



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 05:21 PM UTC

PDB ID : 3J2C / pdb_00003j2c
EMDB ID : EMD-5504
Title : Dissecting the in vivo assembly of the 30S ribosomal subunit reveals the role of RimM
Authors : Guo, Q.; Goto, S.; Chen, Y.; Muto, A.; Himeno, H.; Deng, H.; Lei, J.; Gao, N.
Deposited on : 2012-09-28
Resolution : 13.20 Å (reported)
Based on initial model : 3OFA

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

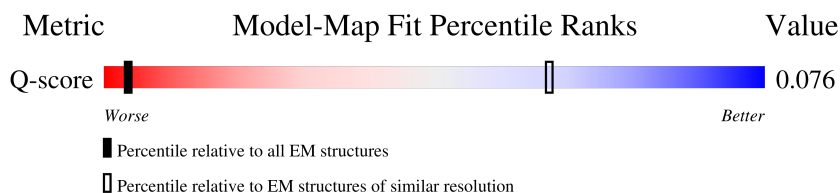
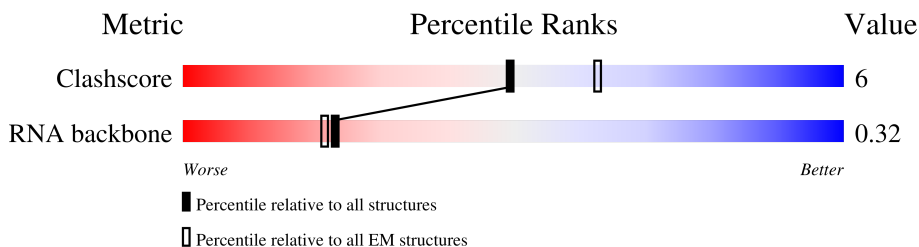
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 13.20 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	61 (12.70 - 13.70)

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	M	462	
2	N	927	
3	O	144	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 49444 atoms, of which 16558 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 16S rRNA head domain.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
1	M	462	14865	4410	4987	1793	3214	461	0	0

- Molecule 2 is a RNA chain called 16S rRNA body domain.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
2	N	927	29941	8884	10017	3681	6433	926	0	0

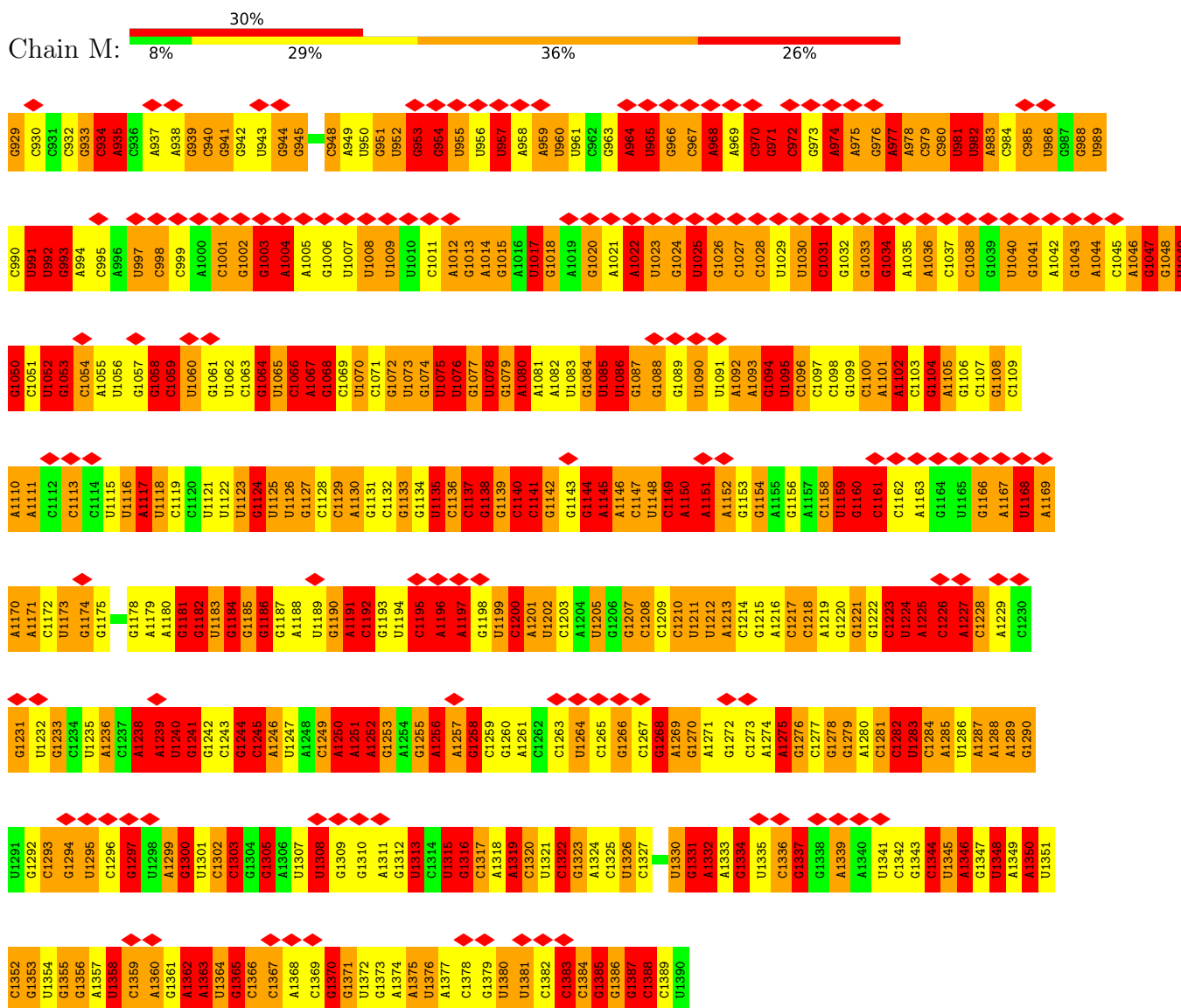
- Molecule 3 is a RNA chain called 16S rRNA body domain.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
3	O	144	4638	1377	1554	562	1002	143	0	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: 16S rRNA head domain

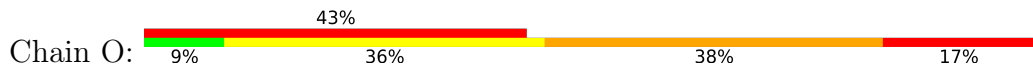


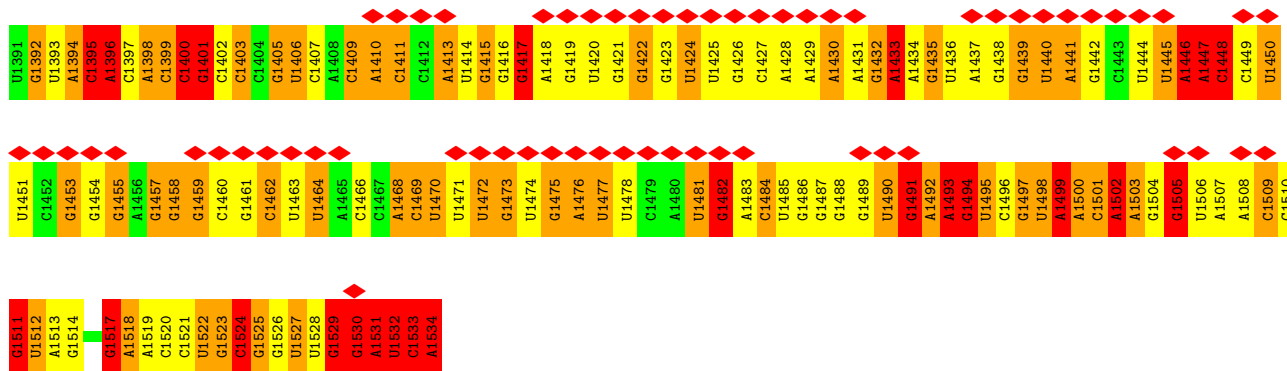
- Molecule 2: 16S rRNA body domain



A2	U62	G122	A182	G242	G302	G362	C422	A482	U543	U603	A663	U723	C783	U843	G903
A3	C63	U123	C183	A243	A303	A363	G423	C483	G544	G604	G664	G724	A784	G844	U904
U4	G64	U125	G184	U244	U304	U364	G424	G484	G545	G605	G665	G725	G785	G845	U905
U5	A65	U125	U185	U245	G305	U365	G425	U485	G546	G606	G666	G726	A786	G846	A906
U6	A66	G126	G186	A246	A306	A366	U426	A486	G547	G607	G667	G727	U787	G847	A907
A7	G67	G127	G187	G247	C307	U367	U427	C487	G549	A609	G669	A729	U789	G849	A909
A8	G68	G128	C188	C248	C308	U368	G428	C488	G550	G610	G670	G730	A790	U850	C910
A9	G69	U129	A189	U249	A309	G369	U429	C489	G551	G611	G671	G731	U791	G851	C911
A10	U70	A130	A190	U250	G310	C370	A430	C490	G552	C612	G672	C732	A792	G852	C912
A11	A71	A131	G191	G251	C311	A371	A431	G491	U553	C613	U673	C733	A793	C853	A913
G11	A72	C132	A192	U252	C312	C372	A432	G492	A553	C614	U674	C734	A794	U854	A914
U12	A73	U133	C193	A253	C313	A373	G433	A493	U554	C615	U675	C735	A795	U855	A915
U13	C73	U134	C194	G254	C314	A374	G434	A494	U555	C616	U676	C736	A796	C856	U916
U14	A74	G134	C194	G255	A315	U375	A435	G495	U556	G616	U677	C737	A797	C857	U917
G15	G75	C135	A195	U256	G316	G376	U436	G496	G557	G617	U678	C738	A798	C858	A918
A16	A76	U137	A197	G257	U317	G377	U437	G497	G558	C618	U679	C739	A799	C859	A919
U17	A77	A138	C198	U258	G318	G378	U438	G498	G559	C619	U680	C740	A800	U860	U920
C18	G78	U139	A199	U259	G319	C379	U439	G499	G560	C620	U681	C741	A801	U861	U921
A19	A79	A140	G200	G260	A320	G380	C440	G500	U561	A621	G681	G741	A802	C862	G922
U20	A80	U140	G201	U261	A321	C381	A441	C501	U562	A622	G682	G742	A803	C863	A923
G21	A81	G141	G202	U262	C322	A382	G442	A502	U563	A623	G683	A743	A804	U864	A924
G22	G82	A143	C203	A263	U323	A383	G443	C503	U564	A624	G684	C744	A805	U865	G925
C23	C83	C143	G204	C264	U324	G384	G444	C504	U565	A625	G685	C745	A806	U866	G926
U24	U84	G144	G204	C264	U324	G384	G444	C504	U566	A626	G686	C746	A807	U867	G927
U25	U85	G145	A205	G265	A325	C385	G445	G505	U567	A627	G687	C747	A808	U868	G928
C25	G86	G146	C206	G266	G326	C386	G446	G506	U568	A628	G688	C748	A809	U869	
A26	G87	G147	C207	G267	A327	U387	G447	C507	U569	A629	G689	C749	A810	U870	
G27	C87	U148	U208	U268	C328	G388	A448	U508	U570	A630	G690	C750	A811	U871	
A28	U88	G148	U209	C269	A329	G389	A449	C509	U571	A631	G691	C751	A812	U872	
U29	C89	U150	U210	U270	G330	U390	G450	C510	U572	A632	G692	C752	A813	U873	
U30	U91	U151	G211	C271	G331	U391	A451	C511	U573	A633	G693	C753	A814	U874	
G31	U91	U152	G212	C272	G332	C392	A452	C512	U574	A634	G694	C754	A815	U875	
A32	C92	C153	C213	U273	U333	A393	G453	C513	U575	A635	G695	C755	A816	U876	
A33	U93	U154	C214	A274	C334	G394	A454	C514	U576	A636	G696	C756	A817	U877	
C34	G94	A155	C215	G275	U335	C395	A455	C515	U577	A637	G697	C757	A818	U878	
G35	C95	U156	U216	C276	A336	C396	A456	C516	U578	A638	G698	C758	A819	U879	
C36	U96	U157	C217	C277	G337	U397	A457	C517	U579	A639	G699	C759	A820	U880	
U37	G97	G158	U218	U278	A338	U398	A458	C518	U580	A640	G700	C760	A821	U881	
G38	C99	U159	U219	A279	C339	G399	A459	C519	U581	A641	G701	C761	A822	U882	
C39	U99	G160	G220	C280	U340	C400	A460	C520	U582	A642	G702	C762	A823	U883	
C40	G100	A161	C221	G281	C341	C401	A461	C521	U583	A643	G703	C763	A824	U884	
G41	U101	G162	C222	A282	C342	G402	A462	C522	U584	A644	G704	C764	A825	U885	
G42	G102	C163	A223	U283	U343	C403	A463	C523	U585	A645	G705	C765	A826	U886	
C43	U103	G164	G224	C284	A344	U404	A464	C524	U586	A646	G706	C766	A827	U887	
A44	G104	A165	C225	C285	C345	U405	A465	C525	U587	A647	G707	C767	A828	U888	
G45	G105	U166	G226	C286	G346	G406	A466	C526	U588	A648	G708	C768	A829	U889	
C46	C106	U167	G227	U287	C347	U407	A467	C527	U589	A649	G709	C769	A830	U890	
C47	G107	A168	A228	A288	C348	A408	A468	C528	U590	A650	G710	C770	A831	U891	
C48	U108	C169	U229	C289	A349	U409	A469	C529	U591	A651	G711	C771	A832	U892	
U49	C110	U170	G230	C290	G350	C410	A470	C530	U592	A652	G712	C772	A833	U893	
A50	A51	G111	U231	U291	G351	A411	U471	A532	U593	A653	G713	C773	A834	U894	
C52	C52	G112	G232	G292	C352	A412	U472	A533	U594	A654	G714	C774	A835	U895	
A53	A53	U173	C234	G293	C353	G413	U473	A534	U595	A655	G715	C775	A836	U896	
G54	G54	G114	U234	U294	C354	A414	A474	A535	U596	A656	G716	C776	A837	U897	
A55	U115	C175	C235	C295	C355	A415	A475	A536	U597	A657	G717	C777	A838	U898	
U56	U116	G176	G236	U296	A356	G416	A476	A537	U598	A658	G718	C778	A839	U899	
G57	G57	G177	G237	G297	G357	U417	C477	A538	U599	A659	G719	C779	A840	U900	
C58	U118	C178	A238	A298	U358	C418	A478	A539	U600	A660	G720	C780	A841	U901	
A59	C58	U119	U239	G299	G359	C419	U479	A540	U601	A661	G721	C781	A842	U902	
A60	U120	U180	U240	A300	G360	U420	U480	A541	U602	A662	G722	C782	A843	U903	
G61	G61	A181	G241	G301	C361	U421	G481	A542	U603	A663	G723	C783	A844	U904	

● Molecule 3: 16S rRNA body domain





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	44392	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Weiner filter	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	80000	Depositor
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor
Maximum map value	4.325	Depositor
Minimum map value	-6.829	Depositor
Average map value	-4.406	Depositor
Map value standard deviation	0.508	Depositor
Recommended contour level	-3.2	Depositor
Map size (\AA)	345.0, 345.0, 345.0	wwPDB
Map dimensions	125, 125, 125	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	2.76, 2.76, 2.76	Depositor

5 Model quality i

5.1 Standard geometry i

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	M	2.02	218/11053 (2.0%)	1.97	486/17234 (2.8%)
2	N	2.04	482/22318 (2.2%)	1.98	989/34825 (2.8%)
3	O	1.98	67/3452 (1.9%)	1.94	151/5383 (2.8%)
All	All	2.03	767/36823 (2.1%)	1.97	1626/57442 (2.8%)

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	M	0	236
2	N	0	522
3	O	0	78
All	All	0	836

The worst 5 of 767 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	N	738	C	C1'-N1	11.02	1.65	1.48
1	M	1294	G	C4'-C3'	10.49	1.68	1.52
2	N	897	C	P-O5'	-9.28	1.45	1.59
2	N	398	U	C1'-N1	8.88	1.61	1.48
1	M	992	U	C3'-O3'	8.71	1.56	1.43

The worst 5 of 1626 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	M	1362	A	P-O3'-C3'	19.50	149.44	120.20
2	N	913	A	P-O3'-C3'	17.08	145.82	120.20
2	N	119	A	P-O3'-C3'	16.70	145.24	120.20
2	N	438	U	P-O3'-C3'	15.72	143.78	120.20
3	O	1530	G	P-O3'-C3'	15.69	143.73	120.20

There are no chirality outliers.

5 of 836 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	M	929	G	Sidechain
1	M	933	G	Sidechain
1	M	934	C	Sidechain
1	M	935	A	Sidechain
1	M	939	G	Sidechain

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	M	9878	4987	4986	67	0
2	N	19924	10017	10006	206	0
3	O	3084	1554	1553	14	0
All	All	32886	16558	16545	281	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 6.

The worst 5 of 281 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:M:998:C:H42	1:M:1042:A:H61	1.38	0.71
2:N:50:A:H1'	2:N:52:C:C6	2.25	0.71
2:N:664:G:H22	2:N:741:G:H1	1.38	0.70
2:N:858:G:H1	2:N:869:G:H2'	1.55	0.70
2:N:411:A:H61	2:N:428:G:H1'	1.57	0.70

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein molecules in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	M	461/462 (99%)	158 (34%)	41 (8%)
2	N	926/927 (99%)	261 (28%)	84 (9%)
3	O	143/144 (99%)	32 (22%)	9 (6%)
All	All	1530/1533 (99%)	451 (29%)	134 (8%)

5 of 451 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	M	932	C
1	M	934	C
1	M	935	A
1	M	944	G
1	M	953	G

5 of 134 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	N	641	U
2	N	733	G
3	O	1513	A
2	N	65	A
2	N	60	A

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](#)

There are no chain breaks in this entry.

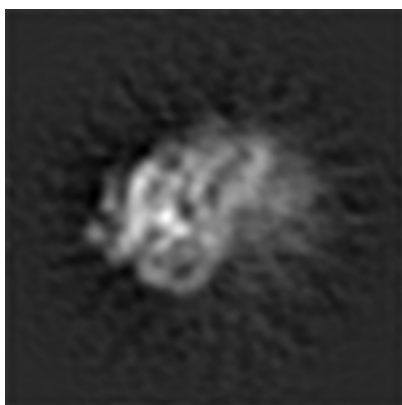
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5504. These allow visual inspection of the internal detail of the map and identification of artifacts.

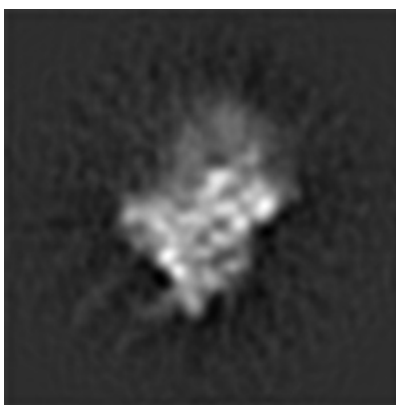
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

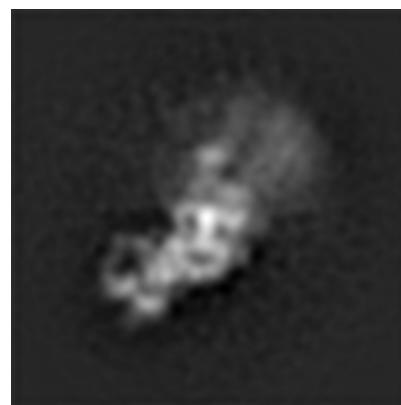
6.1.1 Primary map



X



Y

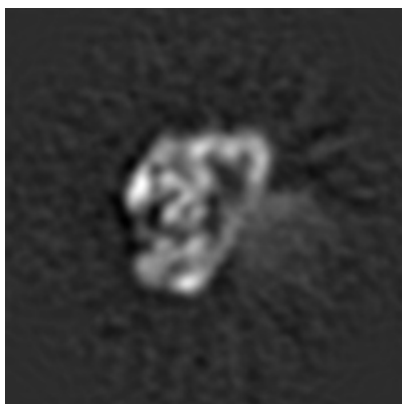


Z

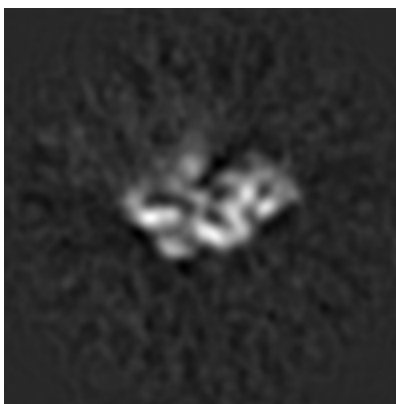
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

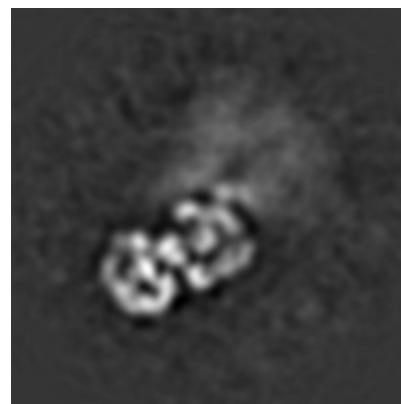
6.2.1 Primary map



X Index: 62



Y Index: 62

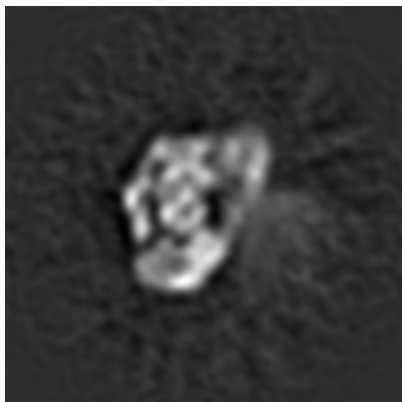


Z Index: 62

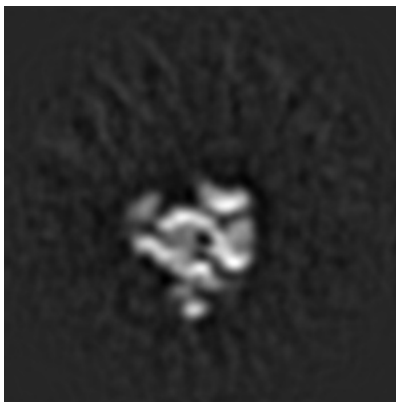
The images above show central slices of the map in three orthogonal directions.

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

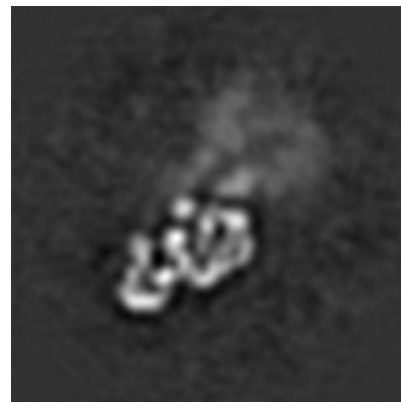
6.3.1 Primary map



X Index: 60



Y Index: 42

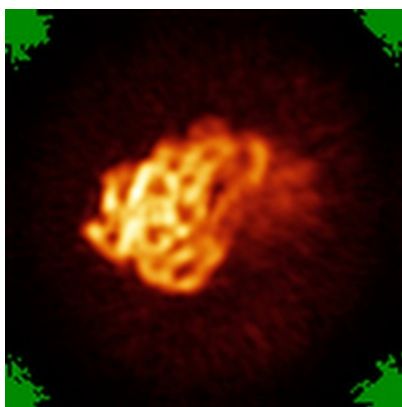


Z Index: 65

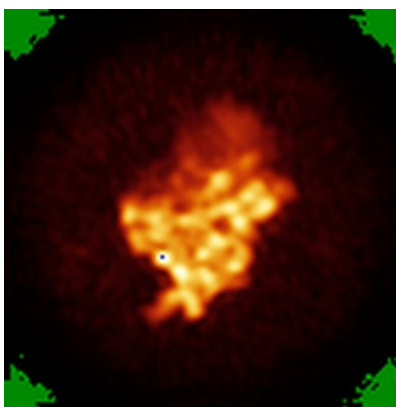
The images above show the largest variance slices of the map in three orthogonal directions.

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

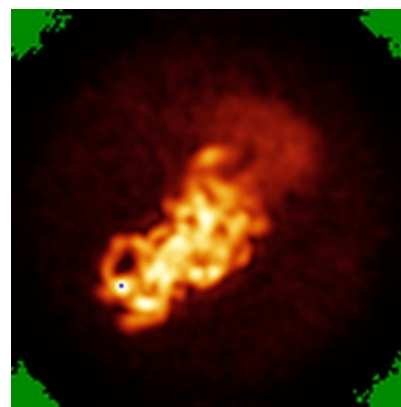
6.4.1 Primary map



X



Y

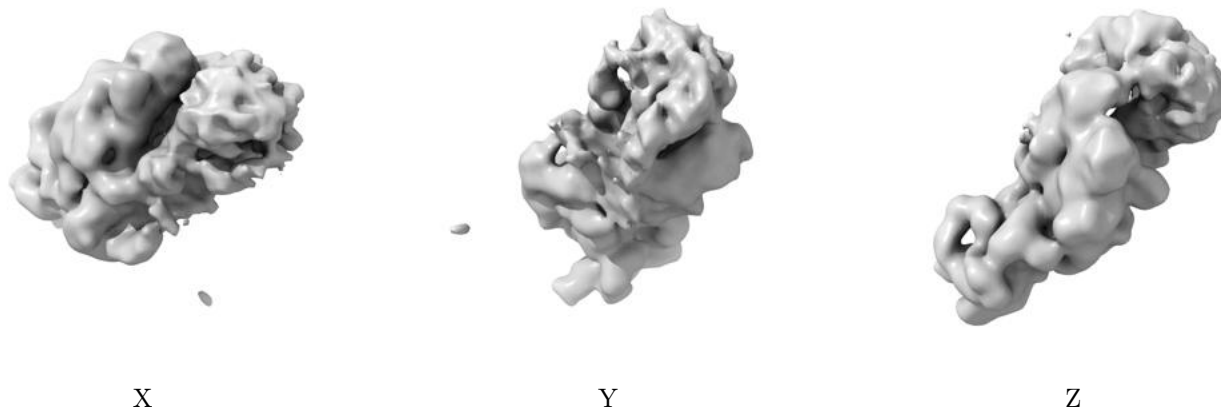


Z

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

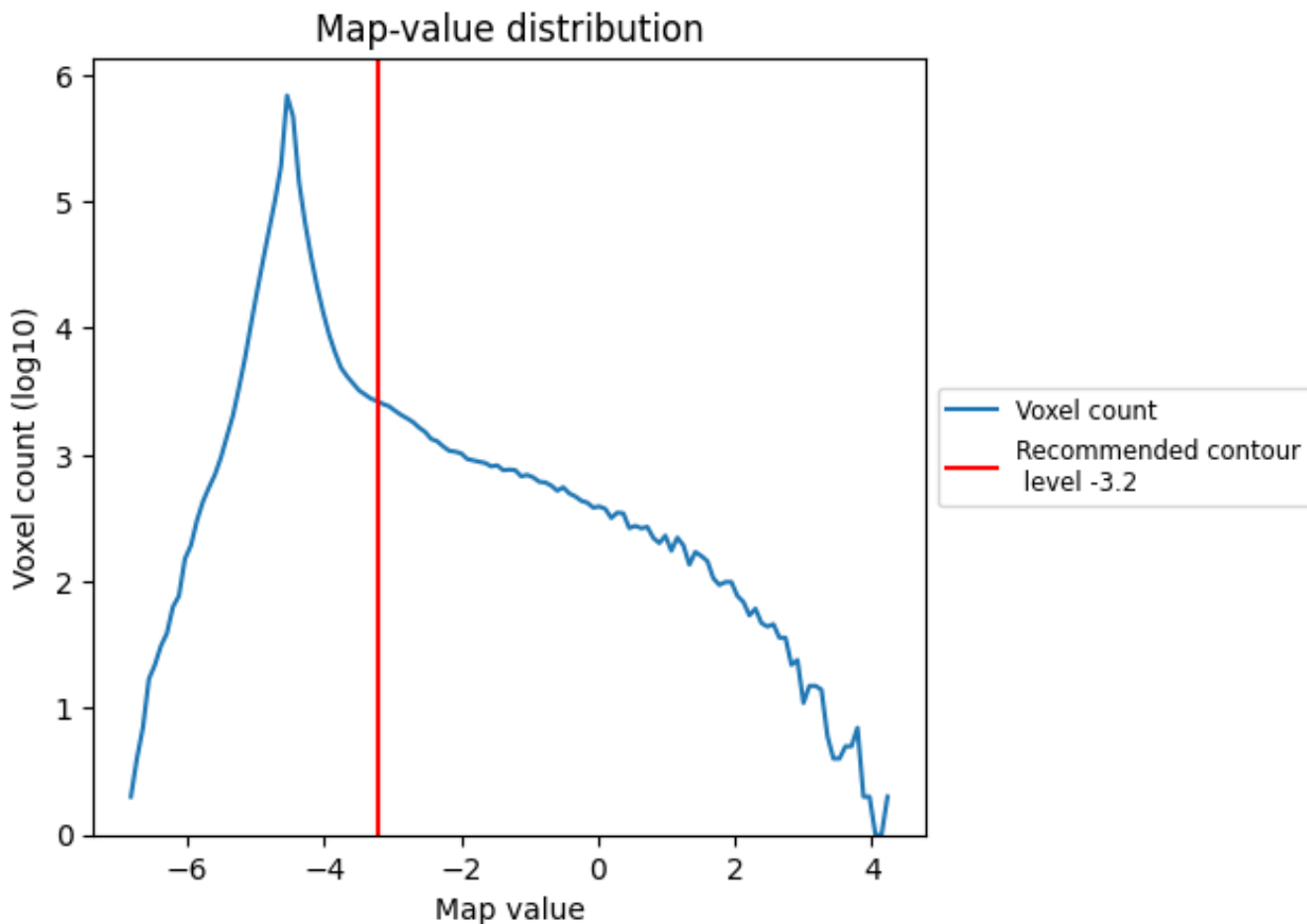
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

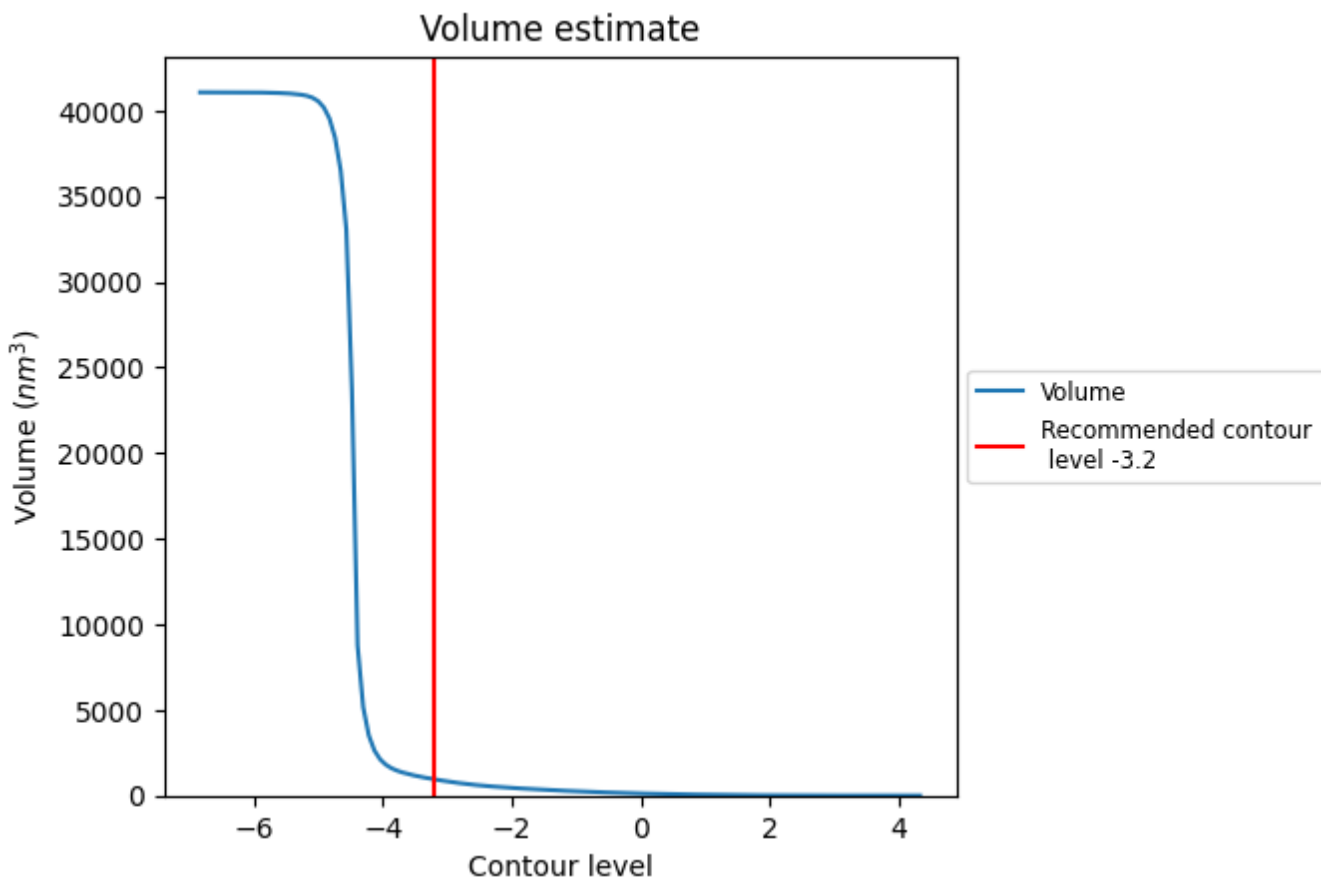
This section contains the results of statistical analysis of the map.

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.

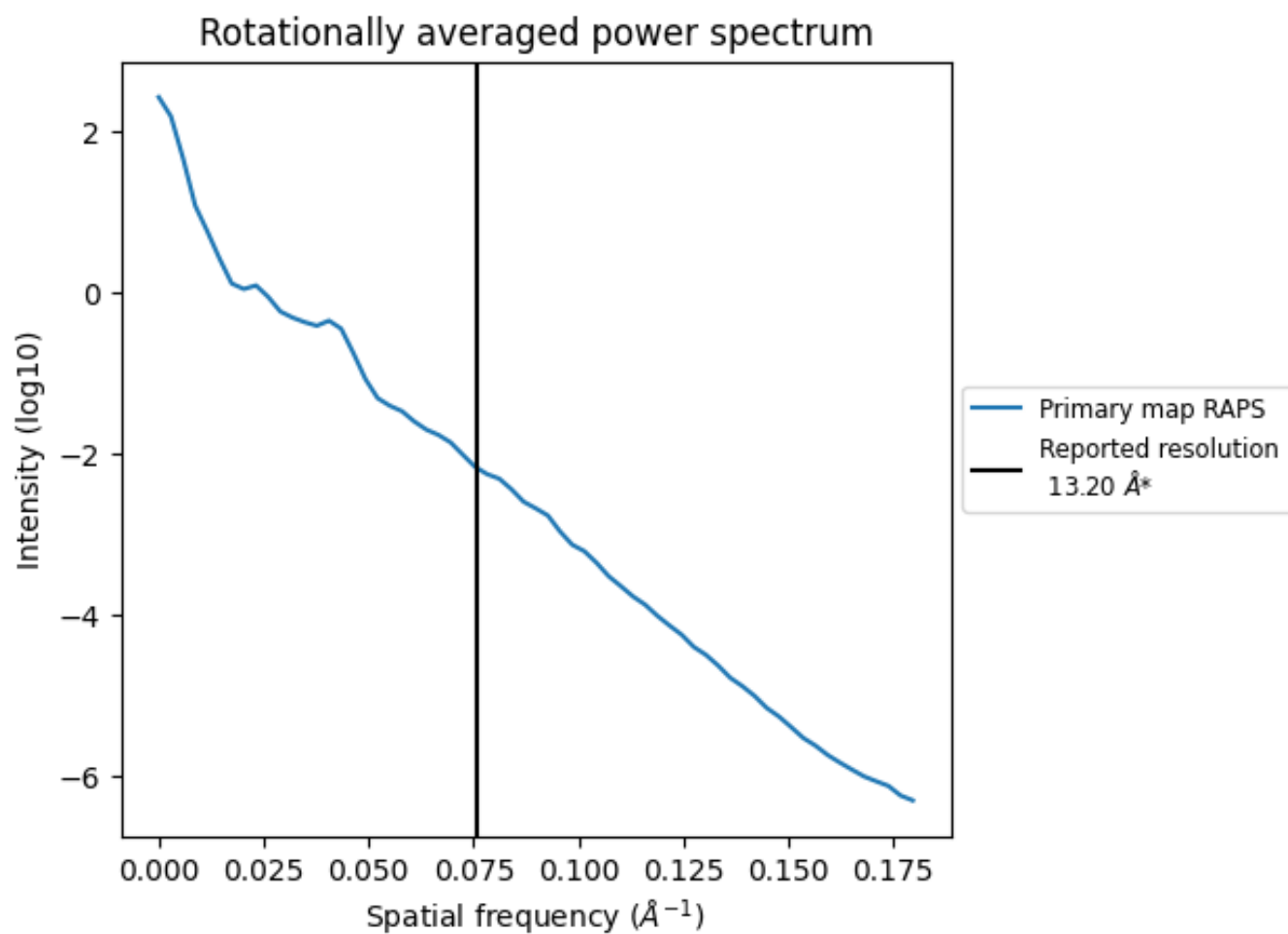
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 949 nm³; this corresponds to an approximate mass of 858 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 0.076 Å⁻¹

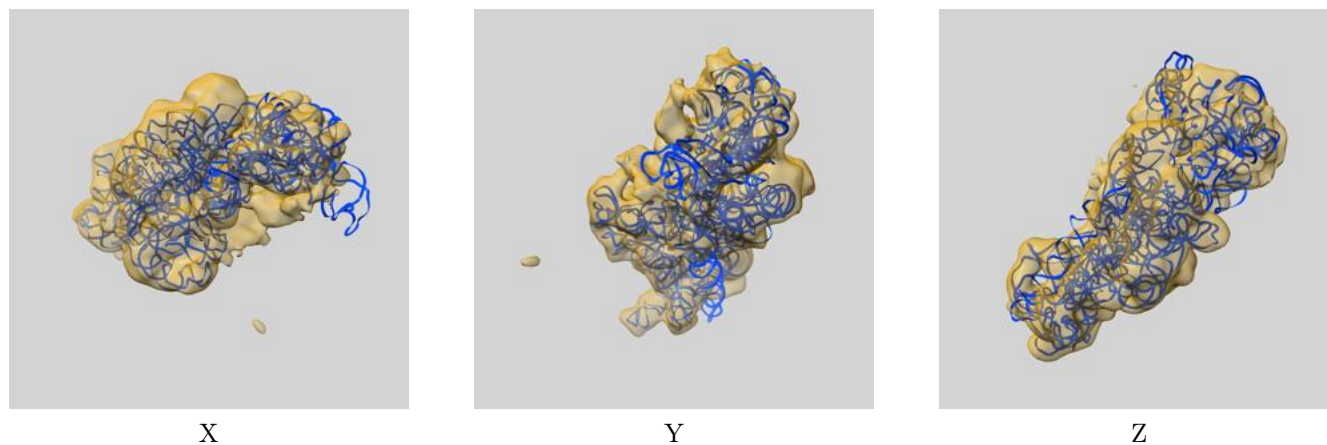
8 Fourier-Shell correlation

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-5504 and PDB model 3J2C. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)



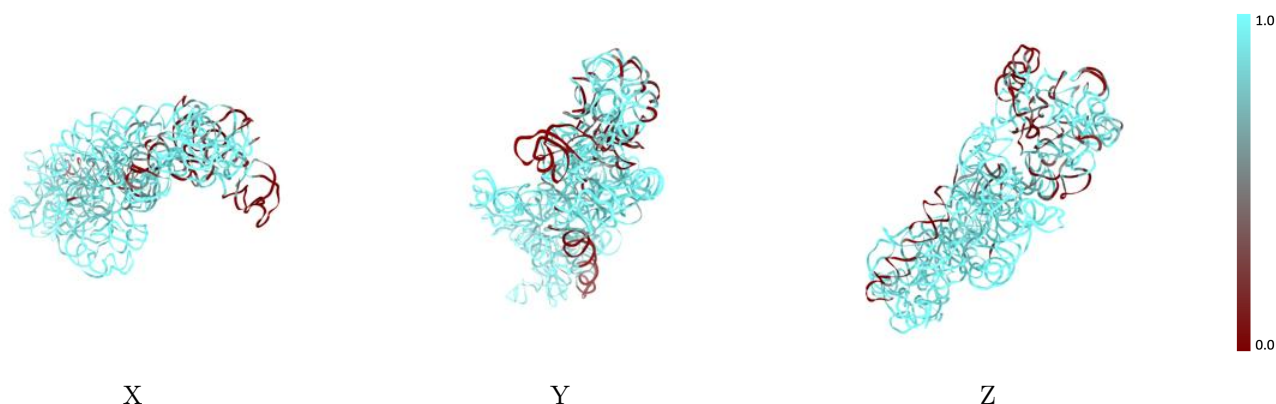
The images above show the 3D surface view of the map at the recommended contour level -3.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



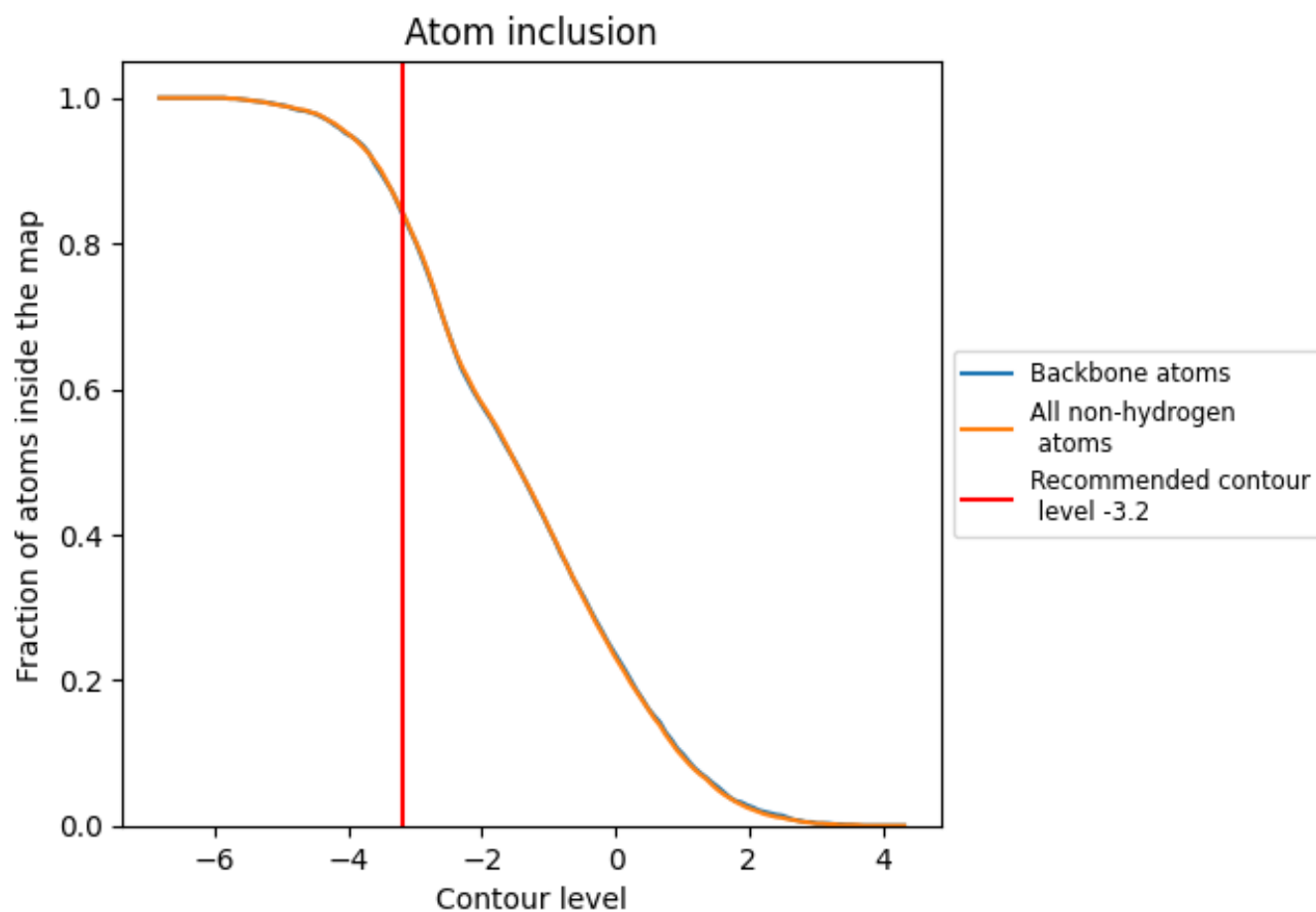
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (-3.2).









9.4 Atom inclusion [i](#)



At the recommended contour level, 84% 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 (-3.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8450	 0.0760
M	 0.6650	 0.0380
N	 0.9860	 0.1040
O	 0.5350	 0.0120

