



wwPDB EM Validation Summary Report ⓘ

Dec 10, 2022 – 08:45 am GMT

PDB ID : 5ANB
EMDB ID : EMD-3146
Title : Mechanism of eIF6 release from the nascent 60S ribosomal subunit
Authors : Weis, F.; Giudice, E.; Churcher, M.; Jin, L.; Hilcenko, C.; Wong, C.C.;
Traynor, D.; Kay, R.R.; Warren, A.J.
Deposited on : 2015-09-06
Resolution : 4.10 Å(reported)

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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.dev43
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) : 2.31.3

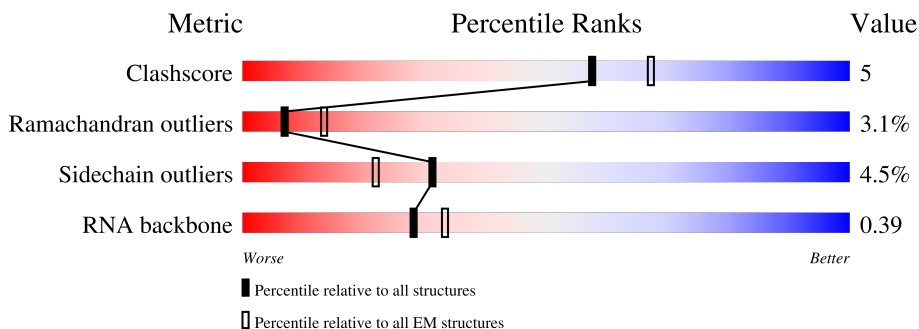
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.10 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.



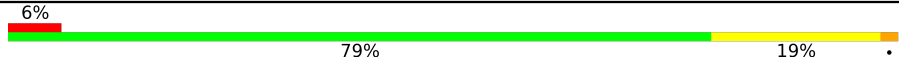
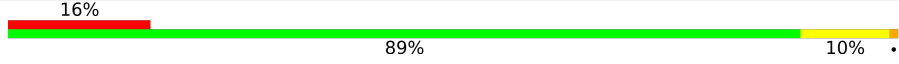
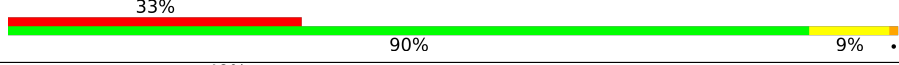
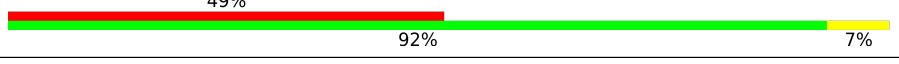

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 ≥ 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	398	
2	B	188	
3	C	205	
4	D	166	
5	E	136	
6	F	217	
7	G	69	

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Mol	Chain	Length	Quality of chain
8	H	52	
9	I	224	
10	J	250	
11	K	1120	
12	N	3741	

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 48493 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 60S RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	398	3176	2018	599	547	12	0	0

- Molecule 2 is a protein called 60S RIBOSOMAL PROTEIN L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	188	1491	944	264	277	6	0	0

- Molecule 3 is a protein called 60S ACIDIC RIBOSOMAL PROTEIN P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	205	1571	998	271	294	8	0	0

- Molecule 4 is a protein called 60S RIBOSOMAL PROTEIN L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	166	1245	790	220	228	7	0	0

- Molecule 5 is a protein called 60S RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	136	1017	640	188	181	8	0	0

- Molecule 6 is a protein called 60S RIBOSOMAL PROTEIN L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	217	1721	1079	332	297	13	0	0

- Molecule 7 is a protein called 60S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	69	586	378	105	99	4	0	0

- Molecule 8 is a protein called UBIQUITIN-60S RIBOSOMAL PROTEIN L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	52	427	269	88	64	6	0	0

- Molecule 9 is a protein called EUKARYOTIC TRANSLATION INITIATION FACTOR 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	I	224	1686	1048	290	338	10	0	0

- Molecule 10 is a protein called RIBOSOME MATURATION PROTEIN SBDS.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	250	2015	1272	352	380	11	0	0

- Molecule 11 is a protein called ELONGATION FACTOR TU GTP-BINDING DOMAIN-CONTAINING PROTEIN 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	K	1120	8800	5547	1518	1682	53	0	0

- Molecule 12 is a RNA chain called 26S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
12	N	1162	24758	11082	4431	8087	1158	0	0

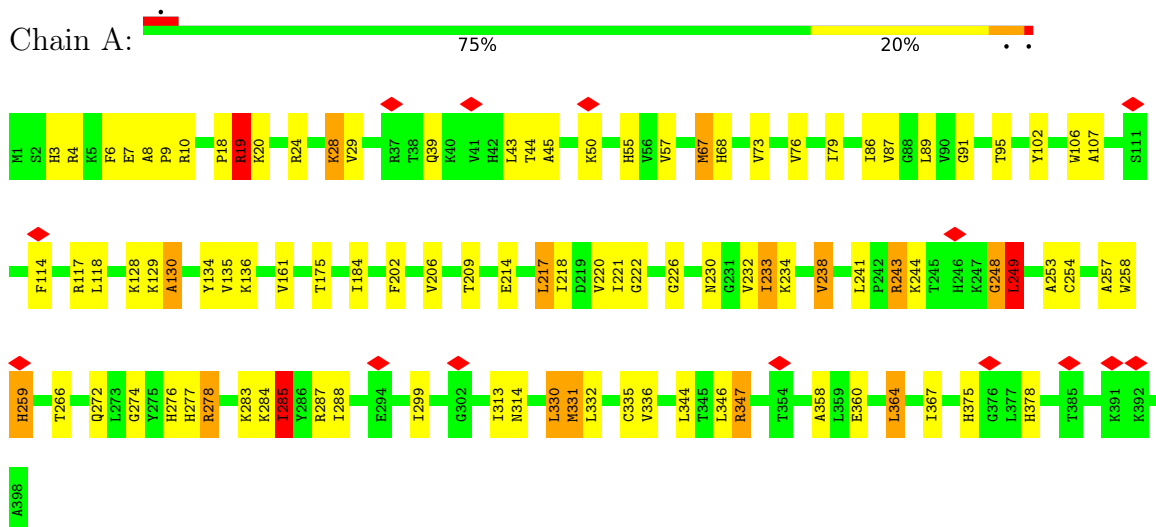
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
N	3119	C	G	conflict	GB FR733594.

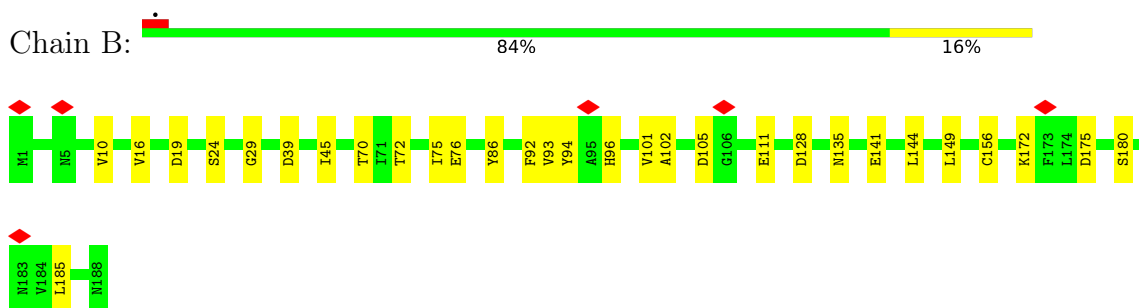
3 Residue-property plots [i](#)

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.

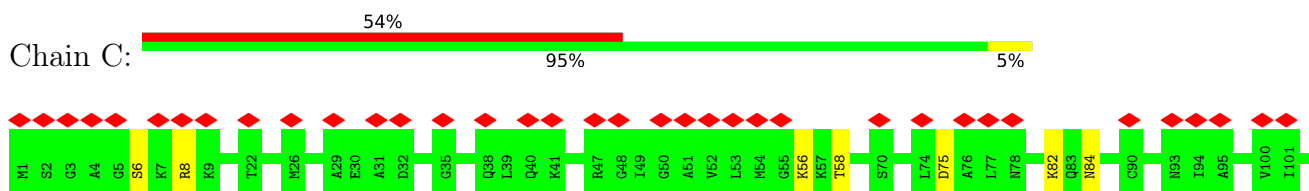
- Molecule 1: 60S RIBOSOMAL PROTEIN L3

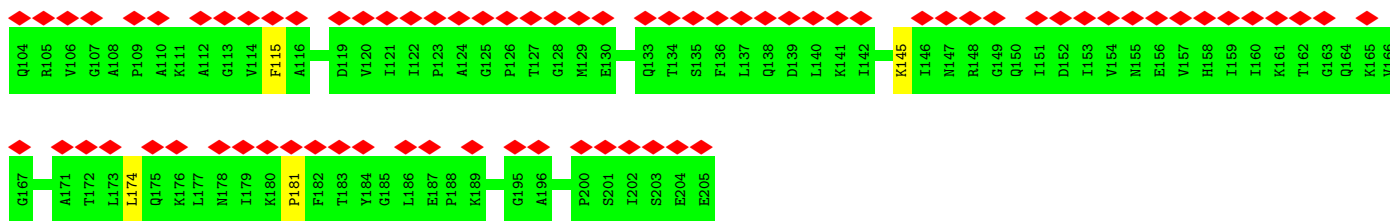


- Molecule 2: 60S RIBOSOMAL PROTEIN L9

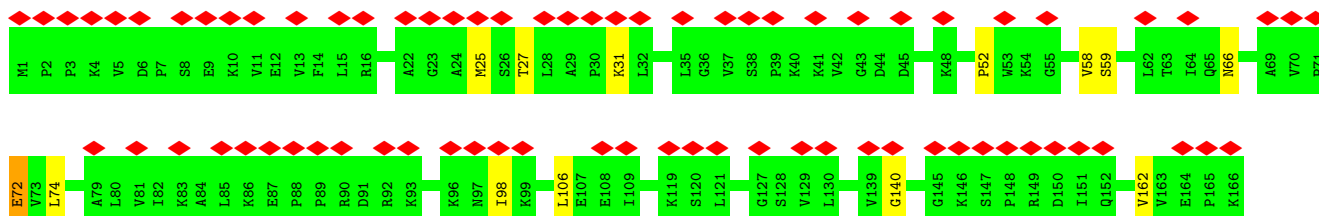
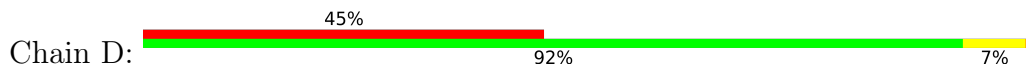


- Molecule 3: 60S ACIDIC RIBOSOMAL PROTEIN P0

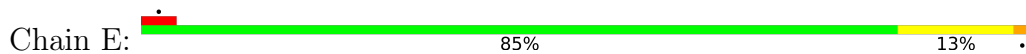




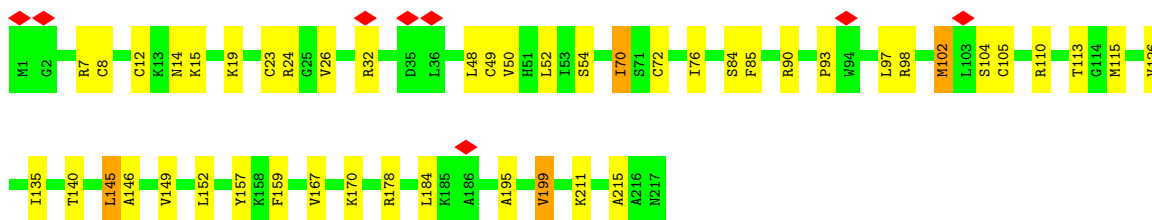
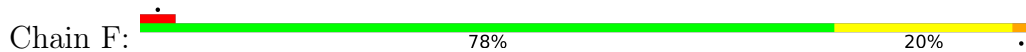
- Molecule 4: 60S RIBOSOMAL PROTEIN L12



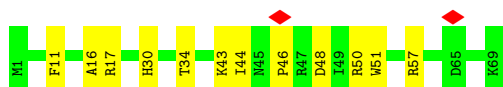
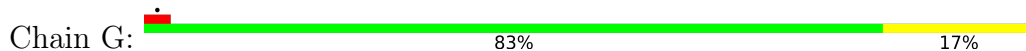
- Molecule 5: 60S RIBOSOMAL PROTEIN L23



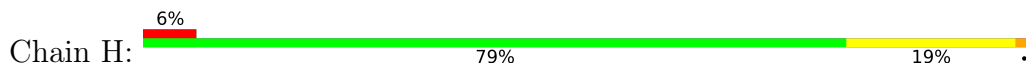
- Molecule 6: 60S RIBOSOMAL PROTEIN L10

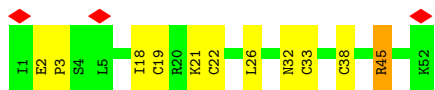


- Molecule 7: 60S RIBOSOMAL PROTEIN L24

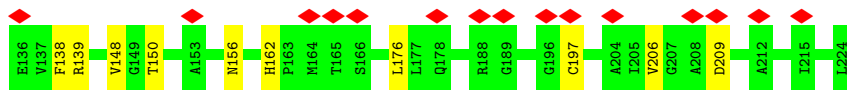
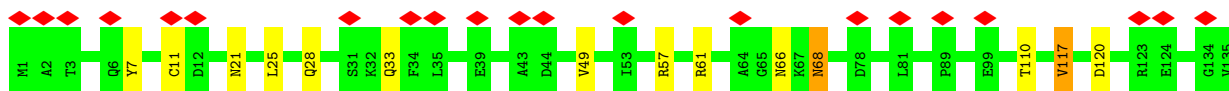
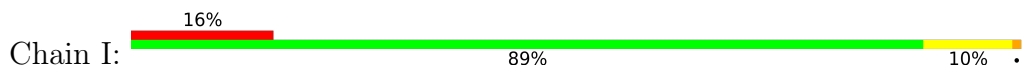


- Molecule 8: UBIQUITIN-60S RIBOSOMAL PROTEIN L40

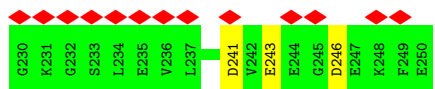
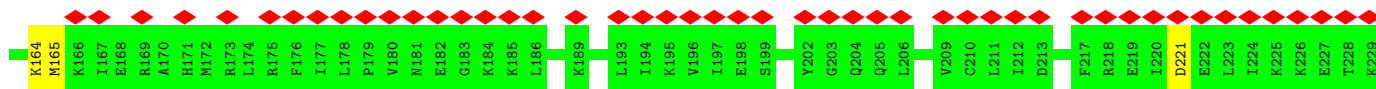
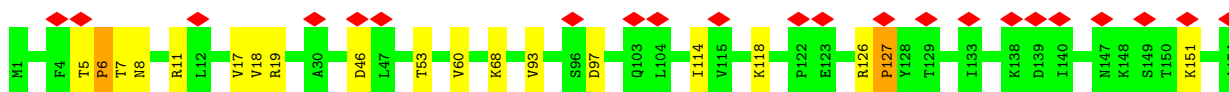
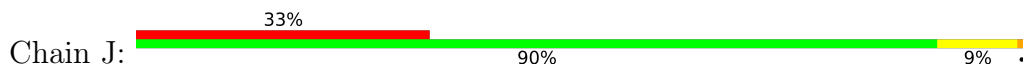




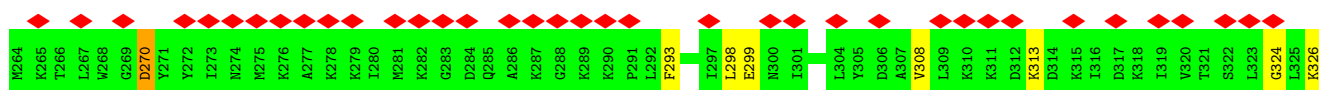
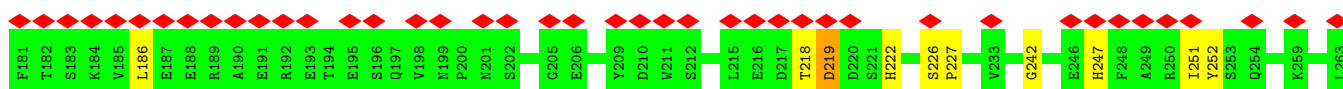
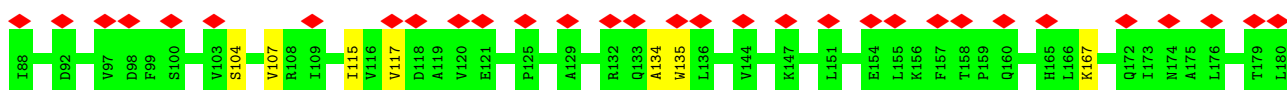
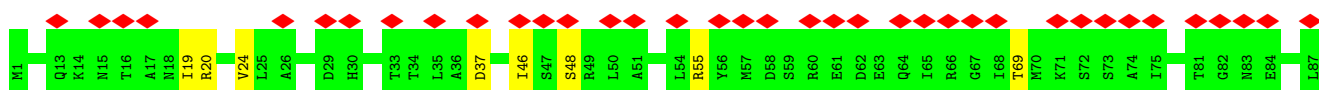
• Molecule 9: EUKARYOTIC TRANSLATION INITIATION FACTOR 6



• Molecule 10: RIBOSOME MATURATION PROTEIN SBDS



• Molecule 11: ELONGATION FACTOR TU GTP-BINDING DOMAIN-CONTAINING PROTEIN 1



U2982	G2983	A2984	G2985	G2986	G2987	G2988	G2989	G2990	G2991	G2992	G2993	G2994	G2995	G2996	G2997	G2998	G2999	A3000	A3007	C3008	A3009	
U2689	A2690	G2691	G2696	U2697	A2698	U2699	U2700	U2701	U2702	U2703	U2704	U2705	U2706	U2707	U2708	U2709	U2710	U2711	U2712	U2713	U2714	U2715
U2600	G2601	U2602	C2603	C2604	G2619	A2624	C2625	C2626	A2627	C2628	U2629	G2630	C2631	A2632	G2635	G2636	G2637	A2638	A2639	C2640	G2641	C2649
A2522	C2523	U2524	A2525	U2526	G2527	A2536	U2537	G2538	G2539	U2540	A2541	G2542	C2543	C2544	A2545	A2546	A2547	U2548	C2553	A2554	U2555	C2556
U2443	U2442	G2443	A2444	G2445	G2446	C2447	U2450	G2451	U2452	G2453	A2454	C2461	C2462	C2463	A2464	G2467	C2468	U2469	C2470	U2471	G2472	A2473
A2481	G2482	G2489	U2492	C2493	A2494	C2497	A2502	C2503	G2504	G2505	U2506	U2507	A2508	A2509	G2512	G2513	C2514	G2515	A2516	G2519	U2520	A2521
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U2568	U2569	U2570	U2571	U2572	U2573	U2574	U2575	U2576	U2577	U2578	U2579	U2580	U2581	U2582	U2583	U2584	U2585	U2586	U2587	U2588	U2589	U2590
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U2752	U2753	U2754	U2755	U2756	U2757	U2758	U2759	U2760	U2761	U2762	U2763	U2764	U2765	U2766	U2767	U2768	U2769	U2770	U2771	U2772	U2773	U2774
U2775	U2776	U2777	U2778	U2779	U2780	U2781	U2782	U2783	U2784	U2785	U2786	U2787	U2788	U2789	U2790	U2791	U2792	U2793	U2794	U2795	U2796	U2797
U2798	U2799	U2800	U2801	U2802	U2803	U2804	U2805	U2806	U2807	U2808	U2809	U2810	U2811	U2812	U2813	U2814	U2815	U2816	U2817	U2818	U2819	U2820
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U2982	U2983	U2984	U2985	U2986	U2987	U2988	U2989	U2990	U2991	U2992	U2993	U2994	U2995	U2996	U2997	U2998	U2999	U3000	U3007	U3008	U3009	U3010

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	11970	Depositor
Resolution determination method	Not provided	
CTF correction method	EACH PARTICLE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	2200	Depositor
Maximum defocus (nm)	2800	Depositor
Magnification	105263	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.646	Depositor
Minimum map value	-0.444	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.028	Depositor
Recommended contour level	0.06	Depositor
Map size (\AA)	399.0, 399.0, 399.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.33, 1.33, 1.33	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	A	0.53	0/3241	0.85	3/4339 (0.1%)
2	B	0.41	0/1510	0.72	0/2030
3	C	0.38	0/1592	0.57	0/2142
4	D	0.38	0/1265	0.61	0/1702
5	E	0.44	0/1032	0.75	0/1386
6	F	0.46	0/1752	0.77	0/2345
7	G	0.52	0/600	0.78	0/801
8	H	0.43	0/433	0.79	0/571
9	I	0.40	0/1706	0.66	0/2325
10	J	0.43	0/2038	0.67	0/2727
11	K	0.41	0/8969	0.64	0/12124
12	N	0.38	1/27702 (0.0%)	0.79	12/43160 (0.0%)
All	All	0.41	1/51840 (0.0%)	0.75	15/75652 (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
1	A	0	1
2	B	0	1
6	F	0	1
10	J	0	1
11	K	0	1
All	All	0	5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	N	3316	C	O3'-P	5.09	1.67	1.61

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	N	2995	G	C2'-C3'-O3'	9.35	130.07	109.50
12	N	2515	G	C2'-C3'-O3'	7.63	126.29	109.50
1	A	249	LEU	CA-CB-CG	7.36	132.22	115.30
12	N	3303	C	C2'-C3'-O3'	7.04	124.98	109.50
12	N	1525	G	C2'-C3'-O3'	6.83	124.63	113.70

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	258	TRP	Peptide
2	B	96	HIS	Peptide
6	F	70	ILE	Peptide
10	J	126	ARG	Peptide
11	K	226	SER	Peptide

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	A	3176	0	3319	51	0
2	B	1491	0	1555	13	0
3	C	1571	0	1657	1	0
4	D	1245	0	1338	0	0
5	E	1017	0	1076	11	0
6	F	1721	0	1778	22	0
7	G	586	0	601	3	0
8	H	427	0	483	7	0
9	I	1686	0	1685	9	0
10	J	2015	0	2112	10	0
11	K	8800	0	8840	16	0
12	N	24758	0	12487	311	0
All	All	48493	0	36931	427	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 5.

The worst 5 of 427 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)
12:N:2989:A:N6	12:N:3046:U:N3	2.19	0.89
12:N:2989:A:N6	12:N:3046:U:H3	1.73	0.87
6:F:50:VAL:HG12	6:F:167:VAL:HG22	1.57	0.86
5:E:45:ARG:NH1	12:N:3379:C:OP1	2.13	0.79
1:A:285:ILE:HD11	1:A:330:LEU:HG	1.68	0.75

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	396/398 (100%)	306 (77%)	65 (16%)	25 (6%)	1	19
2	B	186/188 (99%)	167 (90%)	16 (9%)	3 (2%)	9	43
3	C	203/205 (99%)	180 (89%)	21 (10%)	2 (1%)	15	52
4	D	164/166 (99%)	138 (84%)	21 (13%)	5 (3%)	4	31
5	E	134/136 (98%)	117 (87%)	13 (10%)	4 (3%)	4	31
6	F	215/217 (99%)	169 (79%)	39 (18%)	7 (3%)	4	29
7	G	67/69 (97%)	58 (87%)	7 (10%)	2 (3%)	4	31
8	H	50/52 (96%)	40 (80%)	9 (18%)	1 (2%)	7	39
9	I	222/224 (99%)	200 (90%)	21 (10%)	1 (0%)	29	67
10	J	248/250 (99%)	225 (91%)	17 (7%)	6 (2%)	6	35
11	K	1118/1120 (100%)	921 (82%)	160 (14%)	37 (3%)	4	29
All	All	3003/3025 (99%)	2521 (84%)	389 (13%)	93 (3%)	7	31

5 of 93 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	129	LYS
1	A	130	ALA

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Continued from previous page...

Mol	Chain	Res	Type
5	E	6	ALA
6	F	195	ALA
7	G	46	PRO

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	
1	A	337/337 (100%)	312 (93%)	25 (7%)	13	41
2	B	168/168 (100%)	160 (95%)	8 (5%)	25	53
3	C	172/172 (100%)	165 (96%)	7 (4%)	30	57
4	D	139/139 (100%)	130 (94%)	9 (6%)	17	45
5	E	108/108 (100%)	105 (97%)	3 (3%)	43	65
6	F	180/180 (100%)	168 (93%)	12 (7%)	16	44
7	G	65/65 (100%)	58 (89%)	7 (11%)	6	26
8	H	48/48 (100%)	45 (94%)	3 (6%)	18	46
9	I	190/190 (100%)	181 (95%)	9 (5%)	26	53
10	J	228/228 (100%)	219 (96%)	9 (4%)	32	58
11	K	975/975 (100%)	950 (97%)	25 (3%)	46	67
All	All	2610/2610 (100%)	2493 (96%)	117 (4%)	31	54

5 of 117 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	F	54	SER
11	K	737	ASP
8	H	26	LEU
11	K	724	ASP
11	K	219	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
11	K	340	GLN
11	K	668	GLN
5	E	10	ASN
5	E	5	GLN
11	K	818	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
12	N	1158/3741 (30%)	320 (27%)	46 (3%)

5 of 320 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
12	N	1225	G
12	N	1229	U
12	N	1233	G
12	N	1239	G
12	N	1242	A

5 of 46 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
12	N	3022	A
12	N	3219	U
12	N	3060	A
12	N	3170	A
12	N	3283	G

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 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](#)

There are no chain breaks in this entry.

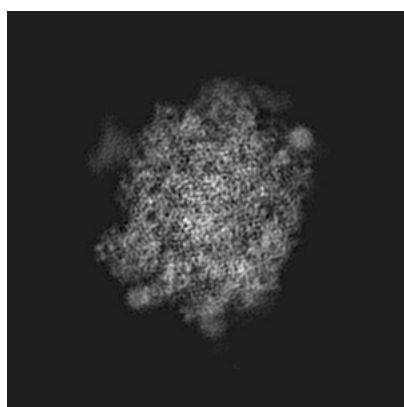
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3146. These allow visual inspection of the internal detail of the map and identification of artifacts.

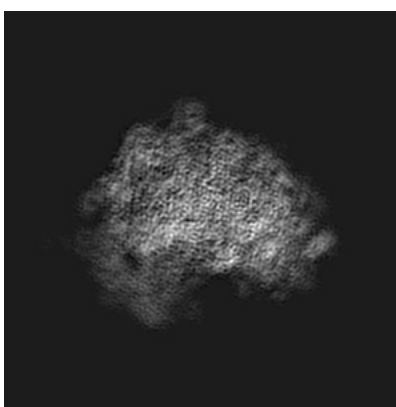
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

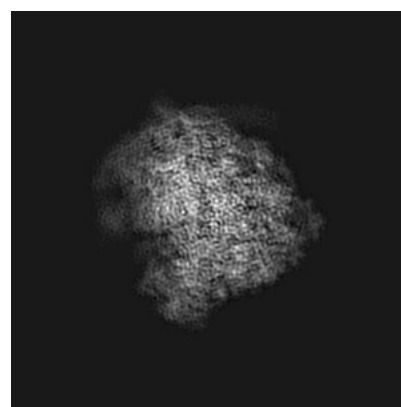
6.1.1 Primary map



X



Y

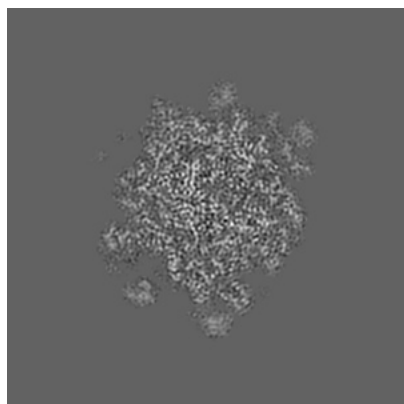


Z

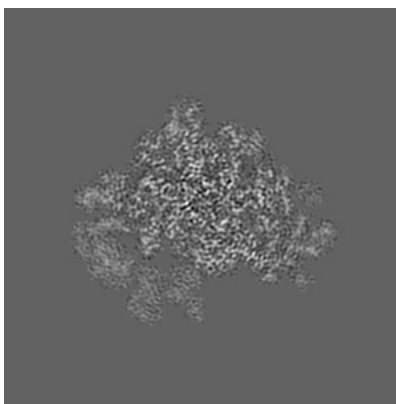
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 150



Y Index: 150

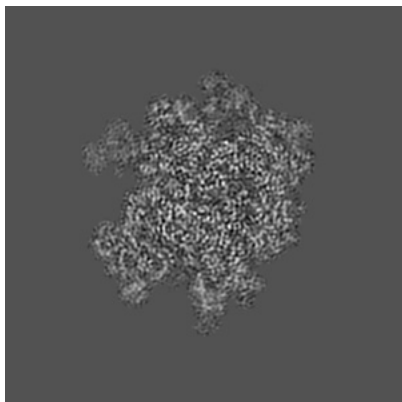


Z Index: 150

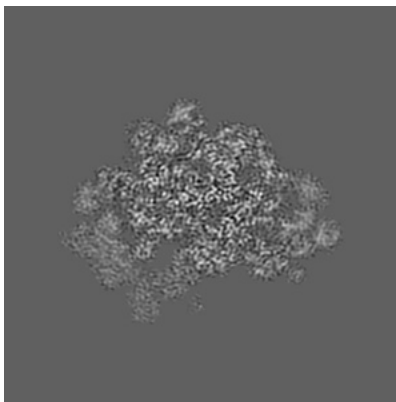
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

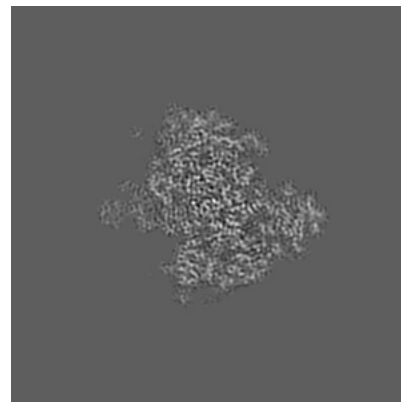
6.3.1 Primary map



X Index: 137



Y Index: 155

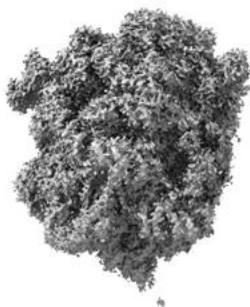


Z Index: 140

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

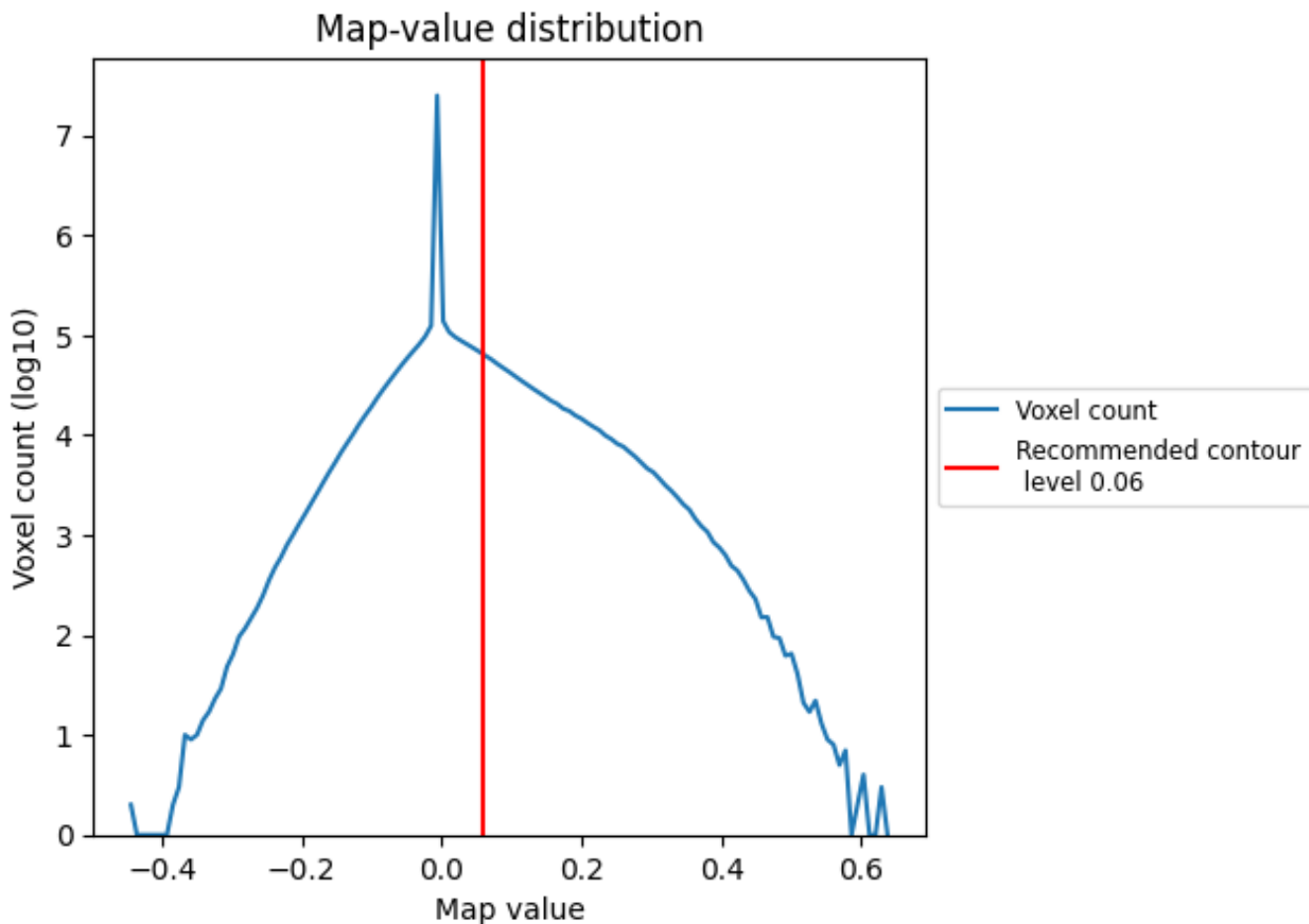
6.5 Mask visualisation

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

7 Map analysis [i](#)

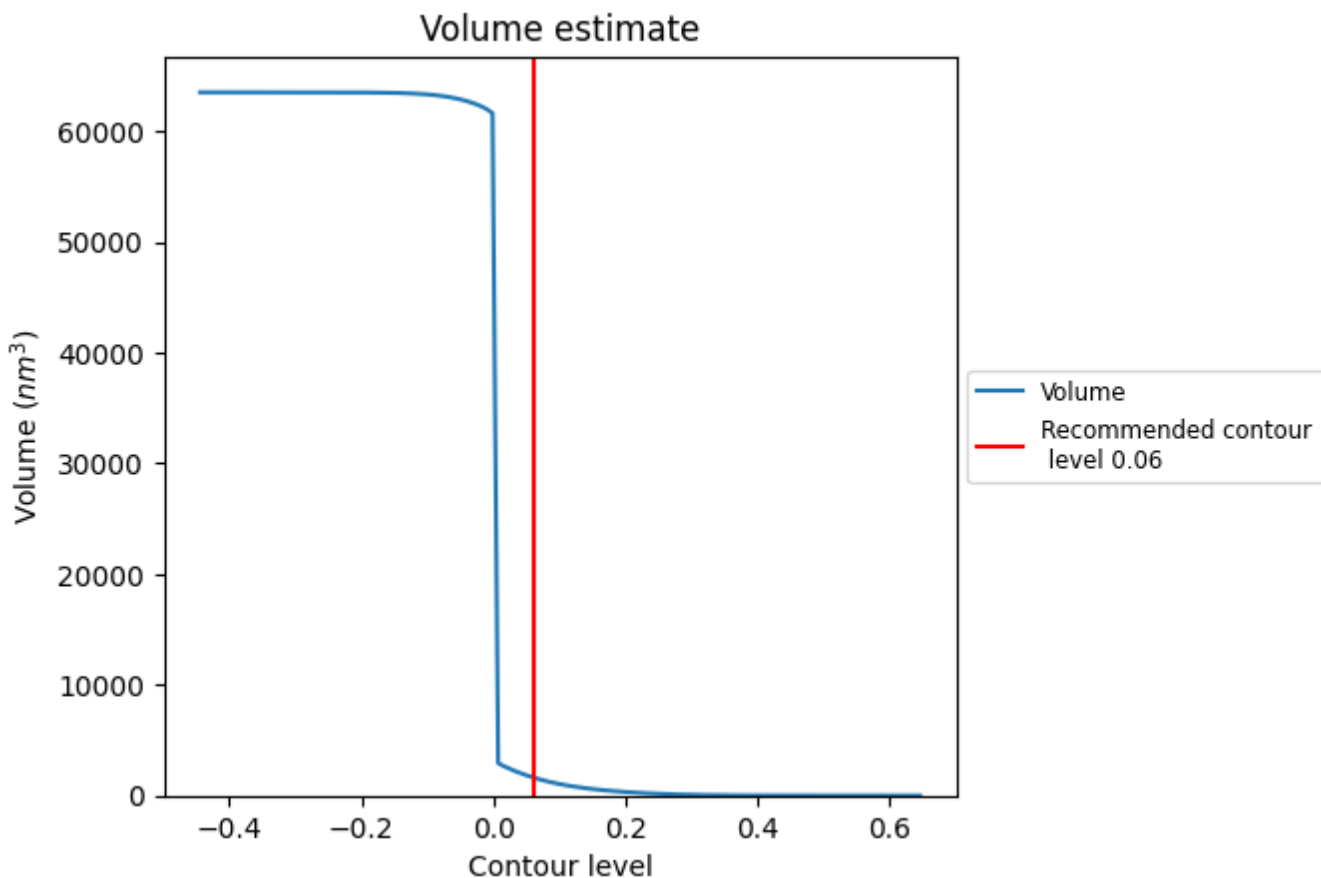
This section contains the results of statistical analysis of the map.

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.

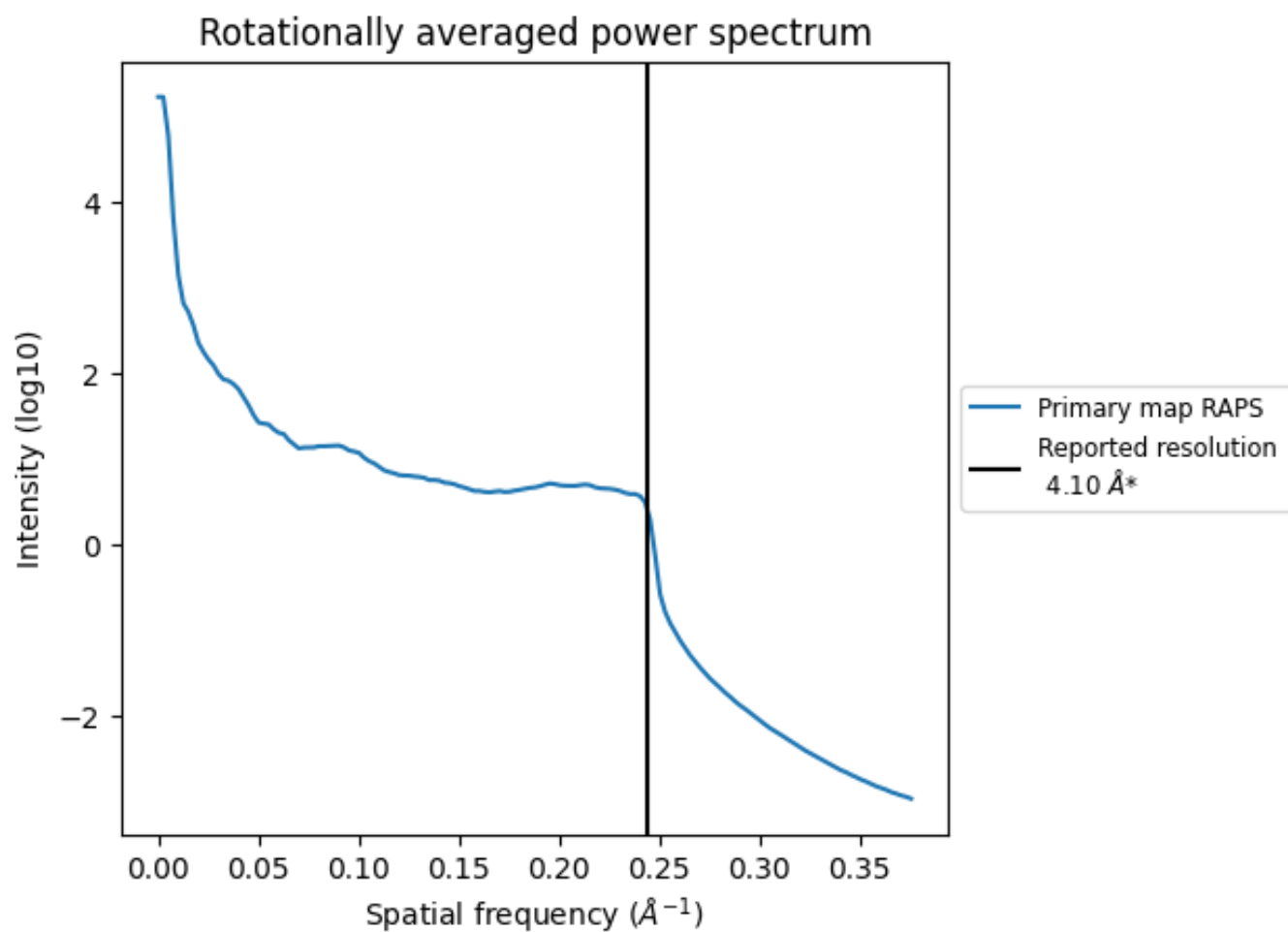
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1641 nm³; this corresponds to an approximate mass of 1483 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 0.244\AA^{-1}

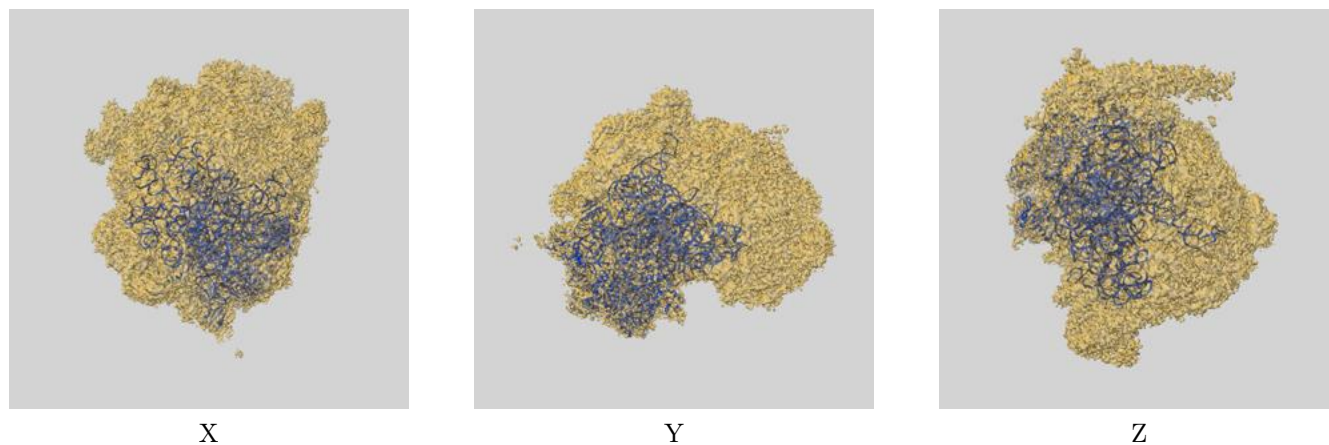
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

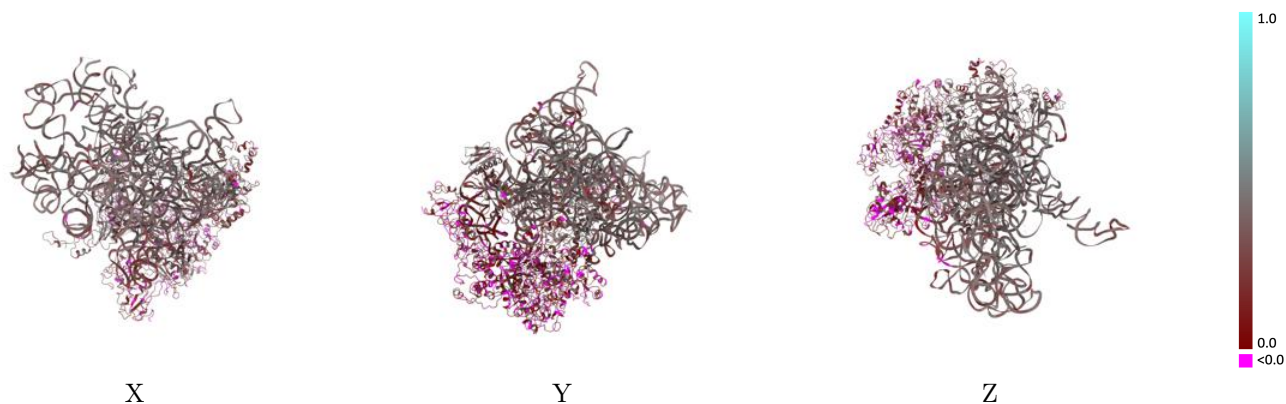
This section contains information regarding the fit between EMDB map EMD-3146 and PDB model 5ANB. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



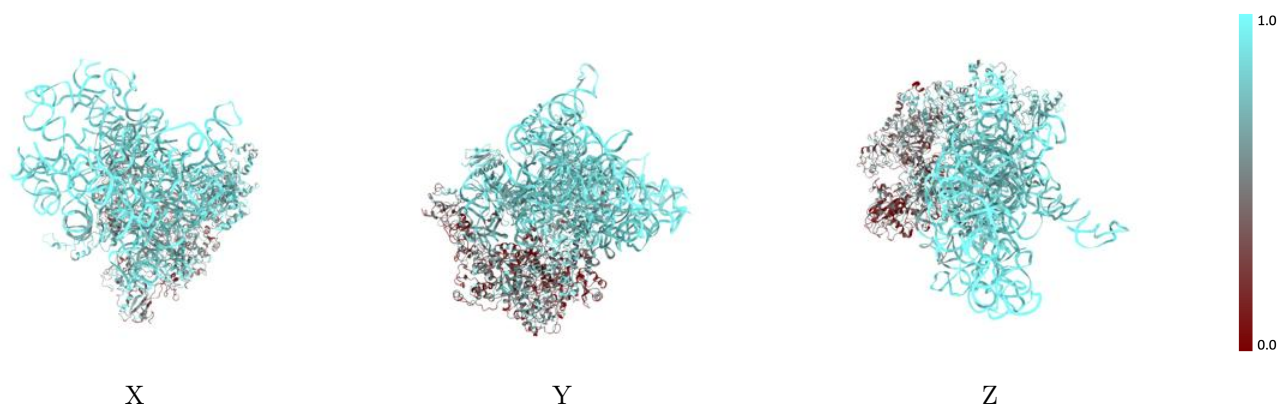
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



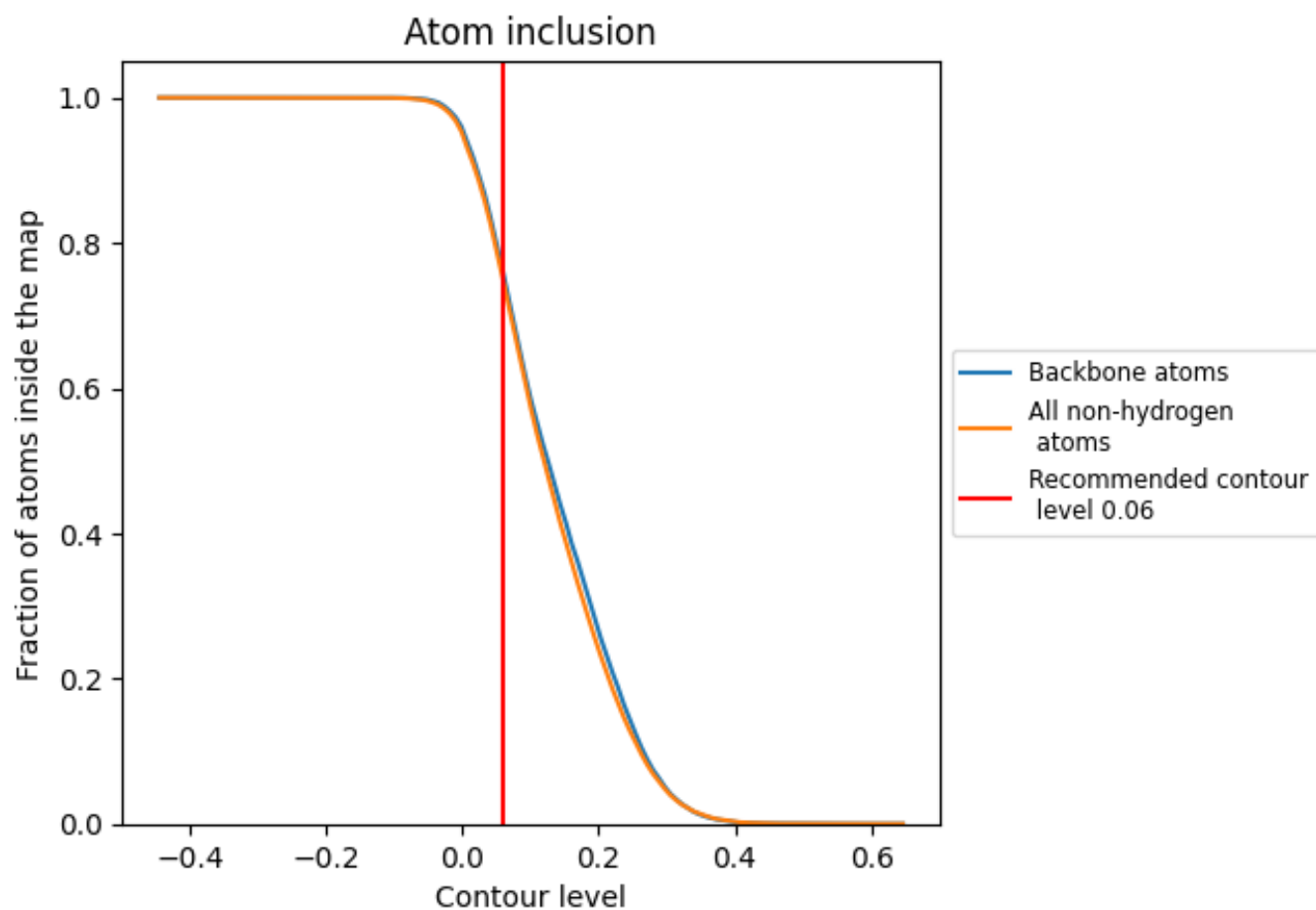
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.06).



























9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 75% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7487	 0.2980
A	 0.8223	 0.3540
B	 0.7936	 0.3380
C	 0.3800	 0.1330
D	 0.4586	 0.1310
E	 0.7934	 0.3840
F	 0.8067	 0.3690
G	 0.8042	 0.3130
H	 0.7627	 0.3590
I	 0.6578	 0.2510
J	 0.5237	 0.2240
K	 0.4131	 0.1290
N	 0.9086	 0.3660

