



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 12:55 PM UTC

PDB ID : 6FSZ / pdb_00006fsz
EMDB ID : EMD-4301
Title : Structure of the nuclear RNA exosome
Authors : Schuller, J.M.; Falk, S.; Conti, E.
Deposited on : 2018-02-20
Resolution : 4.60 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:

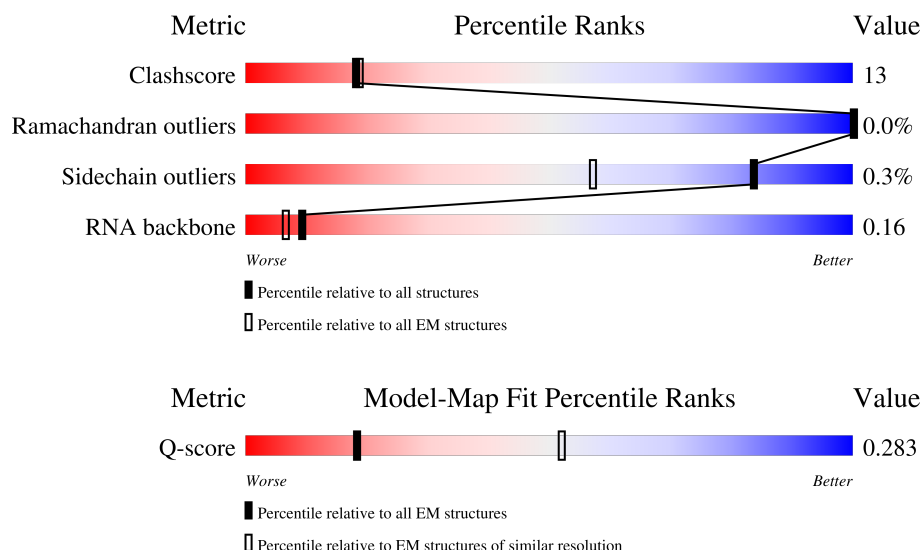
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 4.60 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.



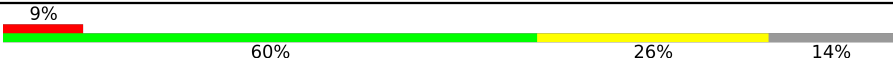
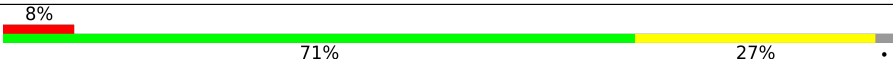
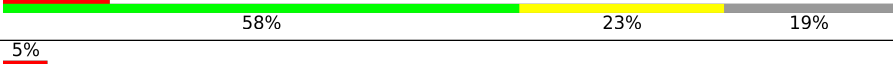
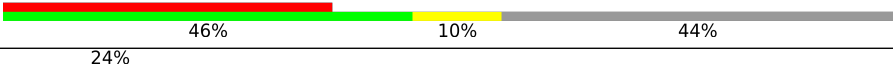
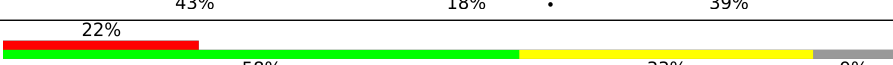
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	2407 (4.10 - 5.10)

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	2	23	
2	AA	303	
3	BB	248	

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Mol	Chain	Length	Quality of chain
4	CC	393	
5	DD	245	
6	EE	267	
7	FF	250	
8	GG	242	
9	HH	361	
10	II	301	
11	JJ	1003	
12	KK	733	
13	LL	184	
14	MM	1073	
15	NN	40	

2 Entry composition

There are 15 unique types of molecules in this entry. The entry contains 36972 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 RNA (5'-R(P*AP*AP*AP*AP*UP*UP*UP*AP*AP*AP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*U)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	23	Total	C	N	O	P	0	0
			378	166	43	146	23		

- Molecule 2 is a protein called Exosome complex component RRP45.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AA	299	Total	C	N	O	S	0	0
			2304	1444	393	451	16		

- Molecule 3 is a protein called Exosome complex component SKI6.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	BB	244	Total	C	N	O	S	0	0
			1886	1177	335	366	8		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BB	-1	GLY	-	expression tag	UNP P46948
BB	0	HIS	-	expression tag	UNP P46948

- Molecule 4 is a protein called Exosome complex component RRP43.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	CC	339	Total	C	N	O	S	1	0
			2589	1640	441	497	11		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CC	102	SER	ALA	conflict	UNP P25359
CC	363	MET	VAL	conflict	UNP P25359

- Molecule 5 is a protein called Exosome complex component RRP46.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	DD	223	Total	C	N	O	S	1	0
			1701	1072	285	334	10		

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DD	-21	GLY	-	expression tag	UNP P53256
DD	-20	HIS	-	expression tag	UNP P53256
DD	-19	GLY	-	expression tag	UNP P53256
DD	-18	ASN	-	expression tag	UNP P53256
DD	-17	ASN	-	expression tag	UNP P53256
DD	-16	LYS	-	expression tag	UNP P53256
DD	-15	GLU	-	expression tag	UNP P53256
DD	-14	PRO	-	expression tag	UNP P53256
DD	-13	ASN	-	expression tag	UNP P53256
DD	-12	THR	-	expression tag	UNP P53256
DD	-11	LYS	-	expression tag	UNP P53256
DD	-10	ASN	-	expression tag	UNP P53256
DD	-9	ARG	-	expression tag	UNP P53256
DD	-8	LEU	-	expression tag	UNP P53256
DD	-7	ASP	-	expression tag	UNP P53256
DD	-6	SER	-	expression tag	UNP P53256
DD	-5	ALA	-	expression tag	UNP P53256
DD	-4	GLU	-	expression tag	UNP P53256
DD	-3	LYS	-	expression tag	UNP P53256
DD	-2	LYS	-	expression tag	UNP P53256
DD	-1	LYS	-	expression tag	UNP P53256
DD	0	LYS	-	expression tag	UNP P53256

- Molecule 6 is a protein called Exosome complex component RRP42.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	EE	267	Total	C	N	O	S	1	0
			2050	1308	338	399	5		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EE	-1	GLY	-	expression tag	UNP Q12277
EE	0	HIS	-	expression tag	UNP Q12277
EE	138	ILE	VAL	conflict	UNP Q12277

- Molecule 7 is a protein called Exosome complex component MTR3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	FF	215	Total	C	N	O	S	0	0
			1638	1023	273	332	10		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
FF	75	SER	THR	conflict	UNP P48240
FF	161	THR	MET	conflict	UNP P48240

- Molecule 8 is a protein called Exosome complex component RRP40.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	GG	237	Total	C	N	O	S	0	0
			1792	1143	295	344	10		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
GG	-1	GLY	-	expression tag	UNP Q08285
GG	0	HIS	-	expression tag	UNP Q08285

- Molecule 9 is a protein called Exosome complex component RRP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	HH	293	Total	C	N	O	S	0	0
			2236	1393	403	428	12		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
HH	-1	ARG	-	expression tag	UNP P38792
HH	0	SER	-	expression tag	UNP P38792

- Molecule 10 is a protein called Exosome complex component CSL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	II	222	Total	C	N	O	S	0	0
			1653	1034	287	325	7		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
II	-8	MET	-	initiating methionine	UNP P53859
II	-7	LYS	-	expression tag	UNP P53859
II	-6	HIS	-	expression tag	UNP P53859
II	-5	HIS	-	expression tag	UNP P53859
II	-4	HIS	-	expression tag	UNP P53859
II	-3	HIS	-	expression tag	UNP P53859
II	-2	HIS	-	expression tag	UNP P53859
II	-1	HIS	-	expression tag	UNP P53859
II	0	PRO	-	expression tag	UNP P53859

- Molecule 11 is a protein called Exosome complex exonuclease DIS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	JJ	948	Total	C	N	O	S	0	0
			7430	4693	1310	1392	35		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
JJ	-1	GLY	-	expression tag	UNP Q08162
JJ	0	ALA	-	expression tag	UNP Q08162
JJ	171	ASN	ASP	conflict	UNP Q08162
JJ	551	ASN	ASP	conflict	UNP Q08162

- Molecule 12 is a protein called Exosome complex exonuclease RRP6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	KK	414	Total	C	N	O	S	0	0
			2517	1544	469	498	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
KK	296	ASN	ASP	engineered mutation	UNP Q12149

- Molecule 13 is a protein called Exosome complex protein LRP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LL	113	Total	C	N	O	S	0	0
			894	565	151	174	4		

- Molecule 14 is a protein called ATP-dependent RNA helicase DOB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	MM	978	Total	C	N	O	S	0	0
			7627	4871	1294	1419	43		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
MM	80	MET	VAL	conflict	UNP P47047

- Molecule 15 is a protein called M-phase phosphoprotein 6 homolog,M-phase phosphoprotein 6 homolog,Nuclear exosome-associated RNA binding protein,M-phase phosphoprotein 6 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	NN	40	Total	C	N	O	0	0
			277	172	51	54		

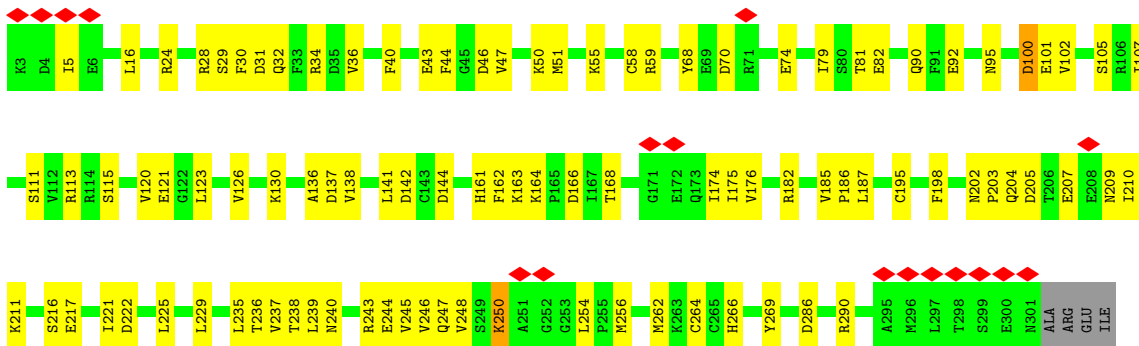
3 Residue-property plots

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.

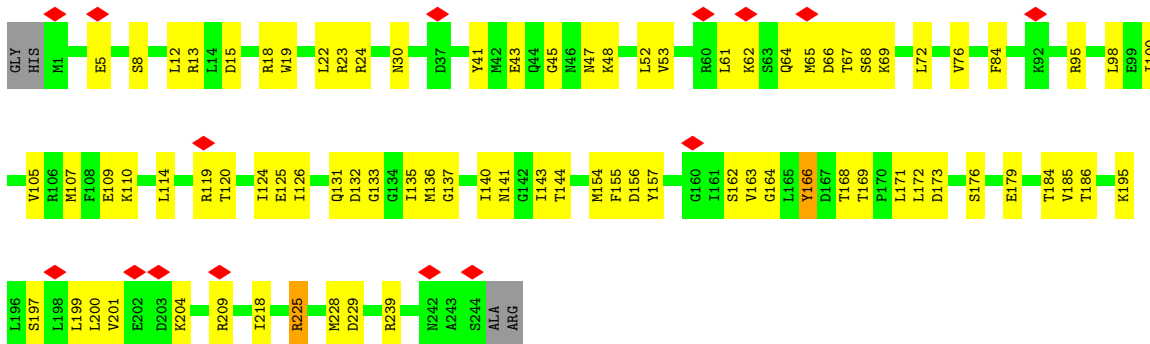
- Molecule 1: RNA (5'-R(P*AP*AP*AP*UP*UP*UP*AP*AP*AP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*U)-3')



- Molecule 2: Exosome complex component RRP45



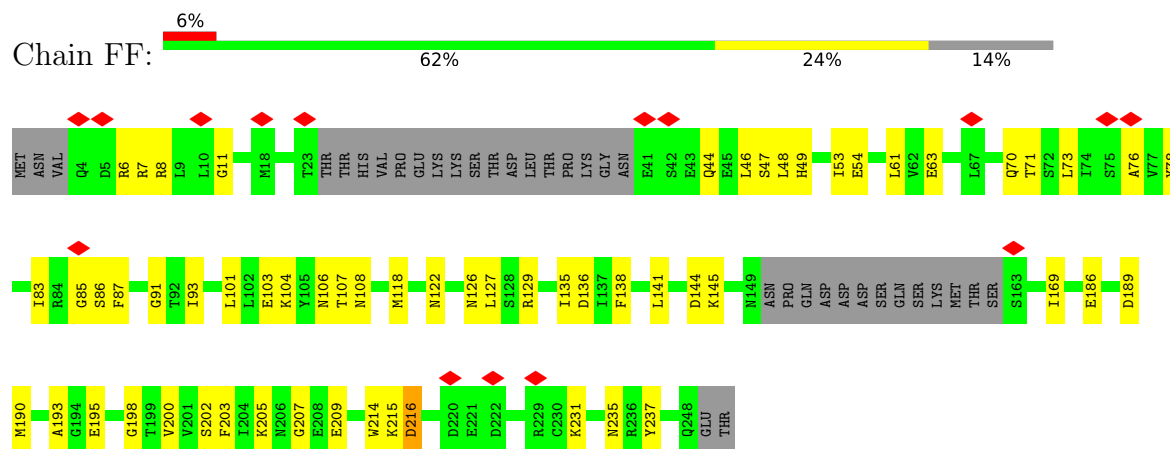
- Molecule 3: Exosome complex component SKI6



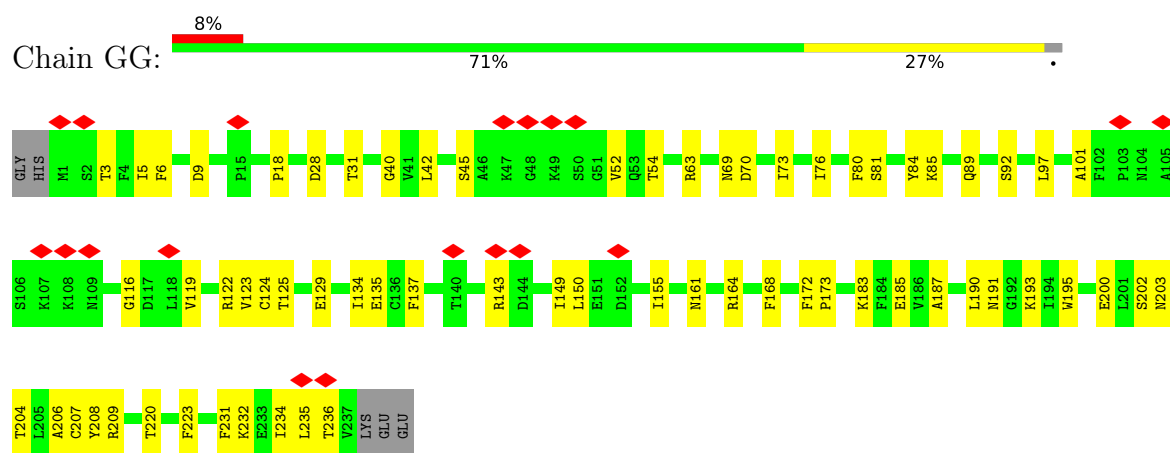
Chain CC:



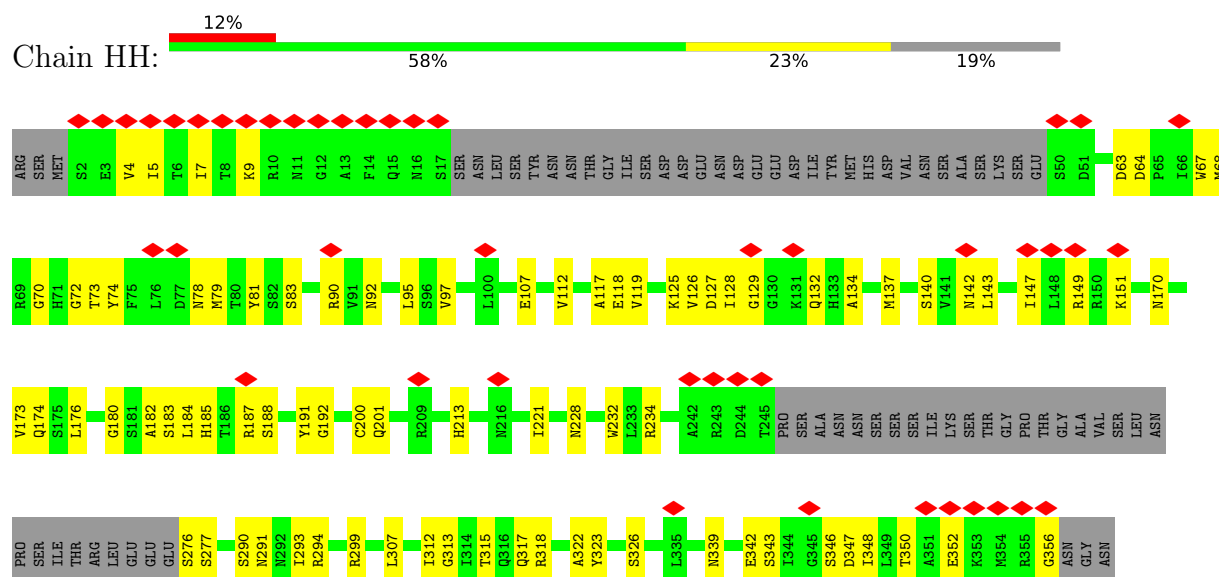
- Molecule 7: Exosome complex component MTR3



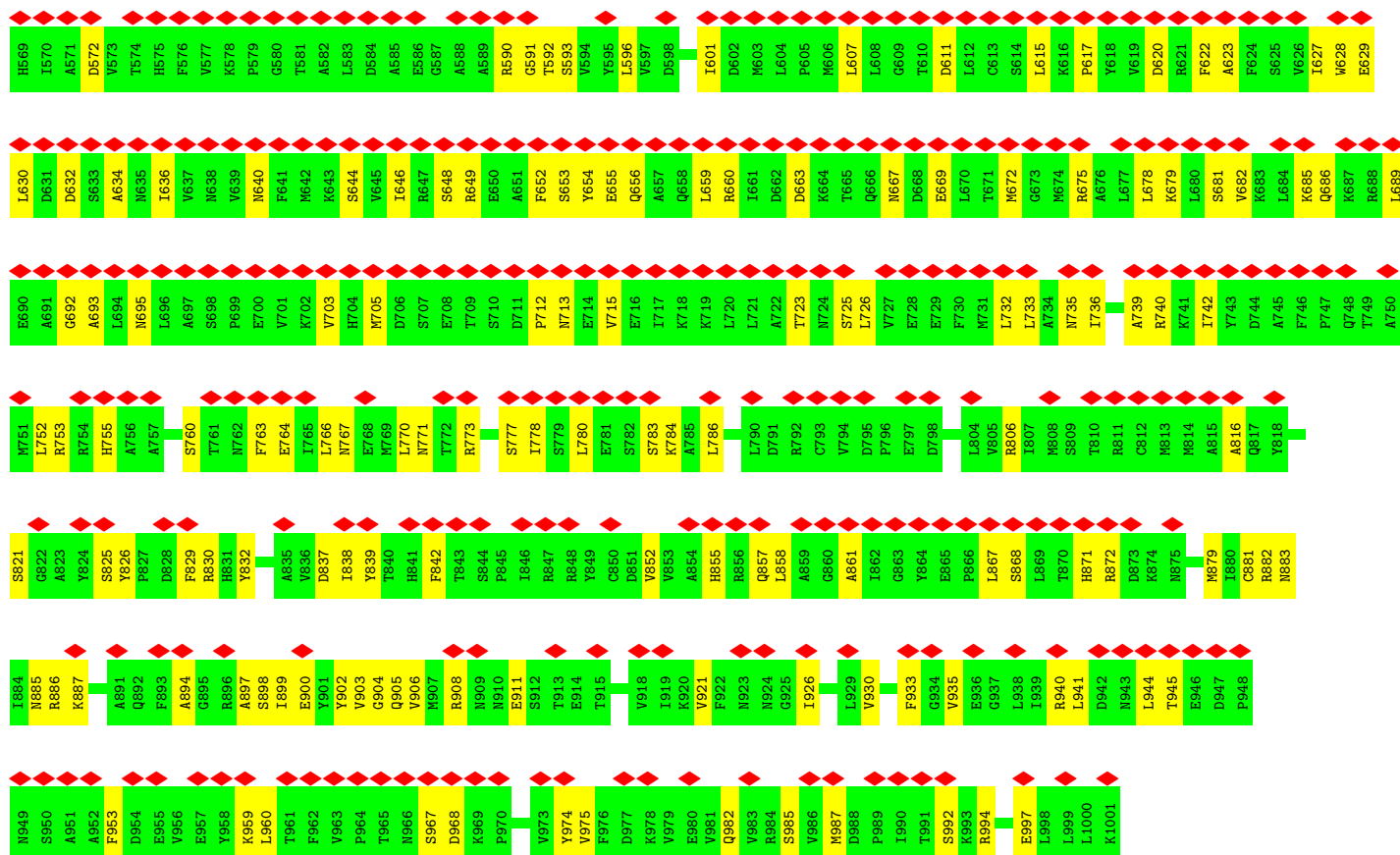
- Molecule 8: Exosome complex component RRP40



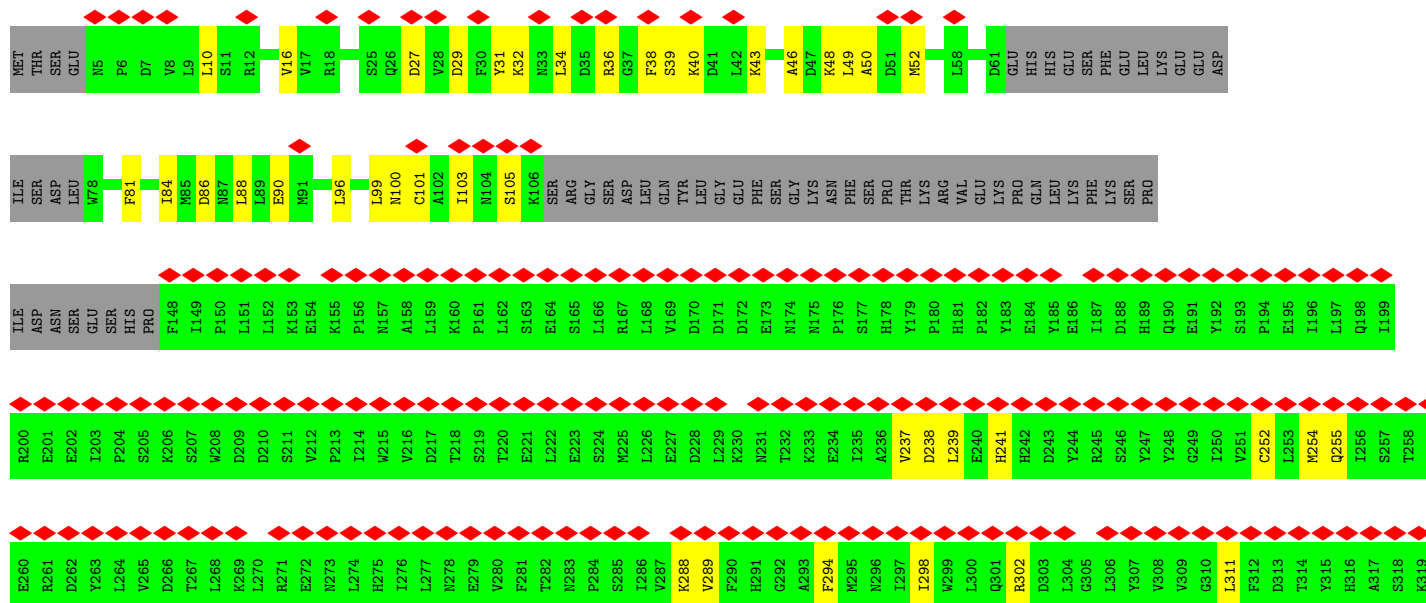
- Molecule 9: Exosome complex component RRP4

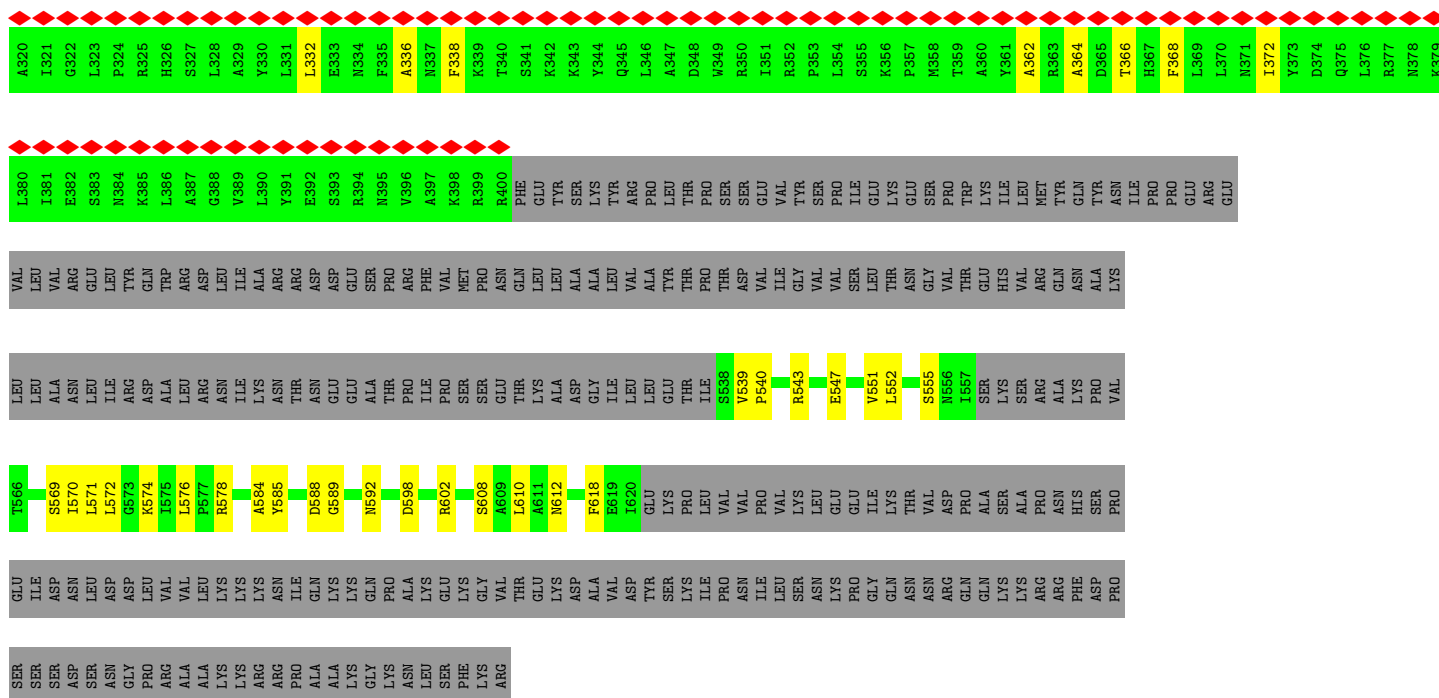


- Molecule 10: Exosome complex component CSL4

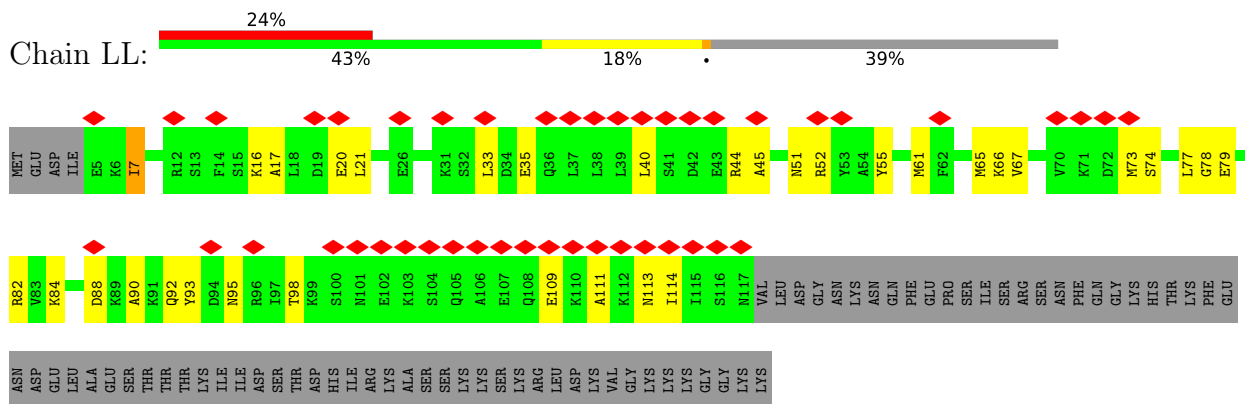


• Molecule 12: Exosome complex exonuclease RRP6

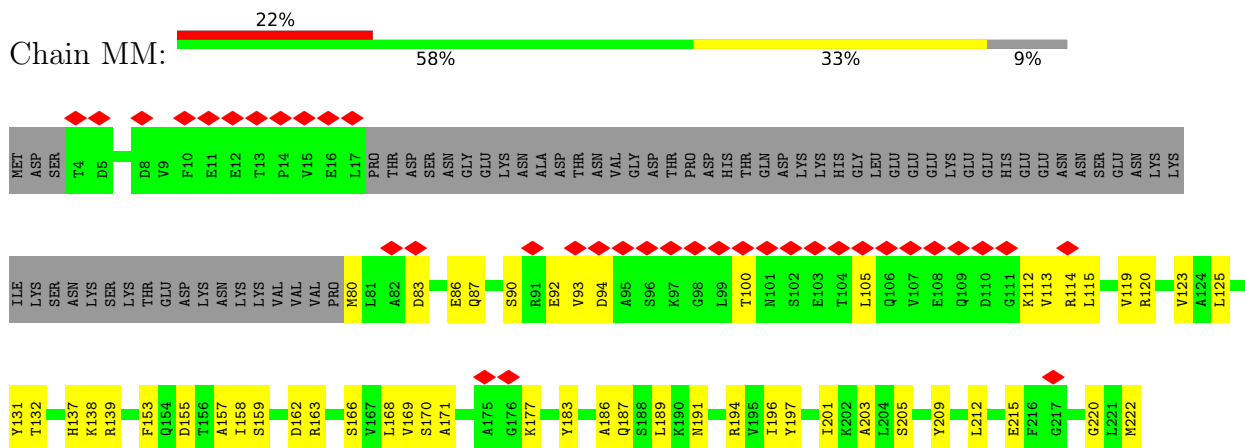


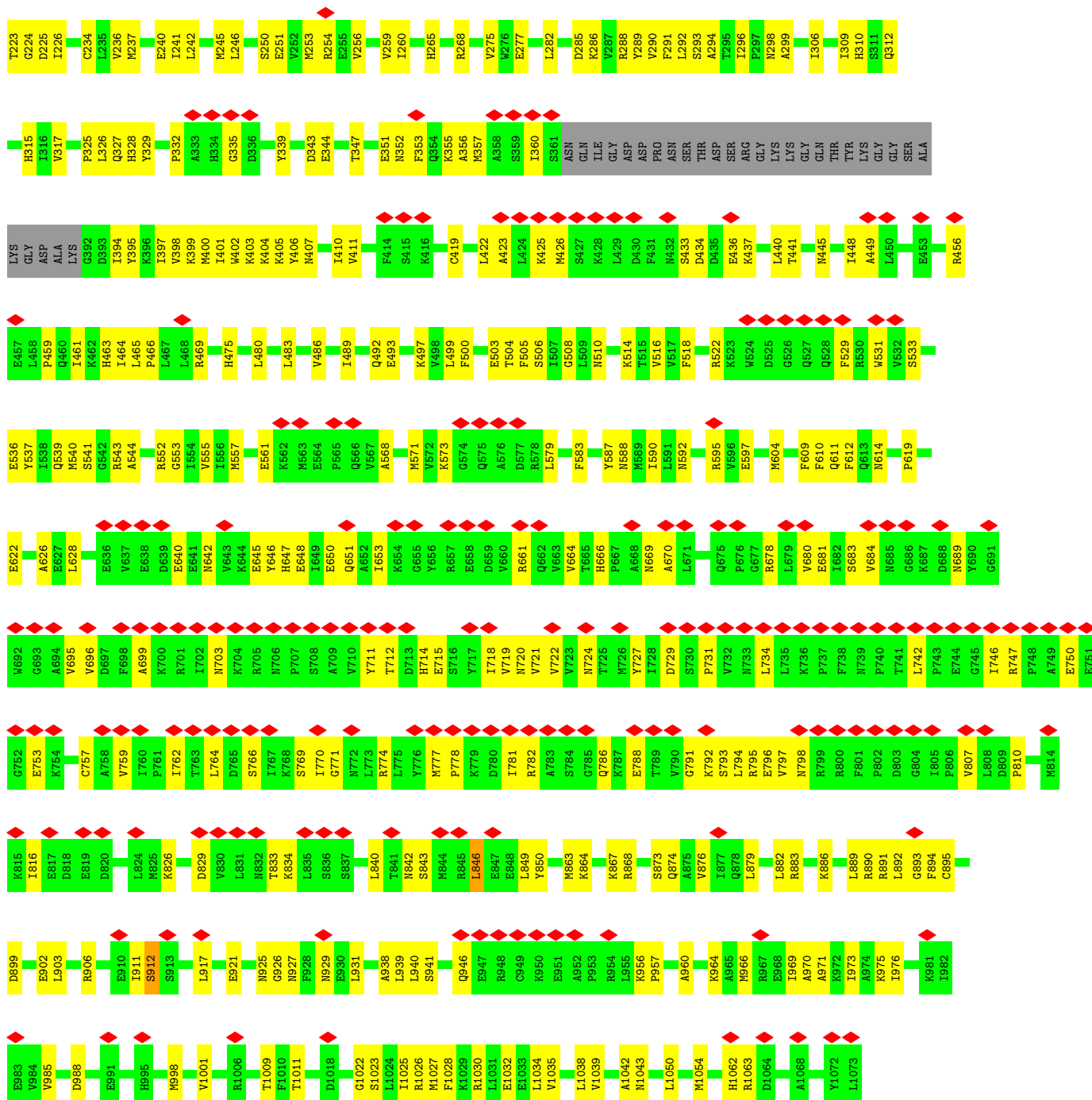


- Molecule 13: Exosome complex protein LRP1



- Molecule 14: ATP-dependent RNA helicase DOB1





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	22439	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 ($e^-/\text{\AA}^2$)	38.4	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	0.117	Depositor
Minimum map value	-0.047	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.035	Depositor
Map size (Å)	594.0, 594.0, 594.0	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.35, 1.35, 1.35	Depositor

5 Model quality

5.1 Standard geometry

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	2	0.41	0/418	0.71	0/645
2	AA	0.58	1/2340 (0.0%)	0.73	0/3161
3	BB	0.58	0/1910	0.76	0/2579
4	CC	0.51	0/2629	0.77	0/3569
5	DD	0.56	0/1722	0.77	0/2339
6	EE	0.51	0/2093	0.75	0/2849
7	FF	0.54	0/1660	0.74	0/2241
8	GG	0.54	0/1828	0.79	2/2486 (0.1%)
9	HH	0.53	0/2269	0.77	0/3066
10	II	0.47	0/1676	0.77	0/2277
11	JJ	0.38	0/7575	0.69	1/10290 (0.0%)
12	KK	0.35	0/2540	0.66	0/3497
13	LL	0.37	0/903	0.70	0/1210
14	MM	0.48	0/7773	0.77	4/10521 (0.0%)
15	NN	0.45	0/225	0.95	1/301 (0.3%)
All	All	0.48	1/37561 (0.0%)	0.74	8/51031 (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
3	BB	0	1
4	CC	0	3
5	DD	0	1
6	EE	0	1
7	FF	0	2
9	HH	0	1
10	II	0	1
11	JJ	0	1
14	MM	0	3
All	All	0	14

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	AA	250	LYS	CA-CB	-7.19	1.43	1.53

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	NN	108	VAL	N-CA-C	-6.09	104.72	113.07
14	MM	612	PHE	N-CA-C	-5.84	107.14	114.56
14	MM	1063	ARG	CA-C-N	5.44	131.92	121.54
14	MM	1063	ARG	C-N-CA	5.44	131.92	121.54
14	MM	912	SER	N-CA-C	-5.42	107.67	114.56

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	BB	166	TYR	Peptide
4	CC	335	ASP	Peptide
4	CC	352	ALA	Peptide
4	CC	54	ILE	Peptide
5	DD	188	GLU	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	2	378	0	190	3	0
2	AA	2304	0	2265	66	0
3	BB	1886	0	1904	62	0
4	CC	2589	0	2607	74	0
5	DD	1701	0	1755	50	0
6	EE	2050	0	2063	59	0
7	FF	1638	0	1590	41	0
8	GG	1792	0	1747	42	0
9	HH	2236	0	2215	56	0
10	II	1653	0	1616	41	0
11	JJ	7430	0	7350	217	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	KK	2517	0	1819	59	0
13	LL	894	0	917	25	0
14	MM	7627	0	7521	236	0
15	NN	277	0	238	6	0
All	All	36972	0	35797	959	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 13.

The worst 5 of 959 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)
5:DD:25:LYS:H	5:DD:96:GLU:HB3	1.50	0.76
9:HH:356:GLY:HA2	13:LL:35:GLU:HB2	1.70	0.73
5:DD:138:ILE:HG12	5:DD:145:ILE:HG12	1.68	0.73
11:JJ:732:LEU:HD23	11:JJ:735:ASN:HD22	1.53	0.73
14:MM:939:LEU:HD11	14:MM:966:MET:HG2	1.70	0.73

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	
2	AA	297/303 (98%)	276 (93%)	21 (7%)	0	100	100
3	BB	242/248 (98%)	224 (93%)	18 (7%)	0	100	100
4	CC	332/393 (84%)	304 (92%)	27 (8%)	1 (0%)	36	71
5	DD	222/245 (91%)	209 (94%)	13 (6%)	0	100	100
6	EE	266/267 (100%)	252 (95%)	14 (5%)	0	100	100
7	FF	209/250 (84%)	191 (91%)	18 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	GG	235/242 (97%)	216 (92%)	19 (8%)	0	100	100
9	HH	287/361 (80%)	262 (91%)	25 (9%)	0	100	100
10	II	214/301 (71%)	198 (92%)	16 (8%)	0	100	100
11	JJ	942/1003 (94%)	875 (93%)	67 (7%)	0	100	100
12	KK	404/733 (55%)	366 (91%)	38 (9%)	0	100	100
13	LL	111/184 (60%)	108 (97%)	3 (3%)	0	100	100
14	MM	972/1073 (91%)	909 (94%)	63 (6%)	0	100	100
15	NN	27/40 (68%)	23 (85%)	4 (15%)	0	100	100
All	All	4760/5643 (84%)	4413 (93%)	346 (7%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	CC	337	GLU

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	
2	AA	255/265 (96%)	252 (99%)	3 (1%)	63	73
3	BB	210/219 (96%)	209 (100%)	1 (0%)	81	81
4	CC	282/349 (81%)	282 (100%)	0	100	100
5	DD	196/216 (91%)	196 (100%)	0	100	100
6	EE	238/241 (99%)	238 (100%)	0	100	100
7	FF	181/219 (83%)	180 (99%)	1 (1%)	78	80
8	GG	194/210 (92%)	194 (100%)	0	100	100
9	HH	243/313 (78%)	241 (99%)	2 (1%)	73	77
10	II	174/249 (70%)	174 (100%)	0	100	100
11	JJ	812/901 (90%)	812 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	KK	150/671 (22%)	150 (100%)	0	100	100
13	LL	99/168 (59%)	97 (98%)	2 (2%)	48	65
14	MM	810/953 (85%)	809 (100%)	1 (0%)	88	88
15	NN	25/25 (100%)	25 (100%)	0	100	100
All	All	3869/4999 (77%)	3859 (100%)	10 (0%)	84	84

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	LL	7	ILE
13	LL	33	LEU
14	MM	846	LEU
3	BB	225	ARG
7	FF	73	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 52 such sidechains are listed below:

Mol	Chain	Res	Type
11	JJ	724	ASN
12	KK	612	ASN
14	MM	832	ASN
11	JJ	775	ASN
12	KK	83	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	22/23 (95%)	15 (68%)	0

5 of 15 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	161	U
1	2	162	U
1	2	163	U
1	2	164	A
1	2	165	A

There are no RNA pucker outliers to report.

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](#)

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
15	NN	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	NN	11:UNK	C	90:PRO	N	57.41

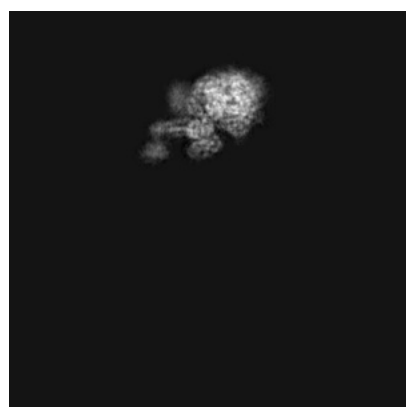
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4301. These allow visual inspection of the internal detail of the map and identification of artifacts.

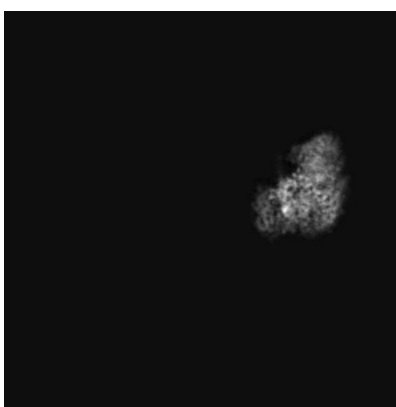
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

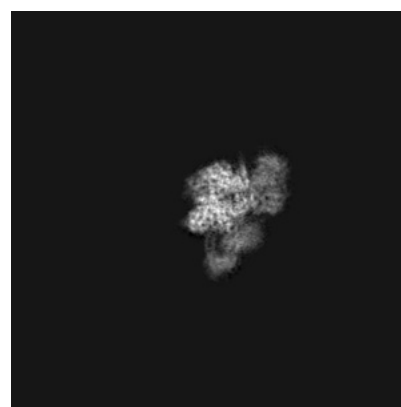
6.1.1 Primary map



X



Y

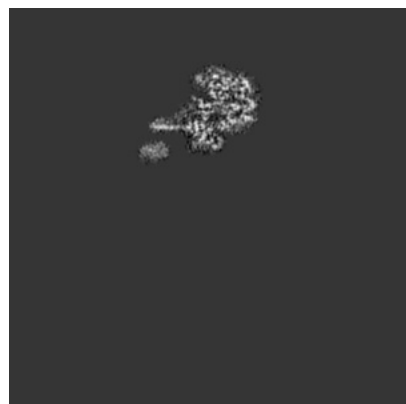


Z

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

6.2 Central slices [i](#)

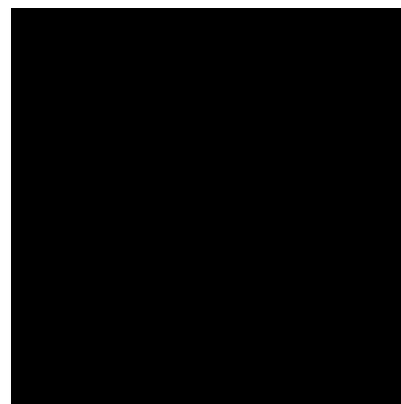
6.2.1 Primary map



X Index: 220



Y Index: 220

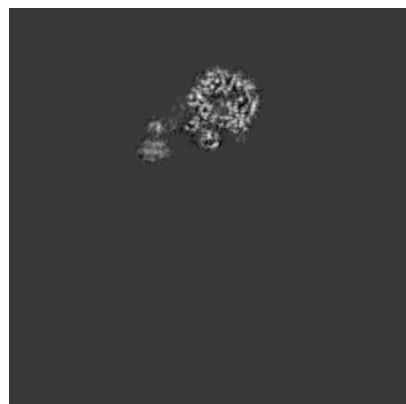


Z Index: 220

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

6.3 Largest variance slices [i](#)

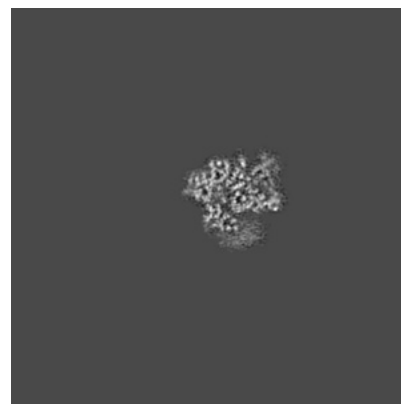
6.3.1 Primary map



X Index: 228



Y Index: 223

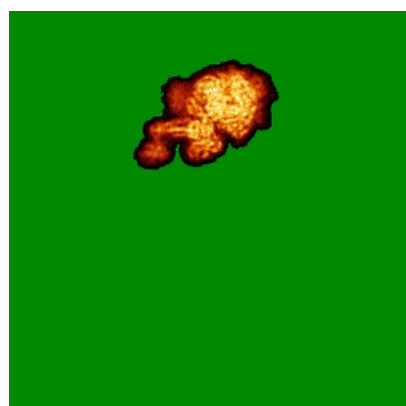


Z Index: 332

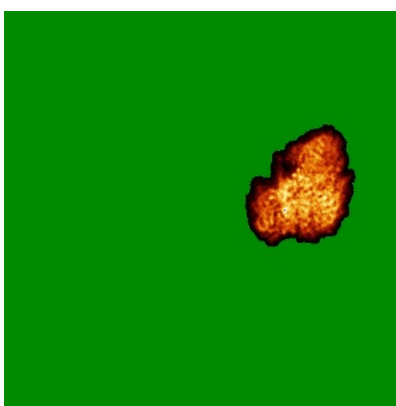
The images above show the largest variance slices of the map in three orthogonal directions.

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

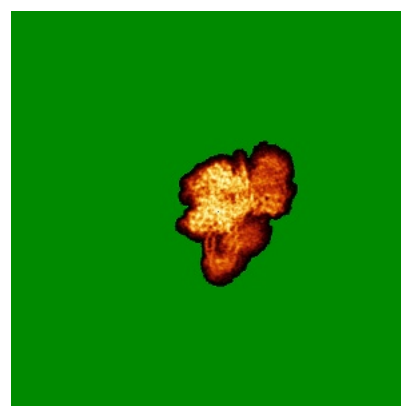
6.4.1 Primary map



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

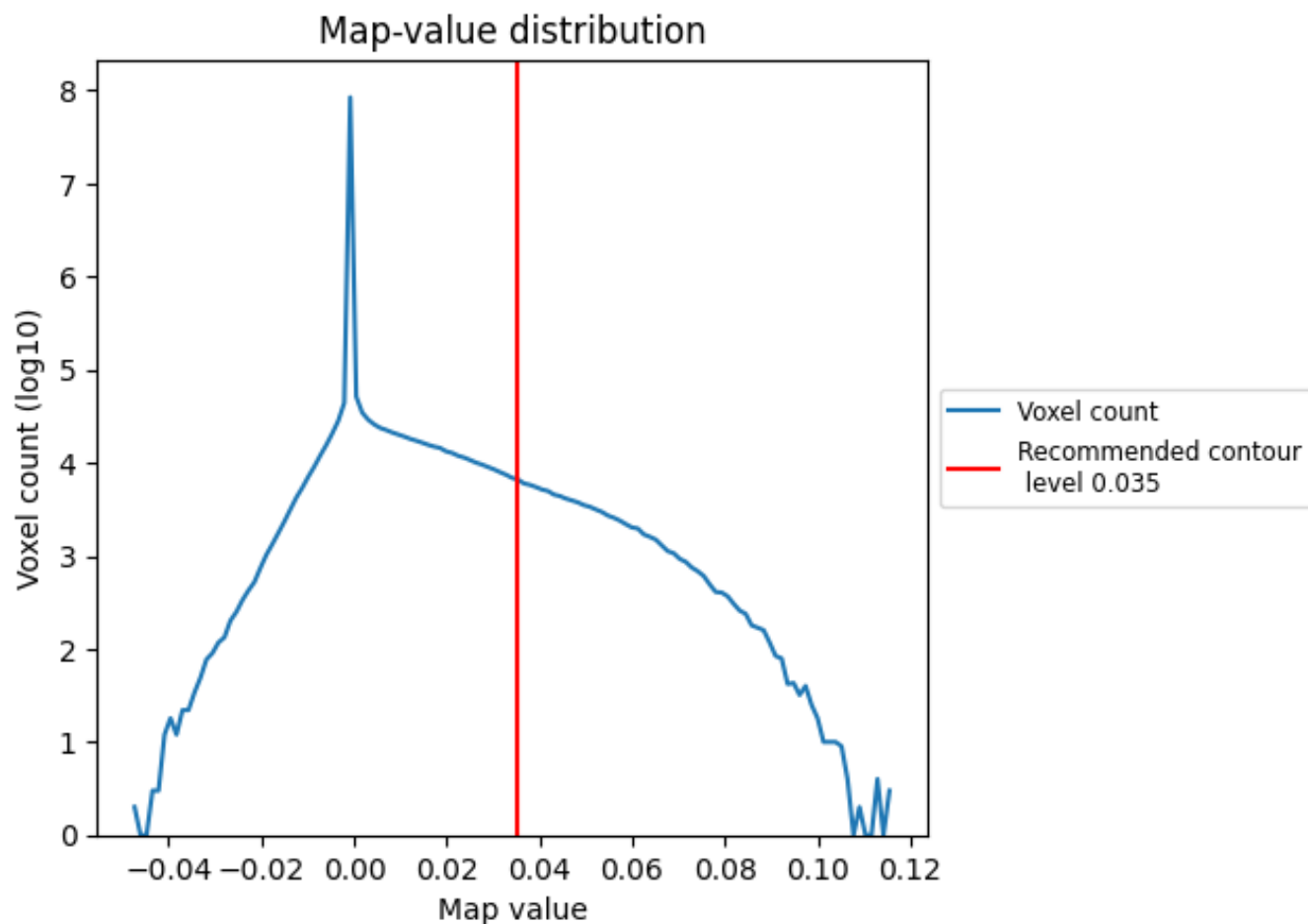
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

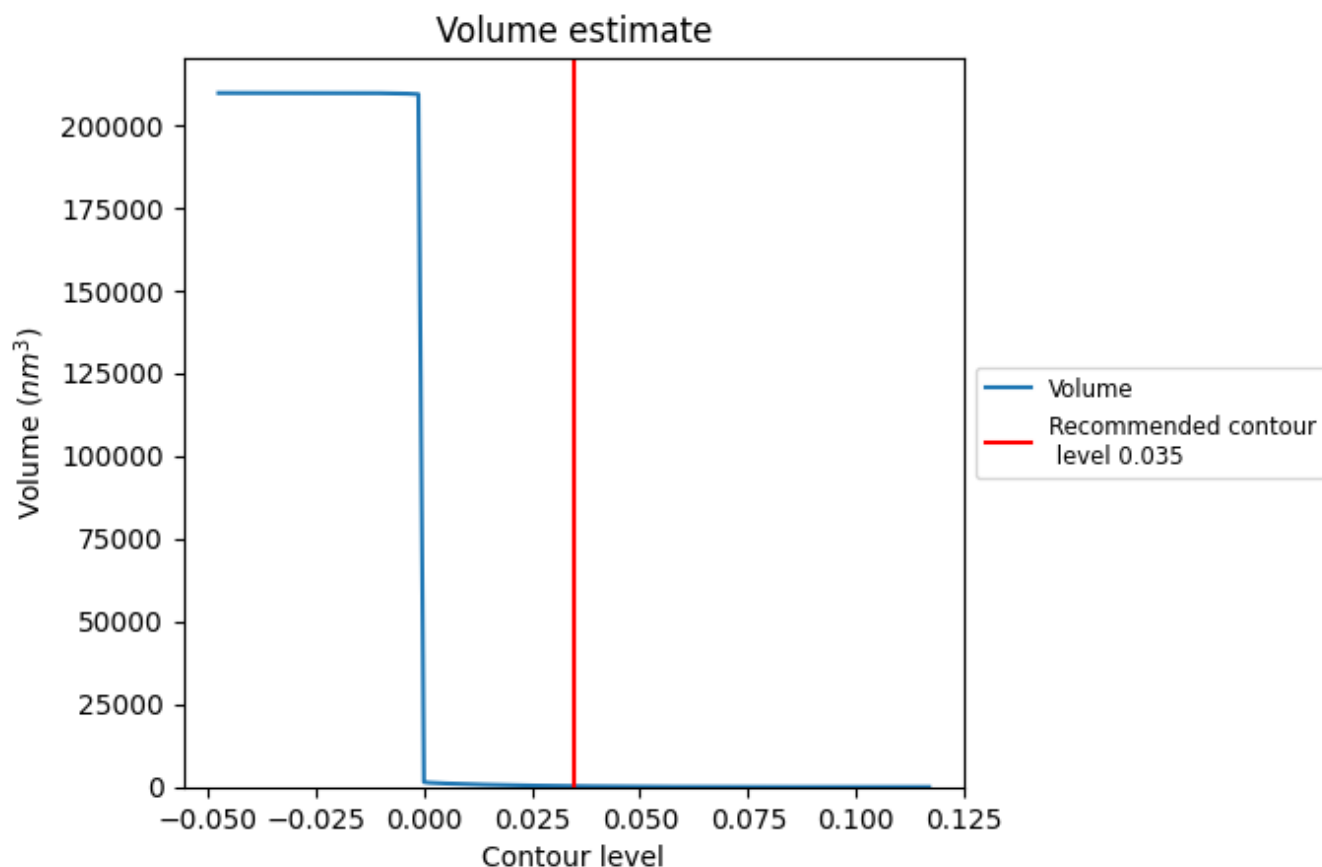
This section contains the results of statistical analysis of the map.

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.

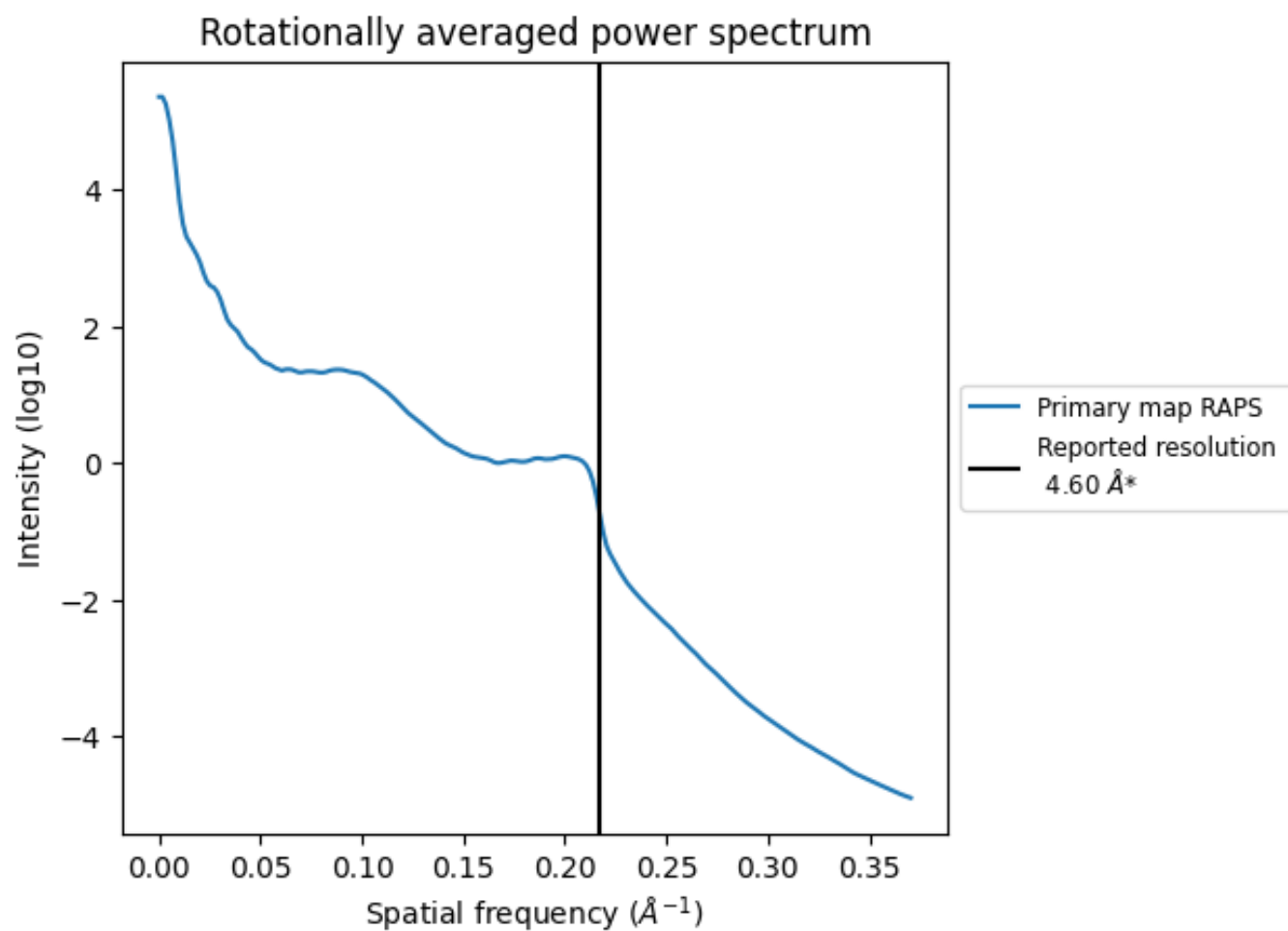
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 244 nm^3 ; this corresponds to an approximate mass of 220 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 0.217 $\text{\AA}^{-1}$

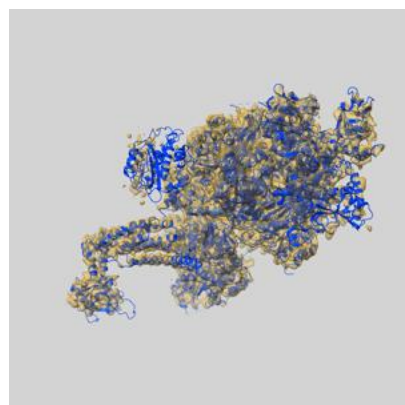
8 Fourier-Shell correlation

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

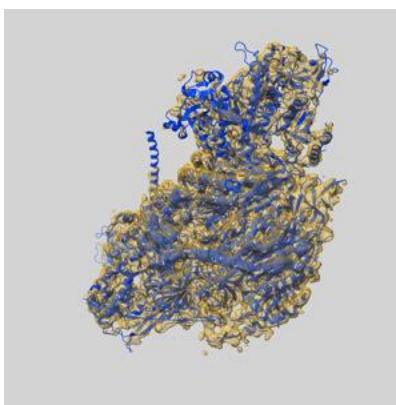
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4301 and PDB model 6FSZ. Per-residue inclusion information can be found in section [3](#) on page [9](#).

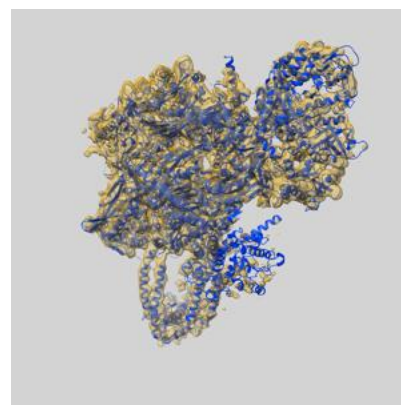
9.1 Map-model overlay [i](#)



X



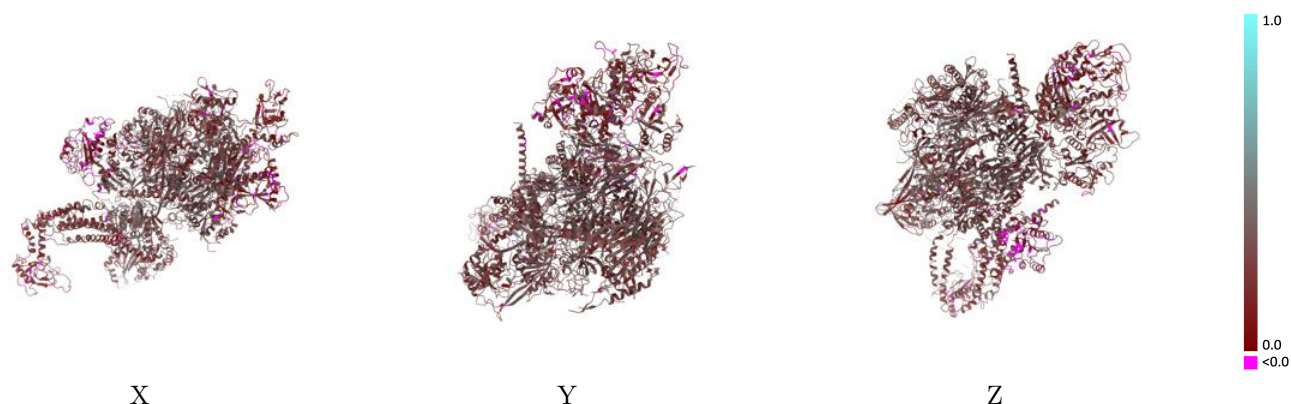
Y



Z

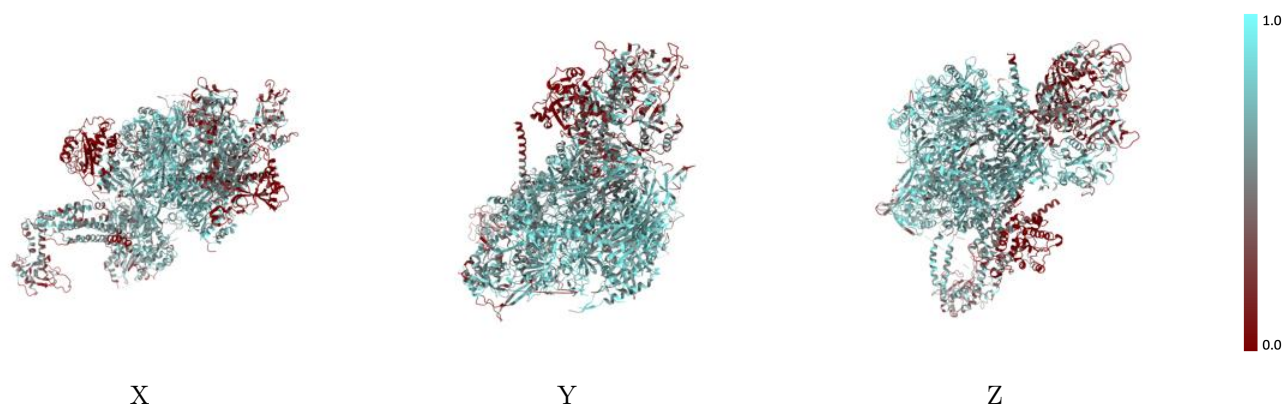
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



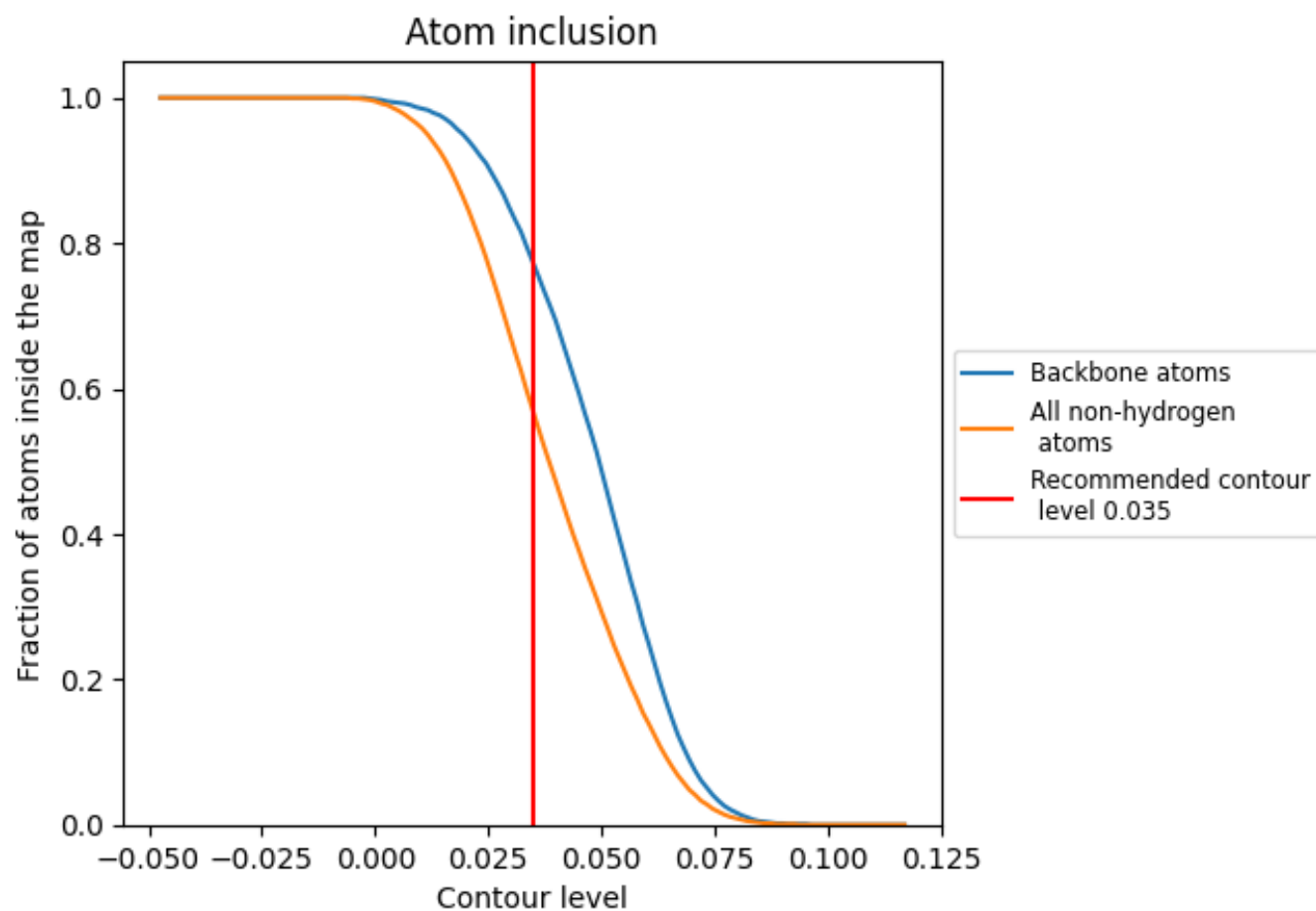
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.035).

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 57% 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 (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5660	 0.2830
2	 0.6220	 0.3030
AA	 0.6860	 0.3290
BB	 0.6760	 0.3310
CC	 0.6770	 0.3090
DD	 0.7110	 0.3230
EE	 0.6840	 0.3220
FF	 0.6910	 0.3140
GG	 0.7040	 0.3170
HH	 0.6390	 0.3220
II	 0.7060	 0.3230
JJ	 0.3910	 0.2410
KK	 0.3270	 0.2140
LL	 0.4240	 0.2320
MM	 0.5550	 0.2630
NN	 0.4850	 0.3000

