



wwPDB EM Validation Summary Report ⓘ

May 25, 2024 – 10:14 am BST

PDB ID : 8QPB
EMDB ID : EMD-18547
Title : Cryo-EM Structure of Pre-B+ATP Complex (core part)
Authors : Zhang, Z.; Kumar, V.; Dybkov, O.; Will, C.L.; Zhong, J.; Ludwig, S.; Urlaub, H.; Kastner, B.; Stark, H.; Luehrmann, R.
Deposited on : 2023-10-01
Resolution : 3.70 Å(reported)

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.dev92
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

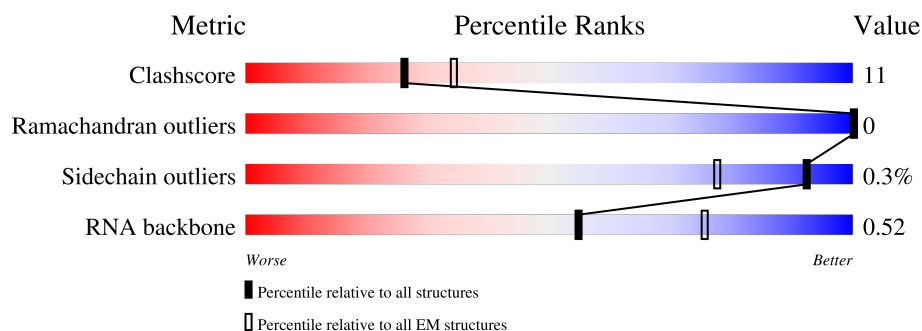
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

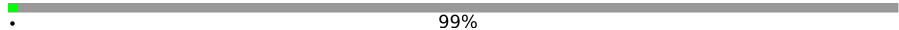


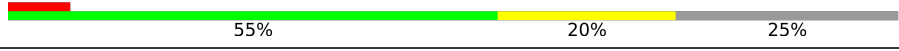



The reported resolution of this entry is 3.70 Å.

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.





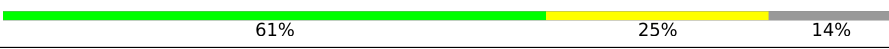


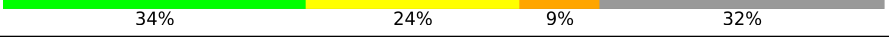
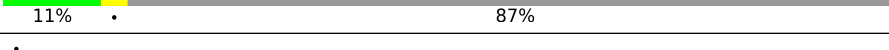
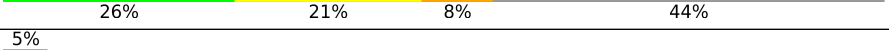
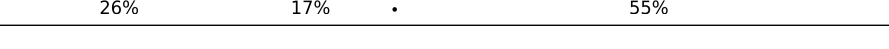
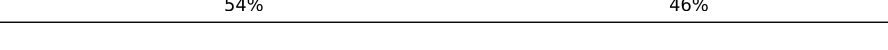
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	B	2136	 99%
2	G	820	 5% 93%
3	J	683	 8% 88%
4	L	499	 7% 55% 20% 25%
5	F	522	 8% 88%
6	N	941	 10% 36% 13% 51%
7	A	2335	 61% 24% 15%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
8	U	565	
9	S	800	
10	C	972	
11	M	128	
12	D	142	
13	5	117	
14	7	793	
15	4	144	
16	6	106	
17	z	13	

2 Entry composition

There are 18 unique types of molecules in this entry. The entry contains 43804 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 U5 small nuclear ribonucleoprotein 200 kDa helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	22	Total	C	N	O	S	0	0
			158	97	28	32	1		

- Molecule 2 is a protein called Probable ATP-dependent RNA helicase DDX23.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	57	Total	C	N	O	S	0	0
			484	304	88	91	1		

- Molecule 3 is a protein called U4/U6 small nuclear ribonucleoprotein Prp3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	J	84	Total	C	N	O	S	0	0
			679	419	138	119	3		

- Molecule 4 is a protein called U4/U6 small nuclear ribonucleoprotein Prp31.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L	376	Total	C	N	O	S	0	0
			2886	1796	526	552	12		

- Molecule 5 is a protein called U4/U6 small nuclear ribonucleoprotein Prp4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	61	Total	C	N	O	S	0	0
			488	297	97	93	1		

- Molecule 6 is a protein called Pre-mRNA-processing factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	N	457	Total	C	N	O	S	0	0
			3502	2191	655	644	12		

- Molecule 7 is a protein called Pre-mRNA-processing-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	1977	Total	C	N	O	S	0	0
			16409	10568	2864	2907	70		

- Molecule 8 is a protein called Ubiquitin carboxyl-terminal hydrolase 39.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	U	456	Total	C	N	O	S	0	0
			3749	2427	635	673	14		

- Molecule 9 is a protein called U4/U6.U5 tri-snRNP-associated protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	S	148	Total	C	N	O	S	0	0
			1164	724	216	222	2		

- Molecule 10 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	C	836	Total	C	N	O	S	0	0
			6592	4211	1110	1238	33		

- Molecule 11 is a protein called NHP2-like protein 1, N-terminally processed.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	M	124	Total	C	N	O	S	0	0
			962	608	171	178	5		

- Molecule 12 is a protein called Thioredoxin-like protein 4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	D	141	Total	C	N	O	S	0	0
			1170	751	194	215	10		

- Molecule 13 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	5	79	Total	C	N	O	P	0	0
			1660	744	275	562	79		

- Molecule 14 is a protein called Splicing factor 3A subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	7	107	Total	C	N	O	S	0	0
			846	522	152	169	3		

- Molecule 15 is a RNA chain called U4 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	4	80	Total	C	N	O	P	0	0
			1699	760	297	562	80		

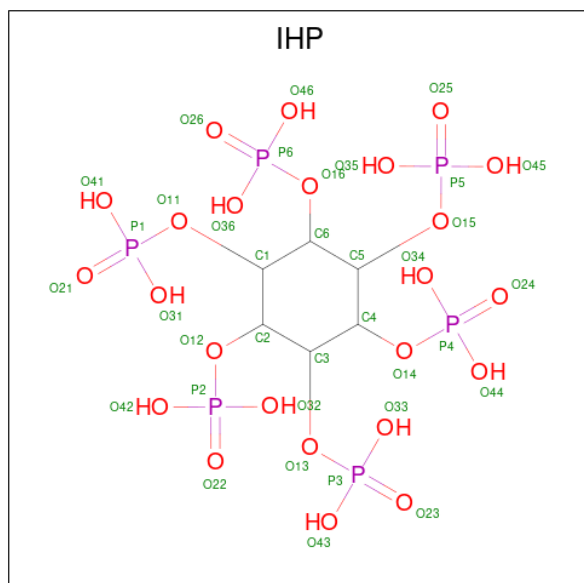
- Molecule 16 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	6	48	Total	C	N	O	P	0	0
			1034	462	196	328	48		

- Molecule 17 is a RNA chain called 5'ss oligo.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	z	13	Total	C	N	O	P	0	0
			286	127	57	89	13		

- Molecule 18 is INOSITOL HEXAKISPHOSPHATE (three-letter code: IHP) (formula: $C_6H_{18}O_{24}P_6$) (labeled as "Ligand of Interest" by depositor).



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.

- [illegible]



ALA	TYR	MET	GLY	CYS	ASP	GLN	GLU	GLY	TYR	LYS	PHE	SER	VAL	ASP	VAL	LYS	GLU	ALA	GLU	THR	ASP	SER	ASP	SER	ASP
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Chain G: 5% . 93%

[illegible]

Chain J:  8% . 88%



T645	L487	N357	D200	R86	MET
P646	L647	R362	W206	L89	ALA
L648	G493	D374	D209	L92	GLY
E649	L494	D375	H210	P96	VAL
R650	L504	E382	Q211	P97	PHE
W651	L507	F383	P212	A98	PRO
ARG	R510	V384	L213	V99	TYR
HIS	RS10	F387	Y219	L100	ARG
SER	L516	D390	T237	K101	GLY
LYS	H517	A403	L238	L102	ASN
GLY	V527	A407	Y239	L103	PRO
VAL	V527	A408	R240	E104	VAL
ALA	SS38	P408	L241	Q112	GLY
LYS	G541	N412	A242	I113	LEU
THR	F544	L413	D259	R114	ALA
THR	H545	R414	M271	I126	LEU
VAL	L546	R419	P281	S127	PRO
LYS	C547	R420	R284	F128	ASP
Q675	V677	A421	D285	V129	TYR
R676	E678	L422	L286	I136	SER
V677	S679	D423	N287	E137	GLU
G678	D682	L424	L288	P138	GLY
S679	E684	P425	N287	V139	LEU
D682	A688	D559	L298	S142	GLN
L683	V689	L426	L298	Q143	GLU
E684	L694	V427	W293	S146	LYS
A688	G697	K428	D298	M147	ALA
V689	F572	N429	D298	L150	ARG
L694	R593	W430	D298	M151	LYS
G697	V441	Q439	D298	R152	TRP
M697	Y594	P440	D298	R153	GLN
K702	K595	K442	D298	E154	GLN
E663	K595	V443	D298	K155	ALA
L864	H610	R444	D298	R156	LYS
G865	H712	V445	D298	D157	ARG
I867	A716	T618	D298	R158	TYR
L878	P732	G619	D298	R159	ALA
K882	M738	G622	D298	H160	GLU
R883	Y742	G626	D298	F161	LYS
Q888	W750	W634	D298	P168	LYS
R889	T751	L638	D298	D180	GLY
E893	N751	M641	D298	R181	PHE
R894	T751	L638	D298	I182	PHE
Q898	Y742	M641	D298	L188	GLY
R899	W750	L638	D298	D180	VAL
E893	N751	M641	D298	R181	ASP
R894	T751	L638	D298	I182	ASP
Q898	Y742	M641	D298	L188	ASP
R899	W750	L638	D298	D180	ASP
E893	N751	M641	D298	R181	ASP
R894	T751	L638	D298	I182	ASP
Q898	Y742	M641	D298	L188	ASP
R899	W750	L638	D298	D180	ASP
E893	N751	M641	D298	R181	ASP
R894	T751	L638	D298	I182	ASP
Q898	Y742	M641	D298	L188	ASP
R899	W750	L638	D298	D180	ASP
E893	N751	M641	D298	R181	ASP
R894	T751	L638	D298	I182	ASP
Q898	Y742	M641	D298	L188	ASP
R899	W750	L638	D298	D180	ASP
E893	N751	M641	D298	R181	ASP
R894	T751	L638	D298	I182	ASP
Q898	Y742	M641	D298	L188	ASP
R899	W750	L638	D298	D180	ASP
E893	N751	M641	D298	R181	ASP
R894	T751	L638	D298	I182	ASP
Q898	Y742	M641	D298	L188	ASP
R899	W750	L638	D298	D180	ASP
E893	N751	M641	D298	R181	ASP
R894	T751	L638	D298	I182	ASP
Q898	Y742	M641	D298	L188	ASP
R899	W750	L638	D298	D180	ASP
E893	N751	M641	D298	R181	ASP
R894	T751	L638	D298	I182	ASP
Q898	Y742	M641	D298	L188	ASP
R899	W750	L638	D298	D180	ASP
E893	N751	M641	D298	R181	ASP
R894	T751	L638	D298	I182	ASP
Q898	Y742	M641	D298	L188	ASP
R899	W750	L638	D298	D180	ASP

ARG	PHE	LEU	GLY	ASP	TRP	VAL	MET	THR	ARG	L2012	L1877	D1782	S1673	L1448	L1328	M1237	E1116	V1015	L901
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	ASN	THR	G2013	D1878	T1783	H1674	P1452	S1329	M1242	N1124	V1016	L905
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	HIS	ASN	E2014	F1879	V1785	Y1679	P1452	M1330	N1243	I1125	I1017	V906
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	ILE	ILE	K1885	Y1786	Y1786	Y1687	K1463	V1333	V1244	G1127	H1024	V907
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	E1888	R1787	V1788	P1686	W1465	L1334	R1245	G1127	R1032	V908
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1889	V1789	V1789	P1686	W1465	L1335	Q1246	G1127	G1033	V909
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	P1892	P1892	H1791	G1700	Y1470	D1347	M1249	C1133	G1033	P913
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1897	K1898	K1792	D1706	L1478	M1357	S1251	D1137	A1037	L914
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	K1898	K1898	E1795	M1710	L1484	M1357	I1259	A1138	A1037	E915
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	V1899	V1899	G1796	M1710	L1484	M1357	V1260	R1139	A1037	K916
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	E1900	E1900	N1797	A1714	T1488	D1362	M1264	R1141	Y1044	R933
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	K1901	K1901	L1601	A1714	L1488	O1363	T1265	D1146	G1045	R933
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	F1902	F1902	L1601	A1714	L1488	L1364	T1265	V1147	D1049	L935
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	P1802	P1802	I1606	M1717	K1491	L1365	I1268	N1148	L1050	L935
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1905	L1905	I1606	M1717	K1491	L1365	I1268	N1148	L1050	L935
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	I1906	I1906	I1606	M1717	K1491	L1365	I1268	N1148	L1050	L935
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	K1907	K1907	P1616	K1723	T1493	Y1369	M1271	L1155	V1052	W939
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	A1908	A1908	P1616	K1723	T1493	Y1369	M1271	L1155	V1052	W939
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	F1808	F1808	S1619	Q1728	T1497	P1374	R1275	W1155	L1055	P942
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	N1809	N1809	S1619	Q1728	T1497	P1374	R1275	W1155	L1055	P942
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	F1810	F1810	M1622	A1731	E1499	E1378	E1276	I1157	H1056	D944
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	N1811	N1811	M1622	A1731	E1499	E1378	E1276	I1157	H1056	D944
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1914	L1914	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1916	L1916	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	I1927	I1927	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	T1931	T1931	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	S1934	S1934	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	I1937	I1937	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	R1941	R1941	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	V1945	V1945	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	A1950	A1950	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1954	L1954	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	K1955	K1955	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	P1956	P1956	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	D1957	D1957	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	K1958	K1958	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	T1959	T1959	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	T1960	T1960	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1964	L1964	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	K1965	K1965	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1966	L1966	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1967	L1967	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1968	L1968	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1969	L1969	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1970	L1970	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1971	L1971	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1972	L1972	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1973	L1973	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1974	L1974	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1975	L1975	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1976	L1976	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1977	L1977	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1978	L1978	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1979	L1979	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1980	L1980	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1981	L1981	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1982	L1982	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1983	L1983	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1984	L1984	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1985	L1985	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1986	L1986	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1987	L1987	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1988	L1988	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1989	L1989	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1990	L1990	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1991	L1991	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1992	L1992	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1993	L1993	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1994	L1994	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1995	L1995	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1996	L1996	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1997	L1997	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1998	L1998	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L1999	L1999	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L2000	L2000	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N960
PHE	LEU	GLY	GLY	GLY	GLY	VAL	GLN	THR	THR	L2001	L2001	L1631	K1732	L1501	V1385	V1278	R1160	E1060	N96

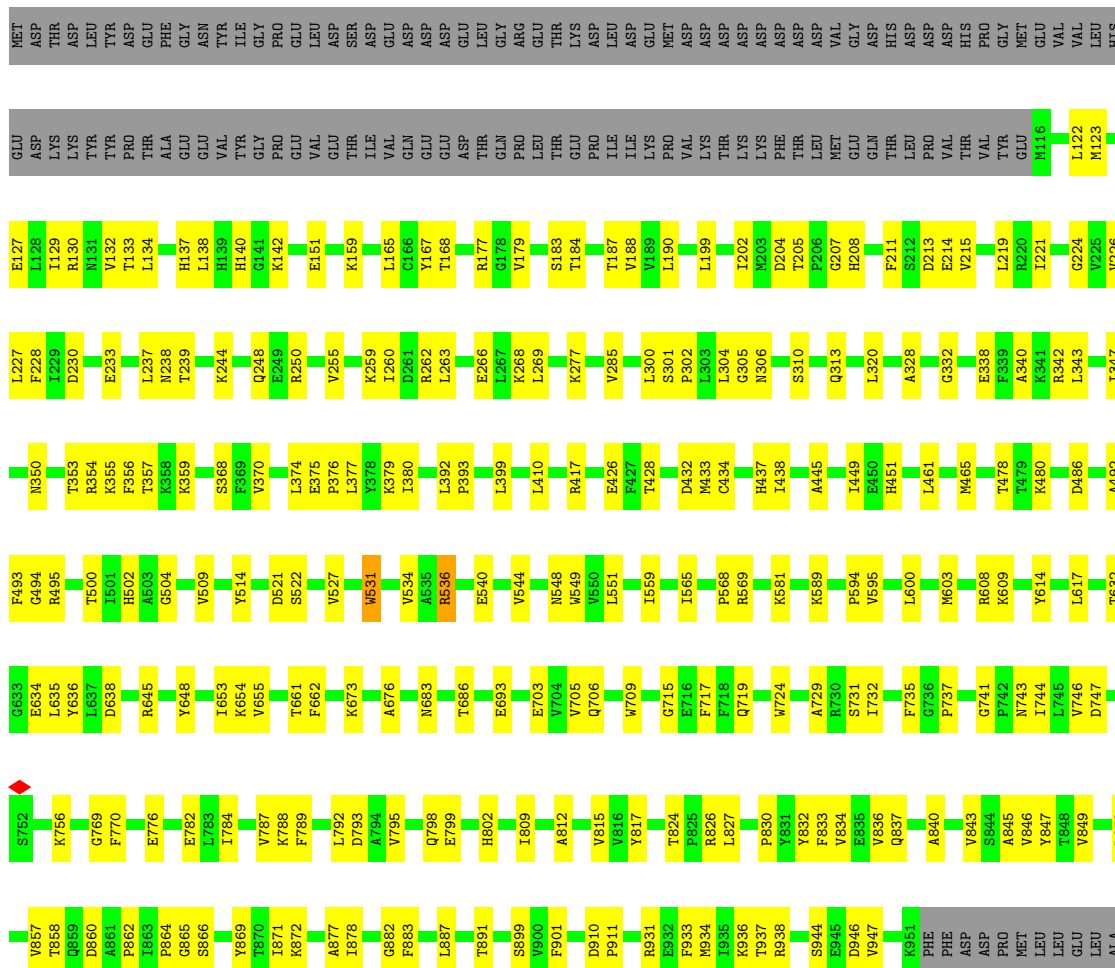


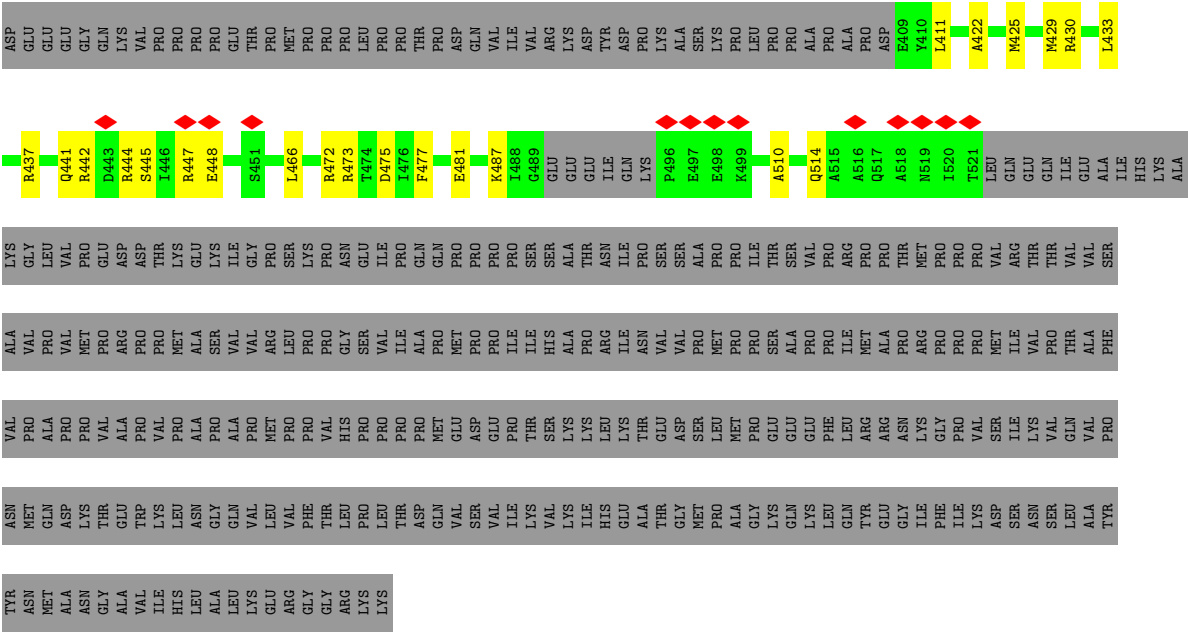
WORLDWIDE
PDB
PROTEIN DATA BANK

TYR	LYS	ALA	ASN	GLU	PRO	LEU
ILE	GLU	PRO	ILE	ASP	ASP	LEU
VAL	ASN	ASN	GLY	PRO	GLY	PRO
LEU	PHE	GLY	TRP	GLU	LEU	GLY
SER	ARG	SER	SER	ARG	PRO	GLY
GLY	GLN	LEU	THR	LYS	GLN	ASP
SER	LEU	PRO	VAL	VAL	GLY	GLN
GLY	LEU	SER	ASN	ALA	LEU	THR
LYS	HIS	ALA	LEU	ILE	GLU	GLN
	ARG	VAL	ASP	VAL	ASP	ASP
	THR	TYR	GLU	PHE	PHE	GLY
	ASN	CYS	GLU	ASN	ASN	GLY
ALA	GLY	ILE	LYS	LYS	ALA	PHE
ASN	LYS	GLU	GLN	THR	GLU	GLY
THR	GLY	ASP	GLN	SER	LEU	SER
ILE	SER	LYS	GLN	GLU	LEU	ARG
THR	GLY	MET	ASP	PHE	LEU	LEU
LYS	LYS	ALA	PHE	CYS	GLN	ARG
	MET	ILE	SER	ARG	LYS	GLY
	LYS	THR	ALA	THR	GLN	ARG
	THR	ASP	SER	LEU	LYS	GLY
	GLU	LYS	SER	GLY	LEU	GLY
	ARG	TYR	THR	GLU	LYS	ARG
	ARG	SER	THR	ILE	GLY	ARG
	MET	ARG	ILE	PRO	ARG	VAL
	LYS	ARG	LEU	TYR	ARG	SER
	LEU	GLU	ASP	GLY	LEU	GLY
	ASP	TYR	GLU	LEU	GLN	VAL
	GLU	ARG	PRO	ALA	LEU	GLU
	ALA	GLY	ILE	GLY	GLN	GLU
	PHE	VAL	VAL	ASN	GLN	LYS
	LEU	THR	ASN	ARG	LEU	GLU
	LEU	GLN	ARG	GLY	PRO	VAL
	LYS	ASP	GLY	GLU	GLN	VAL
	LYS	PHE	LEU	GLN	LEU	PRO
	MET	LYS	ALA	GLU	ARG	GLN
	SER	GLU	ALA	GLU	ASP	PRO
	SER	LYS	ALA	LEU	SER	LEU
	SER	ASP	LEU	MET	GLY	PRO
	ASP	GLY	LEU	ASP	SER	SER
	THR	TYR	LEU	PHE	LYS	ASP
	PRO	LYS	CYS	GLU	VAL	ASP
	LEU	PRO	GLN	ARG	VAL	ASP
	GLY	ASP	ASN	ASP	GLU	ARG
	THR	VAL	LYS	GLY	VAL	VAL
	VAL	ILE	LEU	ARG	LYS	ASN
	ALA	GLU	LEU	SER	LYS	ASN
	LEU	TYR	GLU	ALA	LEU	MET
	GLN	VAL	THR	ASN	GLU	ASP
	GLU	ASP	THR	GLY	SER	SER
	LYS	GLN	VAL	GLY	GLY	ASP
	GLN	THR	GLN	SER	GLN	GLU
	LYS	GLY	LYS	THR	ARG	GLU
	ALA	ARG	VAL	VAL	ILE	GLU
	GLN	LYS	VAL	THR	ASN	GLY
	LYS	THR	THR	GLY	GLY	TRP
	LYS	LEU	ARG	GLY	GLY	GLY
	THR	THR	VAL	GLU	GLU	ALA
	PRO	PRO	LYS	GLU	GLU	PRO

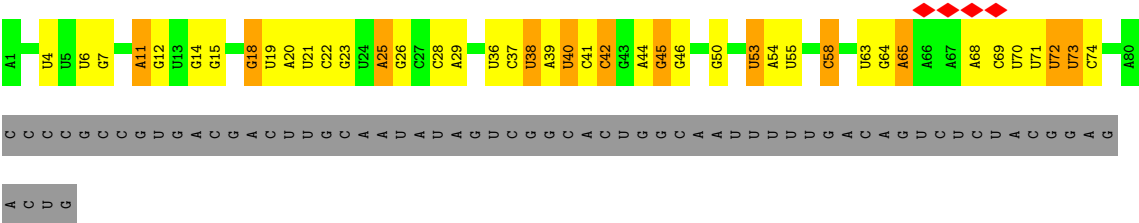
- Molecule 10: 116 kDa U5 small nuclear ribonucleoprotein component

Chain C:  61% 25% 14%

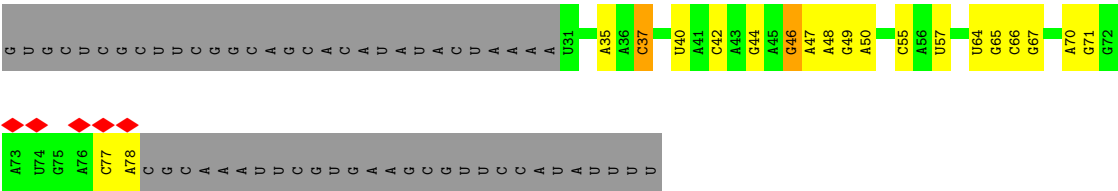




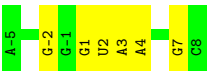
• Molecule 15: U4 snRNA



• Molecule 16: U6 snRNA



• Molecule 17: 5'ss oligo



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	94460	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 ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.130	Depositor
Minimum map value	-0.030	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.027	Depositor
Map size (Å)	556.8, 556.8, 556.8	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.16, 1.16, 1.16	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: IHP

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	B	0.26	0/158	0.63	0/209
2	G	0.24	0/493	0.48	0/659
3	J	0.25	0/686	0.52	0/914
4	L	0.25	0/2924	0.48	0/3938
5	F	0.25	0/491	0.55	0/657
6	N	0.24	0/3565	0.48	0/4818
7	A	0.26	0/16856	0.48	0/22865
8	U	0.25	0/3845	0.46	0/5208
9	S	0.24	0/1172	0.49	0/1567
10	C	0.26	0/6739	0.48	0/9151
11	M	0.25	0/974	0.50	0/1316
12	D	0.27	0/1199	0.45	0/1620
13	5	0.22	0/1850	0.73	0/2875
14	7	0.24	0/858	0.50	0/1152
15	4	0.21	0/1898	0.67	0/2954
16	6	0.21	0/1159	0.72	0/1806
17	z	0.24	0/321	0.67	0/500
All	All	0.25	0/45188	0.51	0/62209

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	B	158	0	166	8	0
2	G	484	0	469	18	0
3	J	679	0	728	31	0
4	L	2886	0	2885	73	0
5	F	488	0	499	13	0
6	N	3502	0	3379	105	0
7	A	16409	0	16326	395	0
8	U	3749	0	3769	97	0
9	S	1164	0	1173	22	0
10	C	6592	0	6615	163	0
11	M	962	0	1012	26	0
12	D	1170	0	1141	37	0
13	5	1660	0	842	24	0
14	7	846	0	837	21	0
15	4	1699	0	858	28	0
16	6	1034	0	521	19	0
17	z	286	0	142	0	0
18	A	36	0	6	1	0
All	All	43804	0	41368	927	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 11.

The worst 5 of 927 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)
10:C:168:THR:H	10:C:536:ARG:HH22	1.03	0.98
3:J:489:ALA:HA	3:J:496:VAL:HG21	1.60	0.82
4:L:88:PRO:HD2	4:L:91:ARG:HE	1.44	0.82
7:A:152:ARG:HH22	7:A:619:GLY:H	1.29	0.81
8:U:174:CYS:O	8:U:178:ASN:HA	1.82	0.79

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	B	20/2136 (1%)	20 (100%)	0	0	100	100
2	G	55/820 (7%)	53 (96%)	2 (4%)	0	100	100
3	J	82/683 (12%)	82 (100%)	0	0	100	100
4	L	372/499 (74%)	366 (98%)	6 (2%)	0	100	100
5	F	59/522 (11%)	59 (100%)	0	0	100	100
6	N	447/941 (48%)	437 (98%)	10 (2%)	0	100	100
7	A	1971/2335 (84%)	1890 (96%)	81 (4%)	0	100	100
8	U	454/565 (80%)	441 (97%)	13 (3%)	0	100	100
9	S	138/800 (17%)	136 (99%)	2 (1%)	0	100	100
10	C	834/972 (86%)	817 (98%)	17 (2%)	0	100	100
11	M	122/128 (95%)	114 (93%)	8 (7%)	0	100	100
12	D	139/142 (98%)	138 (99%)	1 (1%)	0	100	100
14	7	103/793 (13%)	98 (95%)	5 (5%)	0	100	100
All	All	4796/11336 (42%)	4651 (97%)	145 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	17/1908 (1%)	17 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	G	51/721 (7%)	51 (100%)	0	100	100
3	J	72/599 (12%)	72 (100%)	0	100	100
4	L	303/424 (72%)	303 (100%)	0	100	100
5	F	52/442 (12%)	51 (98%)	1 (2%)	57	76
6	N	341/792 (43%)	340 (100%)	1 (0%)	92	96
7	A	1786/2108 (85%)	1781 (100%)	5 (0%)	92	96
8	U	418/511 (82%)	416 (100%)	2 (0%)	88	94
9	S	120/681 (18%)	119 (99%)	1 (1%)	81	89
10	C	738/866 (85%)	736 (100%)	2 (0%)	92	96
11	M	108/111 (97%)	108 (100%)	0	100	100
12	D	129/130 (99%)	128 (99%)	1 (1%)	81	89
14	7	91/709 (13%)	91 (100%)	0	100	100
All	All	4226/10002 (42%)	4213 (100%)	13 (0%)	92	96

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	U	101	ARG
8	U	288	ARG
12	D	98	ASN
10	C	531	TRP
10	C	536	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
8	U	166	ASN
8	U	208	GLN
10	C	548	ASN
8	U	316	GLN
7	A	112	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
13	5	78/117 (66%)	24 (30%)	2 (2%)

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
15	4	79/144 (54%)	24 (30%)	0
16	6	47/106 (44%)	8 (17%)	1 (2%)
17	z	12/13 (92%)	6 (50%)	0
All	All	216/380 (56%)	62 (28%)	3 (1%)

5 of 62 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
13	5	10	U
13	5	14	U
13	5	20	G
13	5	21	A
13	5	22	U

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
13	5	77	G
13	5	78	U
16	6	77	C

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
18	IHP	A	2401	-	36,36,36	0.70	0	54,60,60	1.01	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
18	IHP	A	2401	-	-	5/30/54/54	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

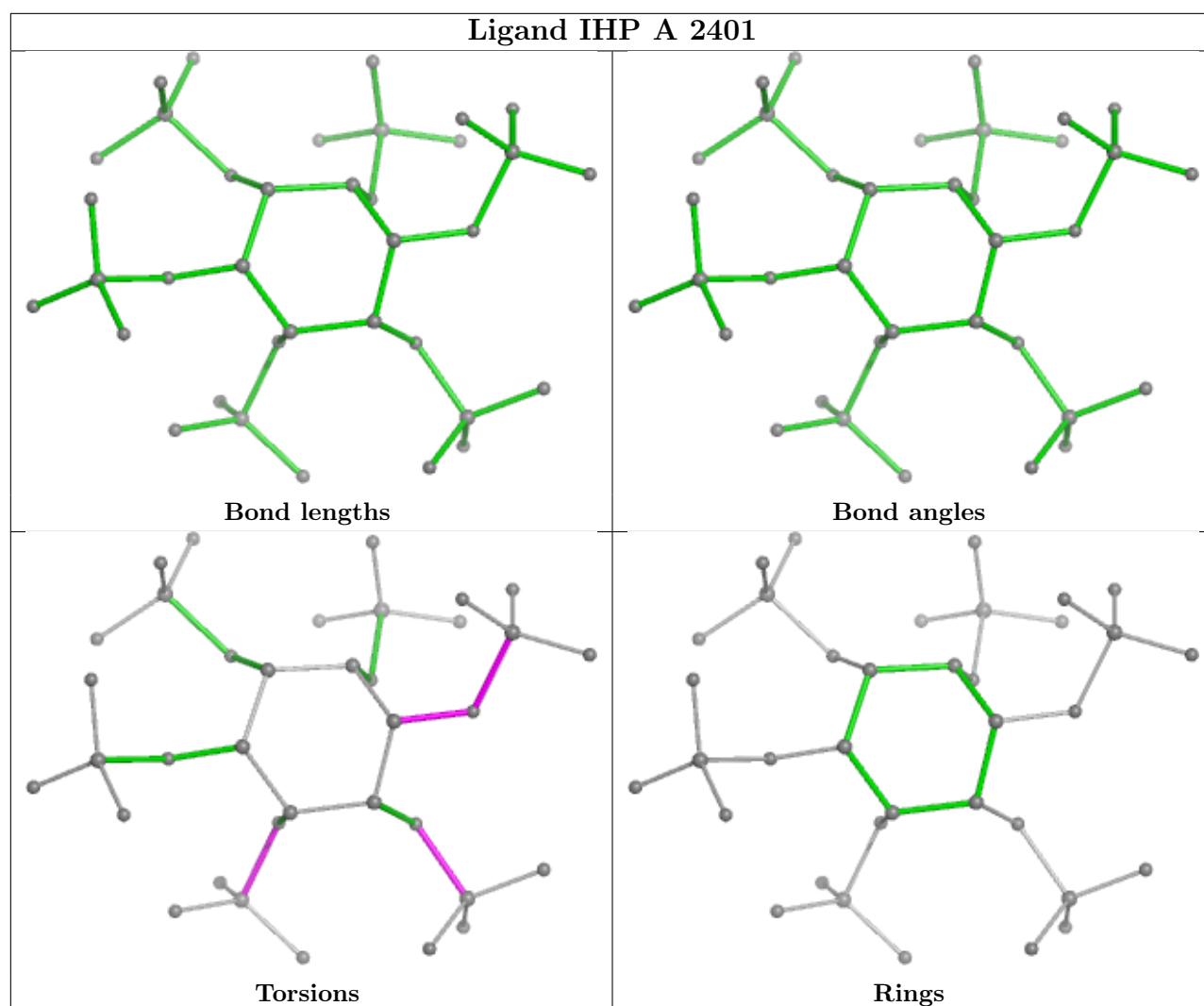
Mol	Chain	Res	Type	Atoms
18	A	2401	IHP	C1-C6-O16-P6
18	A	2401	IHP	C5-C6-O16-P6
18	A	2401	IHP	C4-O14-P4-O44
18	A	2401	IHP	C5-O15-P5-O35
18	A	2401	IHP	C6-O16-P6-O36

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
18	A	2401	IHP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

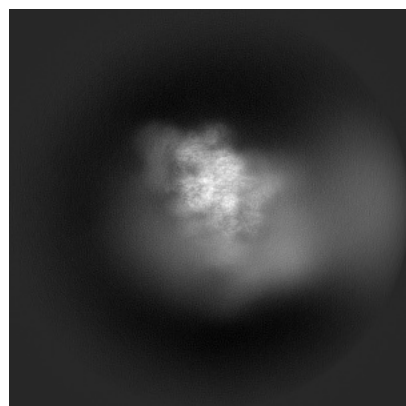
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-18547. These allow visual inspection of the internal detail of the map and identification of artifacts.

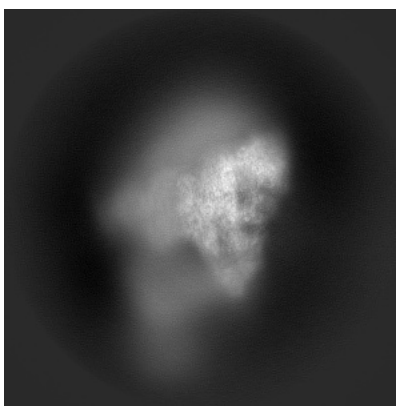
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

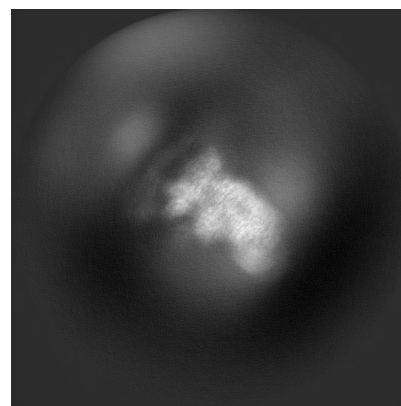
6.1.1 Primary map



X

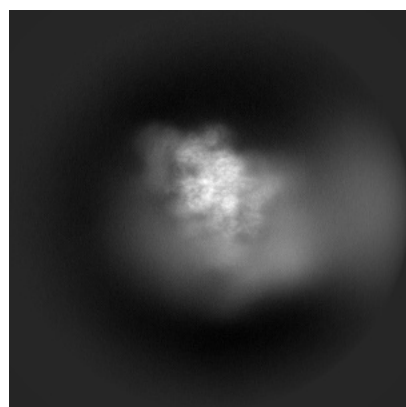


Y

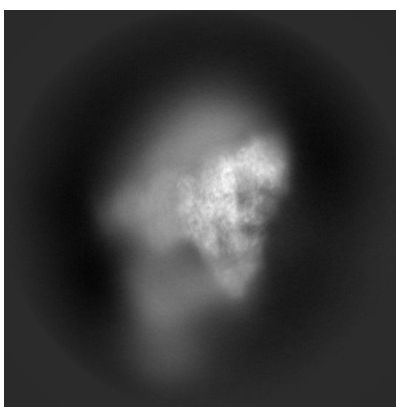


Z

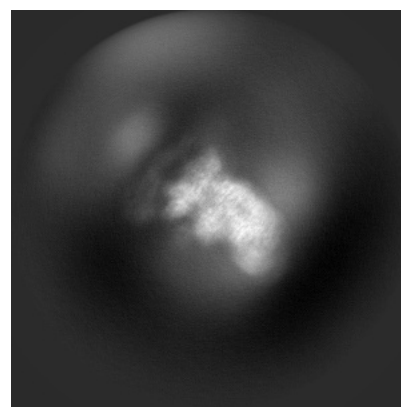
6.1.2 Raw map



X



Y

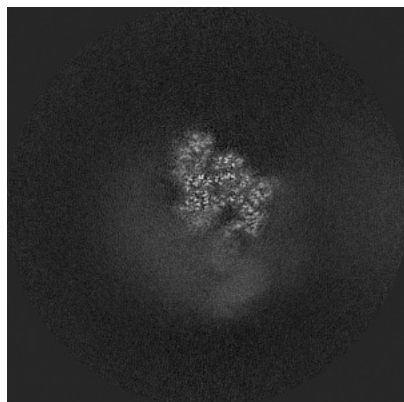


Z

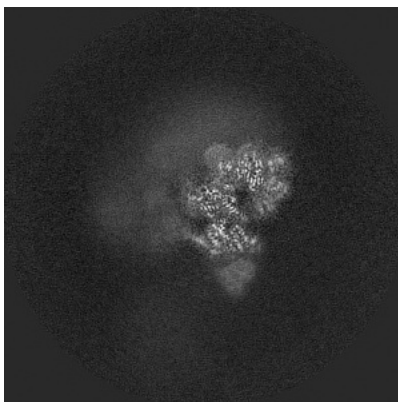
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

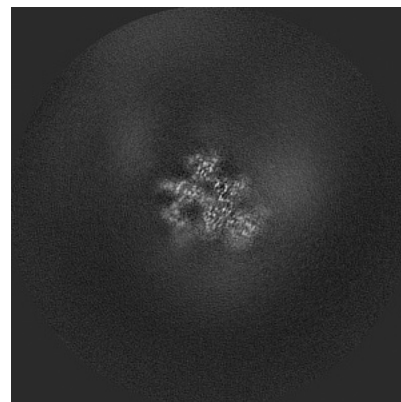
6.2.1 Primary map



X Index: 240

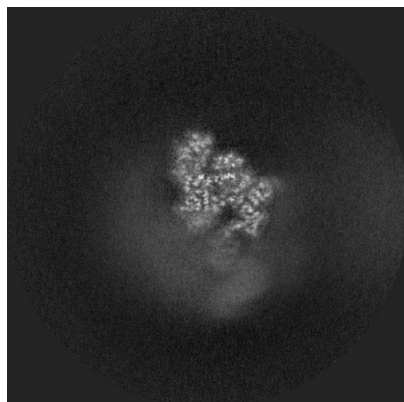


Y Index: 240

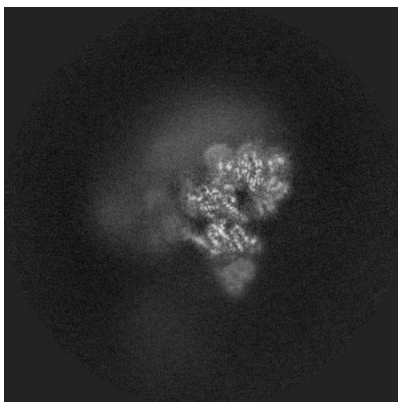


Z Index: 240

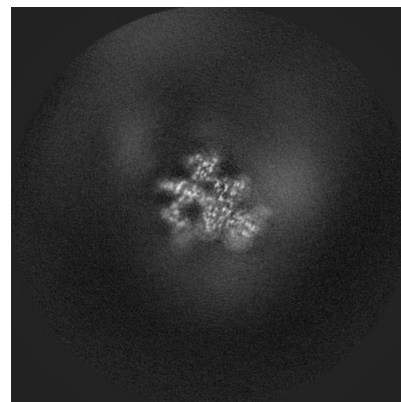
6.2.2 Raw map



X Index: 240



Y Index: 240

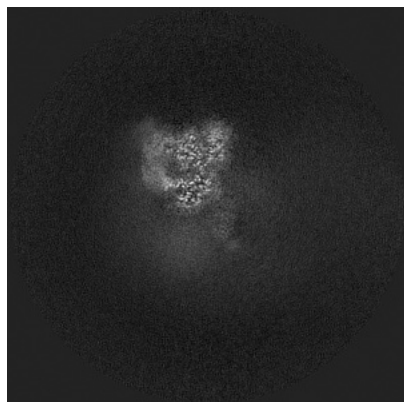


Z Index: 240

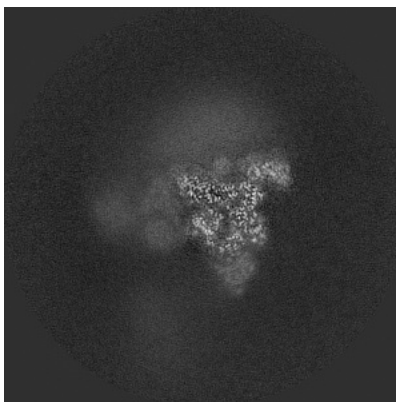
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

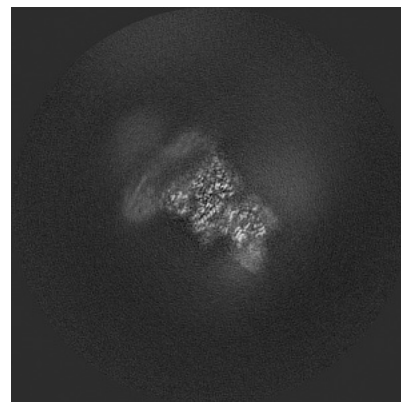
6.3.1 Primary map



X Index: 287

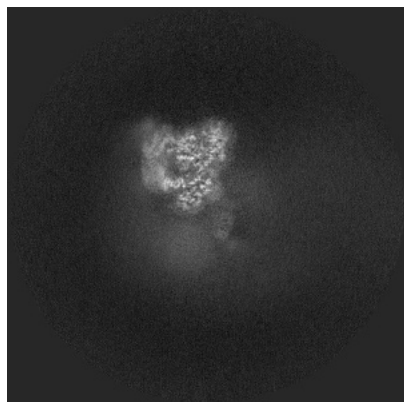


Y Index: 255

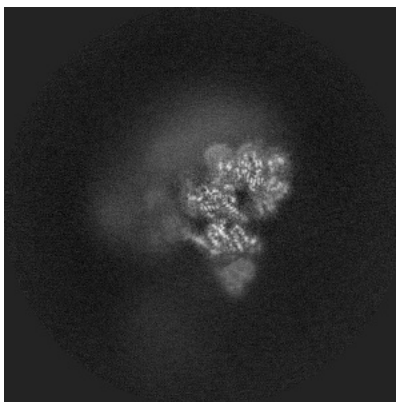


Z Index: 274

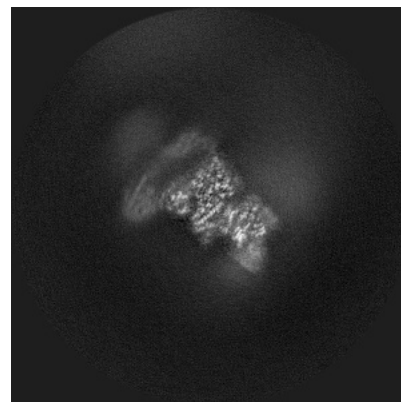
6.3.2 Raw map



X Index: 288



Y Index: 240

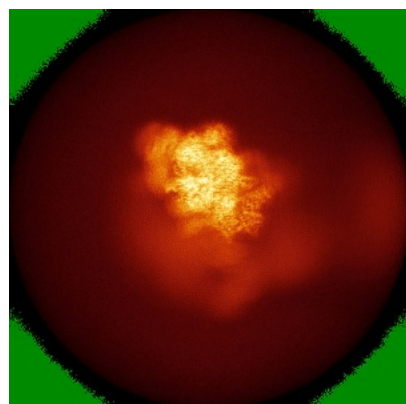


Z Index: 274

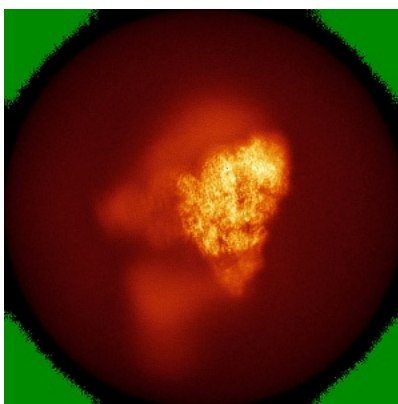
The images above show the largest variance slices of the map in three orthogonal directions.

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

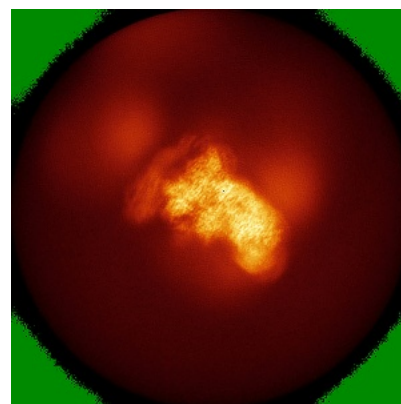
6.4.1 Primary map



X

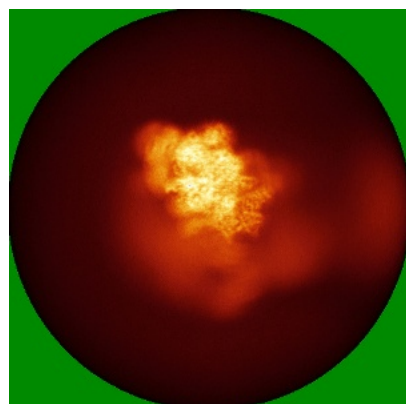


Y

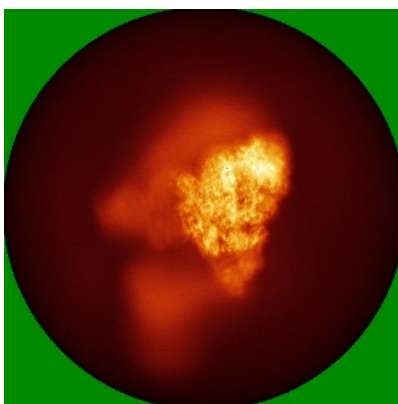


Z

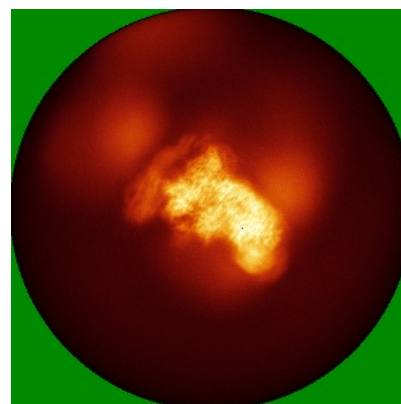
6.4.2 Raw map



X



Y

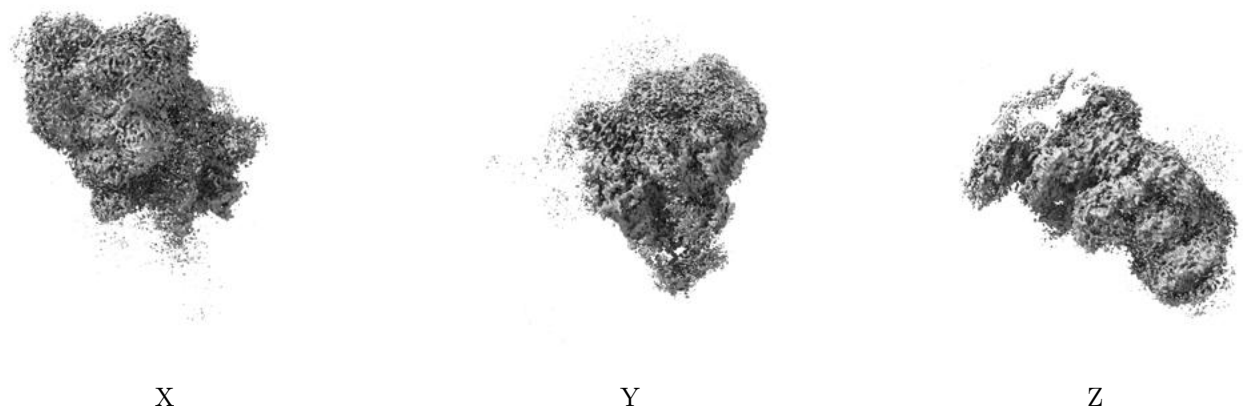


Z

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

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

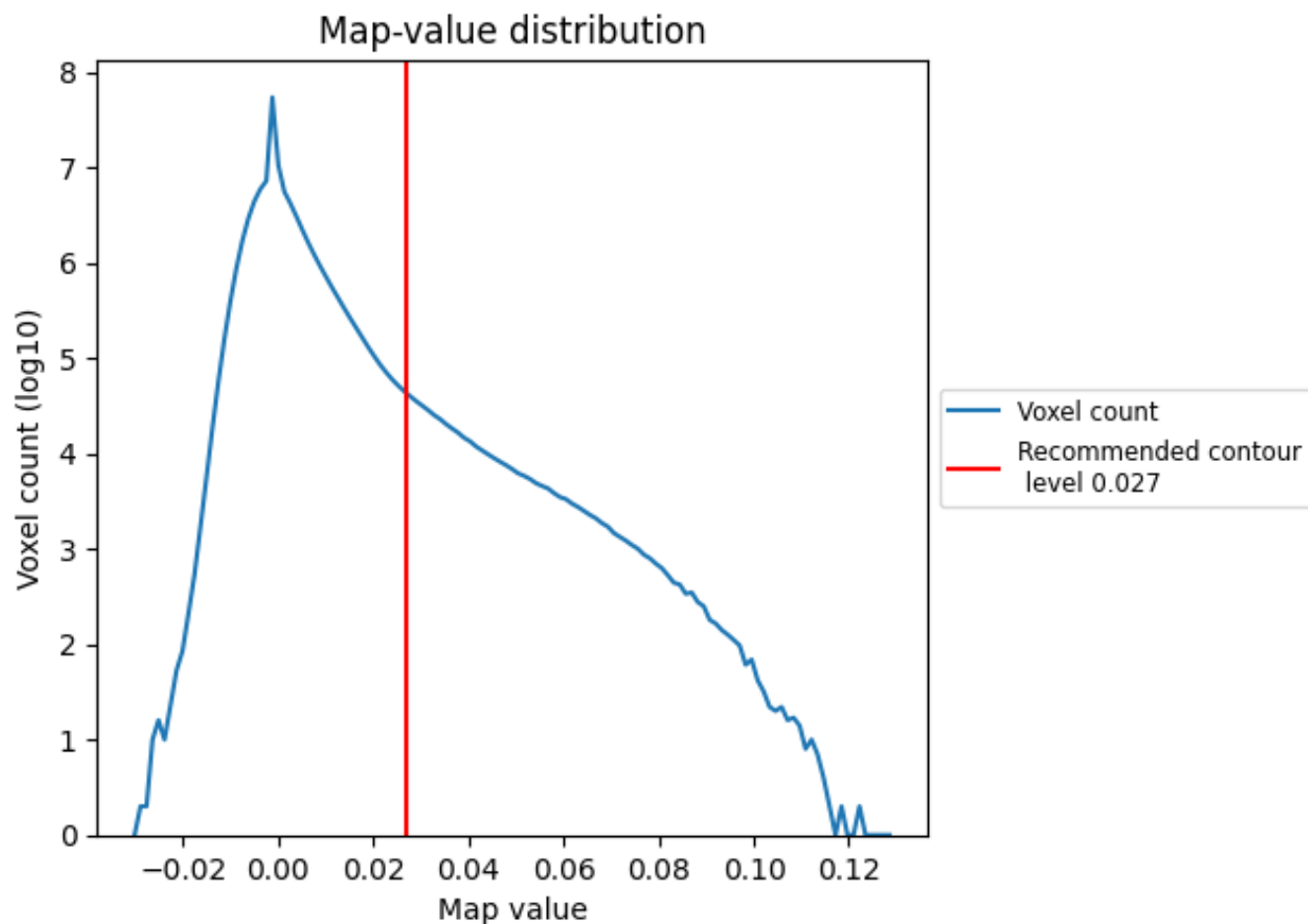
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

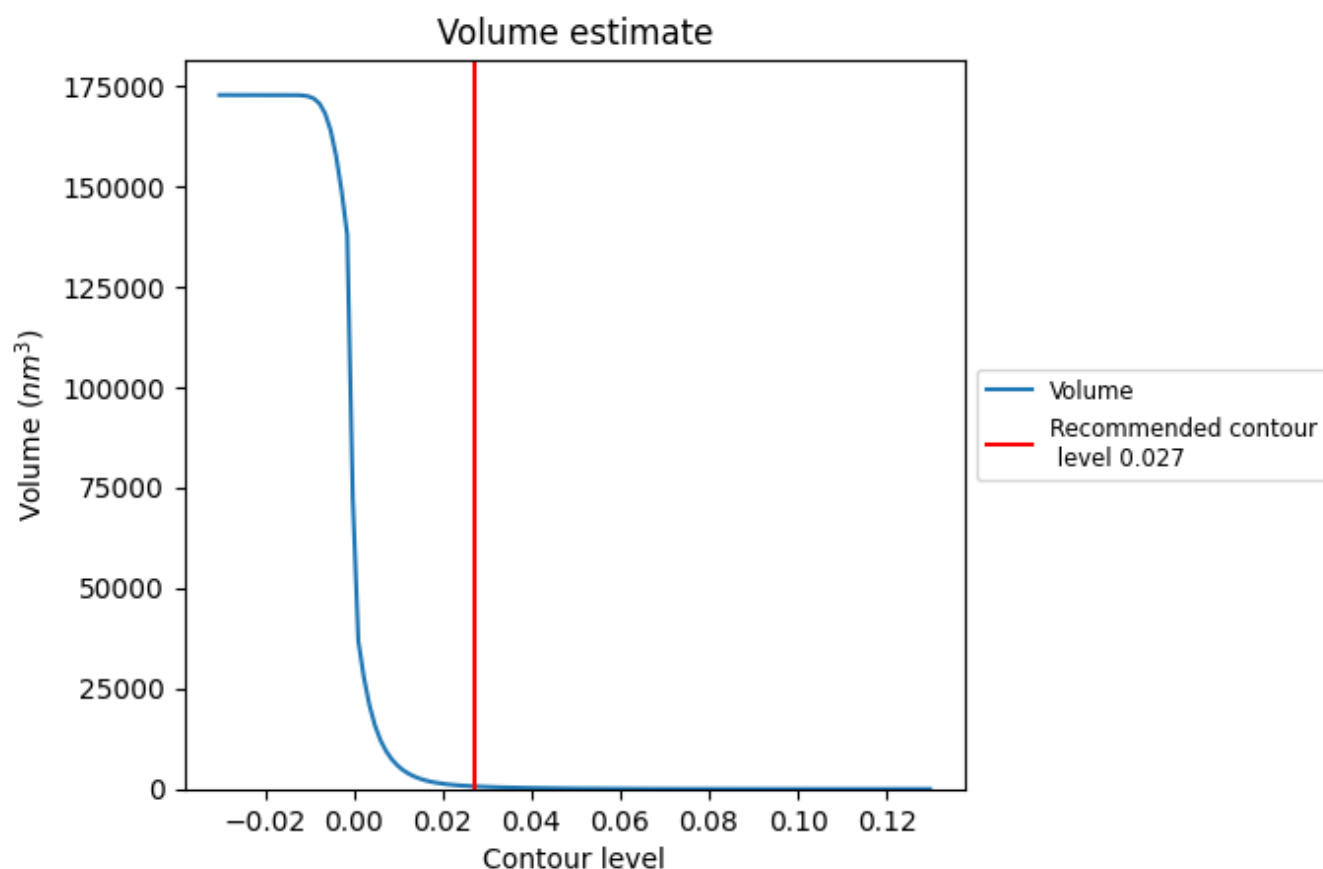
This section contains the results of statistical analysis of the map.

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.

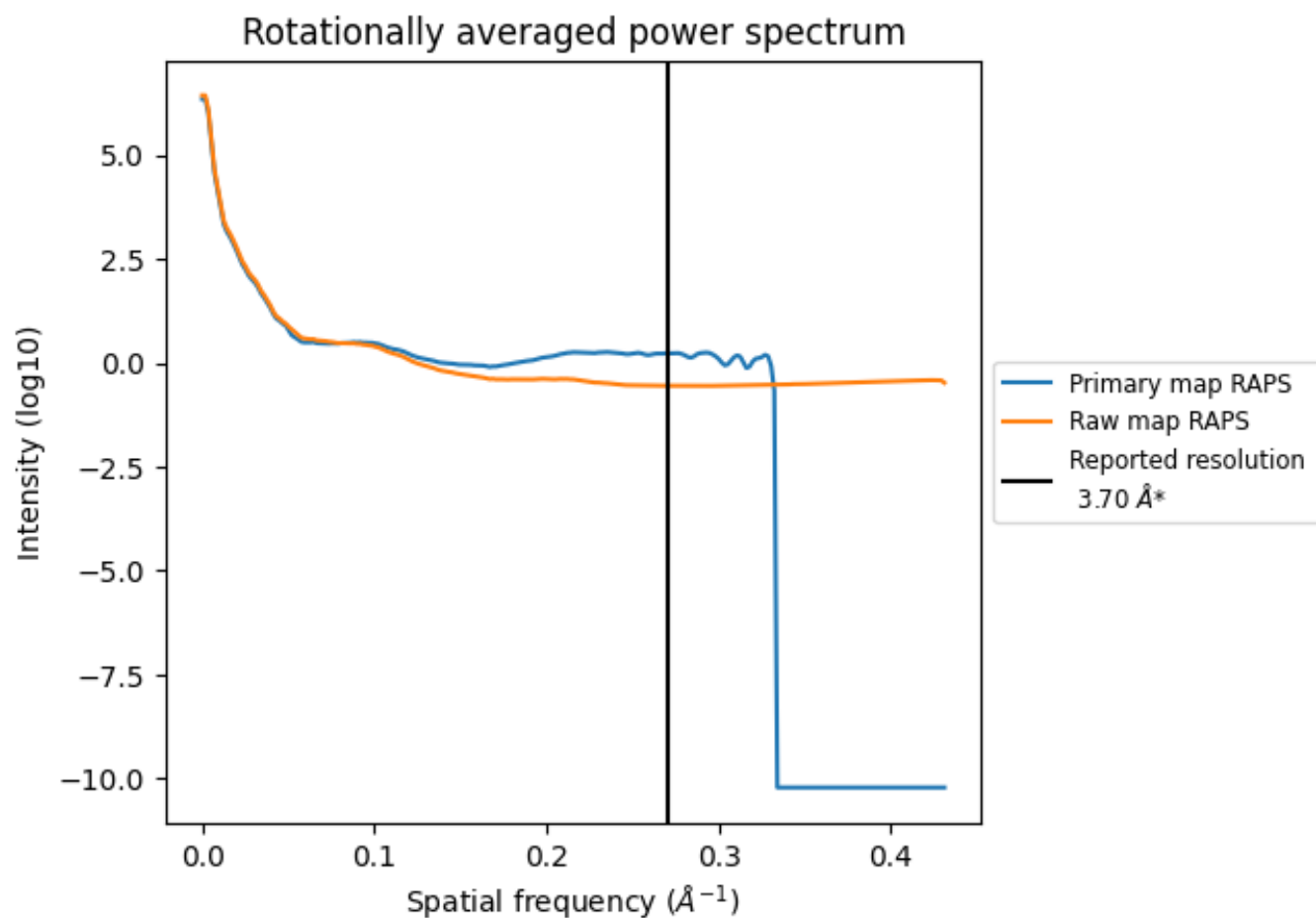
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 667 nm^3 ; this corresponds to an approximate mass of 602 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 ⓘ

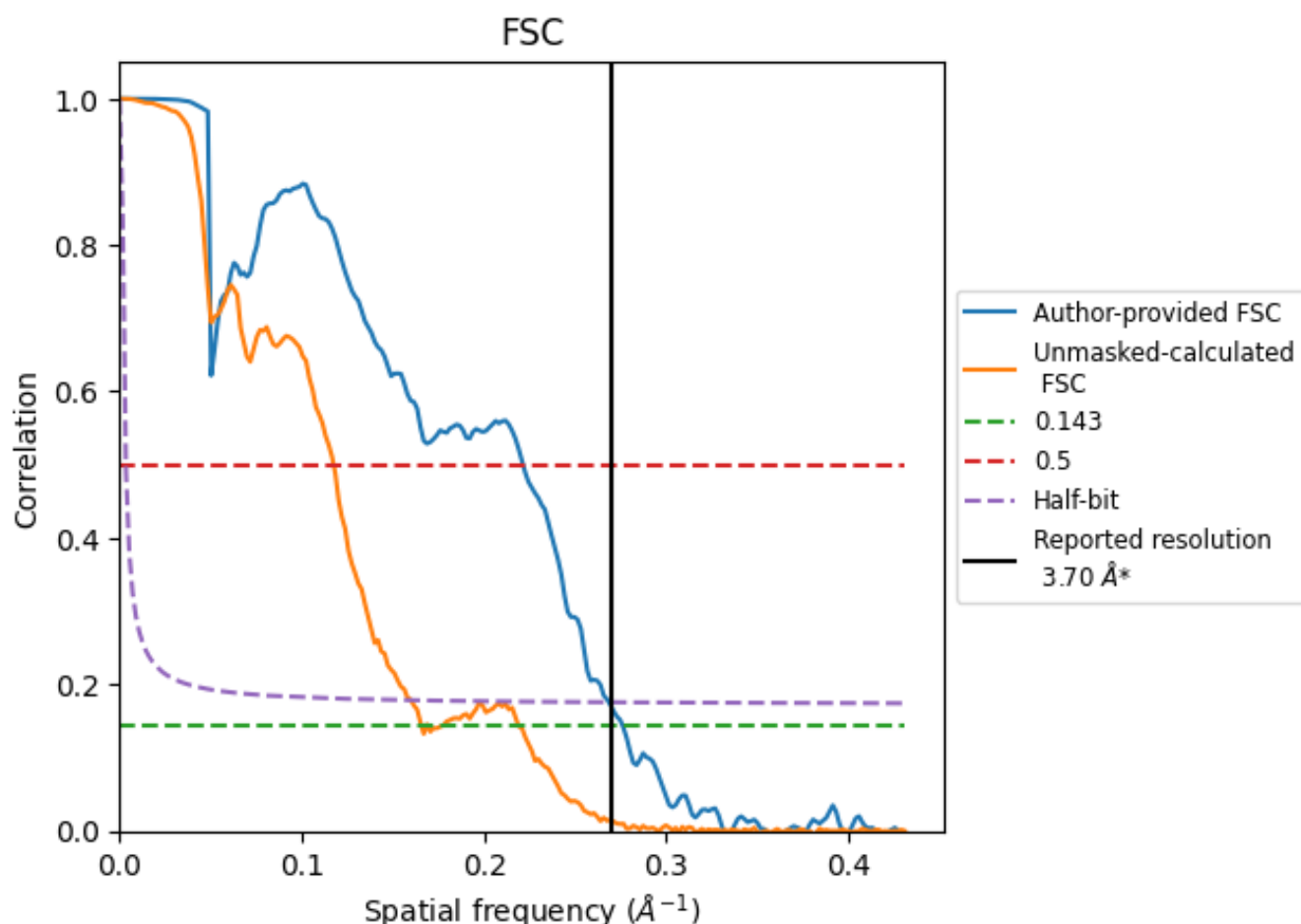


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

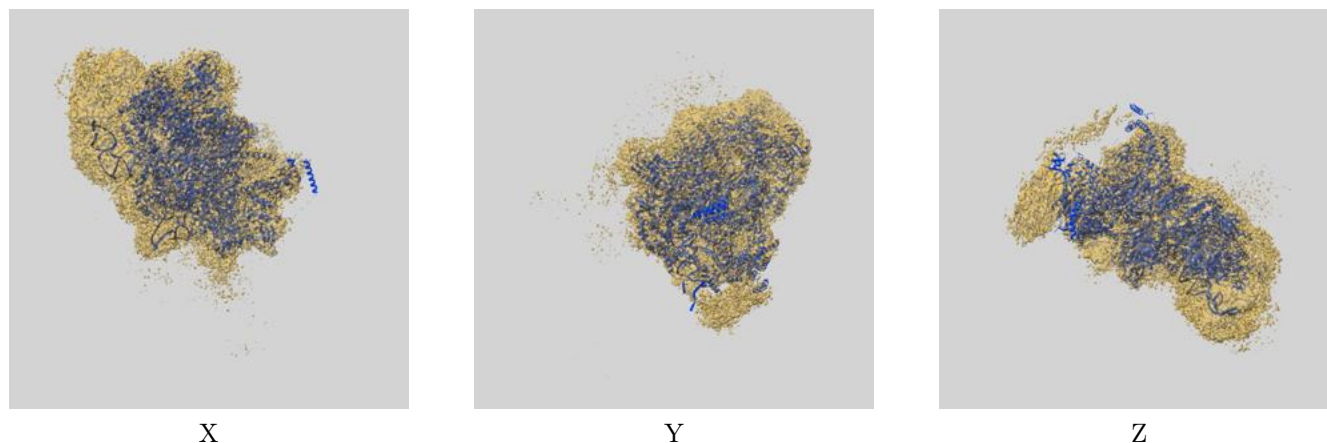
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.62	4.51	3.72
Unmasked-calculated*	6.03	8.50	6.25

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.03 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

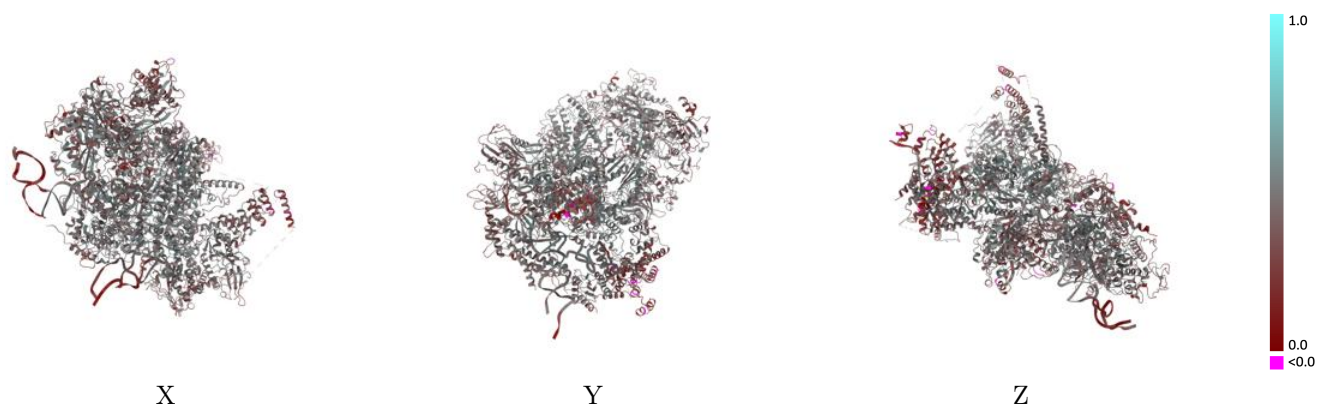
This section contains information regarding the fit between EMDB map EMD-18547 and PDB model 8QPB. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



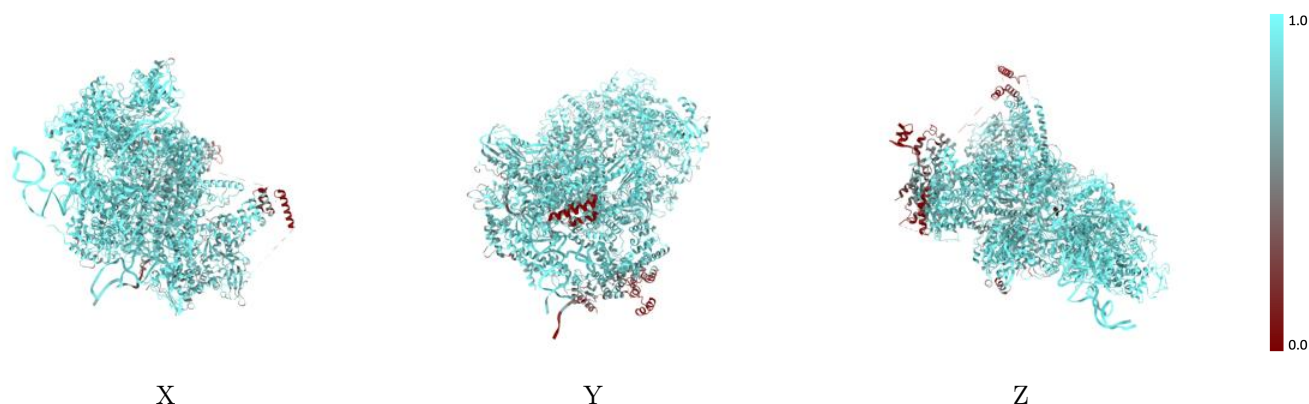
The images above show the 3D surface view of the map at the recommended contour level 0.027 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



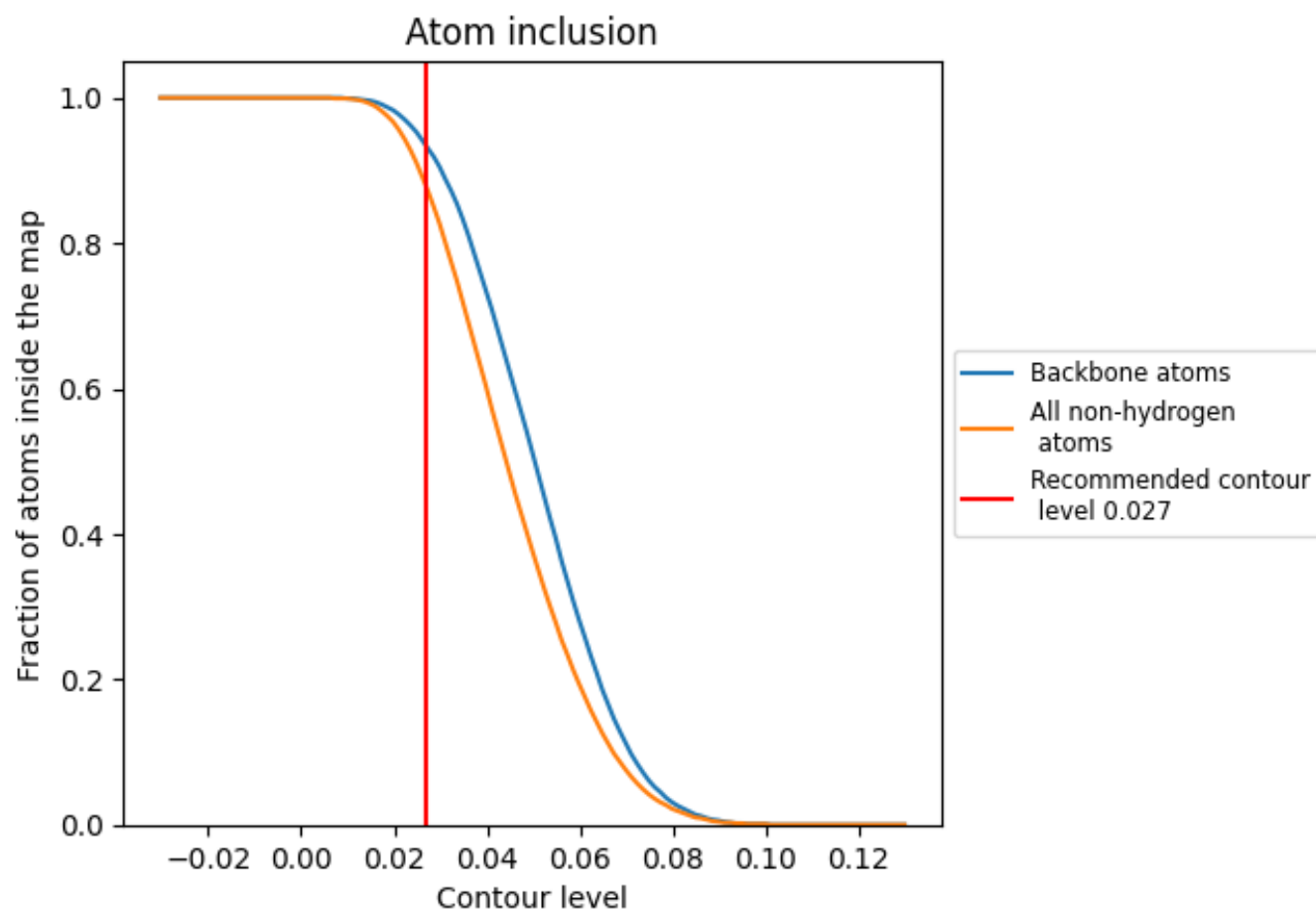
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.027).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 88% 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 (0.027) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8770	<div></div> 0.4230
4	<div></div> 0.8890	<div></div> 0.3960
5	<div></div> 0.9860	<div></div> 0.4040
6	<div></div> 0.8720	<div></div> 0.3990
7	<div></div> 0.7700	<div></div> 0.3800
A	<div></div> 0.9090	<div></div> 0.4570
B	<div></div> 0.8530	<div></div> 0.4010
C	<div></div> 0.9590	<div></div> 0.4230
D	<div></div> 0.9340	<div></div> 0.5000
F	<div></div> 0.8120	<div></div> 0.3510
G	<div></div> 0.9000	<div></div> 0.3210
J	<div></div> 0.9150	<div></div> 0.4390
L	<div></div> 0.8180	<div></div> 0.4070
M	<div></div> 0.6360	<div></div> 0.4180
N	<div></div> 0.7370	<div></div> 0.3710
S	<div></div> 0.6410	<div></div> 0.3590
U	<div></div> 0.8440	<div></div> 0.3830
z	<div></div> 0.9790	<div></div> 0.4300

