



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 05:32 PM UTC

PDB ID : 6ZVK / pdb_00006zvz
EMDB ID : EMD-11459
Title : The Halastavi arva virus (HalV) intergenic region IRES promotes translation by the simplest possible initiation mechanism
Authors : Abaeva, I.S.; Vicens, Q.; Bochler, A.; Soufari, H.; Simonetti, A.; Pestova, T.; Hashem, Y.; Hellen, C.U.T.
Deposited on : 2020-07-24
Resolution : 3.49 Å(reported)

This is a Full wwPDB EM Validation 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>.

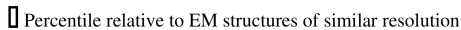
The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
MolProbity : **FAILED**
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

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ELECTRON MICROSCOPY

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	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Q-score	25397	13600 (2.99 - 3.99)

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 228291 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 Ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Z2	138	Total	C	N	O	S	0	0
			1138	727	221	183	7		

- Molecule 2 is a RNA chain called 28S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	e2	3920	Total	C	N	O	P	0	0
			83971	37399	15349	27313	3910		

- Molecule 3 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	d2	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 4 is a RNA chain called 5.8S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	h2	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 5 is a protein called 60S RIBOSOMAL PROTEIN EL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	p2	69	Total	C	N	O	S	0	0
			568	364	103	100	1		

- Molecule 6 is a protein called 60S RIBOSOMAL PROTEIN UL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	w2	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
w2	174	LEU	ILE	conflict	UNP G5B8P1
w2	194	ASP	GLU	conflict	UNP G5B8P1

- Molecule 7 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H2	153	Total	C	N	O	S	0	0
			1243	777	241	216	9		

- Molecule 8 is a protein called 60S RIBOSOMAL PROTEIN EL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	S2	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 9 is a protein called 60S RIBOSOMAL PROTEIN EL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	32	180	Total	C	N	O	S	0	0
			1509	933	328	239	9		

- Molecule 10 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	52	394	Total	C	N	O	S	0	0
			3173	2020	597	543	13		

- Molecule 11 is a protein called 60S RIBOSOMAL PROTEIN EL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	62	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 12 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	72	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 13 is a protein called Ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	82	99	Total	C	N	O	S	0	0
			809	518	141	148	2		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
82	32	GLY	ARG	conflict	UNP G1TSG1
82	36	ALA	GLU	conflict	UNP G1TSG1
82	39	PHE	SER	conflict	UNP G1TSG1
82	54	GLY	ARG	conflict	UNP G1TSG1
82	60	VAL	ALA	conflict	UNP G1TSG1
82	97	ARG	HIS	conflict	UNP G1TSG1

- Molecule 14 is a protein called eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	k2	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 15 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	l2	63	Total	C	N	O	S	0	0
			529	337	103	86	3		

- Molecule 16 is a protein called 60S RIBOSOMAL PROTEIN UL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	m2	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

- Molecule 17 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	o2	134	Total	C	N	O	S	0	0
			1116	700	226	187	3		

- Molecule 18 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	q2	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 19 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	r2	75	Total	C	N	O	S	0	0
			610	378	130	99	3		

- Molecule 20 is a protein called Ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	13	94	Total	C	N	O	S	0	0
			733	464	130	133	6		

- Molecule 21 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	t2	362	Total	C	N	O	S	0	0
			2884	1812	577	481	14		

- Molecule 22 is a protein called eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	u2	107	Total	C	N	O	S	0	0
			889	560	171	156	2		

- Molecule 23 is a protein called eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	v2	128	Total	C	N	O	S	0	0
			1054	667	216	166	5		

- Molecule 24 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	x2	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 25 is a protein called eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	y2	114	Total	C	N	O	S	0	0
			907	566	187	148	6		

- Molecule 26 is a protein called 60S RIBOSOMAL PROTEIN UL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	92	244	Total	C	N	O	S	0	0
			1869	1171	382	310	6		

- Molecule 27 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	A2	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 28 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	B2	102	Total	C	N	O	S	0	0
			831	520	176	130	5		

- Molecule 29 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	C2	86	Total	C	N	O	S	0	0
			706	434	155	112	5		

- Molecule 30 is a protein called ribosomal protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	D2	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 31 is a protein called 60S RIBOSOMAL PROTEIN EL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	E2	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 32 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	F2	104	Total	C	N	O	S	0	0
			852	533	174	139	6		

- Molecule 33 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	G2	292	Total	C	N	O	S	0	0
			2387	1509	437	427	14		

- Molecule 34 is a protein called ribosomal protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	I2	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 35 is a protein called 60S RIBOSOMAL PROTEIN EL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	J2	125	Total	C	N	O	S	0	0
			1002	621	206	169	6		

- Molecule 36 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	K2	198	Total	C	N	O	S	0	0
			1524	969	265	281	9		

- Molecule 37 is a protein called Ribosomal protein L10 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
37	L2	102	Total	C	N	O	S	0	0
			834	527	161	137	9		

- Molecule 38 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	M2	156	Total	C	N	O	S	0	0
			1183	738	221	219	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M2	49	GLY	ALA	conflict	UNP G1SMR7

- Molecule 39 is a protein called Ribosomal_L6e_N domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	R2	35	Total	C	N	O	S	0	0
			285	179	59	45	2		

- Molecule 40 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	T2	201	Total	C	N	O	S	0	0
			1614	1039	301	273	1		

- Molecule 41 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	U2	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 42 is a protein called 60S RIBOSOMAL PROTEIN EL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	V2	233	Total	C	N	O	S	0	0
			1872	1193	361	314	4		

- Molecule 43 is a protein called 60S RIBOSOMAL PROTEIN UL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	W2	190	Total	C	N	O	S	0	0
			1517	954	284	273	6		

- Molecule 44 is a protein called Ribosomal protein L10 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
44	X2	102	Total	C	N	O	S	0	0
			822	524	158	136	4		

- Molecule 45 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Y2	169	Total	C	N	O	S	0	0
			1354	855	252	241	6		

- Molecule 46 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	a7	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a7	47	ALA	-	insertion	UNP G1TPV0
a7	48	PRO	-	insertion	UNP G1TPV0
a7	49	ARG	-	insertion	UNP G1TPV0
a7	50	PRO	-	insertion	UNP G1TPV0
a7	51	ALA	-	insertion	UNP G1TPV0
a7	52	ALA	-	insertion	UNP G1TPV0
a7	53	GLY	-	insertion	UNP G1TPV0
a7	54	PRO	-	insertion	UNP G1TPV0
a7	55	ILE	-	insertion	UNP G1TPV0

- Molecule 47 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	12	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 48 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	22	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 49 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	42	217	Total	C	N	O	S	0	0
			1744	1114	314	307	9		

- Molecule 50 is a RNA chain called INTERNAL RIBOSOME ENTRY SITE.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	E1	153	Total	C	N	O	P	0	0
			3208	1443	529	1083	153		

- Molecule 51 is a protein called Ribosomal_S10 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	I3	104	Total	C	N	O	S	0	0
			822	514	156	148	4		

- Molecule 52 is a protein called 40S RIBOSOMAL PROTEIN ES30.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	s3	43	Total	C	N	O	S	0	0
			350	215	80	54	1		

- Molecule 53 is a protein called Ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	G3	153	Total	C	N	O	S	0	0
			1247	793	234	214	6		

- Molecule 54 is a protein called ribosomal protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	f3	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 55 is a RNA chain called 18S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	K3	1869	Total	C	N	O	P	0	0
			39862	17789	7142	13063	1868		

- Molecule 56 is a protein called 40S RIBOSOMAL PROTEIN ES7.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	P3	189	Total	C	N	O	S	0	0
			1522	969	280	272	1		

- Molecule 57 is a protein called 40S RIBOSOMAL PROTEIN US11.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	a5	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 58 is a protein called ribosomal protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	A3	127	Total	C	N	O	S	0	0
			1061	673	201	180	7		

- Molecule 59 is a protein called 40S RIBOSOMAL PROTEIN US9.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	B3	141	Total	C	N	O	S	0	0
			1124	715	212	194	3		

- Molecule 60 is a protein called 40S RIBOSOMAL PROTEIN ES17.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	C3	129	Total	C	N	O	S	0	0
			1048	658	193	192	5		

- Molecule 61 is a protein called 40S RIBOSOMAL PROTEIN ES21.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	D3	83	Total	C	N	O	S	0	0
			631	387	118	121	5		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D3	3	SER	ASN	conflict	UNP A0A1Z5KTU7
D3	4	ASN	ASP	conflict	UNP A0A1Z5KTU7
D3	33	PRO	GLN	conflict	UNP A0A1Z5KTU7
D3	50	SER	PHE	conflict	UNP A0A1Z5KTU7
D3	76	HIS	ASP	conflict	UNP A0A1Z5KTU7

- Molecule 62 is a protein called ribosomal protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	G5	137	Total	C	N	O	S	0	0
			1140	714	231	194	1		

- Molecule 63 is a protein called 40S RIBOSOMAL PROTEIN ES19.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	H5	141	Total	C	N	O	S	0	0
			1113	701	213	196	3		

- Molecule 64 is a protein called Ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	J5	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 65 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	I5	126	Total	C	N	O	S	0	0
			1024	646	200	173	5		

- Molecule 66 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	L3	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 67 is a protein called ribosomal protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	M3	75	Total	C	N	O	S	0	0
			599	382	111	105	1		

- Molecule 68 is a protein called 40S RIBOSOMAL PROTEIN ES26.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	O3	98	Total	C	N	O	S	0	0
			782	486	161	130	5		

- Molecule 69 is a protein called 40S RIBOSOMAL PROTEIN ES31.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Q3	63	Total	C	N	O	S	0	0
			528	336	99	87	6		

- Molecule 70 is a protein called ribosomal protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	a3	313	Total	C	N	O	S	0	0
			2437	1535	424	466	12		

- Molecule 71 is a protein called Ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	T3	141	Total	C	N	O	S	0	0
			1099	693	219	184	3		

- Molecule 72 is a protein called 40S_SA_C domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	U3	208	Total	C	N	O	S	0	0
			1645	1046	289	302	8		

- Molecule 73 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	V3	213	Total	C	N	O	S	0	0
			1730	1098	309	309	14		

- Molecule 74 is a protein called S5 DRBM domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	W3	218	Total	C	N	O	S	0	0
			1691	1094	289	298	10		

- Molecule 75 is a protein called 60s ribosomal protein l41.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	X3	23	Total	C	N	O	S	0	0
			223	134	61	26	2		

- Molecule 76 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Y3	227	Total	C	N	O	S	0	0
			1765	1124	317	316	8		

- Molecule 77 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	j3	262	Total	C	N	O	S	0	0
			2075	1324	384	358	9		

- Molecule 78 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	N3	191	Total	C	N	O	S	0	0
			1509	943	286	273	7		

- Molecule 79 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	b3	237	Total	C	N	O	S	0	0
			1924	1200	387	330	7		

- Molecule 80 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	c3	206	Total	C	N	O	S	0	0
			1687	1058	332	292	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
c3	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 81 is a protein called Ribosomal protein S9 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
81	d3	185	Total	C	N	O	S	0	0
			1526	969	306	249	2		

- Molecule 82 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	e3	124	Total	C	N	O	S	0	0
			958	600	170	179	9		

- Molecule 83 is a protein called ribosomal protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	F3	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 84 is a protein called S10_ plectin domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	E3	98	Total	C	N	O	S	0	0
			828	539	148	135	6		

- Molecule 85 is a protein called ribosomal protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	H3	53	Total	C	N	O	S	0	0
			445	278	90	72	5		

- Molecule 86 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
86	C2	1	Total	Zn	0
			1	1	
86	E2	1	Total	Zn	0
			1	1	
86	F2	1	Total	Zn	0
			1	1	
86	I2	1	Total	Zn	0
			1	1	
86	O3	1	Total	Zn	0
			1	1	
86	H3	1	Total	Zn	0
			1	1	

MolProbity failed to run properly - this section is therefore empty.

3 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	55589	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	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.250	Depositor
Minimum map value	-0.153	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.027	Depositor
Map size (Å)	396.0, 396.0, 396.0	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	Depositor

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

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

There are no non-standard protein/DNA/RNA residues in this entry.

4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 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.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

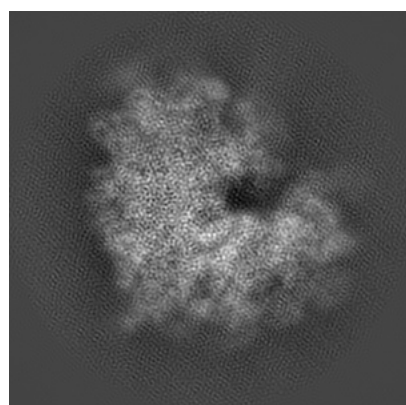
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11459. These allow visual inspection of the internal detail of the map and identification of artifacts.

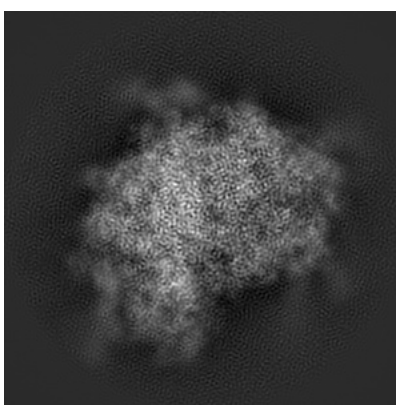
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

5.1 Orthogonal projections [i](#)

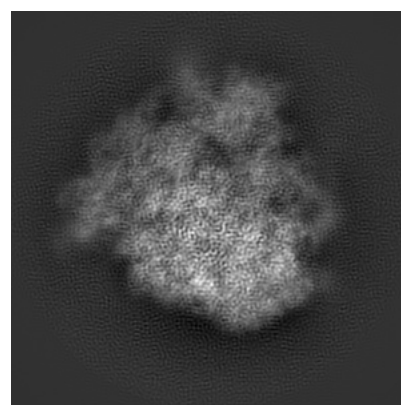
5.1.1 Primary map



X



Y

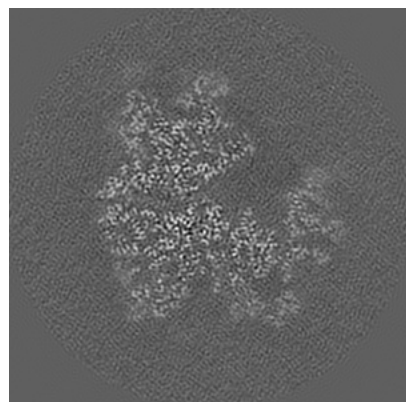


Z

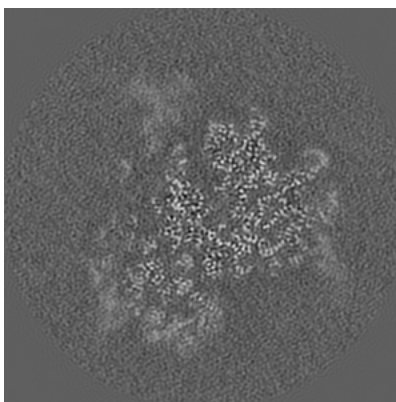
The images above show the map projected in three orthogonal directions.

5.2 Central slices [i](#)

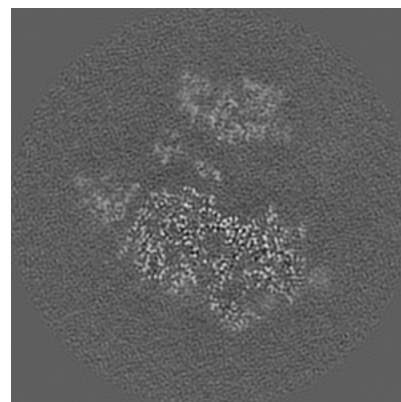
5.2.1 Primary map



X Index: 180



Y Index: 180

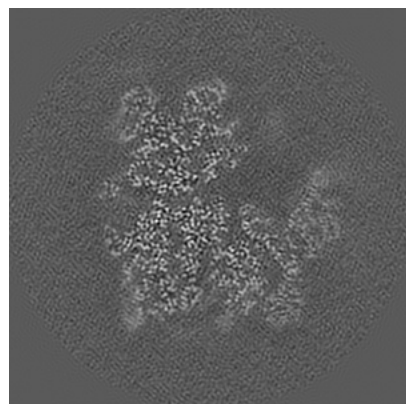


Z Index: 180

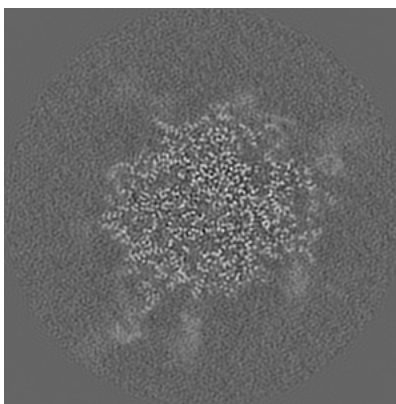
The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices [i](#)

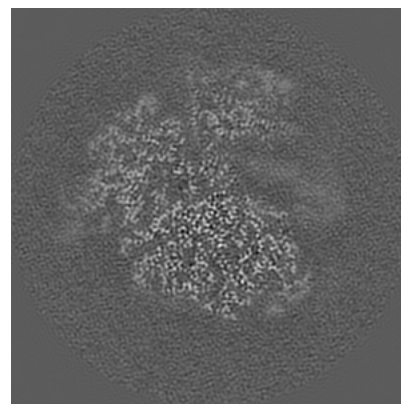
5.3.1 Primary map



X Index: 172



Y Index: 156

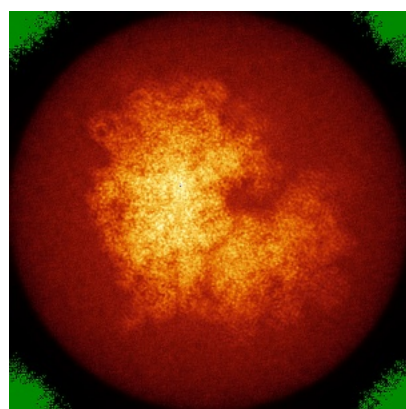


Z Index: 157

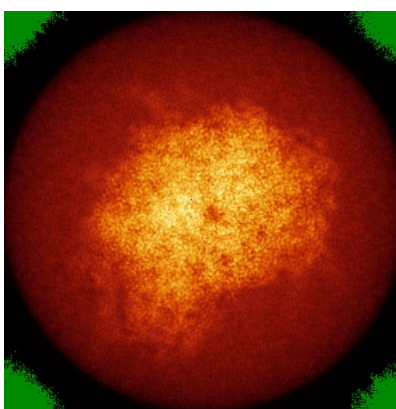
The images above show the largest variance slices of the map in three orthogonal directions.

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

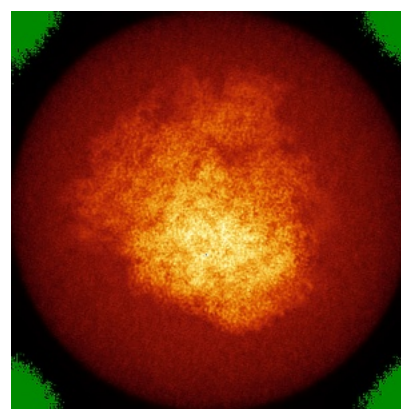
5.4.1 Primary map



X



Y

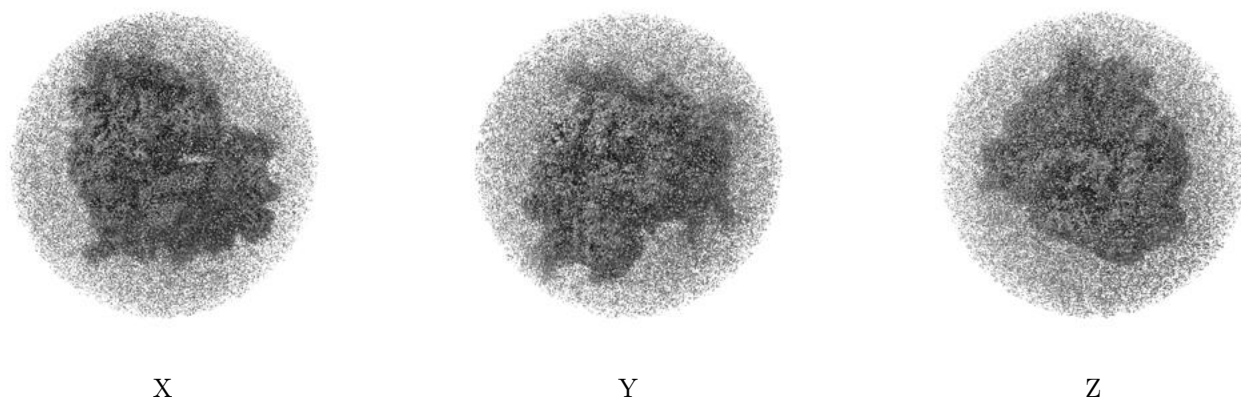


Z

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.

5.5 Orthogonal surface views [i](#)

5.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.027. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

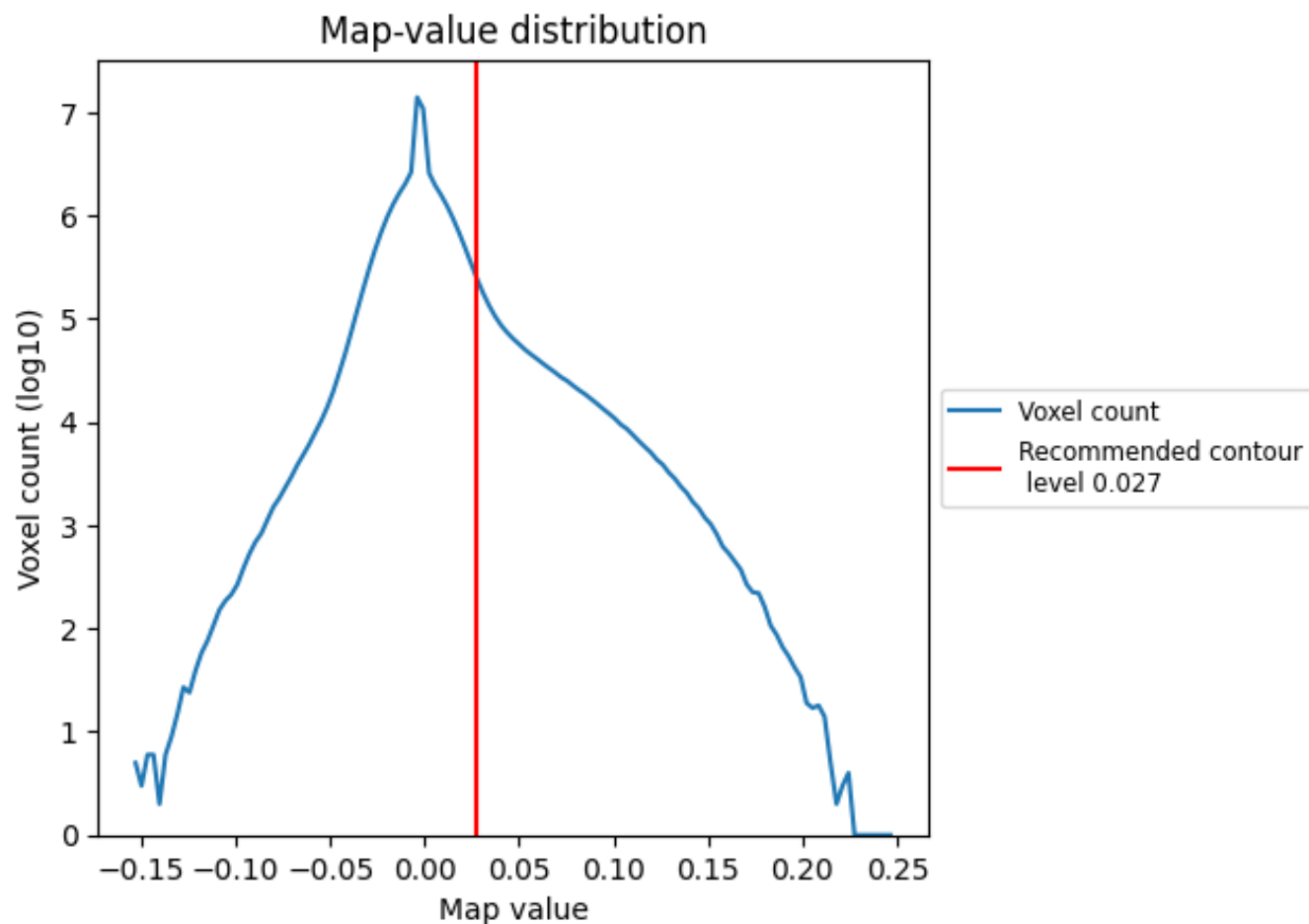
5.6 Mask visualisation [i](#)

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

6 Map analysis [i](#)

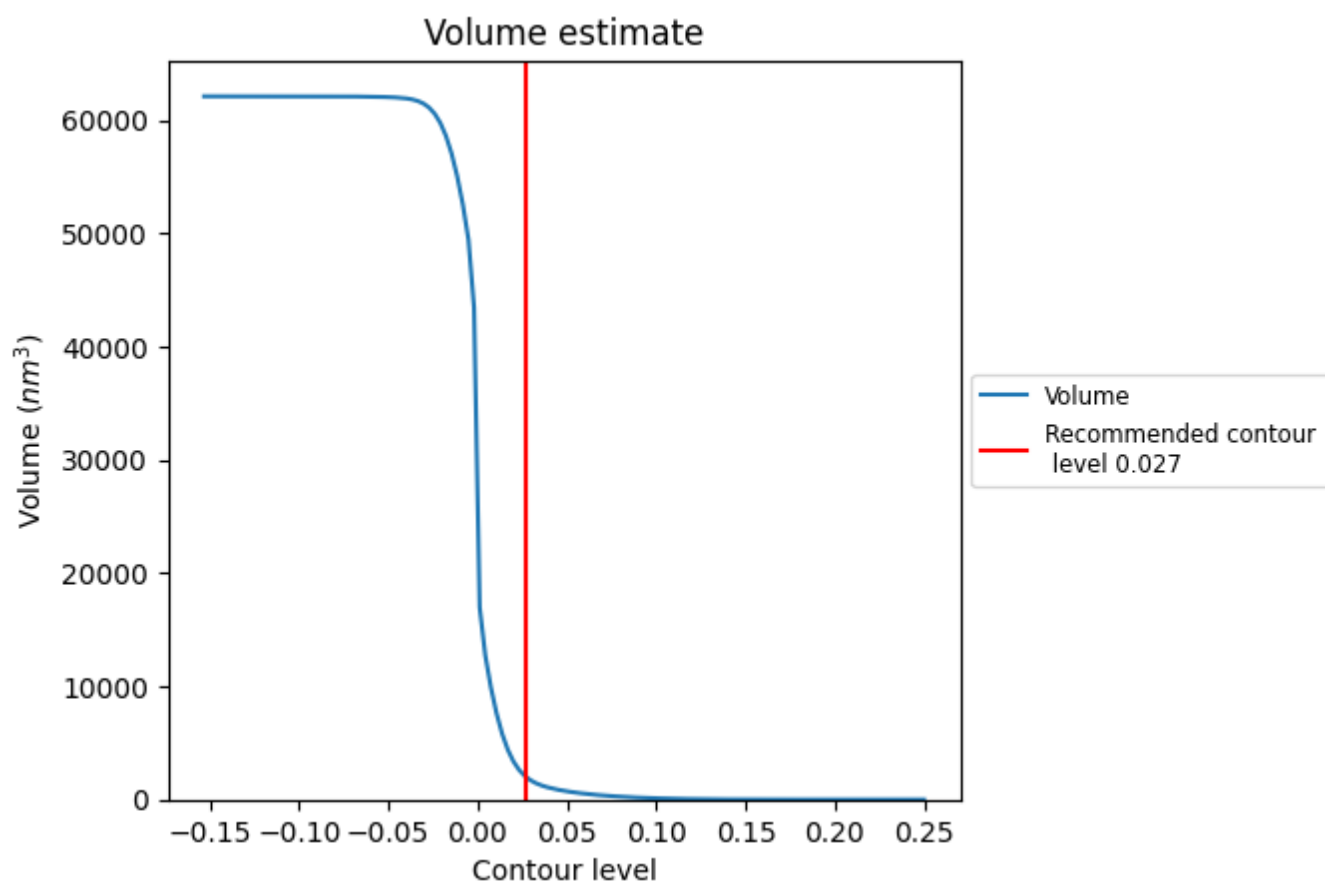
This section contains the results of statistical analysis of the map.

6.1 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.

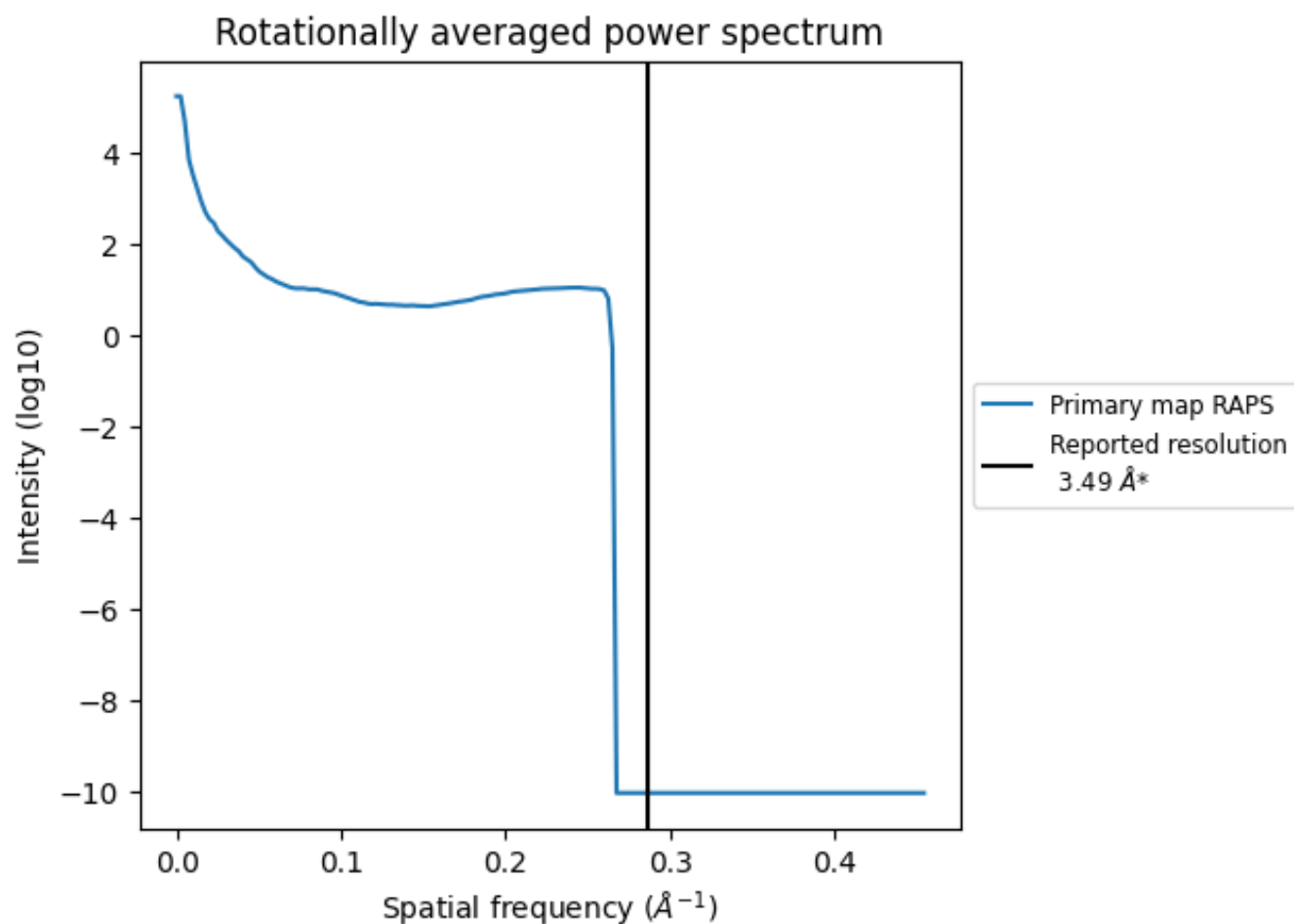
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 2019 nm³; this corresponds to an approximate mass of 1823 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.

6.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.287 Å⁻¹

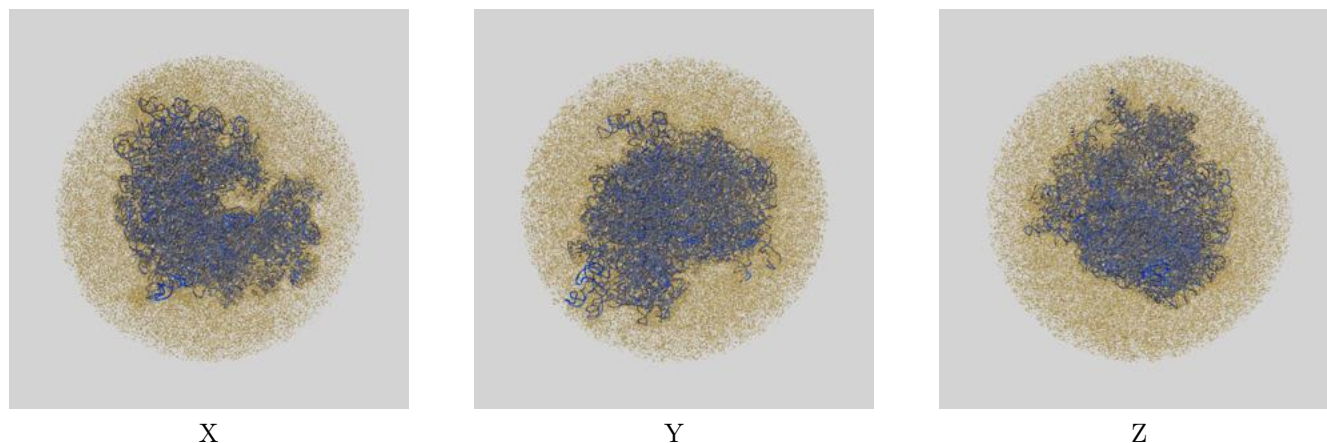
7 Fourier-Shell correlation

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

8 Map-model fit [i](#)

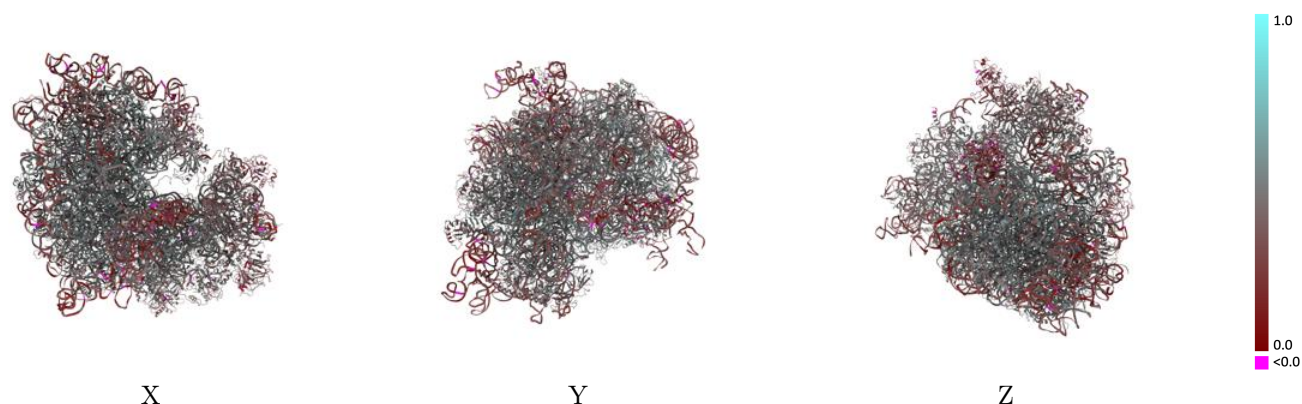
This section contains information regarding the fit between EMDB map EMD-11459 and PDB model 6ZVK. Per-residue inclusion information can be found in section ?? on page ??.

8.1 Map-model overlay [i](#)



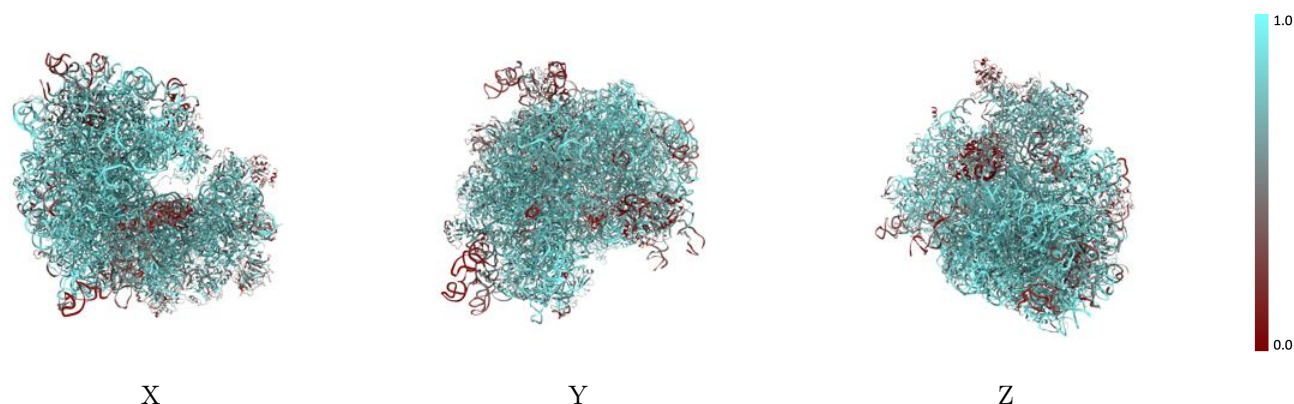
The images above show the 3D surface view of the map at the recommended contour level 0.027 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



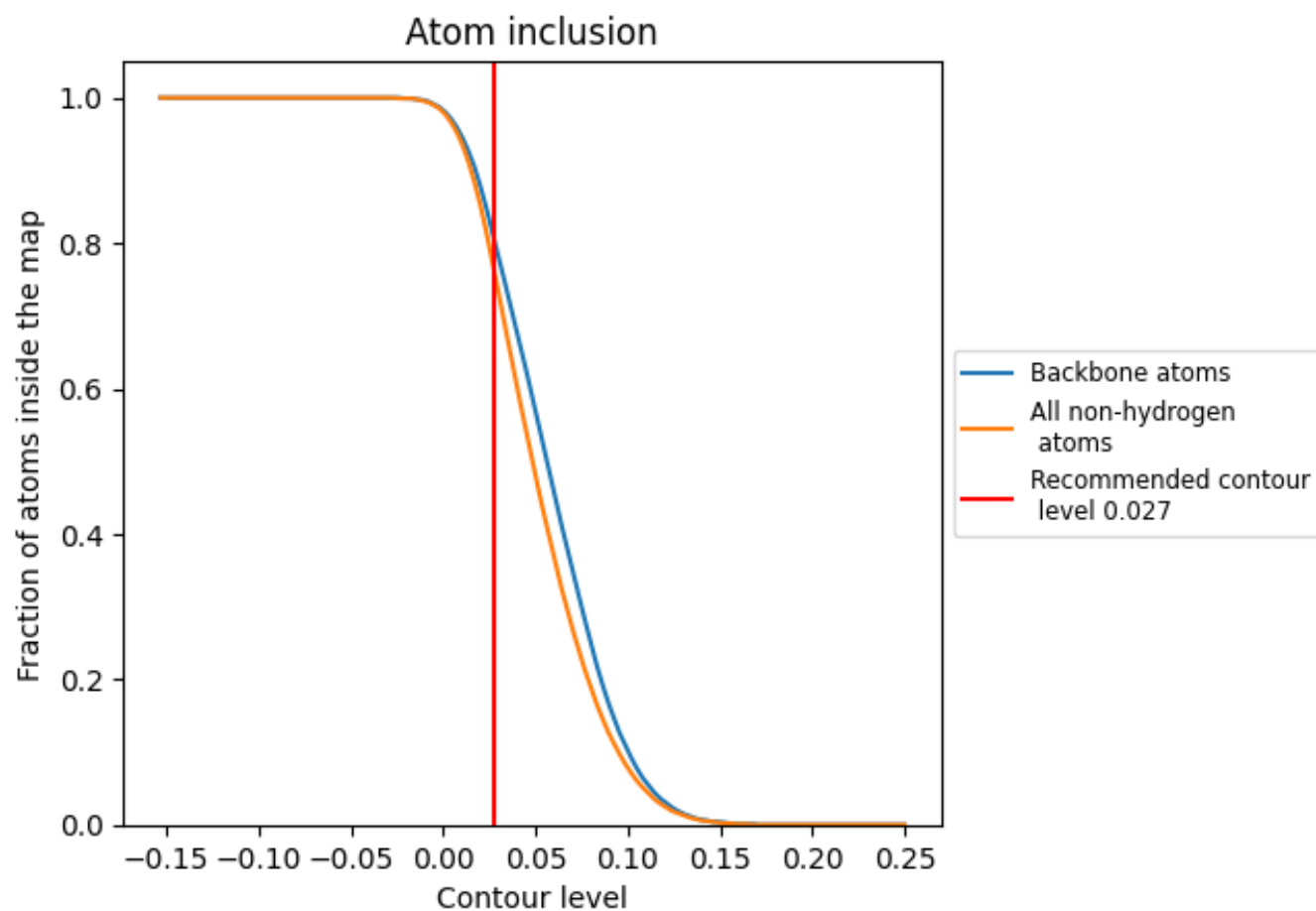
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

8.3 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 (0.027).

8.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 77% of all non-hydrogen atoms, are inside the map.

8.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.027) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7700	 0.4210
12	 0.8610	 0.5110
13	 0.8380	 0.5090
22	 0.8430	 0.4990
32	 0.8010	 0.4890
42	 0.2820	 0.2550
52	 0.8590	 0.5130
62	 0.8370	 0.5040
72	 0.8230	 0.5000
82	 0.8140	 0.4540
92	 0.8670	 0.5300
A2	 0.8350	 0.5050
A3	 0.6300	 0.3780
B2	 0.7820	 0.4710
B3	 0.7190	 0.4240
C2	 0.9120	 0.5470
C3	 0.6380	 0.3970
D2	 0.8790	 0.5140
D3	 0.7080	 0.4280
E1	 0.3000	 0.2390
E2	 0.8440	 0.5000
E3	 0.6170	 0.3510
F2	 0.8250	 0.5080
F3	 0.8030	 0.4960
G2	 0.8010	 0.4480
G3	 0.7010	 0.4430
G5	 0.6940	 0.4010
H2	 0.8630	 0.5260
H3	 0.7450	 0.4530
H5	 0.7020	 0.4030
I2	 0.8270	 0.5250
I3	 0.6070	 0.3920
I5	 0.7540	 0.4260
J2	 0.8400	 0.4970
J5	 0.8280	 0.5020



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Chain	Atom inclusion	Q-score
K2	 0.1920	 0.2260
K3	 0.7830	 0.3910
L2	 0.8150	 0.5100
L3	 0.7280	 0.4320
M2	 0.1860	 0.2130
M3	 0.6080	 0.3530
N3	 0.7060	 0.4320
O3	 0.8410	 0.5010
P3	 0.5880	 0.3830
Q3	 0.2440	 0.2300
R2	 0.7140	 0.4100
S2	 0.8410	 0.5070
T2	 0.7030	 0.4090
T3	 0.8060	 0.5040
U2	 0.8410	 0.4960
U3	 0.7290	 0.4460
V2	 0.7700	 0.4720
V3	 0.7930	 0.4770
W2	 0.8000	 0.4880
W3	 0.7900	 0.4720
X2	 0.8100	 0.4740
X3	 0.8560	 0.5030
Y2	 0.8130	 0.4680
Y3	 0.6460	 0.4120
Z2	 0.8460	 0.4970
a3	 0.5530	 0.3430
a5	 0.7970	 0.4820
a7	 0.7550	 0.4420
b3	 0.7060	 0.4130
c3	 0.7490	 0.4540
d2	 0.9130	 0.4440
d3	 0.7950	 0.4670
e2	 0.8030	 0.4050
e3	 0.2450	 0.2300
f3	 0.6360	 0.4080
h2	 0.8750	 0.4400
j3	 0.7620	 0.4610
k2	 0.8390	 0.5300
l2	 0.8550	 0.5160
m2	 0.8260	 0.5000
o2	 0.8350	 0.5000
p2	 0.7540	 0.4600

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Chain	Atom inclusion	Q-score
q2	 0.8480	 0.5090
r2	 0.6830	 0.4040
s3	 0.7670	 0.4640
t2	 0.8510	 0.5040
u2	 0.8050	 0.4920
v2	 0.8440	 0.5110
w2	 0.8360	 0.5010
x2	 0.8600	 0.5210
y2	 0.8200	 0.4820