



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 10:48 PM UTC

PDB ID : 8QPB / pdb_00008qpb
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)

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A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

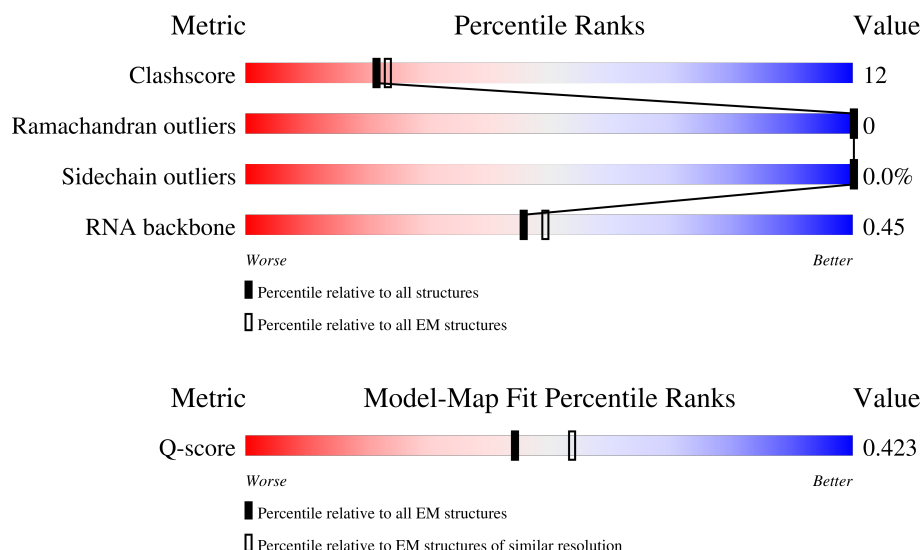
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

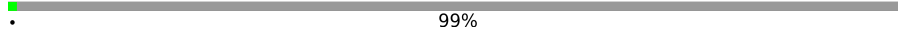
The reported resolution of this entry is 3.70 Å.

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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	 93%
3	J	683	 88%

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Mol	Chain	Length	Quality of chain
4	L	499	
5	F	522	
6	N	941	
7	A	2335	
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		

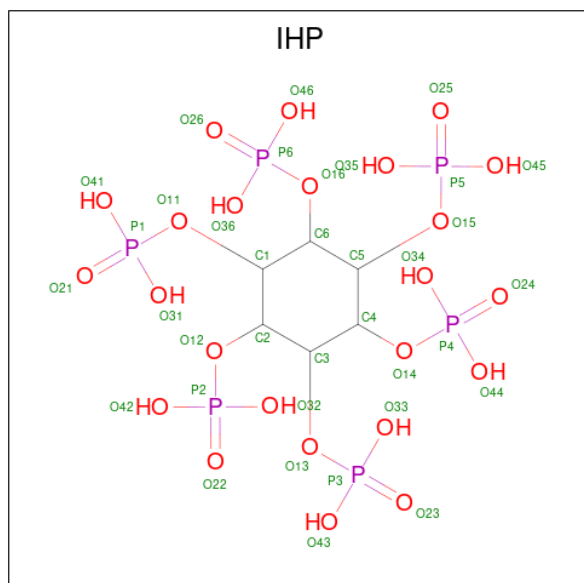
- Molecule 16 is a RNA chain called U6 snRNA.

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 (CCD ID: IHP) (formula: $C_6H_{18}O_{24}P_6$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
18	A	1	Total	C	O	P	0
			36	6	24	6	

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]



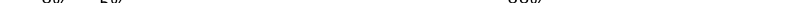
ALA	TYR	MET	GLY	CYS	ASP	GLN	GLU	GLY	TYR	LYS	PHE	SER	VAL	ASP	VAL	LYS	GLU	ALA	GLU	THR	ASP	SER	ASP	SER	ASP
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- Molecule 2: Probable ATP-dependent RNA helicase DDX23

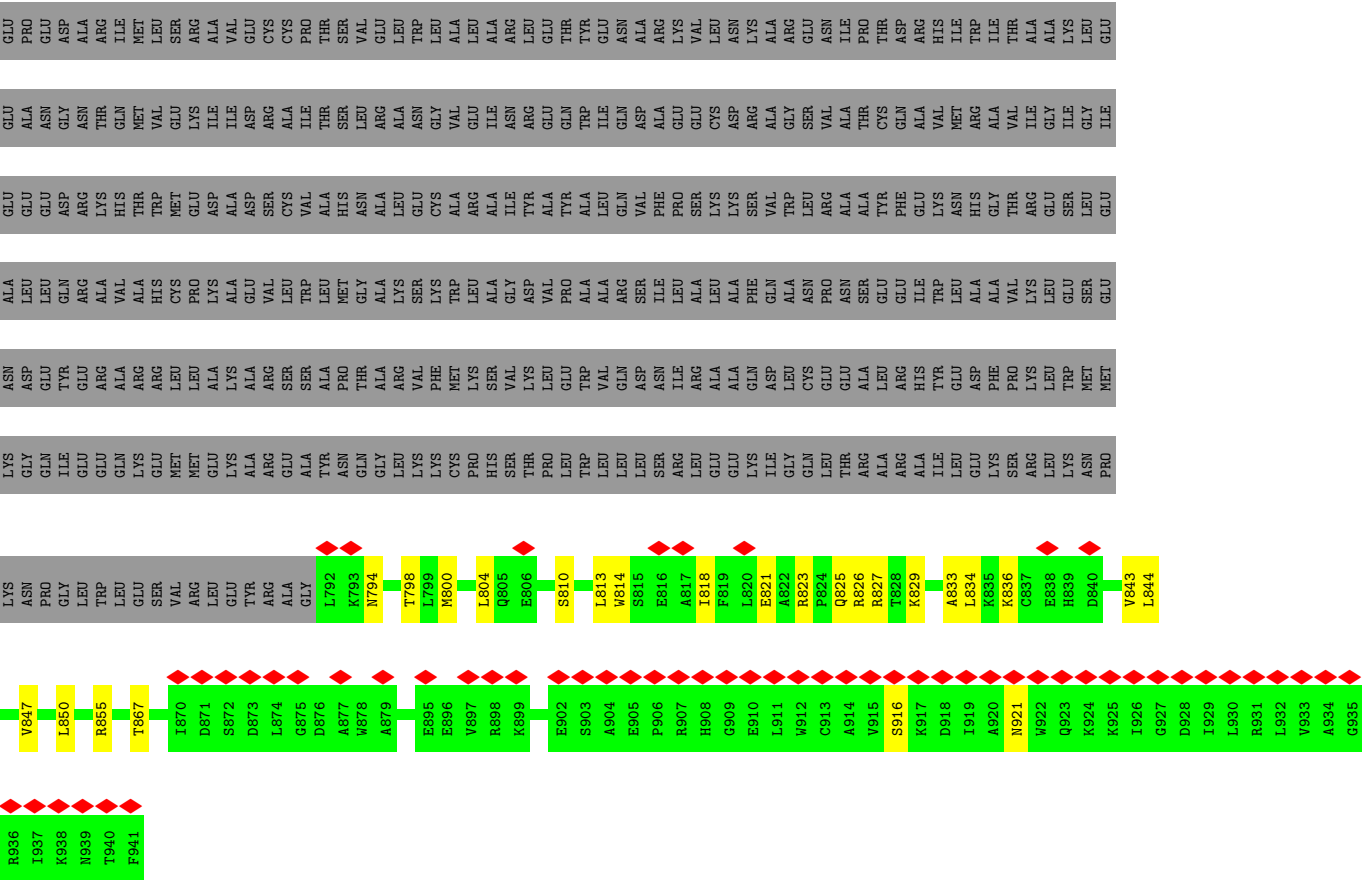
Chain G: 5% 93%

[illegible]

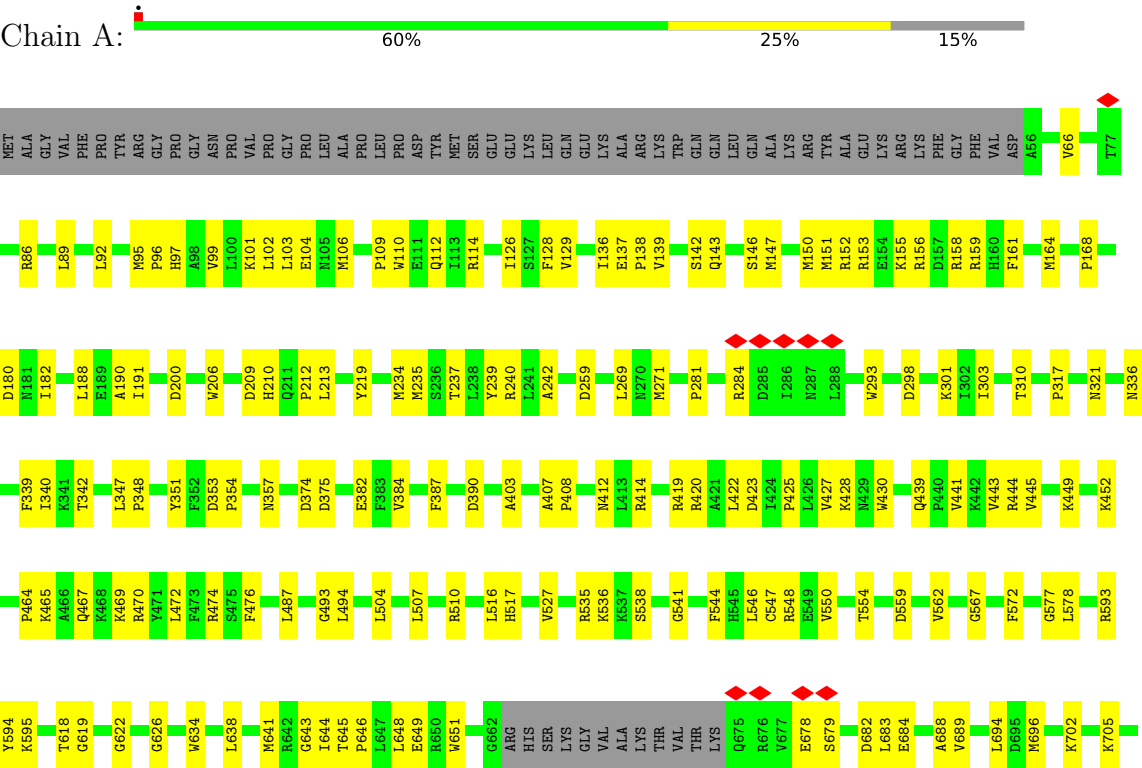
- Molecule 3: U4/U6 small nuclear ribonucleoprotein Prp3

Chain J:  8% 5% 88%



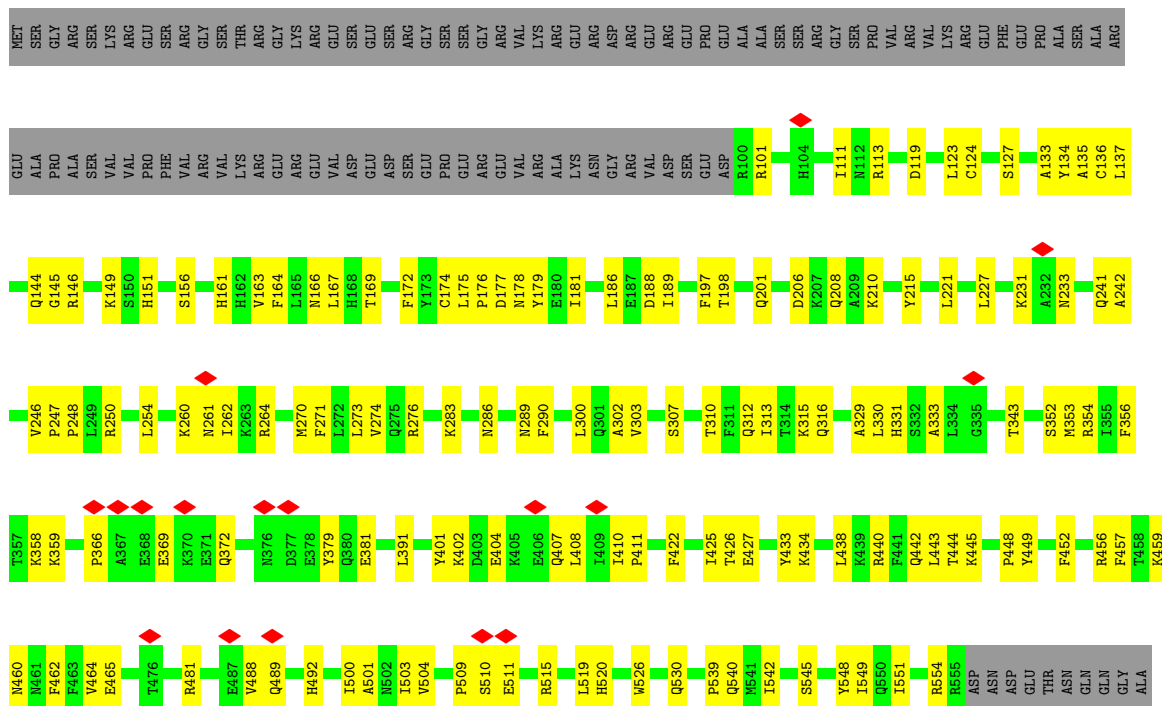


● Molecule 7: Pre-mRNA-processing-splicing factor 8

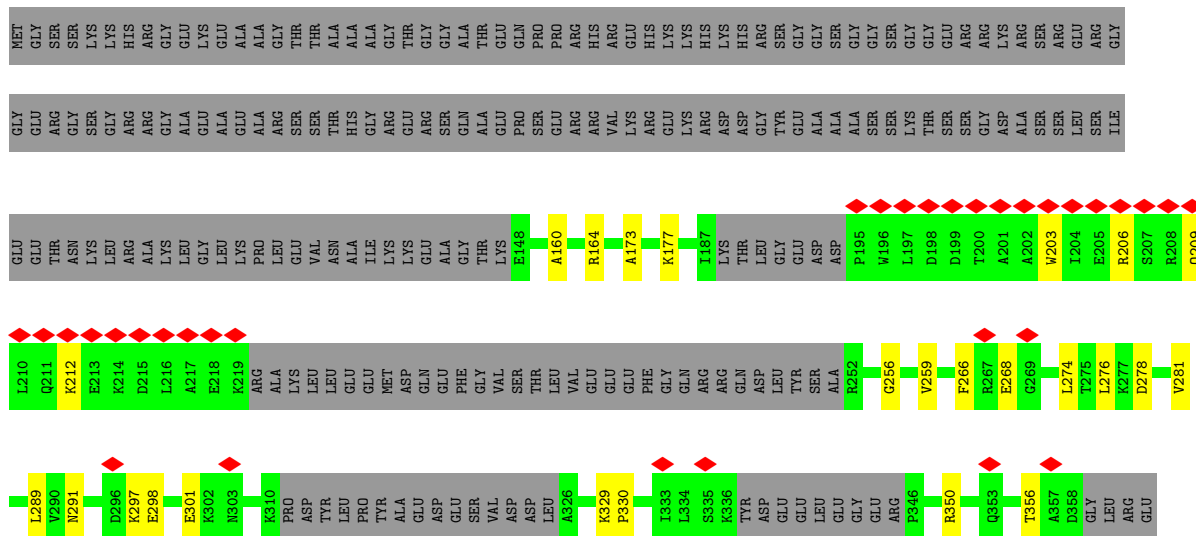


ASP	R1941	K1838	L1747	W1637	K1517	L1403	C1291	F1187	P1084	N974	R861	H712
GLU	V1945	W1839	L1751	W1638	Q1522	T1404	E1292	M1188	I1085	V975	E862	A716
ILE	K1840	S1640	L1753	S1640	Q1522	S1411	M1293	M1189	R1086	N976	E863	L1087
THR	A1950	T1841	L1753	R1641	M1531	S1411	K1294	M1189	L1087	N976	L864	L1087
SER	L1954	E1844	E1757	S1643	T1535	R1414	Q1296	E1193	G1089	N984	G865	P732
THR	K1955	L1848	P1758	L1644	L1536	G1415	M1304	I1196	R1090	N985	L866	W738
ALA	P1956	L1849	T1759	L1645	W1537	I1416	S1305	L1197	Y1091	E986	L867	W738
GLY	D1957	T1849	E1760	Y1660	P1540	T1421	P1308	P1198	I1092	N988	L878	Y742
LEU	K1958	S1851	P1761	W1661	T1541	L1422	H1209	H1209	I1097	L992	K882	W750
TYR	T1959	K1859	Y1762	I1662	T1541	F1423	F1311	P1198	F1098	N993	R883	T751
VAL	T1960	K1859	L1763	D1663	R1544	Q1424	F1311	W1214	R1100	R995	Q888	N752
SER	L1989	V1863	L1771	I1664	R1544	Q1424	F1311	W1214	F1101	V1001	R889	E759
PRO	K1994	T1864	F1772	Q1665	F1551	K1425	V1314	T1225	T1102	V1001	R760	R760
ASP	K1994	R1865	F1772	L1666	Q1552	D1426	F1316	T1225	A1103	I1005	R893	R763
ASN	N1998	M1868	Q1775	R1667	Q1552	T1429	Y1317	G1228	E1105	I1005	R894	R763
GLN	V1999	M1868	Q1775	W1668	L1555	T1429	T1318	G1228	E1105	I1005	R894	R763
ALA	E2006	P1871	W1776	G1669	L1556	K1434	E1321	R1231	I1110	T1010	F898	T766
VAL	I2007	L1872	I1776	D1670	L1557	G1435	G1324	V1232	I1110	A1011	M899	T770
GLU	R2008	E1873	W1776	Y1671	T1558	V1438	L1325	D1233	E1116	K1012	D900	T770
LEU	D2009	L1877	D1781	I1671	G1559	R1439	M1327	D1234	E1116	V1016	L901	C772
ASN	I2010	F1878	D1782	Y1671	T1558	V1438	L1328	D1234	E1116	I1017	L905	L776
LEU	G2012	T1878	W1783	I1671	L1558	V1438	M1330	Q1246	E1116	A1011	G906	G777
ARG	G2013	K1885	W1786	G1696	L1556	K1463	L1333	Q1246	E1116	K1012	P907	G777
THR	M2014	E1888	R1787	P1696	L1556	L1464	L1334	Q1246	E1116	V1016	P907	G777
ASN	E2015	L1889	W1788	G1700	W1582	W1465	L1334	Q1246	E1116	K1012	P907	G777
THR	I2016	L1889	T1789	I1703	Q1583	W1465	L1334	Q1246	E1116	K1012	P907	G777
GLY	Q2022	P1892	H1791	I1703	Q1583	W1465	L1334	Q1246	E1116	K1012	P907	G777
THR	A2027	L1897	K1792	D1706	L1589	L1478	D1347	Q1246	E1116	K1012	P907	G777
GLU	GLU	K1898	E1795	N1710	V1590	T1484	M1357	Q1246	E1116	K1012	P907	G777
ILE	ILE	V1899	G1796	N1710	M1591	T1484	M1357	Q1246	E1116	K1012	P907	G777
ASP	ASP	E1900	G1796	N1710	M1591	T1484	M1357	Q1246	E1116	K1012	P907	G777
LEU	LEU	K1901	G1796	N1710	M1591	T1484	M1357	Q1246	E1116	K1012	P907	G777
THR	THR	F1902	L1798	A1714	V1596	F1490	L1365	T1265	D1146	L1050	R820	R820
GLY	GLY	L1905	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLN	GLN	L1906	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1907	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLY	GLY	L1908	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLN	GLN	L1909	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1910	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
LEU	LEU	M1914	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLU	GLU	V1915	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
ALA	ALA	L1916	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1917	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
LEU	LEU	L1918	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLN	GLN	L1919	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
VAL	VAL	L1920	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1921	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLY	GLY	L1922	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
LEU	LEU	L1923	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLY	GLY	L1924	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1925	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLY	GLY	L1926	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1927	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
LEU	LEU	L1928	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLY	GLY	L1929	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1930	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLY	GLY	L1931	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1932	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
LEU	LEU	L1933	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLY	GLY	L1934	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1935	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLY	GLY	L1936	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1937	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLY	GLY	L1938	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1939	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLY	GLY	L1940	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1941	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLY	GLY	L1942	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1943	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLY	GLY	L1944	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1945	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLY	GLY	L1946	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1947	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLY	GLY	L1948	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1949	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLY	GLY	L1950	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1951	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLY	GLY	L1952	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1953	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLY	GLY	L1954	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1955	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
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GLY	GLY	L1958	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1959	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLY	GLY	L1960	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1961	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLY	GLY	L1962	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1963	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
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THR	THR	L1965	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLY	GLY	L1966	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1967	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLY	GLY	L1968	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1969	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLY	GLY	L1970	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1971	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLY	GLY	L1972	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1973	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLY	GLY	L1974	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1975	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLY	GLY	L1976	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
THR	THR	L1977	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825
GLY	GLY	L1978	P1802	N1717	L1601	K1491	Y1369	I1268	N1148	V1052	I825	I825

- Molecule 8: Ubiquitin carboxyl-terminal hydrolase 39



- Molecule 9: U4/U6.U5 tri-snRNP-associated protein 1



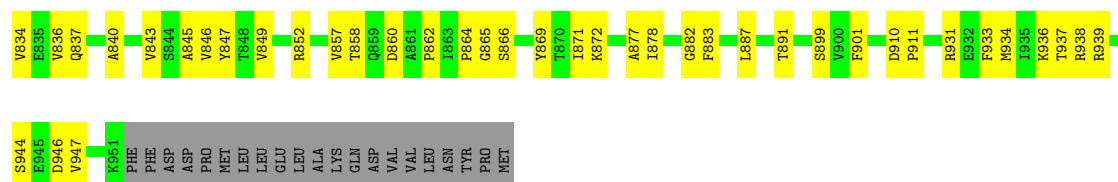
Tyr	Lys	Ala	Asn	Glu	Pro	Leu	Pro	Leu	Arg
Ile	Glu	Pro	Ile	Asp	Pro	Leu	Pro	Leu	Glu
Val	Ala	Asn	Gly	Pro	Gly	Leu	Gly	Leu	Glu
Leu	Phe	Lys	Trp	Arg	Trp	Leu	Arg	Leu	Glu
Gly	Gln	Leu	Thr	Lys	Gln	Asp	Gln	Asp	Ile
Ser	Leu	Pro	Val	Gly	Val	Gln	Val	Gln	Arg
Gly	Leu	Ser	Asn	Ala	Leu	Leu	Leu	Thr	Ala
Ser	His	Ala	Leu	Ile	Ile	Gln	Glu	Asp	Lys
Ser	His	Val	Asp	Val	Val	Glu	Glu	Asp	Leu
Met	Phe	Tyr	Glu	Phe	Phe	Asp	Asp	Gly	Leu
Asn	His	Cys	Glu	Asn	Asn	Glu	Glu	Asp	Arg
Ala	Gly	Ile	Lys	Ala	Ala	Ala	Ala	Phe	Gln
Asn	Lys	Glu	Gln	Thr	Thr	Gly	Gly	Phe	Gln
Thr	Gly	Asp	Gln	Ser	Ser	Leu	Leu	Ser	Gln
Ile	Ser	Val	Asn	Glu	Glu	Glu	Glu	Arg	Ser
Thr	Gly	Met	Asp	Phe	Phe	Leu	Leu	Leu	Arg
Thr	Lys	Ala	Phe	Cys	Cys	Gln	Gln	Arg	Ser
Lys	Met	Ile	Ser	Arg	Arg	Lys	Lys	Gly	Thr
	Lys	Asp	Ala	Thr	Thr	Gln	Gln	Arg	Val
	Thr	Asp	Ser	Leu	Leu	Leu	Leu	Gly	Gly
	Glu	Lys	Ser	Gly	Glu	Glu	Glu	Arg	Pro
	Glu	Tyr	Thr	Ile	Thr	Lys	Lys	Arg	Arg
	Leu	Arg	Ile	Pro	Pro	Gly	Gly	Val	Leu
	Leu	Arg	Leu	Gly	Leu	Leu	Leu	Val	Leu
	Leu	Thr	Asn	Thr	Asn	Gln	Gln	Pro	Glu
	Leu	Thr	Arg	Glu	Glu	Gln	Gln	Met	Val
	Lys	Asp	Gly	Glu	Gln	Leu	Leu	Pro	Val
	Lys	Phe	Leu	Gln	Leu	Leu	Pro	Pro	Thr
	Met	Lys	Ala	Glu	Arg	Gln	Gln	Gln	Phe
	Ser	Glu	Ala	Leu	Leu	Leu	Lys	Lys	Glu
	Ser	Glu	Ala	Leu	Leu	Leu	Pro	Glu	Glu
	Ser	Thr	Asn	Leu	Leu	Leu	Pro	Leu	Lys
	Ser	Asp	Leu	Met	Met	Gly	Gly	Pro	Lys
	Thr	Tyr	Leu	Asp	Phe	Asp	Ser	Asp	Arg
	Pro	Lys	Cys	Glu	Thr	Lys	Lys	Asp	Arg
	Leu	Pro	Gln	Arg	Val	Val	Val	Asp	Arg
	Gly	Asp	Asn	Asp	Glu	Arg	Lys	Thr	Val
	Thr	Val	Lys	Glu	Ile	Val	Val	Glu	Ile
	Ala	Lys	Gly	Glu	Val	Val	Val	Asn	Lys
	Leu	Ile	Leu	Ser	Lys	Arg	Lys	Met	Lys
	Leu	Glu	Thr	Ala	Leu	Thr	Leu	Asp	Glu
	Leu	Thr	Thr	Thr	Val	Ser	Ser	Gly	Lys
	Gln	Thr	Val	Ser	Gln	Gly	Arg	Asp	Val
	Lys	Gly	Lys	Ser	Arg	Ser	Arg	Glu	Val
	Ala	Arg	Val	Glu	Arg	Glu	Arg	Glu	Val
	Leu	Gly	Val	Leu	Glu	Glu	Glu	Glu	Val
	Thr	Leu	Ala	Asp	Thr	Trp	Trp	Gly	Arg
	Pro	Thr	Lys	Gly	Gly	Arg	Glu	Gly	Ala
	Pro	Pro	Val	Glu	Asp	Asp	Glu	Ala	Asp
			Lys	Thr	Lys	Lys	Pro	Pro	Pro

- Molecule 10: 116 kDa U5 small nuclear ribonucleoprotein component

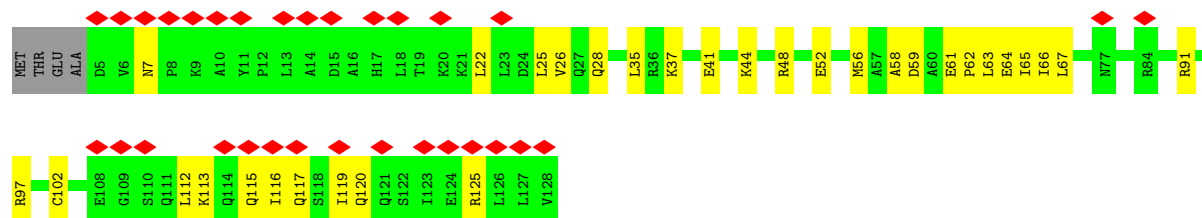
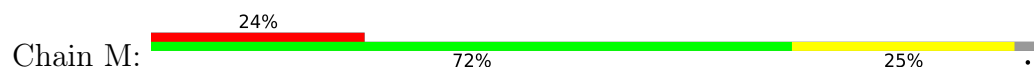
Chain C:



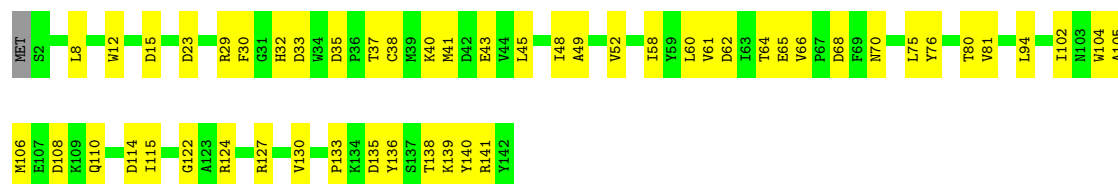
P737	K609	Y481	R350	L227	E127	GLU	MET
G741	Y614	Y482	R350	F228	L128	ASP	THR
P742	L617	D486	T353	D230	I129	LYS	THR
I744	T632	A492	R354	E233	N131	LYS	LEU
L745	G633	F493	F356		V132	TVR	TVR
D747	G634	G494	T357	L237	T133	PRO	ASP
	L635	R495	R358	N238	L134	ALA	GLU
	Y636		R359	T239		GLY	PHE
S752	L637	T500	S368		H137	GLU	GLY
	D638	H502	F369	K244	L138	GLU	ASN
K756	A503	E503	F370		H139	VAL	TVR
L758	G504	G504		Q248	H140	TVR	ILE
			L374	E249	G141	GLY	GLY
			L375	R250	K142	PRO	PRO
S761	R645	V509	E375		E151	VAL	LEU
G769	F646	Y514	P376	V255		GLU	ASP
F770	Y648	Y514	L377		K159	THR	SER
Q771	D521	D521	T378	K259		ILE	ASP
W772	L653	S522	L380	L260	L165	VAL	GLU
	K654	V655		D261	C166	GLN	ASP
E776	V655		L392	R262	Y167	GLU	ASP
			F393	L263	T168	GLU	ASP
E782	T661	M531			R177	ASP	GLU
L783	F662	I532	L399	E286	G178	THR	LEU
I784	K673	V534	L410	K288	V179	GLN	GLY
				L269		LEU	ARG
V787	A676	M536	R417		S183	THR	THR
K788	N683	E540	E426	K277	T184	GLU	LYS
F789			F427			PRO	ASP
	T686	V544	T428	V285	T187	ILE	LEU
L792	E693	N548	G429	L300	V188	ILE	ASP
D793	Y794	M549	F430	S301	V189	LYS	GLU
V795	E703	W704	V431	P302	L190	PRO	MET
Q798	V705	L551	D432	L303		VAL	ASP
E799	Q706		M433	G305	L199	LYS	ASP
			C434	N306		THR	ASP
H802	W709	T559	H437		I202	LYS	ASP
			I438	S310	M203	PHE	ASP
I809	G715	P565	A445		D204	THR	ASP
A812	F716	B569		Q313	T205	LEU	ASP
V815	F717		I449		G207	MET	VAL
V816	F718	K581	E450	L320	H208	GLU	GLY
Y817	Q719	K589	H451			GLN	ASP
	W724		Y453		F211	THR	HIS
T824		P594		A328	S212	LEU	ASP
P825	A729	V595	L461	E214	D213	PRO	ASP
R826	F730	L600	M465	G332	E214	VAL	ASP
L827	I732	M603	M465		V215	THR	HIS
P830				E338		VAL	PRO
K831	F735		T478		L219	THR	GLY
R832			T479	F339	R220	GLU	MET
				K341	I221	GLU	GLU
				R342			VAL
				L343			VAL
					G224	L122	VAL
					V225	M116	LEU
						M123	LEU
							HIS



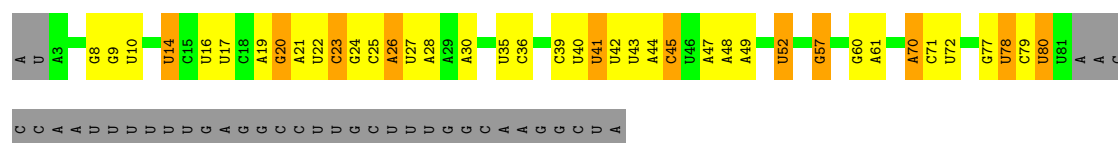
- Molecule 11: NHP2-like protein 1, N-terminally processed



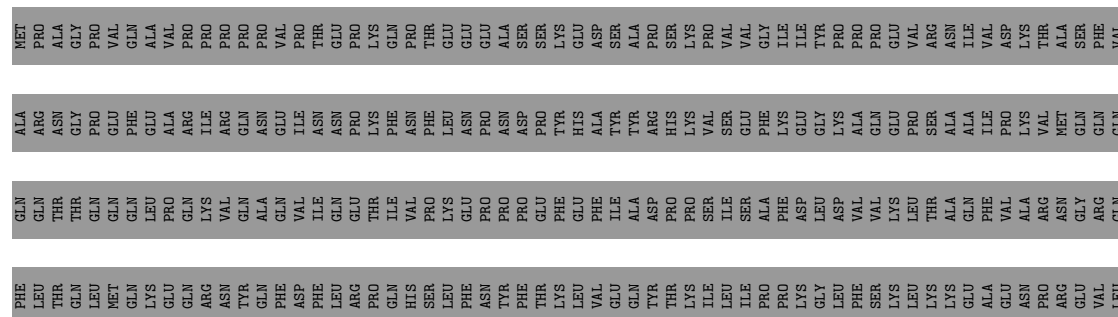
- Molecule 12: Thioredoxin-like protein 4A

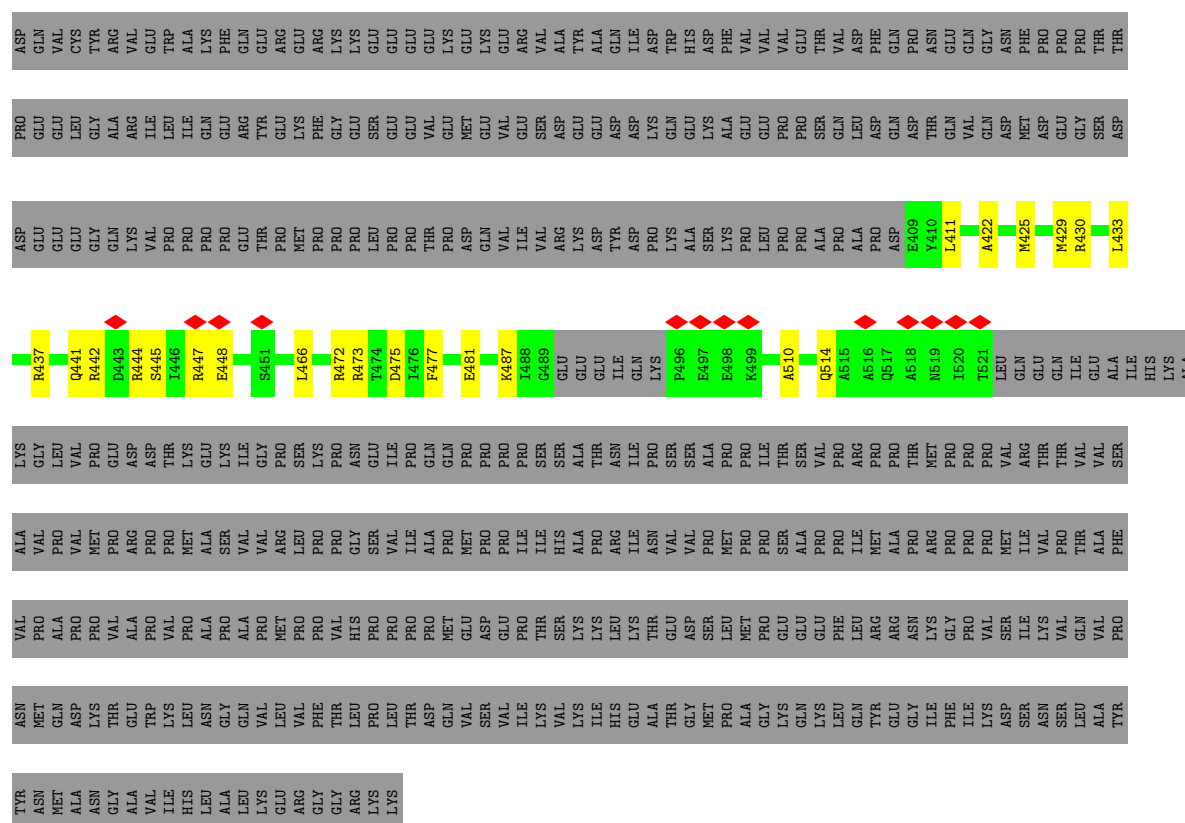


- Molecule 13: U5 snRNA

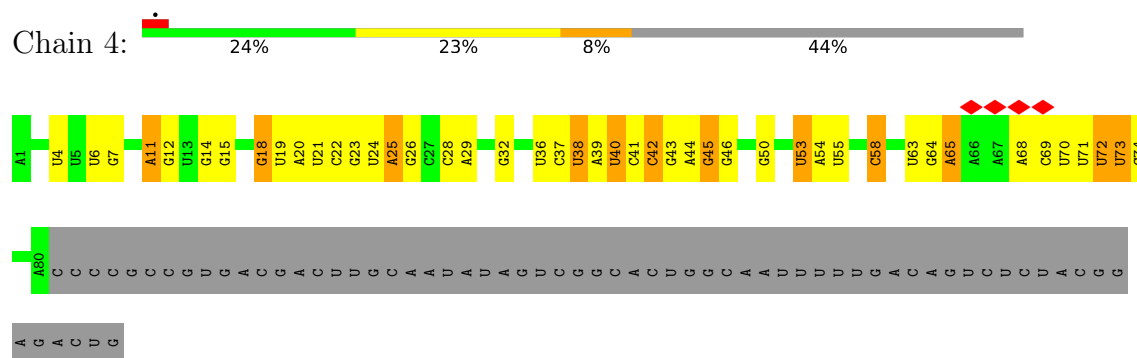


- Molecule 14: Splicing factor 3A subunit 1

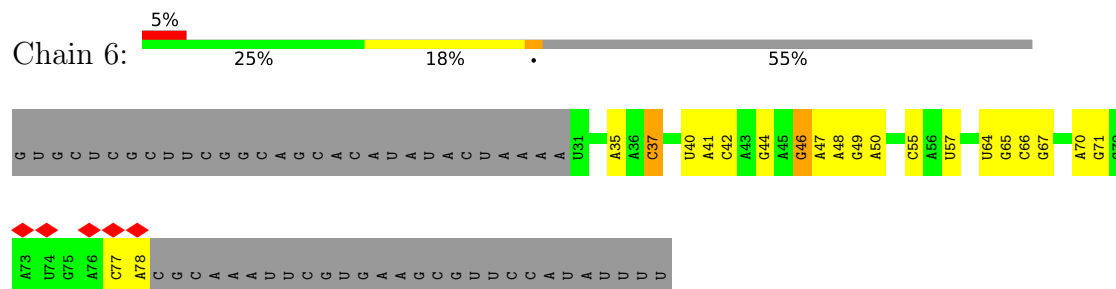




- Molecule 15: U4 snRNA



- Molecule 16: U6 snRNA



- Molecule 17: 5'ss oligo



A-5
G-4
U-3
G-2
G-1
G1
U2
A3
A4
GS
A6
G7
C8

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 ($\text{\AA}$)	556.8, 556.8, 556.8	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	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	0.13	0/158	0.36	0/209
2	G	0.08	0/493	0.23	0/659
3	J	0.12	0/686	0.27	0/914
4	L	0.12	0/2924	0.28	0/3938
5	F	0.10	0/491	0.27	0/657
6	N	0.11	0/3565	0.26	0/4818
7	A	0.14	0/16856	0.30	0/22865
8	U	0.10	0/3845	0.29	0/5208
9	S	0.11	0/1172	0.25	0/1567
10	C	0.13	0/6739	0.32	0/9151
11	M	0.13	0/974	0.34	0/1316
12	D	0.13	0/1199	0.26	0/1620
13	5	0.11	0/1850	0.20	0/2875
14	7	0.11	0/858	0.28	0/1152
15	4	0.10	0/1898	0.14	0/2954
16	6	0.10	0/1159	0.21	0/1806
17	z	0.11	0/321	0.14	0/500
All	All	0.12	0/45188	0.28	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	32	0
4	L	2886	0	2885	75	0
5	F	488	0	499	13	0
6	N	3502	0	3379	110	0
7	A	16409	0	16326	422	0
8	U	3749	0	3769	100	0
9	S	1164	0	1173	23	0
10	C	6592	0	6615	175	0
11	M	962	0	1012	29	0
12	D	1170	0	1141	36	0
13	5	1660	0	842	25	0
14	7	846	0	837	22	0
15	4	1699	0	858	32	0
16	6	1034	0	521	21	0
17	z	286	0	142	8	0
18	A	36	0	6	0	0
All	All	43804	0	41368	980	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 12.

The worst 5 of 980 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
10:C:123:MET:HE1	10:C:532:ILE:HG21	1.61	0.83
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

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

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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%)	52 (100%)	0	100	100
6	N	341/792 (43%)	341 (100%)	0	100	100
7	A	1786/2108 (85%)	1786 (100%)	0	100	100
8	U	418/511 (82%)	418 (100%)	0	100	100
9	S	120/681 (18%)	120 (100%)	0	100	100
10	C	738/866 (85%)	737 (100%)	1 (0%)	88	88
11	M	108/111 (97%)	108 (100%)	0	100	100
12	D	129/130 (99%)	129 (100%)	0	100	100
14	7	91/709 (13%)	91 (100%)	0	100	100
All	All	4226/10002 (42%)	4225 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	C	531	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 48 such sidechains are listed below:

Mol	Chain	Res	Type
7	A	1875	HIS
8	U	492	HIS
7	A	1944	HIS
8	U	241	GLN
9	S	293	ASN

5.3.3 RNA ⓘ

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

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
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 oligosaccharides 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	60,60,60	1.05	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	-	-	4/30/54/54	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

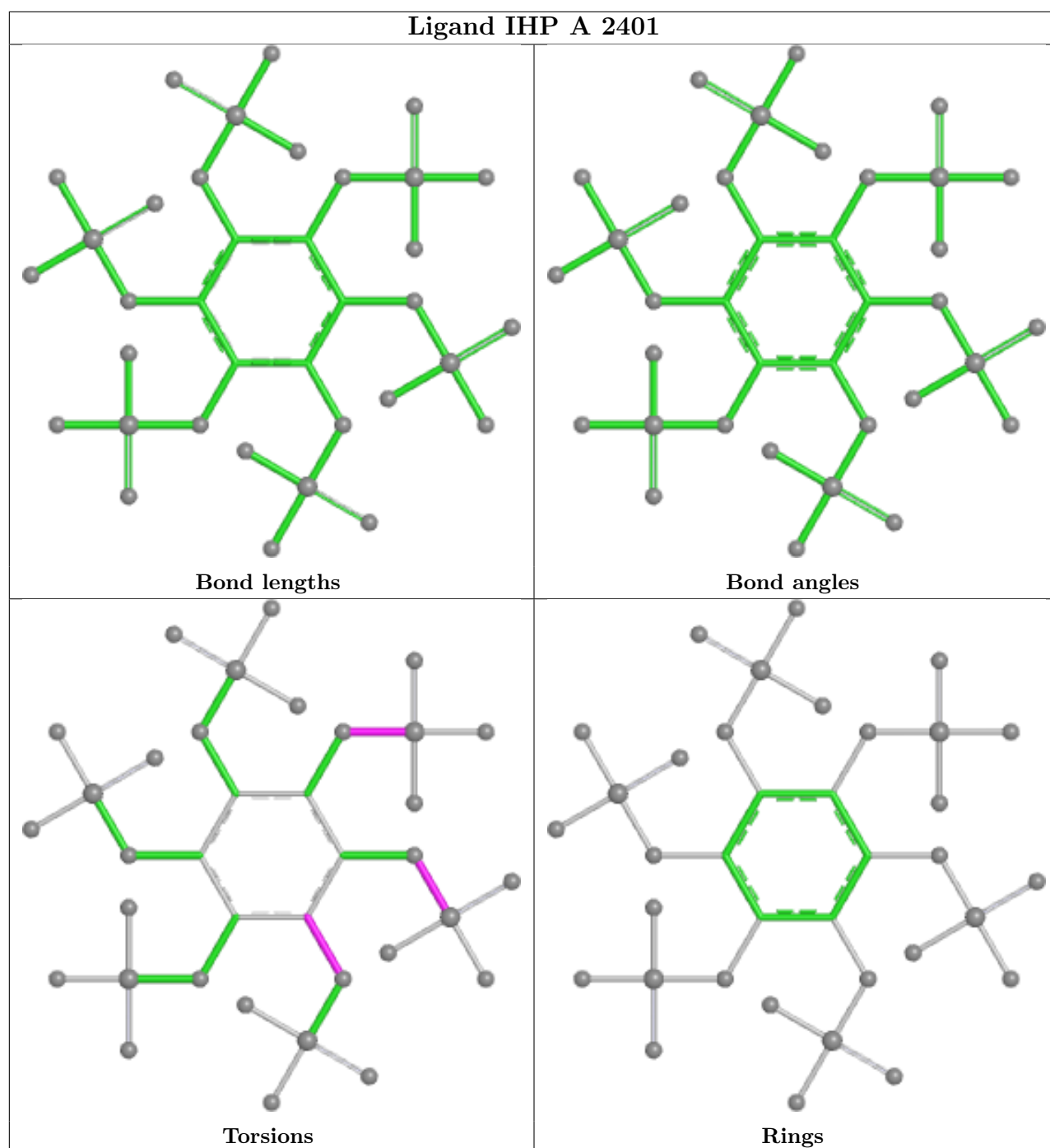
All (4) torsion outliers are listed below:

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

There are no ring outliers.

No monomer is involved in short contacts.

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.

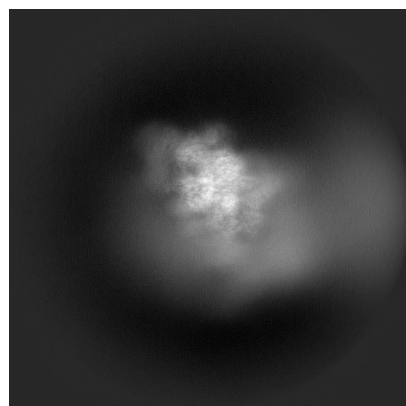
6 Map visualisation [i](#)

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.

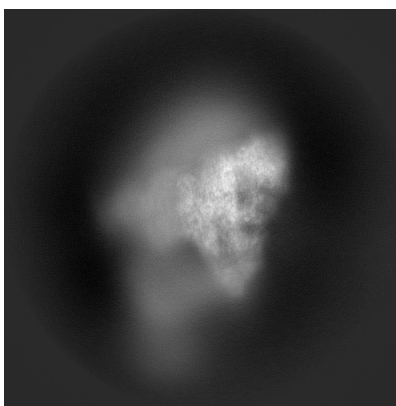
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

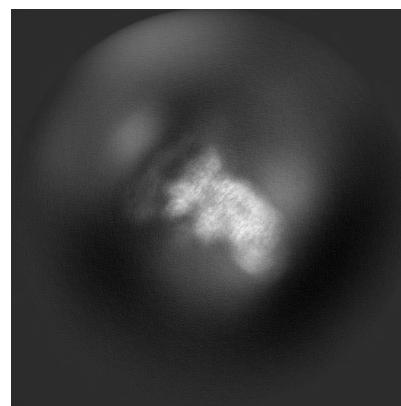
6.1.1 Primary map



X

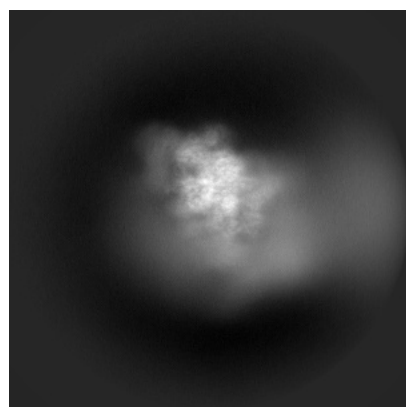


Y

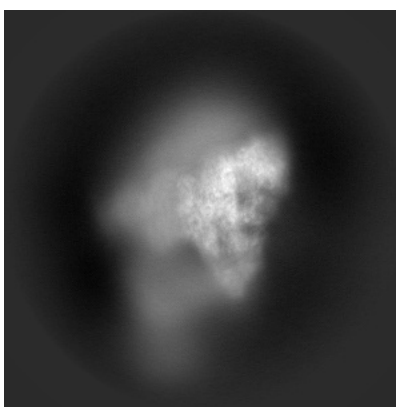


Z

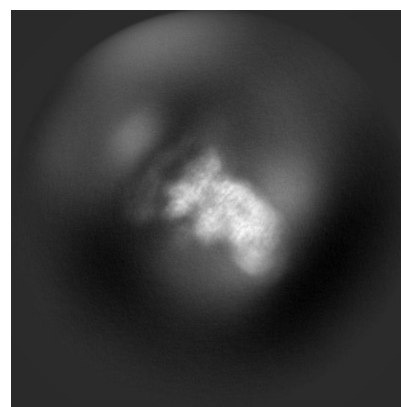
6.1.2 Raw map



X



Y

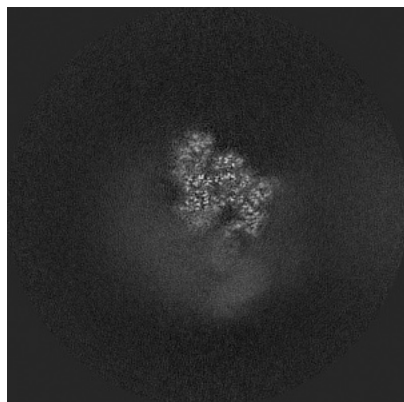


Z

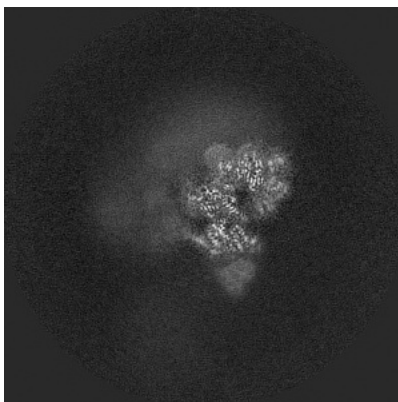
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

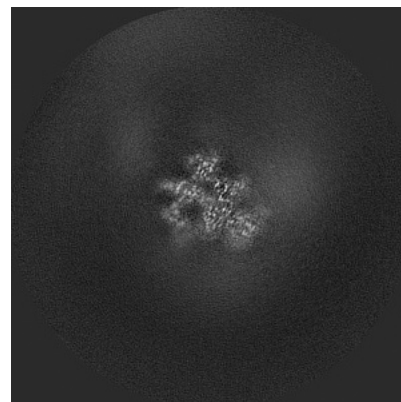
6.2.1 Primary map



X Index: 240

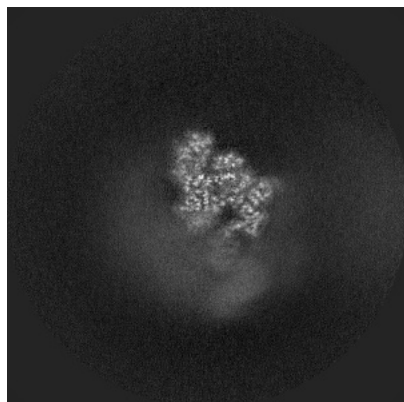


Y Index: 240

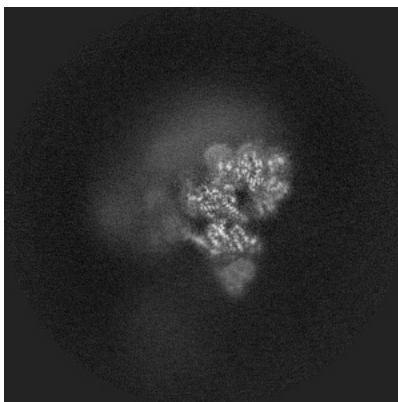


Z Index: 240

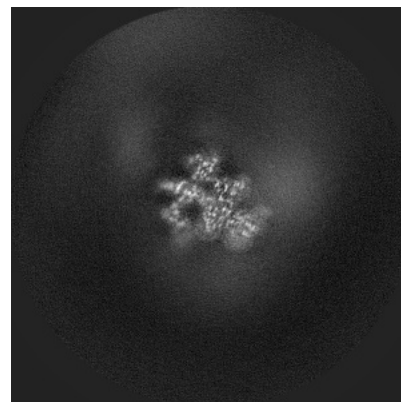
6.2.2 Raw map



X Index: 240



Y Index: 240

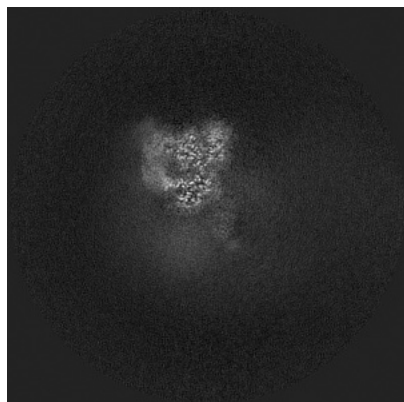


Z Index: 240

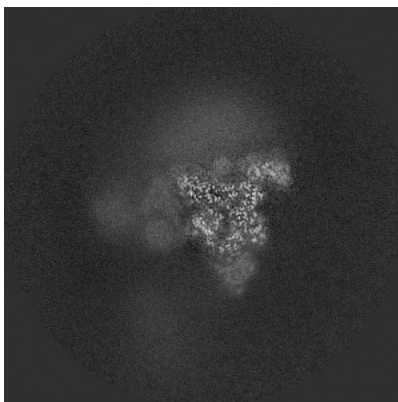
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

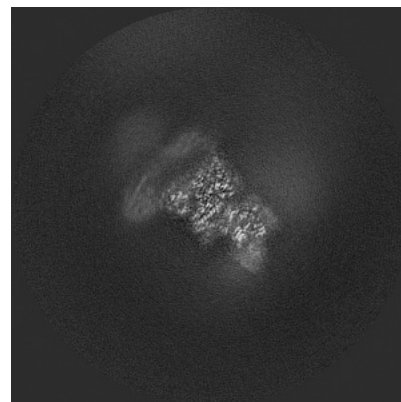
6.3.1 Primary map



X Index: 287

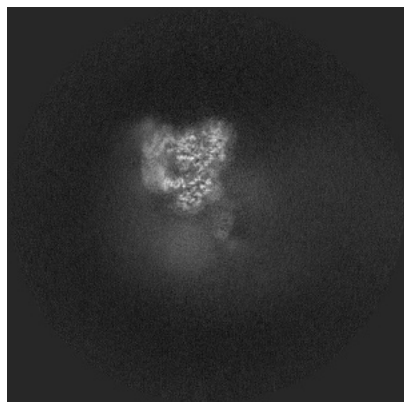


Y Index: 255

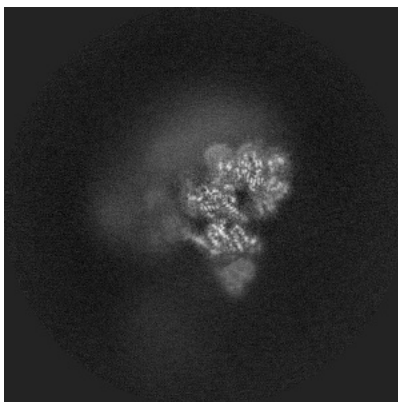


Z Index: 274

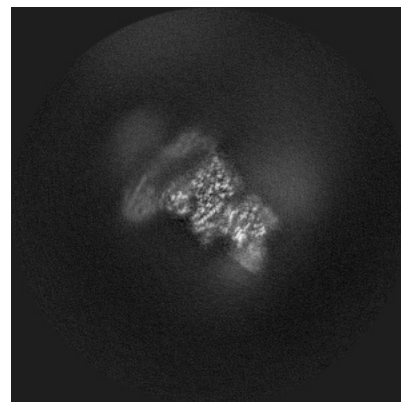
6.3.2 Raw map



X Index: 288



Y Index: 240

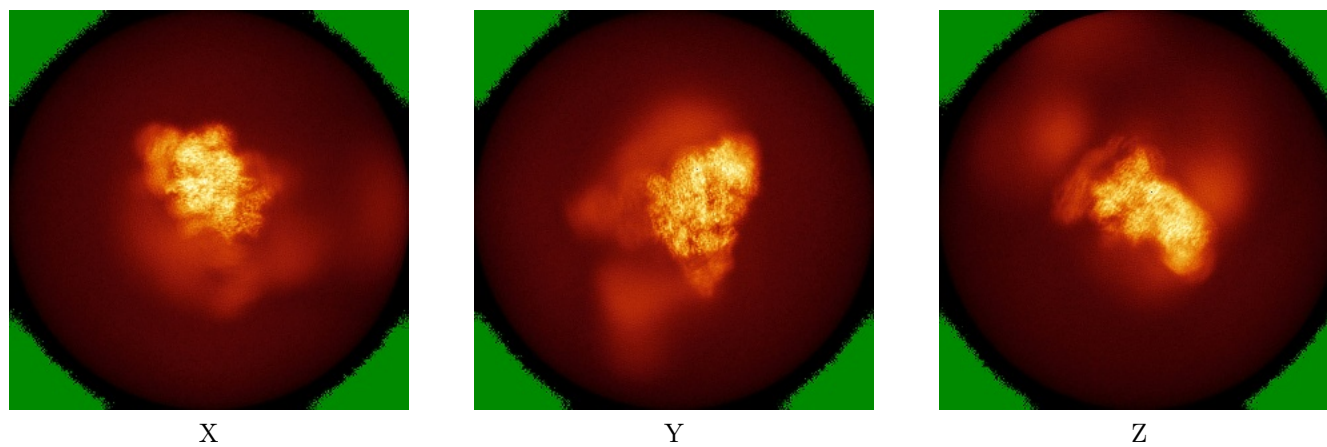


Z Index: 274

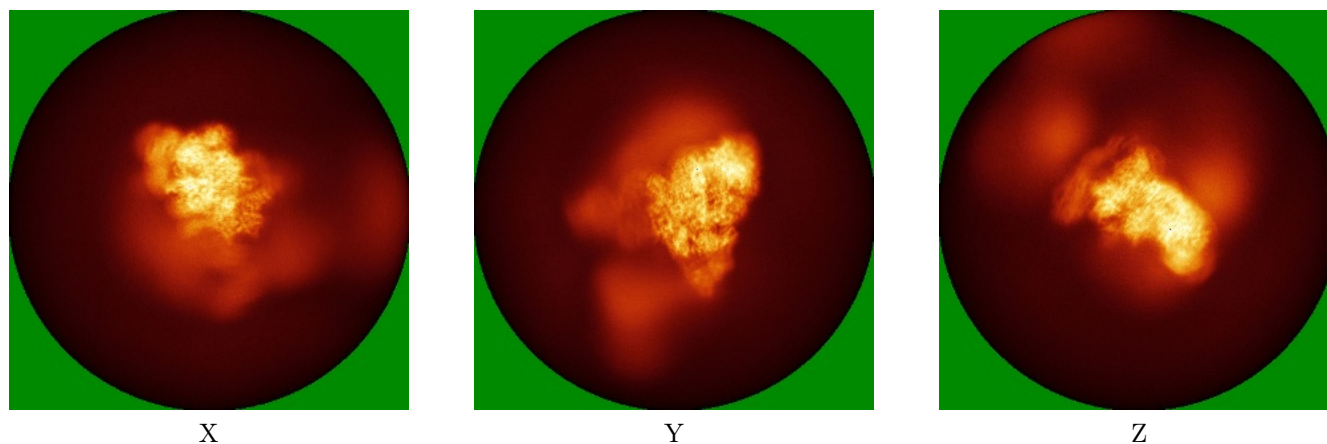
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

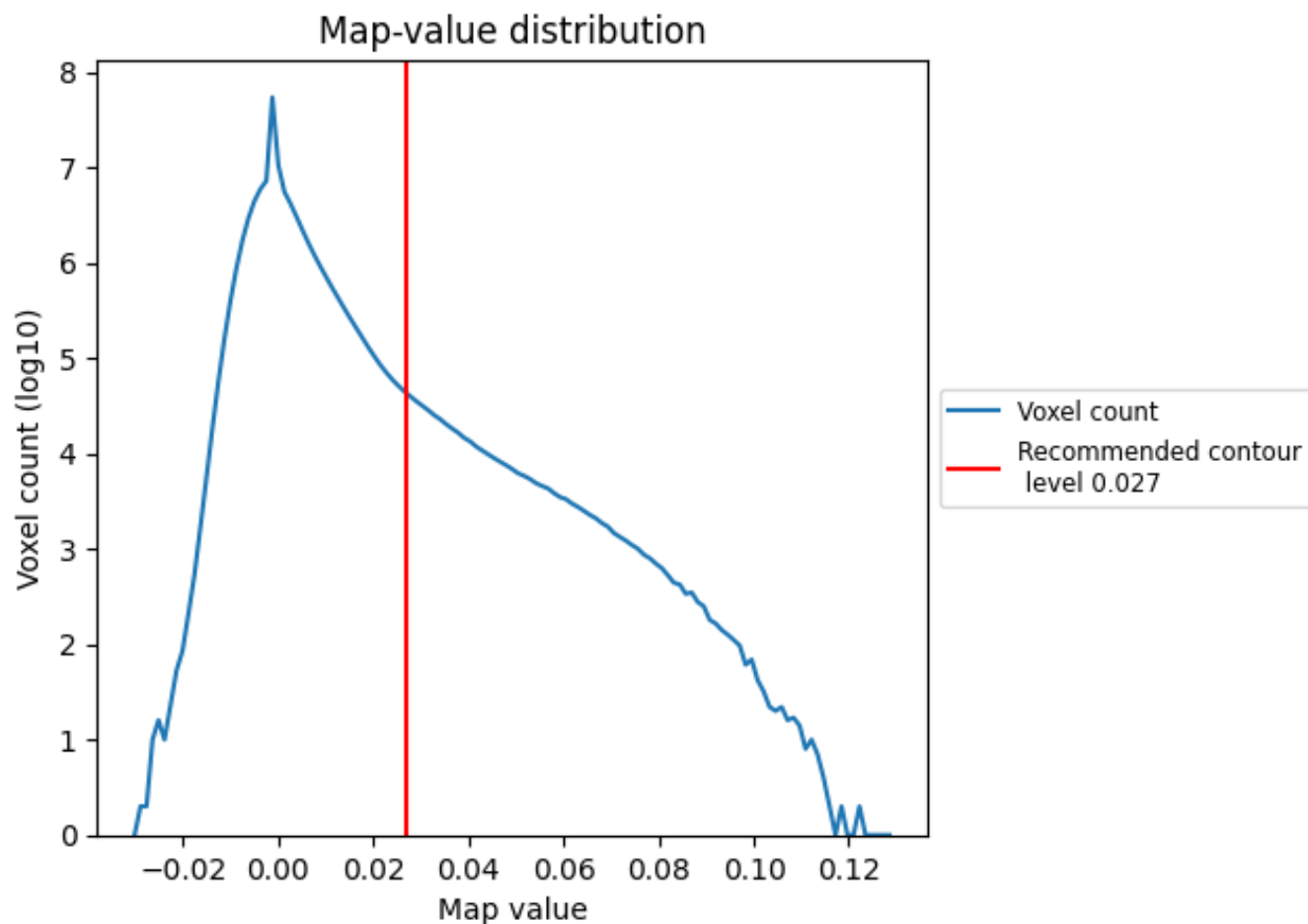
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

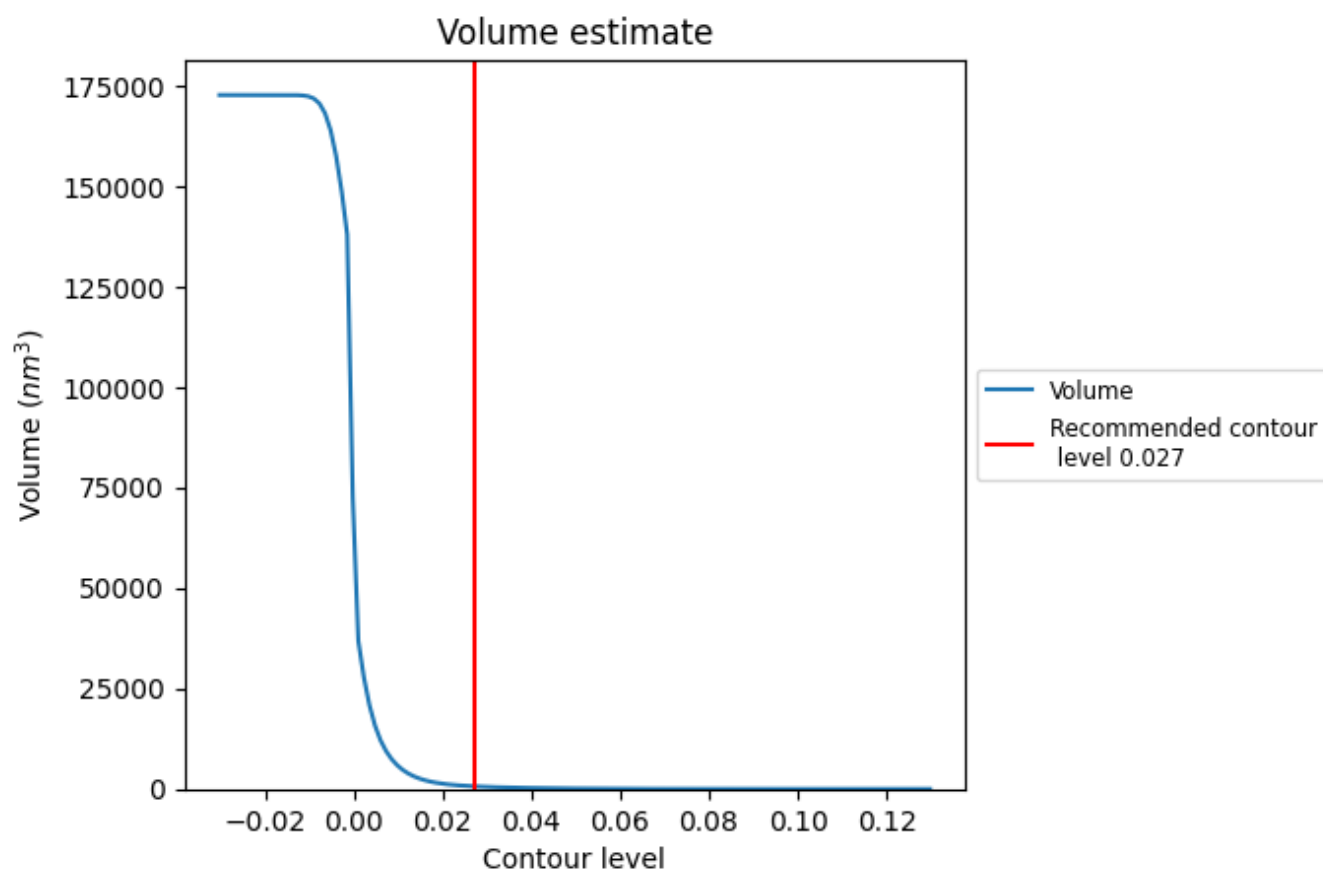
This section contains the results of statistical analysis of the map.

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.

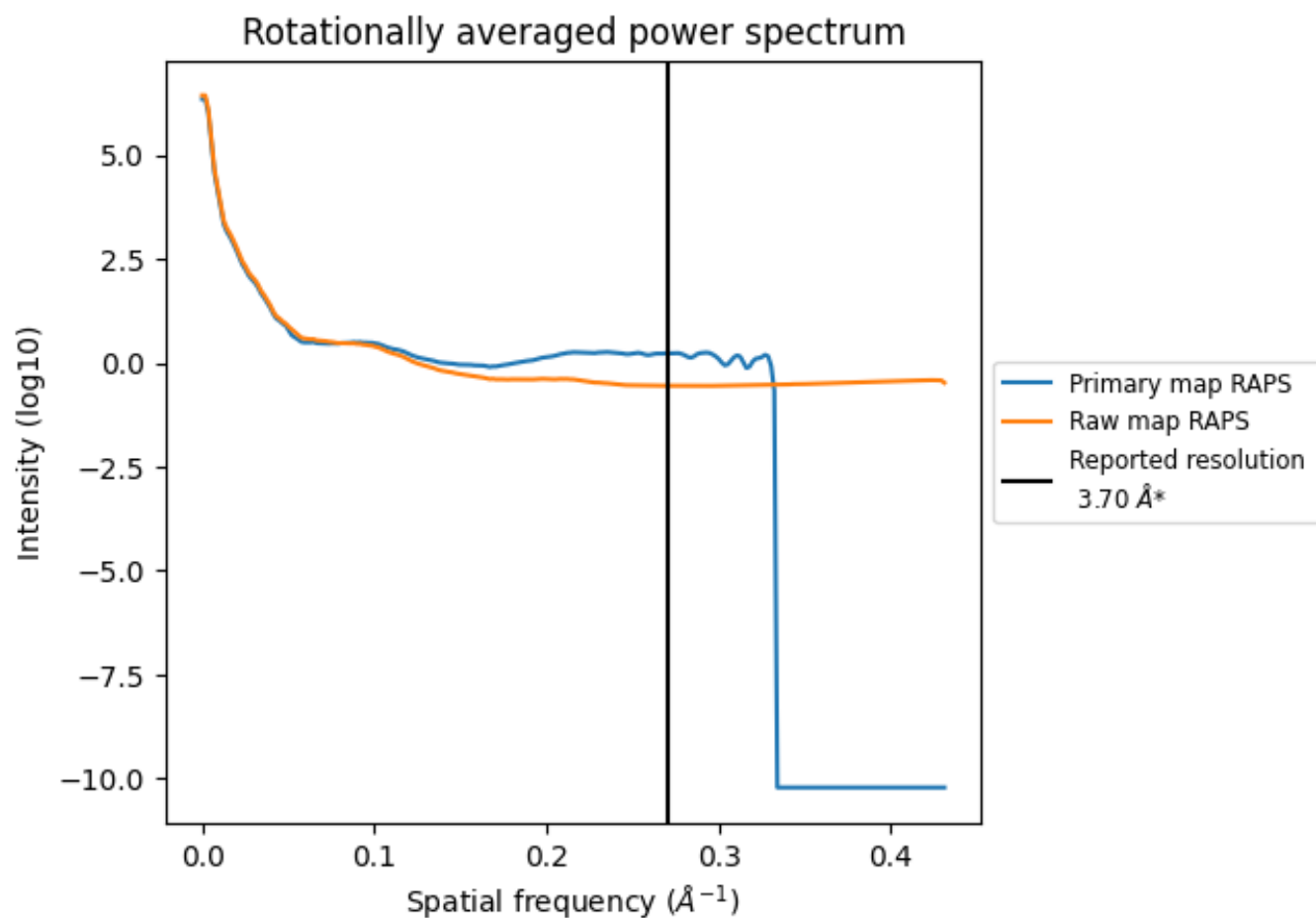
7.2 Volume estimate [i](#)



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 ⓘ

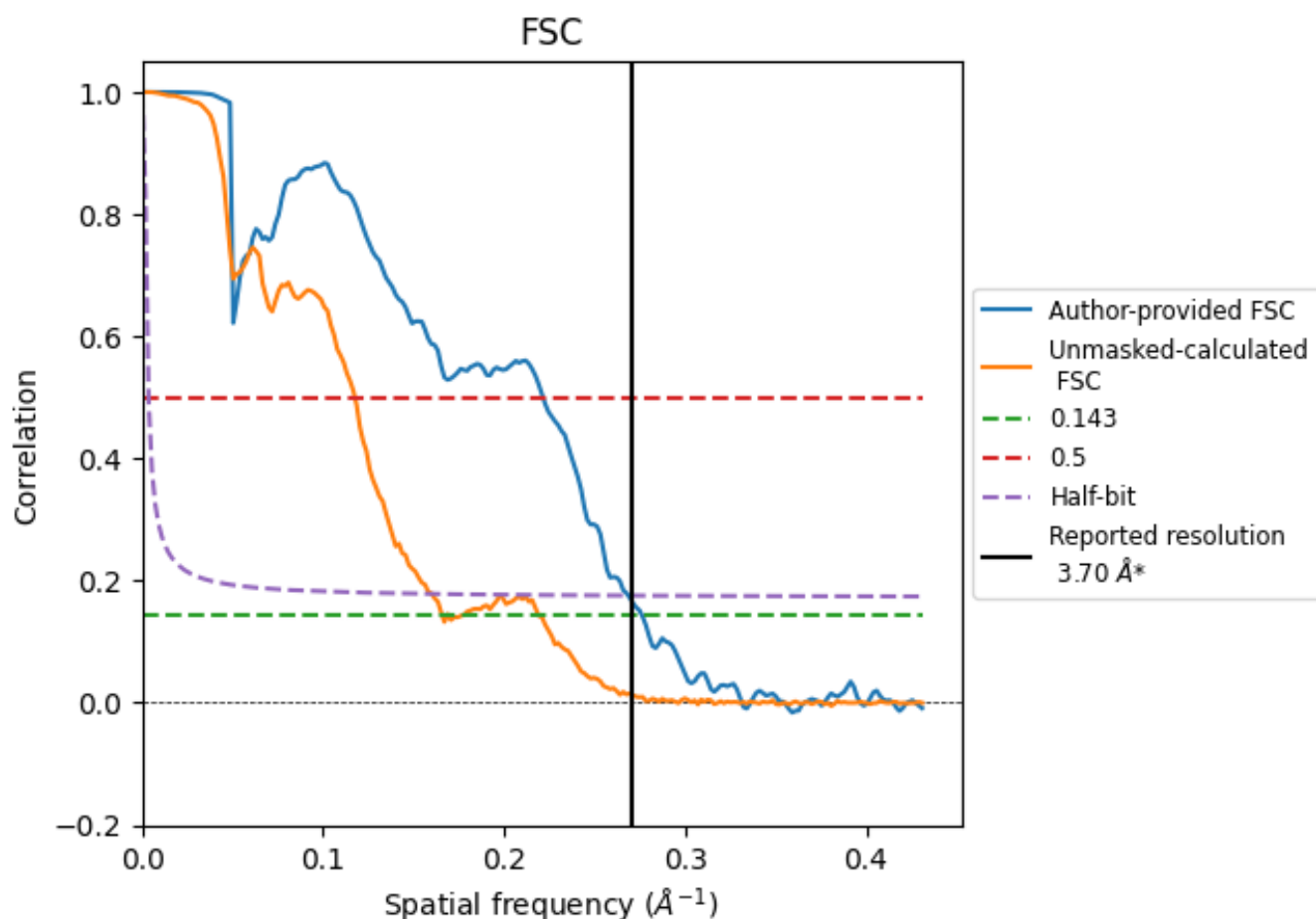


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

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 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

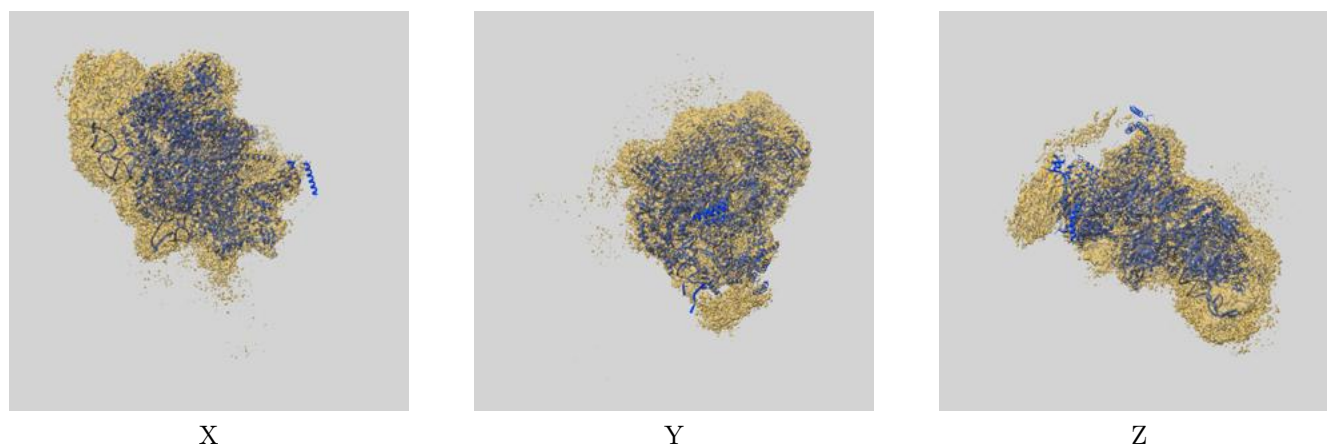
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.62	4.51	3.72
Unmasked-calculated*	6.03	8.50	6.25

*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](#)

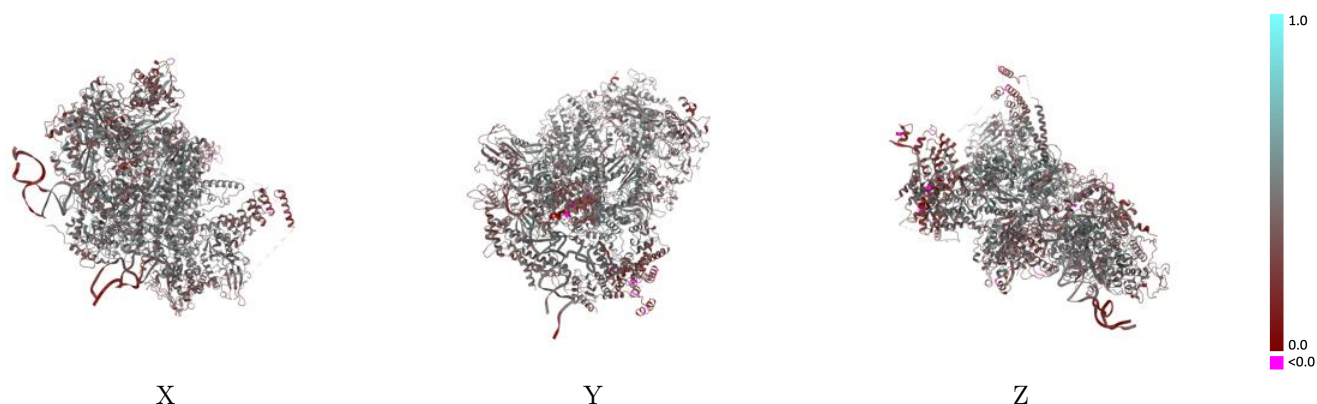
This section contains information regarding the fit between EMDB map EMD-18547 and PDB model 8QPB. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



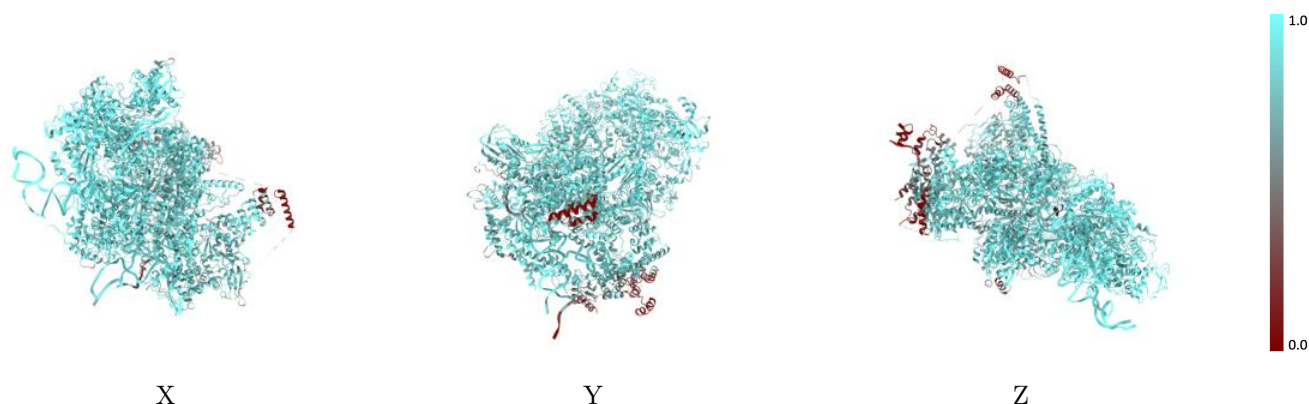
The images above show the 3D surface view of the map at the recommended contour level 0.027 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



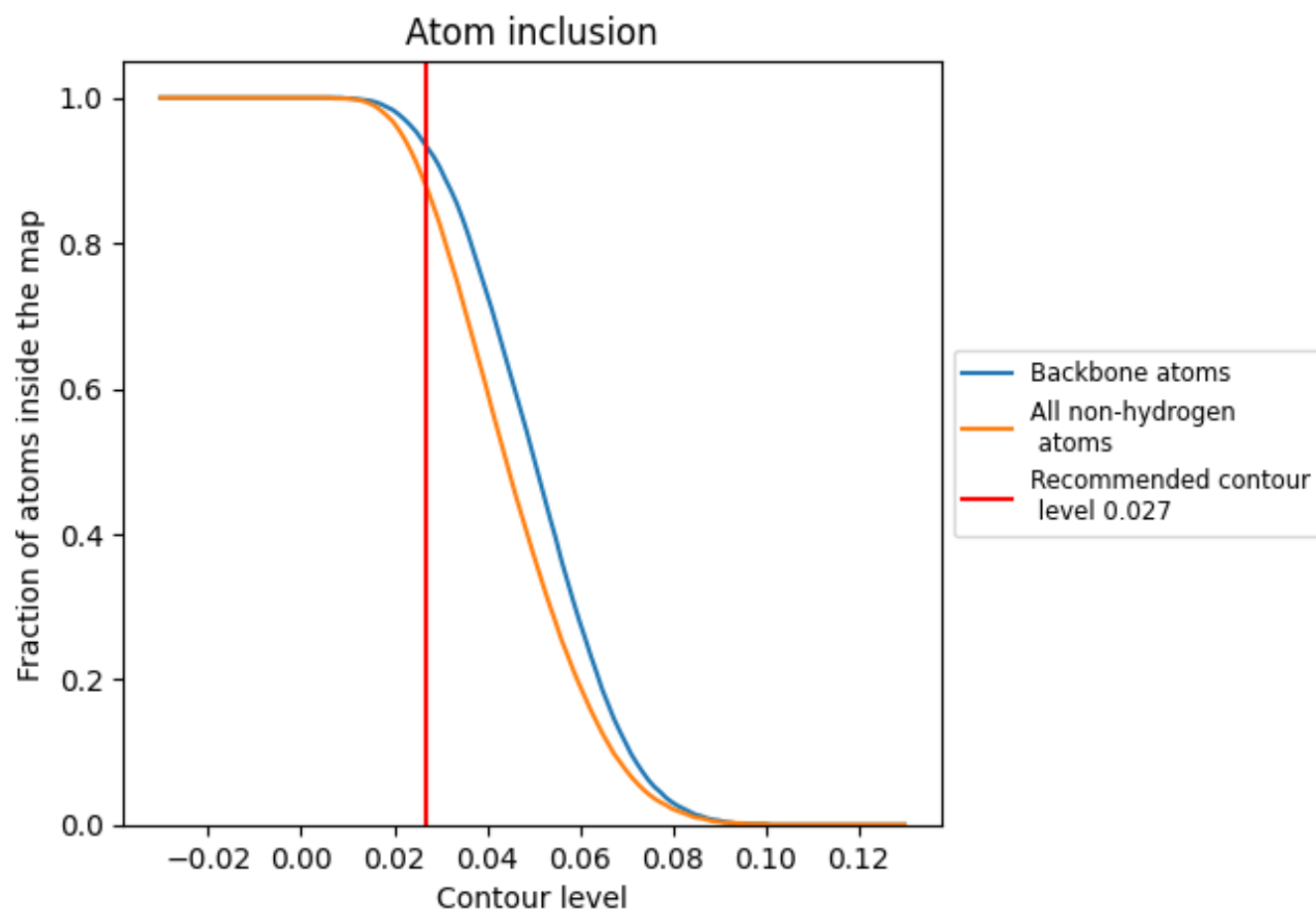
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	0.8770	0.4230
4	0.8890	0.3960
5	0.9860	0.4040
6	0.8720	0.3990
7	0.7700	0.3800
A	0.9090	0.4570
B	0.8530	0.4010
C	0.9590	0.4230
D	0.9340	0.5000
F	0.8120	0.3510
G	0.9000	0.3210
J	0.9150	0.4390
L	0.8180	0.4070
M	0.6360	0.4180
N	0.7370	0.3710
S	0.6410	0.3590
U	0.8440	0.3830
z	0.9790	0.4300

