



Full wwPDB EM Validation Report ⓘ

Nov 19, 2022 – 01:41 PM EST

PDB ID : 3JCR
EMDB ID : EMD-6581
Title : 3D structure determination of the human*U4/U6.U5* tri-snRNP complex
Authors : Agafonov, D.E.; Kastner, B.; Dybkov, O.; Hofele, R.V.; Liu, W.T.; Urlaub, H.; Luhrmann, R.; Stark, H.
Deposited on : 2016-01-21
Resolution : 7.00 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:

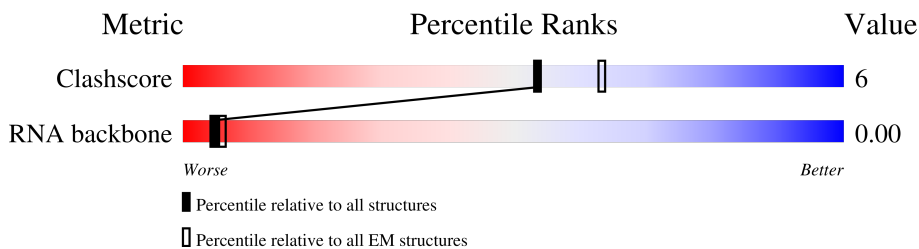
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 7.00 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
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	G	941	8% 43% 56%
2	D	357	78% 84% 15%
3	C	2136	17% 88% 12%
4	E	142	40% 94% 5%
5	A	2335	18% 94% 5%
6	F	820	41% 52% 47%
7	B	972	12% 86% 13%
8	O	240	15% 37% 63%
8	o	240	22% 37% 63%

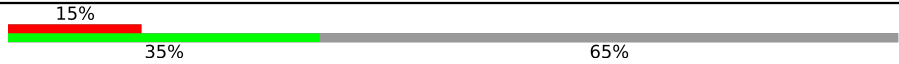

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Mol	Chain	Length	Quality of chain
9	P	119	29% 78% 22%
9	p	119	61% 79% 21%
10	Q	118	25% 75% 25%
10	q	118	60% 75% 25%
11	R	126	18% 70% 30%
11	r	126	38% 70% 30%
12	S	92	36% 85% 15%
12	s	92	59% 85% 15%
13	T	86	34% 85% 15%
13	t	86	80% 97% .
14	U	76	34% 96% .
14	u	76	41% 96% .
15	8	96	66% 73% 27%
16	6	80	81% 88% 12%
17	5	91	82% 84% 16%
18	4	139	55% 58% 42%
19	3	102	75% 81% 19%
20	2	95	94% 95% 5%
21	7	103	74% 77% 23%
22	K	683	12% 18% 81%
23	L	521	21% 58% 41%
24	J	499	22% 46% 52%
25	I	128	23% 95% ..
26	V	565	18% 75% 24%
27	M	145	47% 71% 29%

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Mol	Chain	Length	Quality of chain
28	N	106	
29	H	116	

2 Entry composition [i](#)

There are 29 unique types of molecules in this entry. The entry contains 9403 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 hPrp6.

Mol	Chain	Residues	Atoms	AltConf	Trace
1	G	418	Total C 418 418	0	418

- Molecule 2 is a protein called U5-40K.

Mol	Chain	Residues	Atoms	AltConf	Trace
2	D	302	Total C 302 302	0	302

- Molecule 3 is a protein called hBrr2.

Mol	Chain	Residues	Atoms	AltConf	Trace
3	C	1885	Total C 1885 1885	0	1885

- Molecule 4 is a protein called hDim1.

Mol	Chain	Residues	Atoms	AltConf	Trace
4	E	135	Total C 135 135	0	135

- Molecule 5 is a protein called hPrp8.

Mol	Chain	Residues	Atoms	AltConf	Trace
5	A	2222	Total C 2222 2222	0	2222

- Molecule 6 is a protein called hPrp28.

Mol	Chain	Residues	Atoms	AltConf	Trace
6	F	435	Total C 435 435	0	435

- Molecule 7 is a protein called hSnu114.

Mol	Chain	Residues	Atoms	AltConf	Trace
7	B	844	Total C 844 844	0	844

- Molecule 8 is a protein called SmB.

Mol	Chain	Residues	Atoms	AltConf	Trace
8	O	89	Total C 89 89	0	89
8	o	89	Total C 89 89	0	89

- Molecule 9 is a protein called SmD1.

Mol	Chain	Residues	Atoms	AltConf	Trace
9	P	93	Total C 93 93	0	93
9	p	94	Total C 94 94	0	94

- Molecule 10 is a protein called SmD2.

Mol	Chain	Residues	Atoms	AltConf	Trace
10	Q	89	Total C 89 89	0	89
10	q	89	Total C 89 89	0	89

- Molecule 11 is a protein called SmD3.

Mol	Chain	Residues	Atoms	AltConf	Trace
11	R	88	Total C 88 88	0	88
11	r	88	Total C 88 88	0	88

- Molecule 12 is a protein called SmE.

Mol	Chain	Residues	Atoms	AltConf	Trace
12	S	78	Total C 78 78	0	78

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Mol	Chain	Residues	Atoms	AltConf	Trace
12	s	78	Total C 78 78	0	78

- Molecule 13 is a protein called SmF.

Mol	Chain	Residues	Atoms	AltConf	Trace
13	T	73	Total C 73 73	0	73
13	t	83	Total C 83 83	0	83

- Molecule 14 is a protein called SmG.

Mol	Chain	Residues	Atoms	AltConf	Trace
14	U	73	Total C 73 73	0	73
14	u	73	Total C 73 73	0	73

- Molecule 15 is a protein called LSm8.

Mol	Chain	Residues	Atoms	AltConf	Trace
15	8	70	Total C 70 70	0	70

- Molecule 16 is a protein called LSm6.

Mol	Chain	Residues	Atoms	AltConf	Trace
16	6	70	Total C 70 70	0	70

- Molecule 17 is a protein called LSm5.

Mol	Chain	Residues	Atoms	AltConf	Trace
17	5	76	Total C 76 76	0	76

- Molecule 18 is a protein called LSm4.

Mol	Chain	Residues	Atoms	AltConf	Trace
18	4	80	Total C 80 80	0	80

- Molecule 19 is a protein called LSm3.

Mol	Chain	Residues	Atoms	AltConf	Trace
19	3	83	Total C 83 83	0	83

- Molecule 20 is a protein called LSm2.

Mol	Chain	Residues	Atoms	AltConf	Trace
20	2	90	Total C 90 90	0	90

- Molecule 21 is a protein called LSm7.

Mol	Chain	Residues	Atoms	AltConf	Trace
21	7	79	Total C 79 79	0	79

- Molecule 22 is a protein called hPrp3.

Mol	Chain	Residues	Atoms	AltConf	Trace
22	K	131	Total C 131 131	0	131

- Molecule 23 is a protein called hPrp4.

Mol	Chain	Residues	Atoms	AltConf	Trace
23	L	307	Total C 307 307	0	307

- Molecule 24 is a protein called hPrp31.

Mol	Chain	Residues	Atoms	AltConf	Trace
24	J	239	Total C 239 239	0	239

- Molecule 25 is a protein called hSnu13.

Mol	Chain	Residues	Atoms	AltConf	Trace
25	I	126	Total C 126 126	0	126

- Molecule 26 is a protein called hSad1.

Mol	Chain	Residues	Atoms	AltConf	Trace
26	V	431	Total C 431 431	0	431

- Molecule 27 is a RNA chain called U4 snRNA.

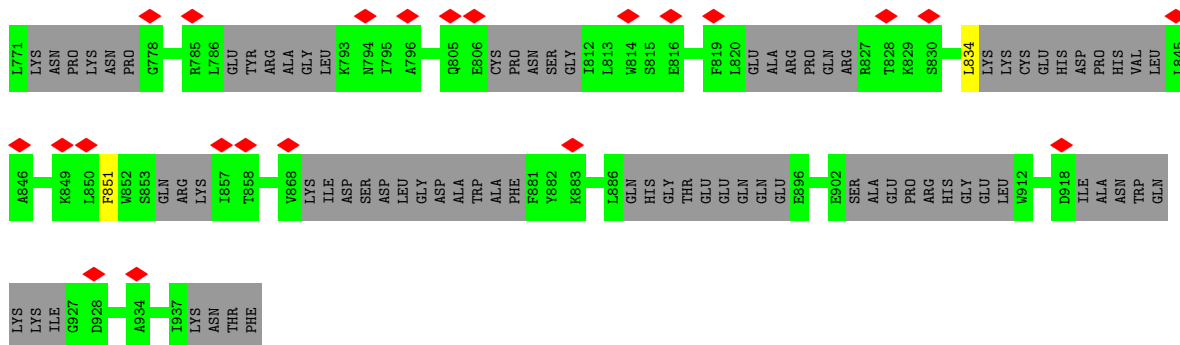
Mol	Chain	Residues	Atoms	AltConf	Trace
27	M	103	Total P 103 103	0	103

- Molecule 28 is a RNA chain called U6 snRNA.

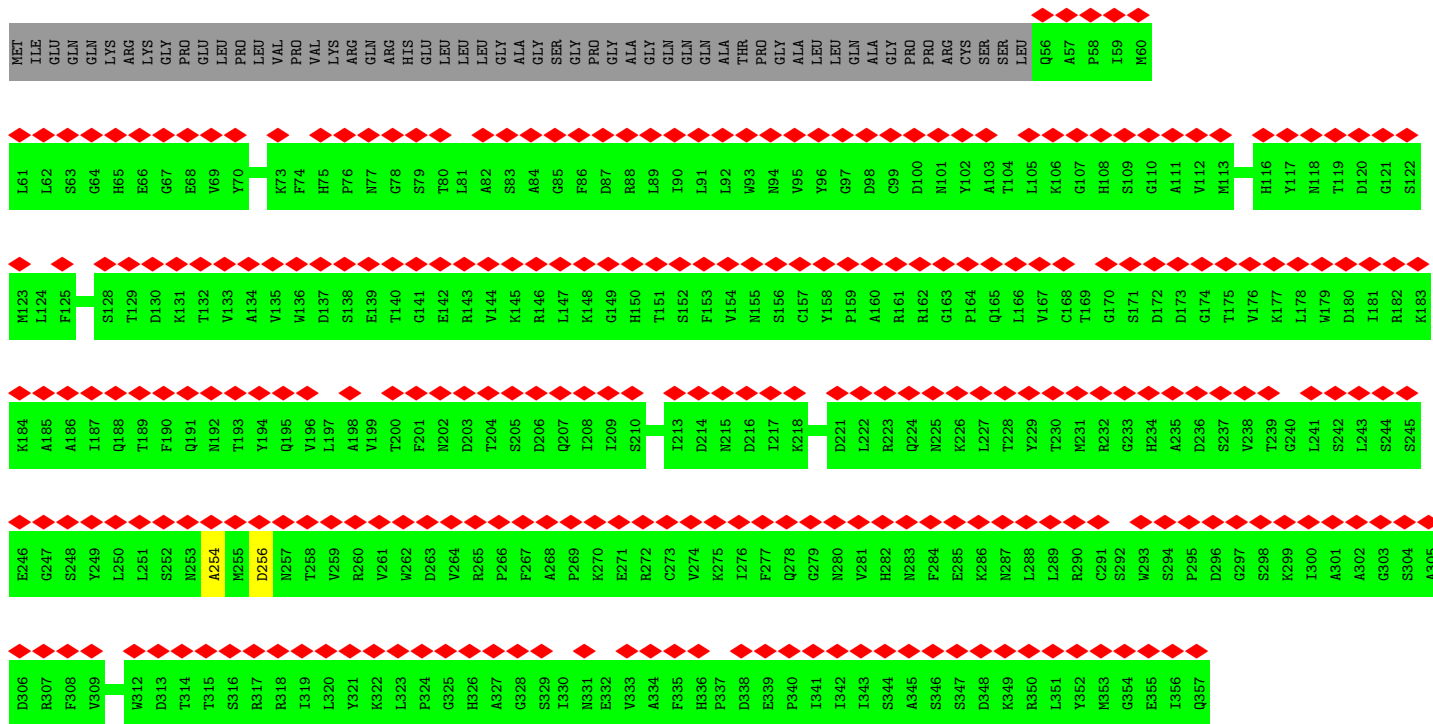
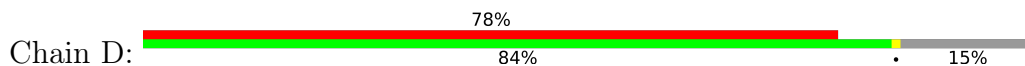
Mol	Chain	Residues	Atoms	AltConf	Trace
28	N	37	Total P 37 37	0	37

- Molecule 29 is a RNA chain called U5 snRNA.

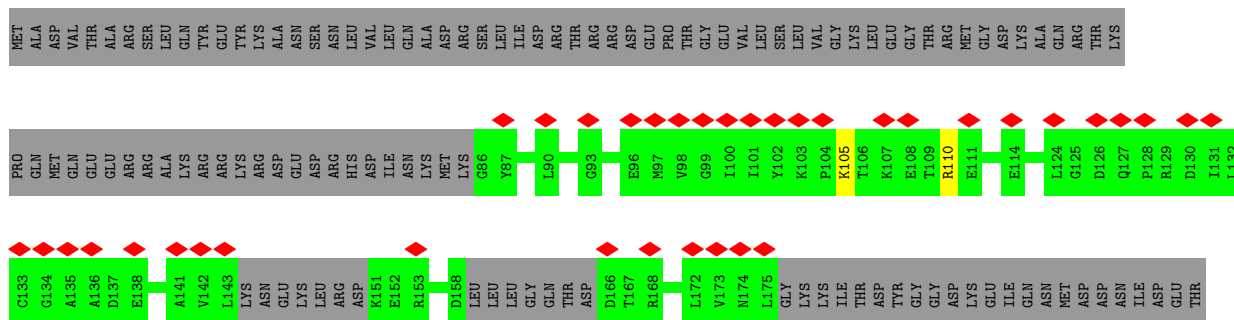
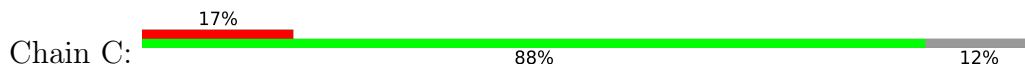
Mol	Chain	Residues	Atoms	AltConf	Trace
29	H	63	Total P 63 63	0	63



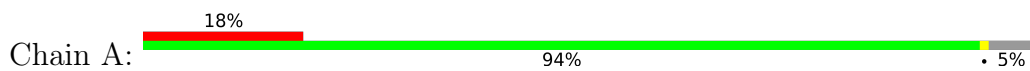
• Molecule 2: U5-40K



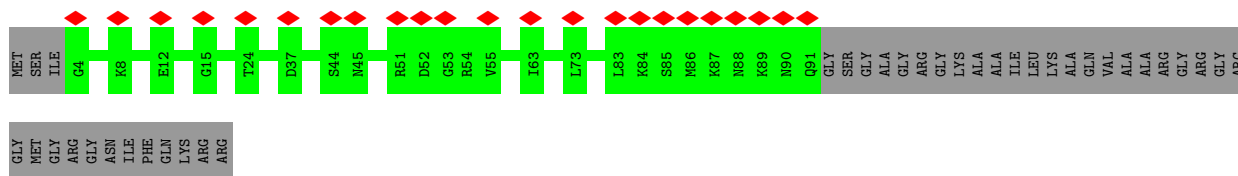
• Molecule 3: hBrr2



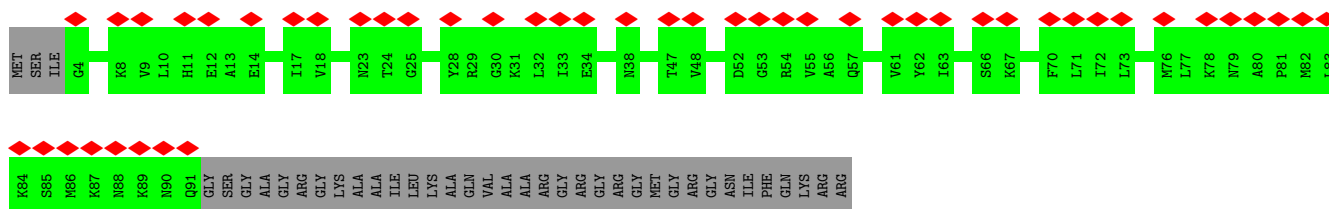
• Molecule 5: hPrp8



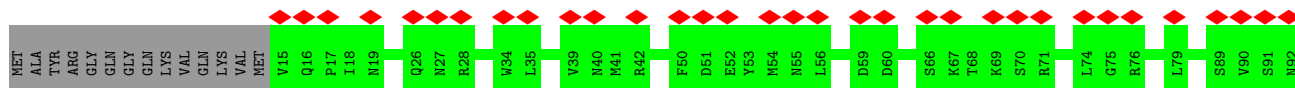
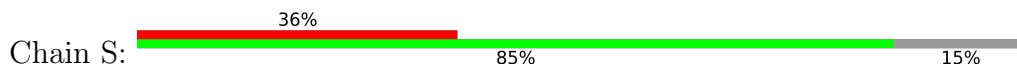
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M61	D72	R79	H83	L89	L92	E104	F128	D157	R158	R159	H160	F161	K162	P175	L176	D177	Y178	A179	A190	P197	E198	L246	V250	D251	D252	L371	D253	Y256	L257	A262	T265	M271	A272	K278	P281	L282	V283	R284	D285	I286	N287	L288	Q289	D290	E291	D292	W293	N294	E295	D298	Y318	L319	V327	T330	P335	T342	E343	D344	F350	N357	R362	H363	S364	V365	K366	S367	Q368	E369	P370	L371	P372	D373	D374	D375	E376	E377	F378	E379	V384	E385	P386	F387	L388	K389	P392	L393	R414	A437	G438	V441	A458	L459	P463	Y471	T479	S484	G493	R510	V527	K528	T529	L530	T531	T532	K533	E534	C547	G577	L588	T589	G590	V621	G622	K623	G626	A632	G633	P646	L647	M654	A657	F660	E661	G662	R663	H664	S665	K666	G667	V668	A669	K670	T671	V672	K674	Q675	R676	V677	E678	S679	R686	V689	M690	I693	P698	E699	G700	I701	K702	R707	I724	P725	W726	P729	G730	L731	P732	T733	K746	W750	T753	N757	G764	A765	I766	V767	D768	V807	E861	G862	R863	H864	S831	T836	V852	K853	S854	N857	D872	E893	I896	D910	V911	G971	E982	K987	T991	D1021	I1030	I1031	Q1035	F1036	L1055	L1072	Q1075	A1078	I1110	T1115	P1118	D1119	P1120	E1123	I1124	I1125	V1126	N1130	K1131	K1132	D1137	M1140	L1141	L1142	V1165	T1166	T1167	V1168	V1177	L1186	F1187	L1197	G1200	E1205	E1206	F1207	T1208	H1209	D1234	A1250	S1251	G1252	S1253	T1254	T1255	F1256	T1257	I1268	E1276	A1277	V1278	V1279	I1285	A1477	L1478	G1479	G1492	P1496	T1497	A1506	S1507	G1508	F1509	E1510	E1511	S1512	M1513	W1515	K1516	D1347	V1348	G1349	I1350	T1351	G1356	M1357	S1358	H1359	E1360	E1361	D1362	I1365	P1366	L1391	E1395	A1396	R1401	E1406	D1410	I1416	D1433	D1441	Q1446	V1447	L1448	G1462	A1477	L1478	G1479	G1492	P1496	T1497	A1506	S1507	G1508	F1509	E1510	E1511	S1512	M1513	W1515	K1516	K1517	L1518	T1519	M1520	A1521	S1524	M1527	L1536	P1540	A1545	M1546	V1547	Y1548	G1550	F1551	L1557	M1562	K1565	F1597	D1598	D1602	E1607	I1614	S1625	D1628	S1634	A1646	D1647	S1648	T1655	T1658	T1689	D1690	M1691	M1692	S1693	I1694	P1698	M1710	G1721	A1736	N1737	P1738	S1755	S1756	E1757	P1758	T1759	E1760	P1761	N1774	Q1775	V1780	D1781	D1782	T1783	I1790	Y1795	G1796	L1798	T1799	T1800	N1804	G1805	A1806	T1814	G1829	Q1830	K1831	R1832	L1833	A1837	K1838	W1839	K1840	T1841	V1845	A1846	S1851	L1852	P1853	V1854	E1855	V1863	R1865	K1866	P1867	L1868	T1869	M1870	N1871	S1872	L1873	E1874	G1875	H1876	I1877	V1878	F1879	K1880	L1881	M1882	V1883	G1884	S1885	E1886	L1887	L1888	L1889	E1900	D1904	T1910	E1911	P1912	Q1913	L1924	K1925	T1926	M1946	R1949	A1950	P1956	D1957	K1958	T1959	T1960	I1961	I1967	T1972	D1973	E1974	L1986	K1993	K1994	M1995	M1996	V1997	M1998	A2000	S2001	L2002	E2006	F2067	S2068	S2069	K2070	A2080	A2081	T2087	D2096	T2100	G2101	L2120	R2121	A2122	Q2123	T2124	A2125	S2132	P2133	P2134	D2135	M2136	P2137	K2140	N2183	D2202	D2207	G2208	L2230	Q2240	G2245	K2249	G2250	V2259	Q2276	P2301	H2313	F2314	LEU	ASN	PHE	ALA	LEU



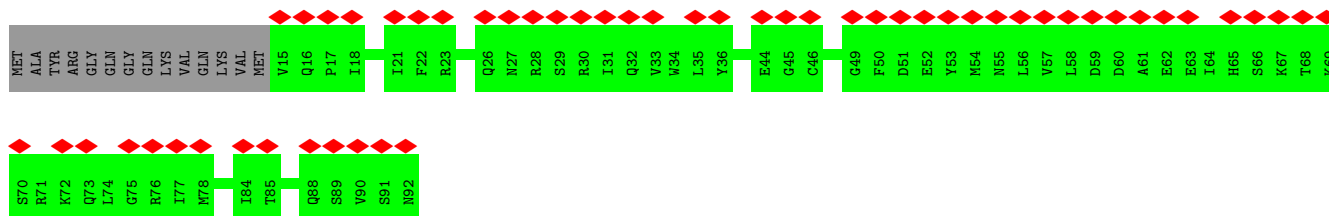
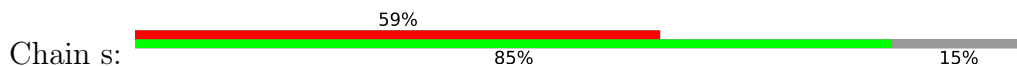
• Molecule 11: SmD3



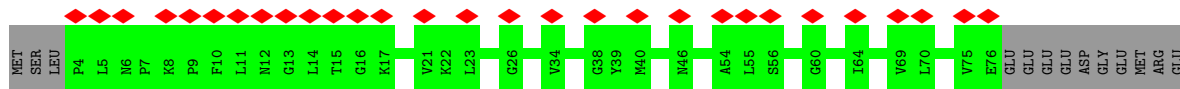
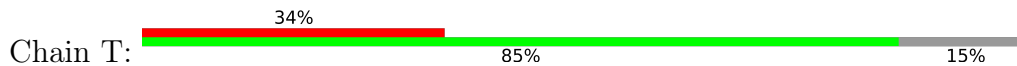
• Molecule 12: SmE



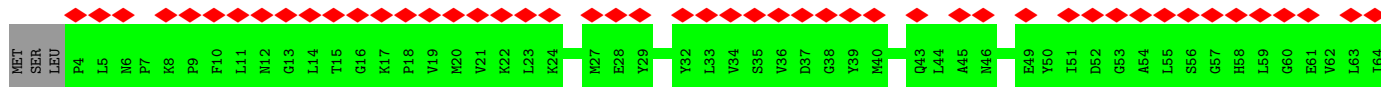
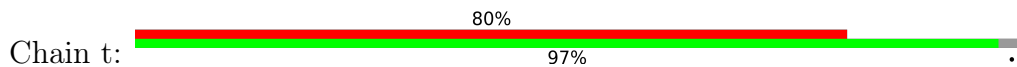
• Molecule 12: SmE

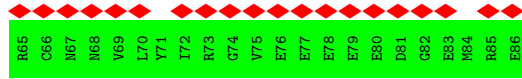


• Molecule 13: SmF

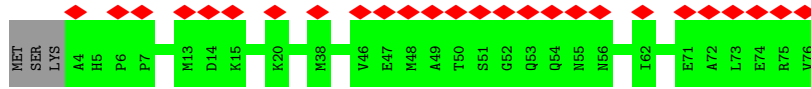


• Molecule 13: SmF

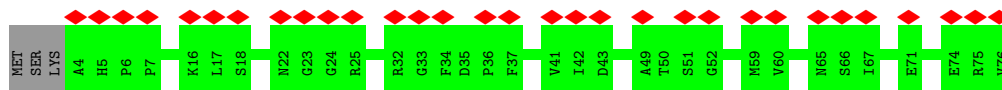




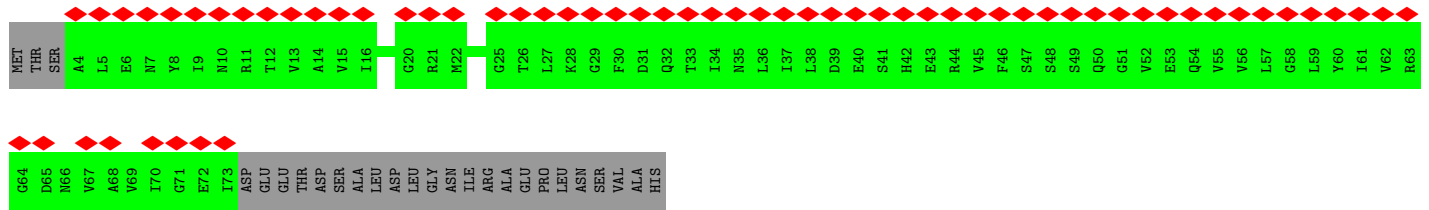
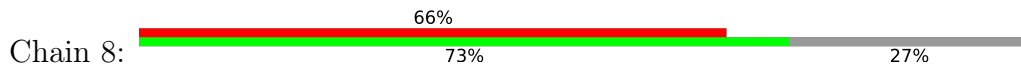
• Molecule 14: SmG



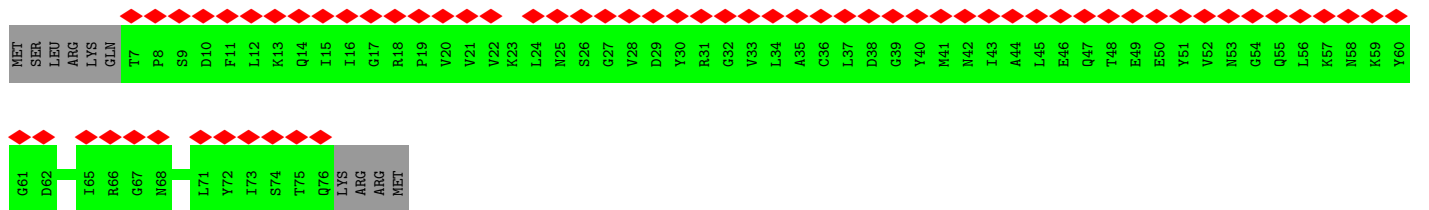
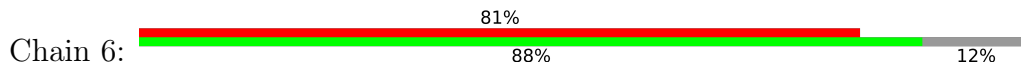
• Molecule 14: SmG



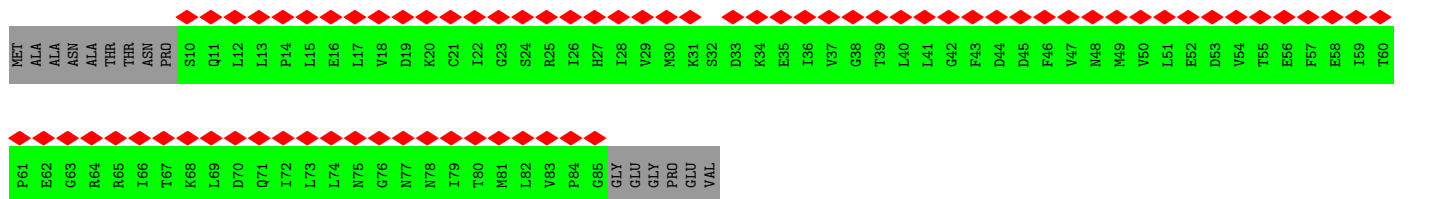
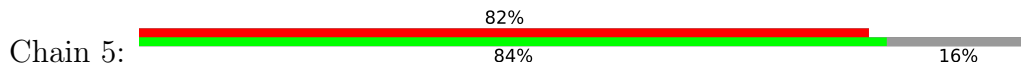
• Molecule 15: LSm8



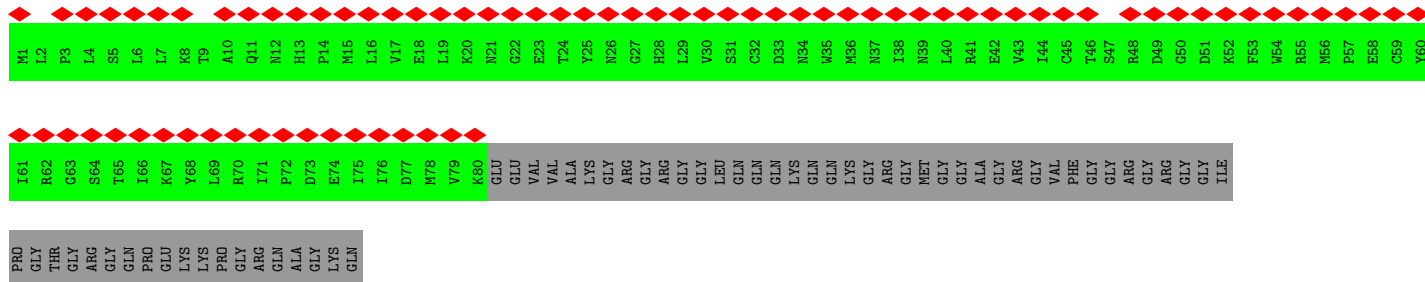
• Molecule 16: LSm6



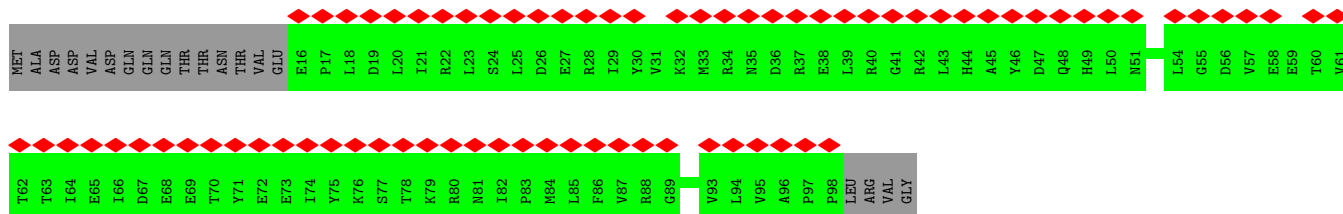
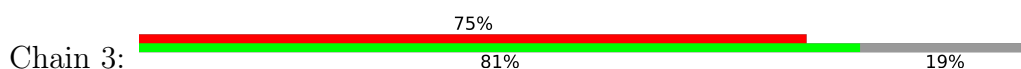
• Molecule 17: LSm5



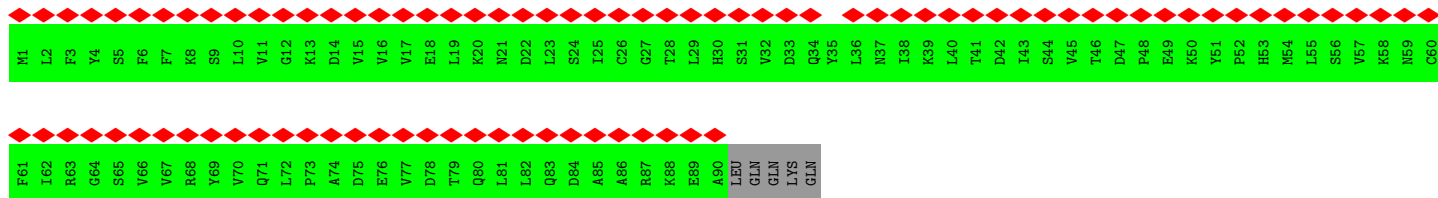
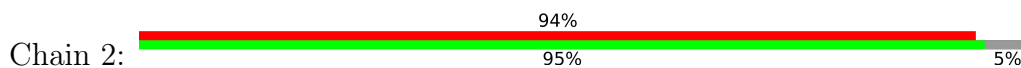
● Molecule 18: LSm4



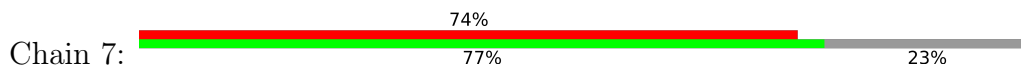
● Molecule 19: LSm3



● Molecule 20: LSm2

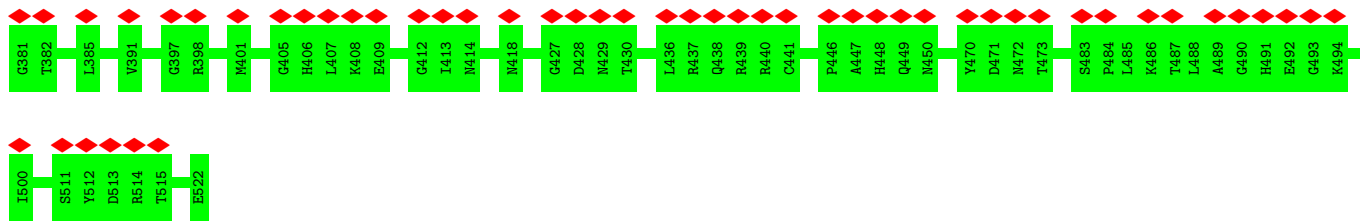


● Molecule 21: LSm7

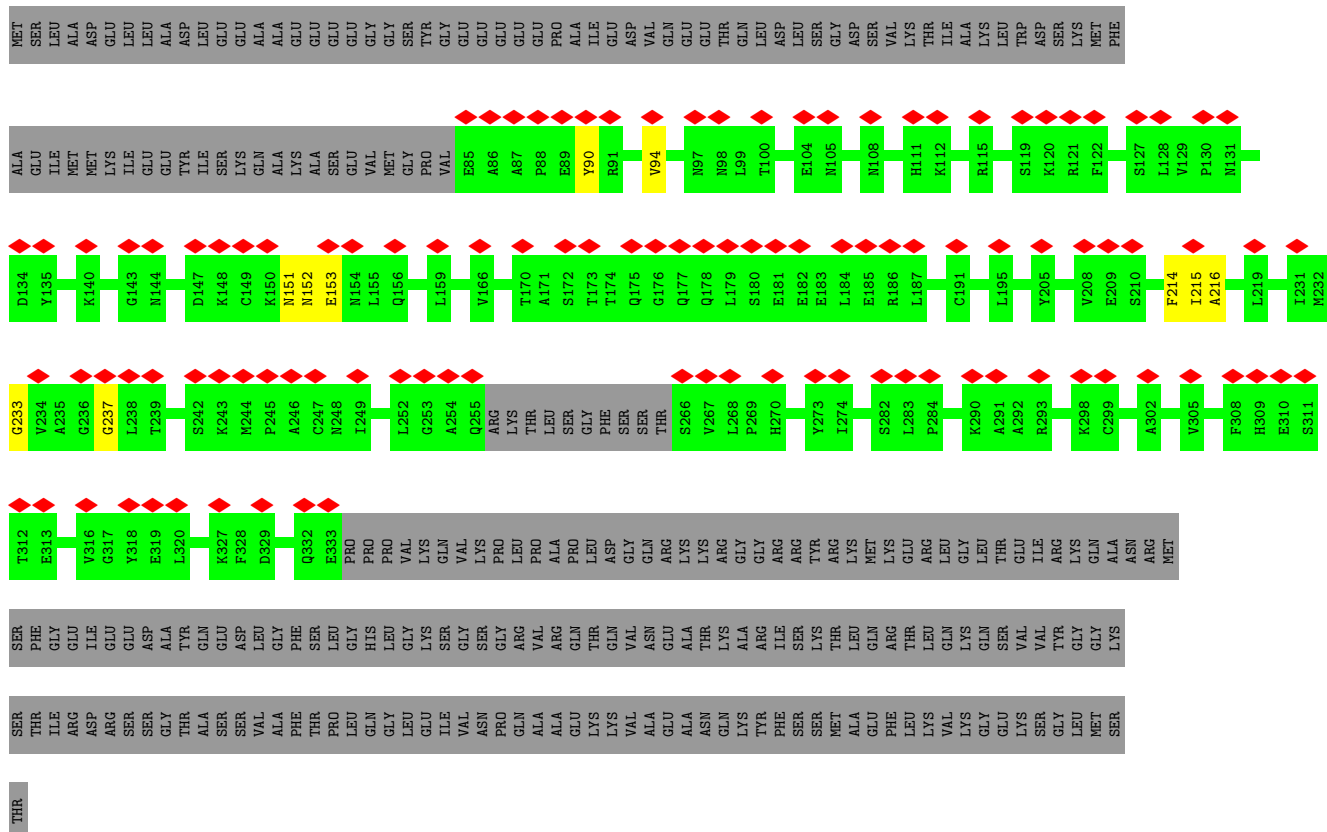


● Molecule 22: hPrp3

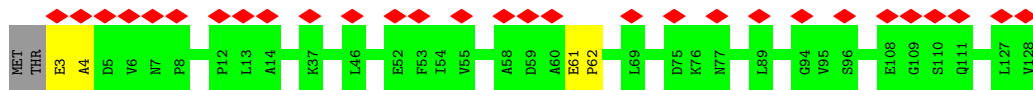
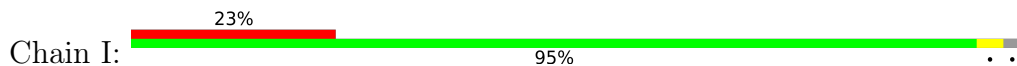




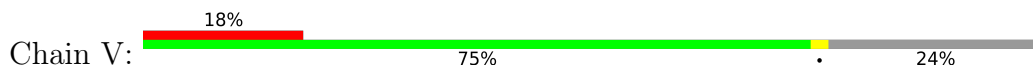
• Molecule 24: hPrp31

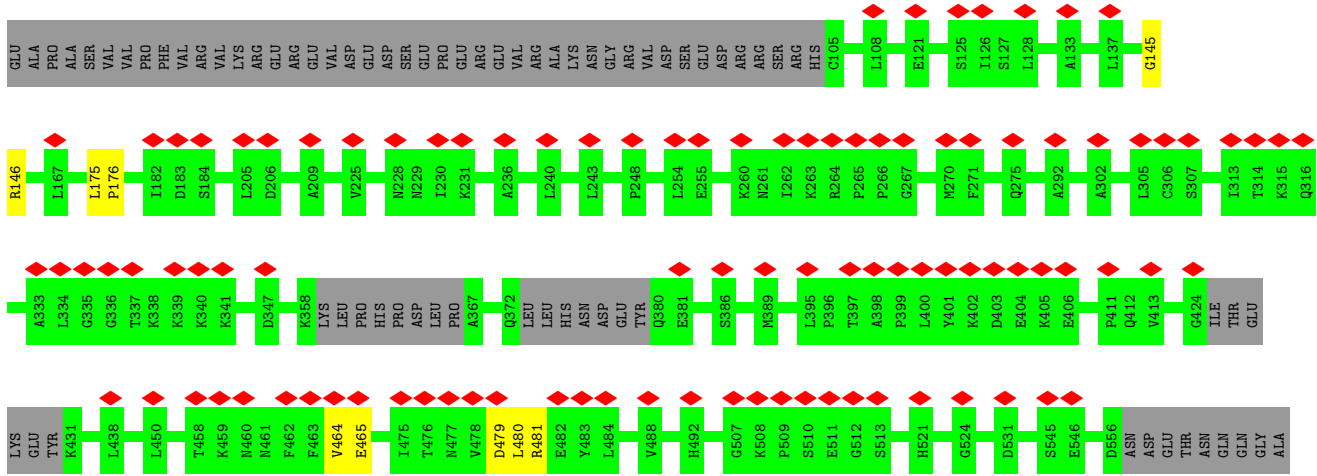


• Molecule 25: hSnu13

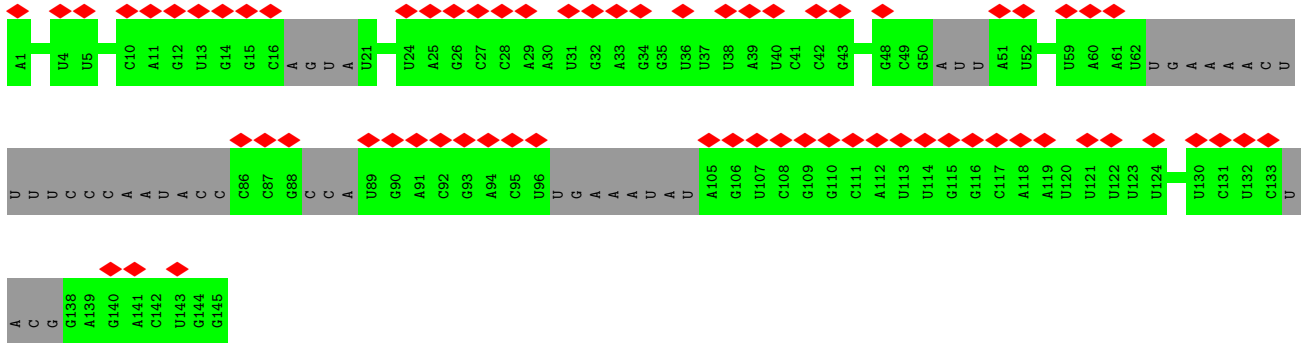


• Molecule 26: hSad1

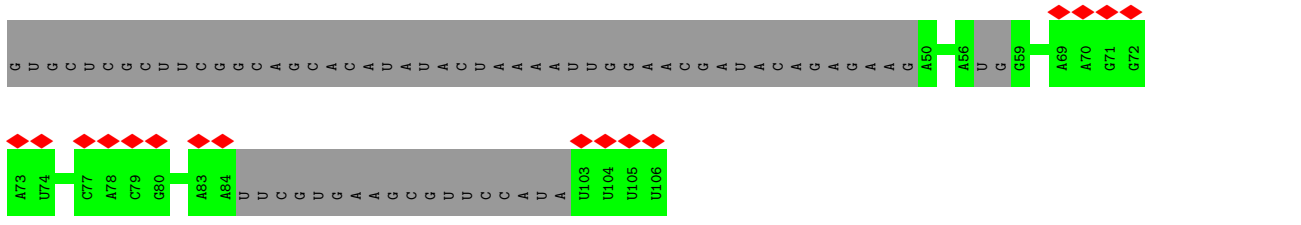




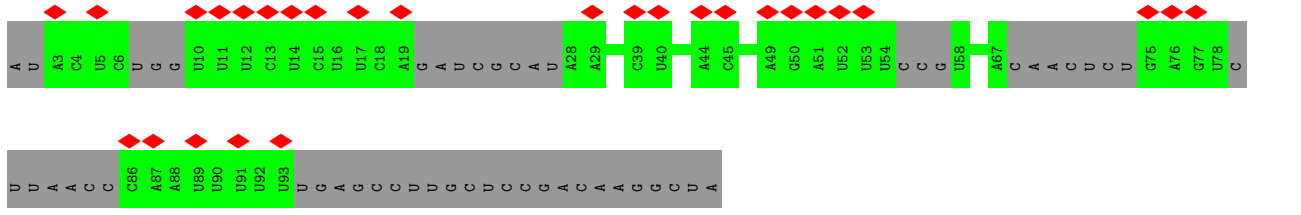
• Molecule 27: U4 snRNA



• Molecule 28: U6 snRNA



• Molecule 29: U5 snRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	141109	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	5350	Depositor
Magnification	74000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.653	Depositor
Minimum map value	-0.382	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.027	Depositor
Recommended contour level	0.13	Depositor
Map size (\AA)	440.0, 440.0, 440.0	wwPDB
Map dimensions	220, 220, 220	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	2.0, 2.0, 2.0	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

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	G	418	0	0	6	0
2	D	302	0	0	3	0
3	C	1885	0	0	1	0
4	E	135	0	0	1	0
5	A	2222	0	0	20	0
6	F	435	0	0	6	0
7	B	844	0	0	4	0
8	O	89	0	0	0	0
8	o	89	0	0	0	0
9	P	93	0	0	0	0
9	p	94	0	0	0	0
10	Q	89	0	0	0	0
10	q	89	0	0	0	0
11	R	88	0	0	0	0
11	r	88	0	0	0	0
12	S	78	0	0	0	0
12	s	78	0	0	0	0
13	T	73	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	t	83	0	0	0	0
14	U	73	0	0	0	0
14	u	73	0	0	0	0
15	8	70	0	0	0	0
16	6	70	0	0	0	0
17	5	76	0	0	0	0
18	4	80	0	0	0	0
19	3	83	0	0	0	0
20	2	90	0	0	0	0
21	7	79	0	0	0	0
22	K	131	0	0	10	0
23	L	307	0	0	10	0
24	J	239	0	0	7	0
25	I	126	0	0	2	0
26	V	431	0	0	6	0
27	M	103	0	0	0	0
28	N	37	0	0	0	0
29	H	63	0	0	0	0
All	All	9403	0	0	52	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (52) 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)
24:J:94:VAL:CA	24:J:233:GLY:CA	1.95	1.44
5:A:294:ASN:CA	5:A:1141:ARG:CA	1.96	1.43
4:E:95:GLY:CA	5:A:707:ARG:CA	1.95	1.42
22:K:669:TYR:CA	23:L:294:VAL:CA	1.98	1.39
24:J:215:ILE:CA	24:J:216:ALA:CA	2.03	1.36
24:J:153:GLU:CA	26:V:479:ASP:CA	2.11	1.28
5:A:295:GLU:CA	5:A:1142:LEU:CA	2.11	1.27
5:A:675:GLN:CA	5:A:676:ARG:CA	2.27	1.13
5:A:678:GLU:CA	5:A:750:TRP:CA	2.29	1.10
5:A:158:ARG:CA	6:F:372:ILE:CA	2.39	1.00
1:G:652:GLU:CA	1:G:661:ALA:CA	2.40	0.99
5:A:292:ASP:CA	5:A:1140:MET:CA	2.51	0.88
22:K:667:GLU:CA	23:L:310:LEU:CA	2.53	0.86
24:J:151:ASN:CA	26:V:481:ARG:CA	0.84	0.84
2:D:254:ALA:CA	5:A:30:LEU:CA	2.56	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:350:PHE:CA	7:B:270:PRO:CA	2.57	0.82
5:A:384:VAL:CA	7:B:355:LYS:CA	2.60	0.79
24:J:214:PHE:CA	24:J:216:ALA:CA	2.60	0.78
6:F:637:GLU:CA	6:F:638:ARG:CA	2.65	0.75
22:K:659:GLU:CA	23:L:313:ASP:CA	2.68	0.71
24:J:152:ASN:CA	26:V:480:LEU:CA	0.67	0.67
1:G:318:LEU:CA	5:A:1798:LEU:CA	2.73	0.66
1:G:434:VAL:CA	1:G:455:LYS:CA	2.74	0.65
22:K:673:ALA:CA	23:L:266:LEU:CA	2.76	0.63
5:A:293:TRP:CA	5:A:1141:ARG:CA	2.77	0.62
1:G:519:VAL:CA	1:G:551:VAL:CA	2.78	0.62
3:C:105:LYS:CA	3:C:110:ARG:CA	2.78	0.61
1:G:834:LEU:CA	1:G:851:PHE:CA	2.79	0.60
6:F:665:PRO:CA	6:F:666:PRO:CA	2.80	0.60
6:F:629:ILE:CA	6:F:630:GLY:CA	0.59	0.58
26:V:145:GLY:CA	26:V:146:ARG:CA	2.82	0.57
5:A:725:PRO:CA	5:A:726:TRP:CA	2.84	0.56
24:J:90:TYR:CA	24:J:237:GLY:CA	2.84	0.56
25:I:3:GLU:CA	25:I:4:ALA:CA	2.87	0.53
25:I:61:GLU:CA	25:I:62:PRO:CA	2.87	0.52
2:D:256:ASP:CA	5:A:29:LYS:CA	2.87	0.52
5:A:388:LEU:CA	5:A:389:LYS:CA	2.88	0.52
22:K:658:ARG:CA	23:L:313:ASP:CA	2.88	0.52
26:V:175:LEU:CA	26:V:176:PRO:CA	2.91	0.49
22:K:670:TRP:CA	23:L:310:LEU:CA	2.90	0.48
22:K:657:ALA:CA	23:L:313:ASP:CA	2.91	0.48
5:A:1795:GLU:CA	5:A:1796:GLY:CA	2.92	0.47
5:A:159:ARG:CA	6:F:372:ILE:CA	2.93	0.47
22:K:545:VAL:CA	23:L:291:PRO:CA	0.45	0.45
5:A:357:ASN:CA	7:B:864:PRO:CA	2.95	0.45
1:G:545:GLU:CA	1:G:558:CYS:CA	2.95	0.44
2:D:256:ASP:CA	5:A:30:LEU:CA	2.96	0.43
5:A:1123:GLU:CA	7:B:597:PRO:CA	2.97	0.43
22:K:666:ALA:CA	23:L:309:SER:CA	2.96	0.43
6:F:638:ARG:CA	6:F:639:VAL:CA	2.98	0.42
22:K:544:SER:CA	23:L:292:LYS:CA	2.98	0.42
26:V:464:VAL:CA	26:V:465:GLU:CA	2.98	0.41

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
27	M	0/145	-	-
28	N	0/106	-	-
29	H	0/116	-	-
All	All	0/367	-	-

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

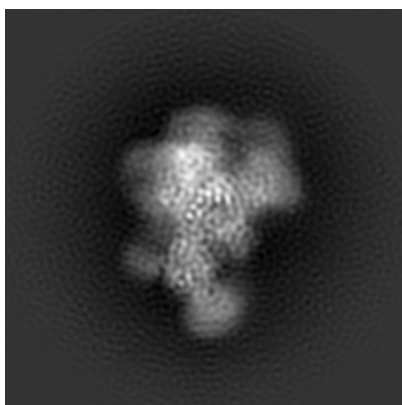
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6581. These allow visual inspection of the internal detail of the map and identification of artifacts.

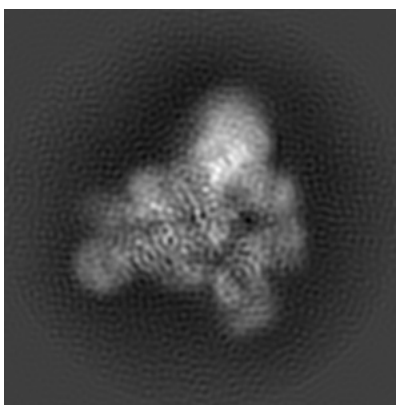
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

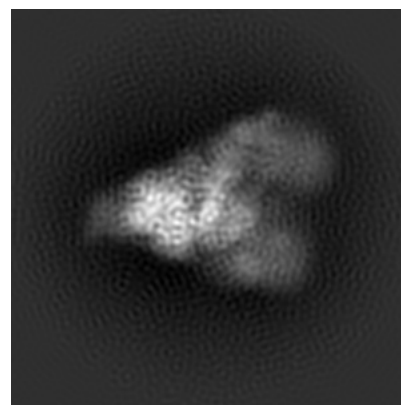
6.1.1 Primary map



X



Y

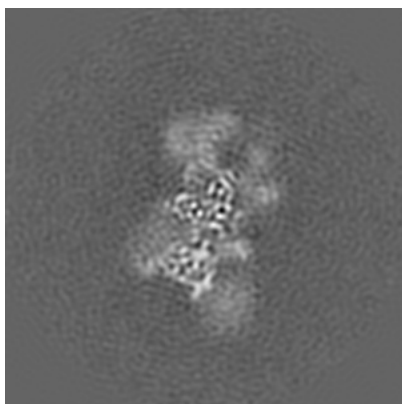


Z

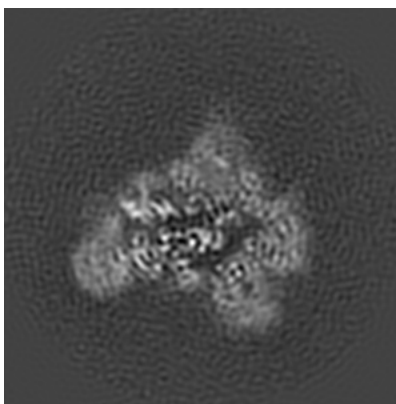
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

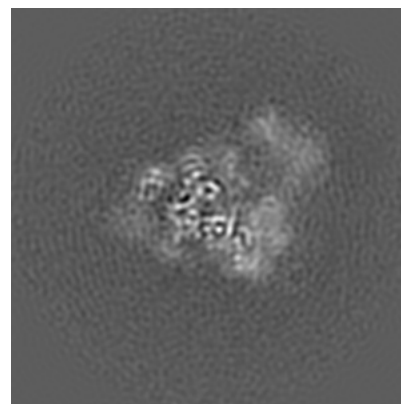
6.2.1 Primary map



X Index: 110



Y Index: 110

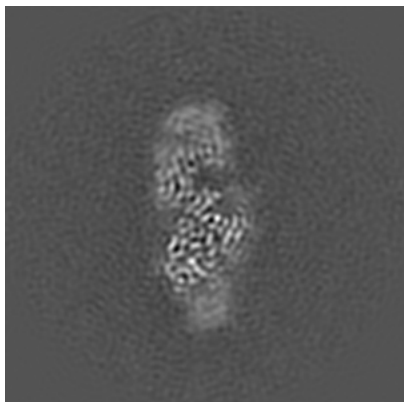


Z Index: 110

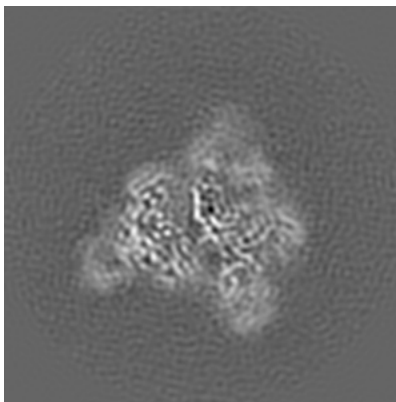
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

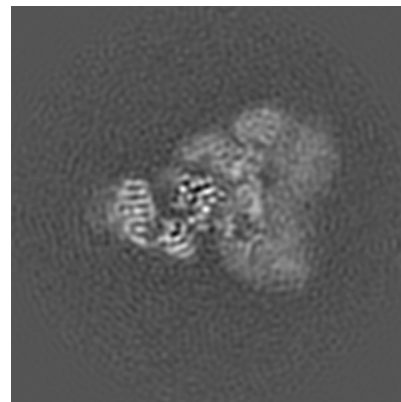
6.3.1 Primary map



X Index: 90



Y Index: 101



Z Index: 119

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.13. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

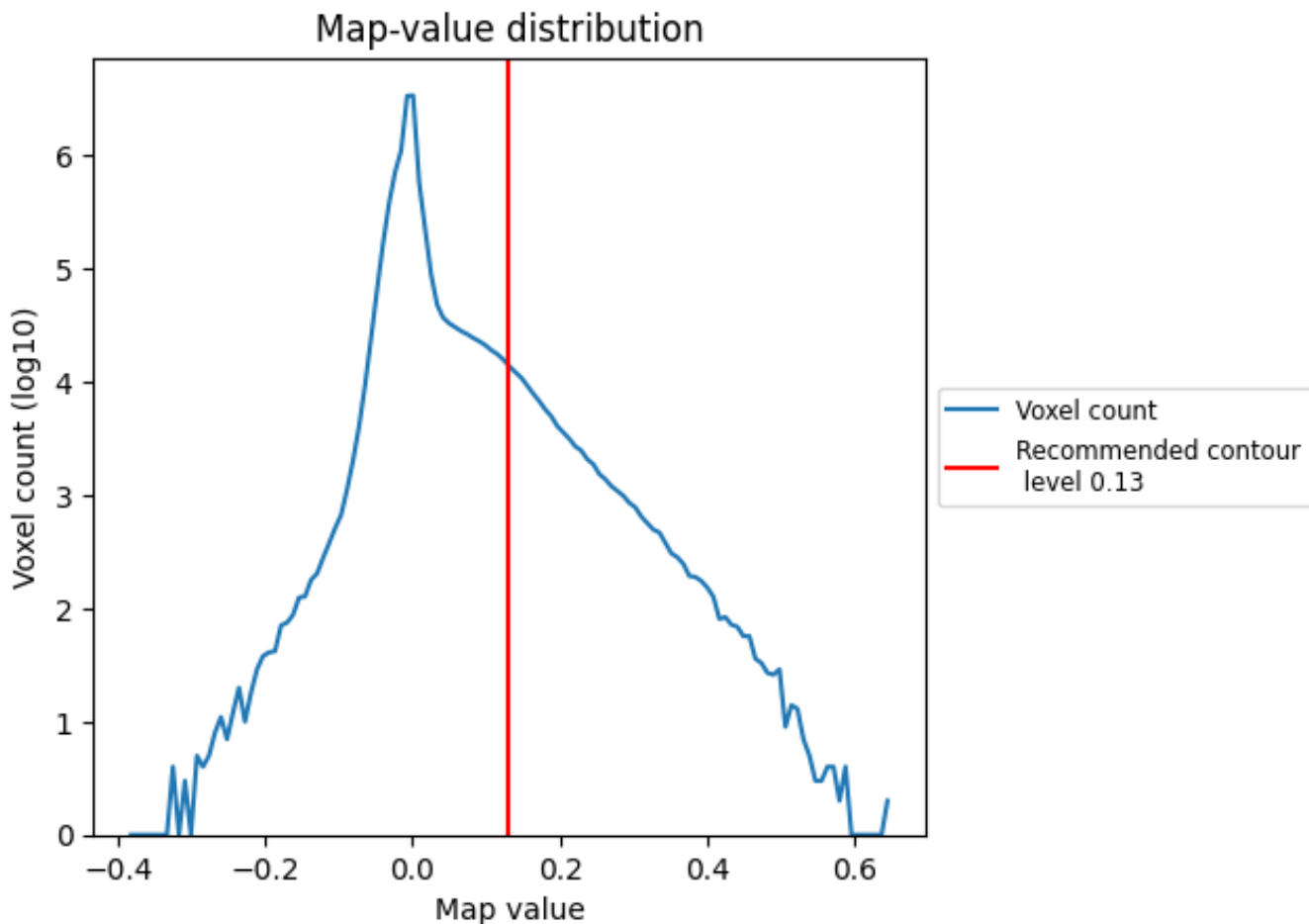
6.5 Mask visualisation

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

7 Map analysis [i](#)

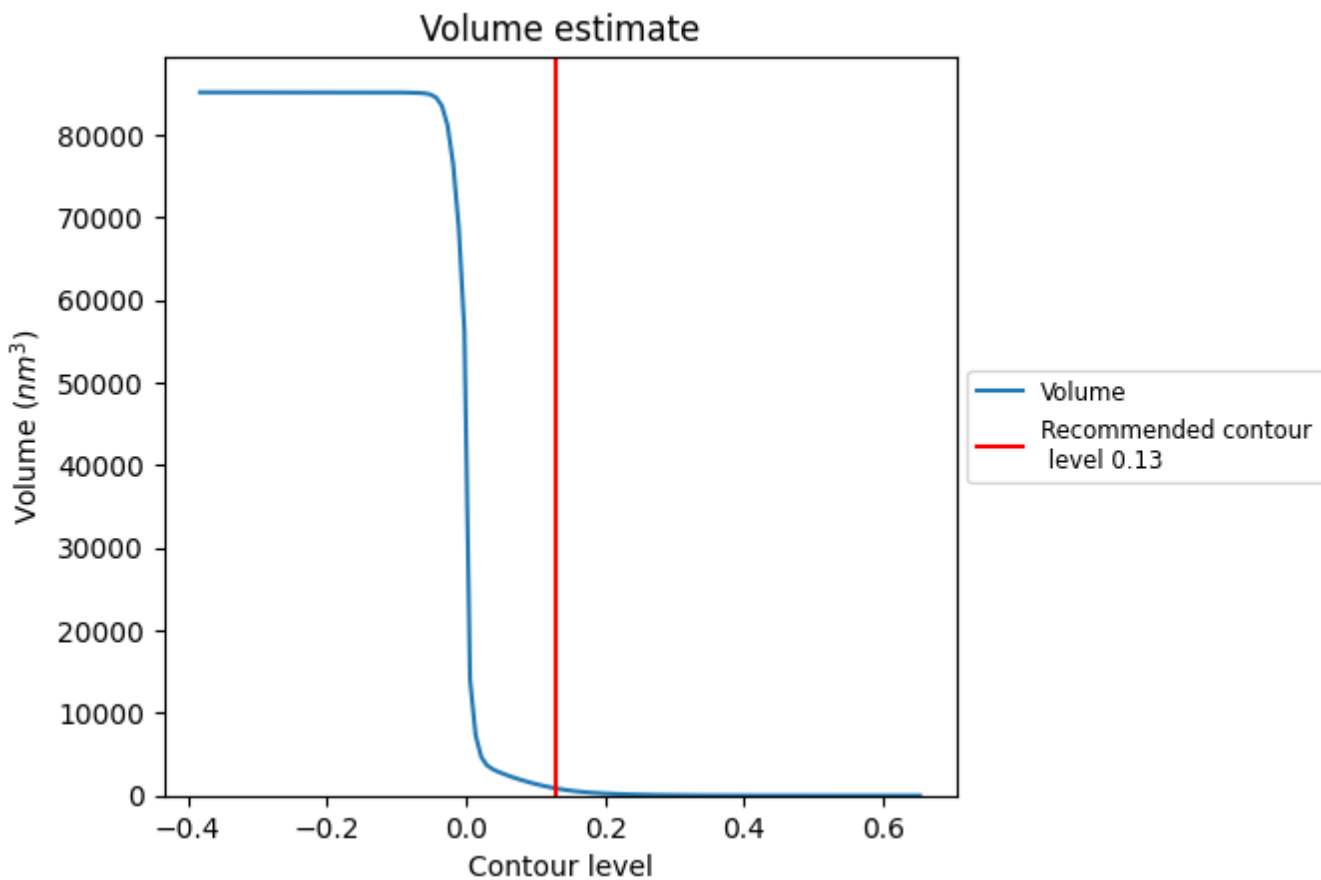
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

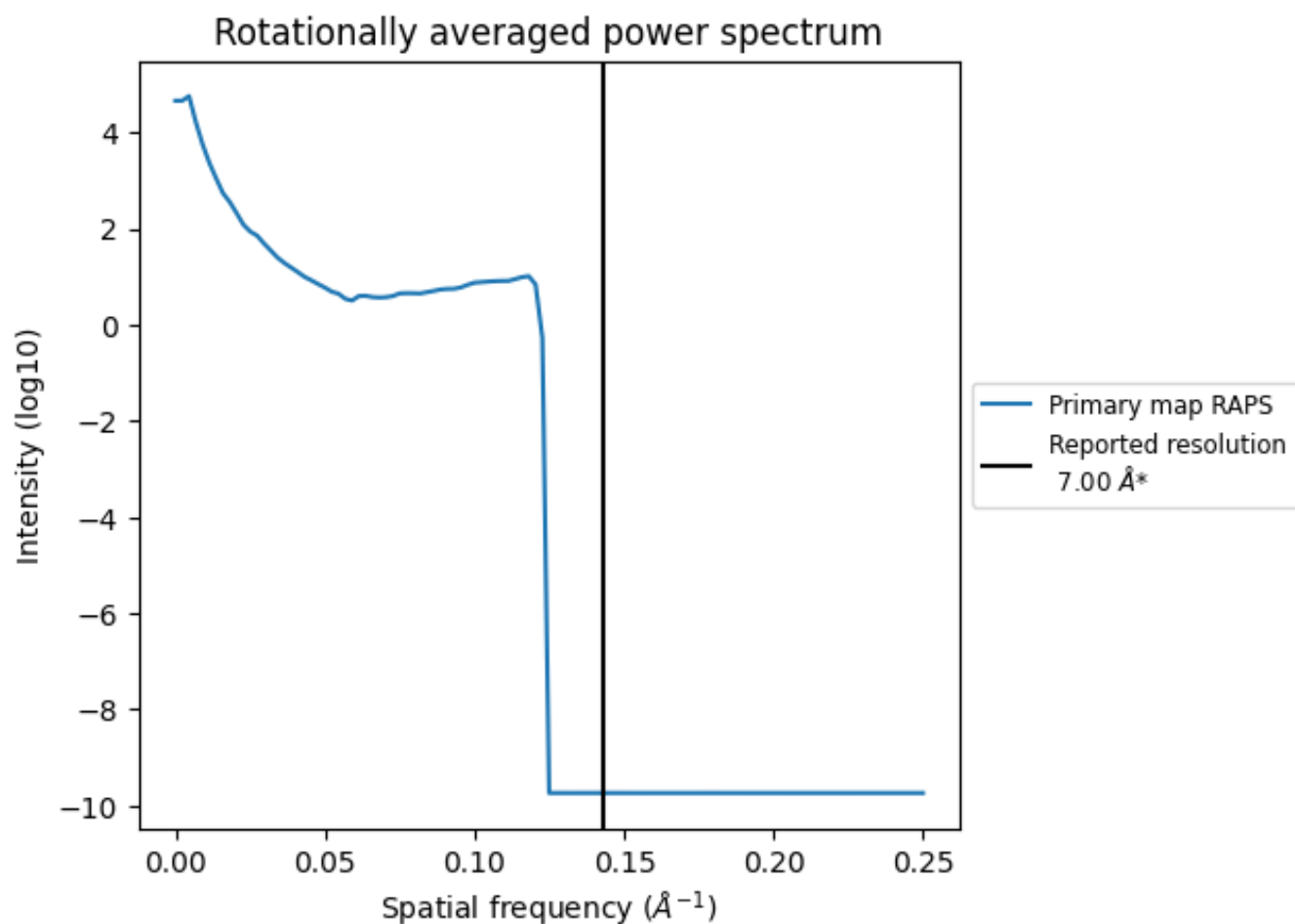
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 860 nm³; this corresponds to an approximate mass of 777 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [\(i\)](#)



*Reported resolution corresponds to spatial frequency of 0.143 Å⁻¹

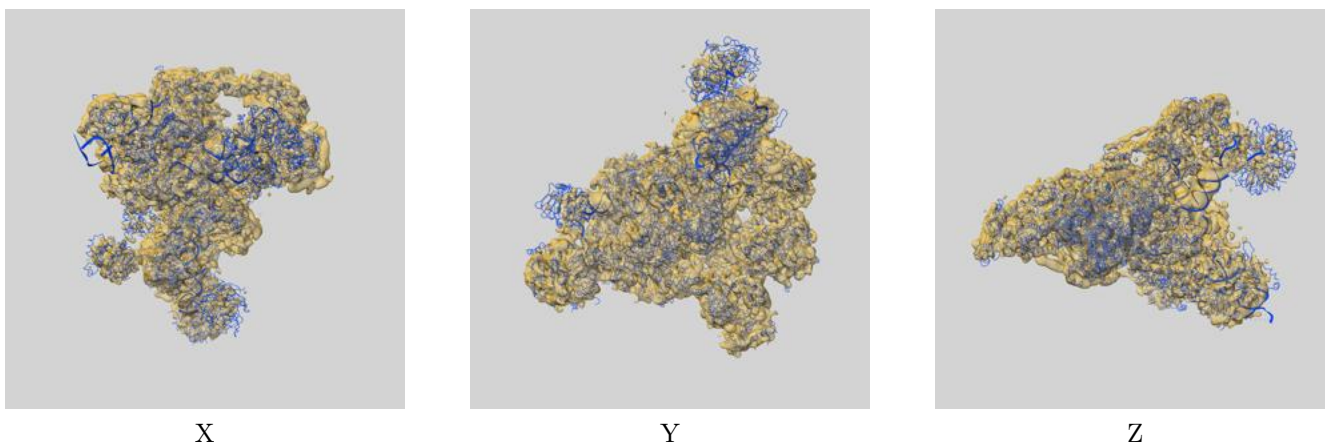
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

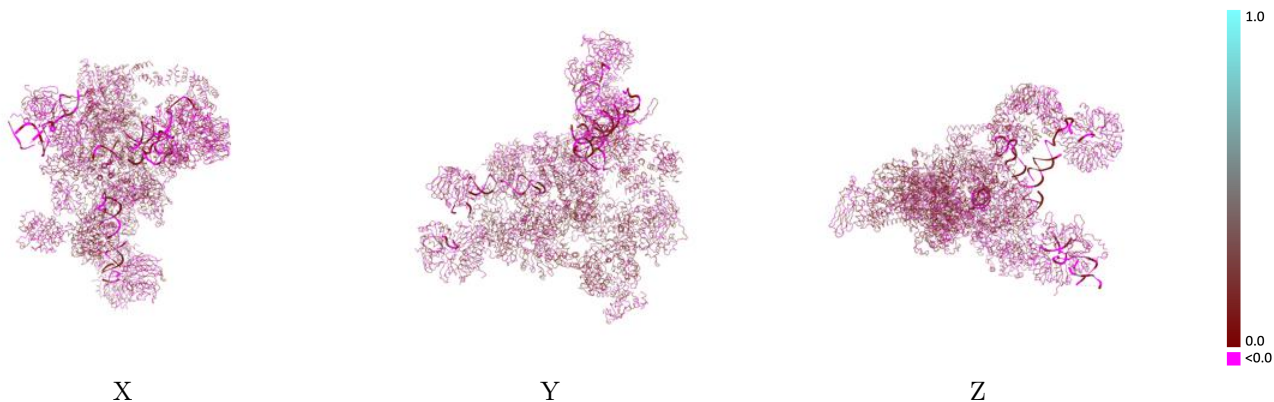
This section contains information regarding the fit between EMDB map EMD-6581 and PDB model 3JCR. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



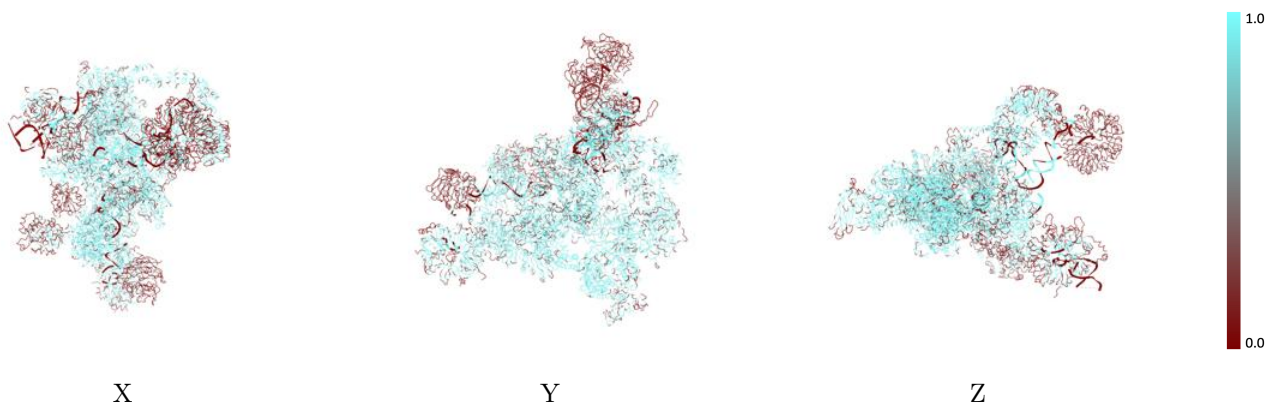
The images above show the 3D surface view of the map at the recommended contour level 0.13 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



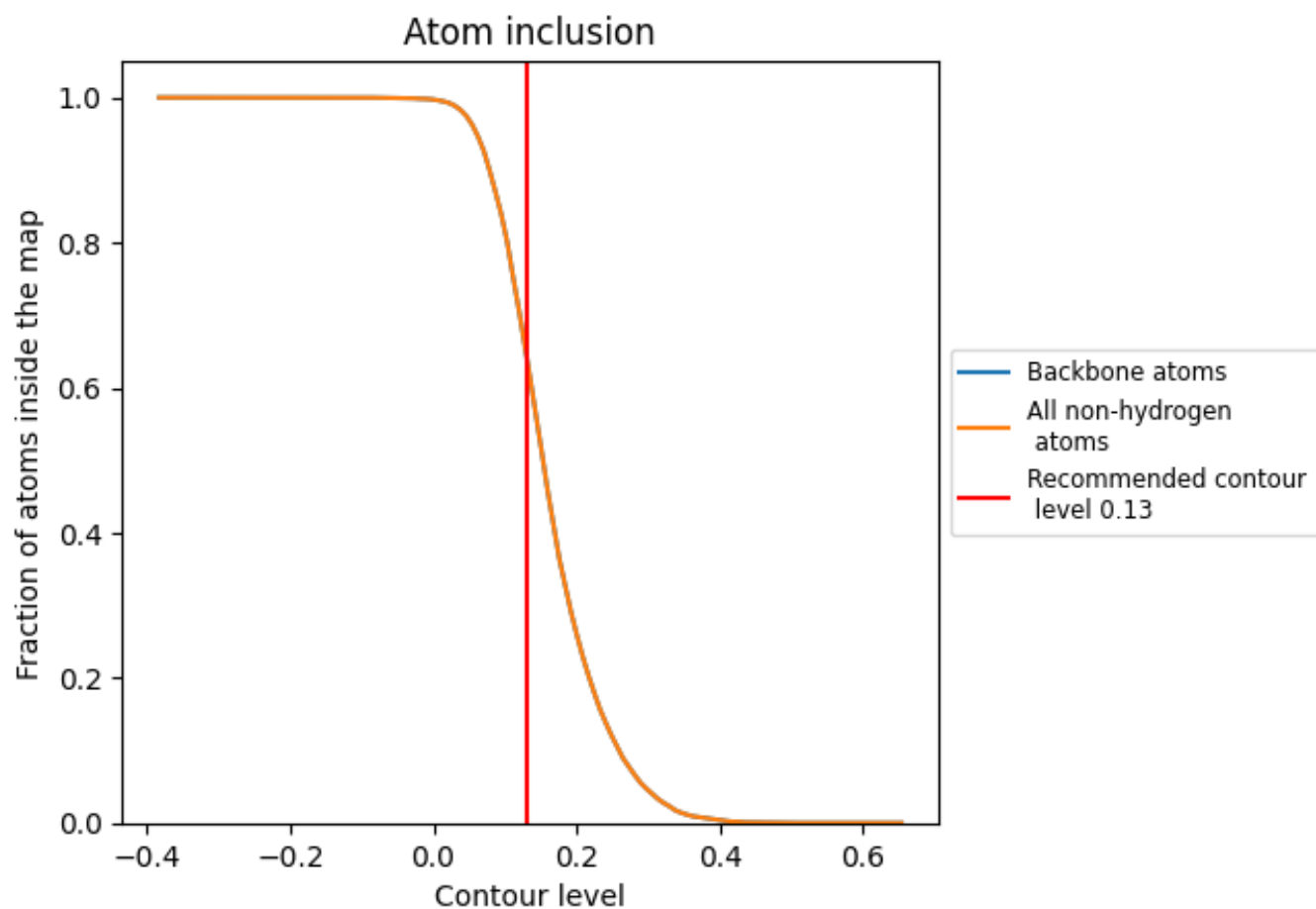
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.13).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 65% 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 (0.13) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6452	 0.0910
2	 0.0111	 0.0190
3	 0.0843	 0.0170
4	 0.0375	 0.0140
5	 0.0132	 0.0110
6	 0.0714	 0.0210
7	 0.0380	 -0.0040
8	 0.1000	 0.0080
A	 0.8074	 0.1250
B	 0.8578	 0.1270
C	 0.8037	 0.1130
D	 0.0795	 0.0290
E	 0.5778	 0.0700
F	 0.2345	 0.0460
G	 0.8110	 0.0990
H	 0.5556	 0.0440
I	 0.7698	 0.1180
J	 0.5439	 0.0800
K	 0.3664	 0.0170
L	 0.6515	 0.0340
M	 0.3398	 0.0260
N	 0.5676	 0.0170
O	 0.5843	 0.0940
P	 0.6237	 0.0990
Q	 0.6629	 0.0960
R	 0.7386	 0.1090
S	 0.5769	 0.0660
T	 0.6027	 0.0890
U	 0.6438	 0.1020
V	 0.7680	 0.1080
o	 0.4157	 0.0430
p	 0.2340	 0.0330
q	 0.2022	 0.0130
r	 0.4545	 0.0020
s	 0.3077	 0.0390



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Chain	Atom inclusion	Q-score
t	 0.1687	 0.0170
u	 0.5753	 0.0900