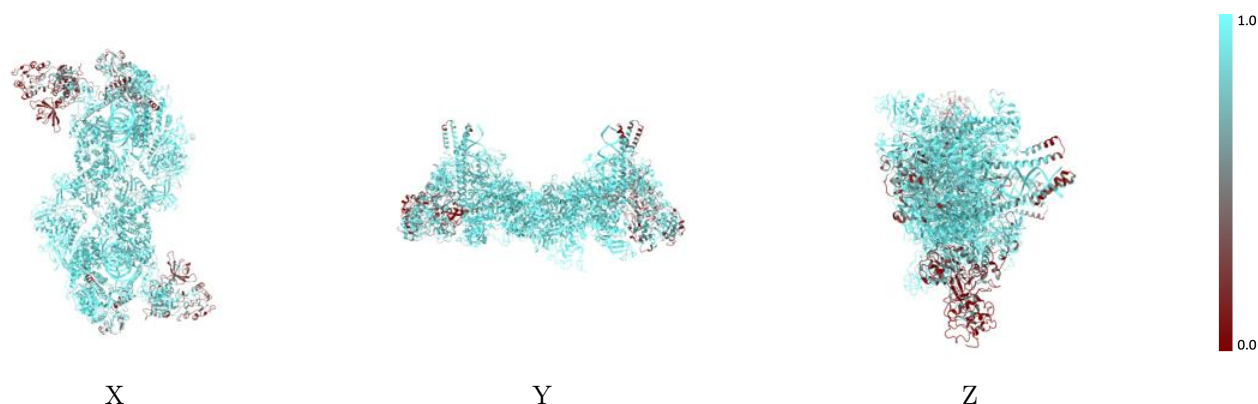
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



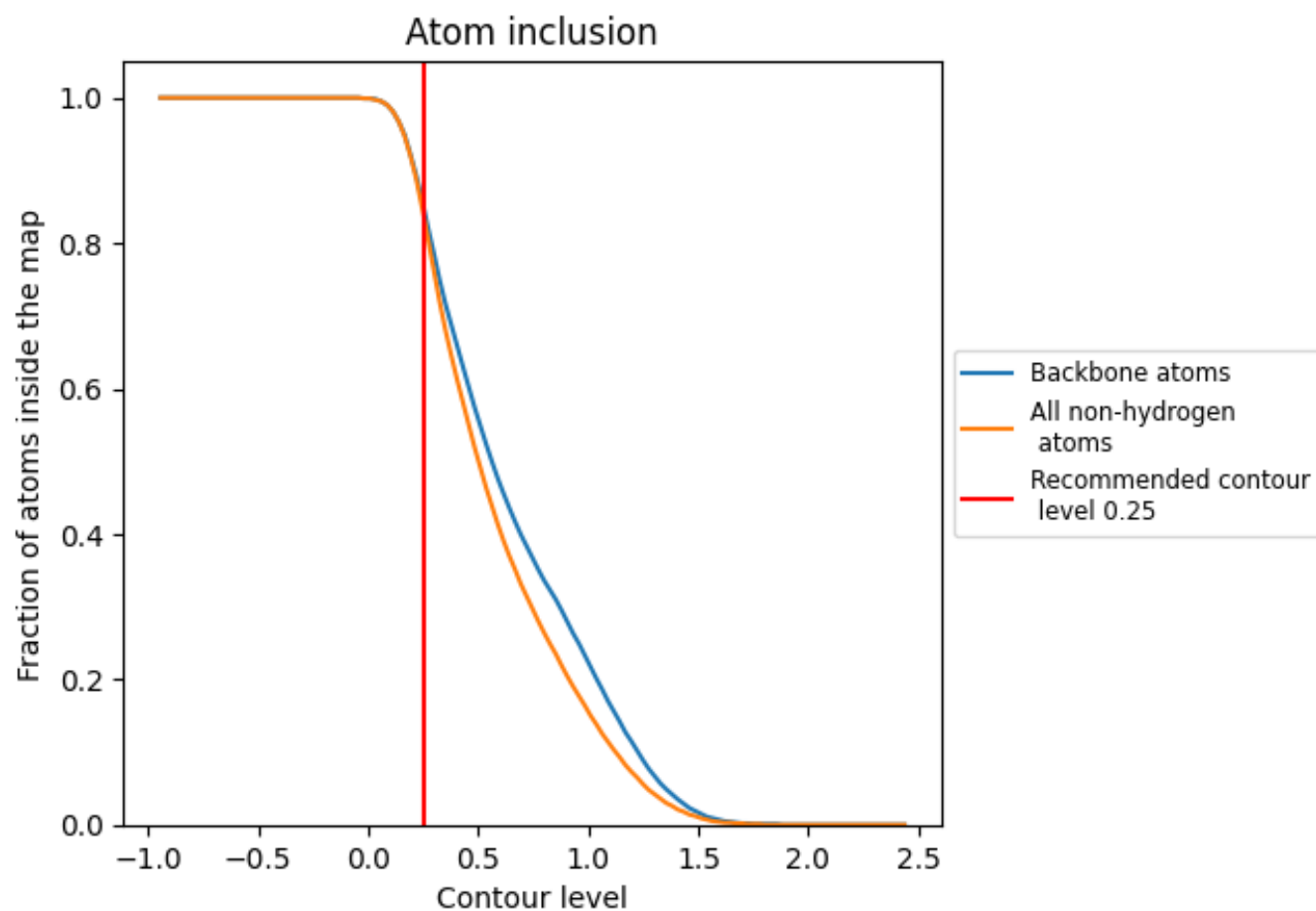
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 84% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8400	 0.3840
A	 0.9720	 0.5200
B	 0.8540	 0.3890
C	 0.9550	 0.5070
D	 0.8710	 0.3790
E	 0.6990	 0.2140
F	 0.3210	 0.1710
G	 0.9480	 0.3630
H	 0.9930	 0.4660
I	 0.9060	 0.2680
J	 0.9710	 0.2770
K	 0.9850	 0.5130
L	 0.8940	 0.2740
M	 0.9650	 0.2800
N	 0.9780	 0.5320
O	 0.9270	 0.4190
P	 0.9580	 0.5070
Q	 0.9200	 0.4000
R	 0.8710	 0.3000
S	 0.5360	 0.1800
T	 0.9320	 0.3380
U	 0.9920	 0.4590
X	 0.9670	 0.4760

