



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 06:06 PM UTC

PDB ID : 7SYN / pdb_00007syn
EMDB ID : EMD-25534
Title : Structure of the HCV IRES bound to the 40S ribosomal subunit, head opening.
Structure 8(delta dII)
Authors : Brown, Z.P.; Abaeva, I.S.; De, S.; Hellen, C.U.T.; Pestova, T.V.; Frank, J.
Deposited on : 2021-11-25
Resolution : 4.00 Å(reported)
Based on initial models : 5FLX, 6D9J

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:

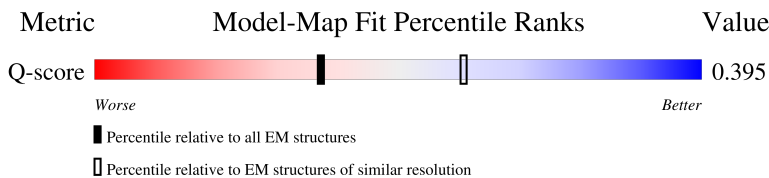
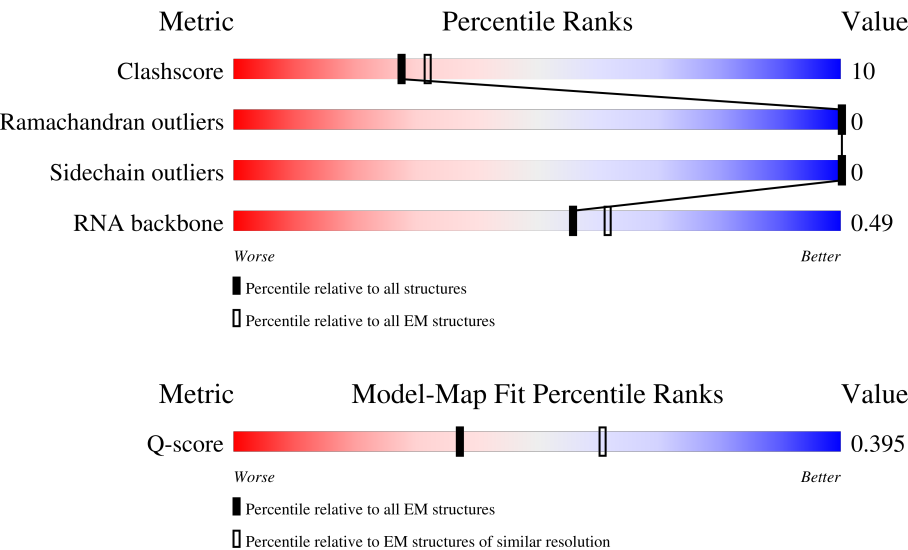
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.00 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.



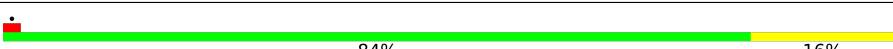
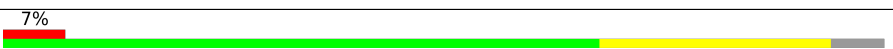
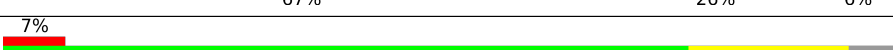
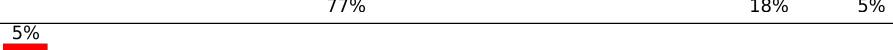
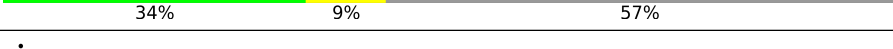
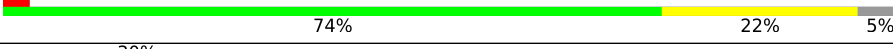
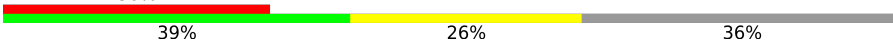
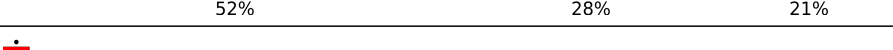
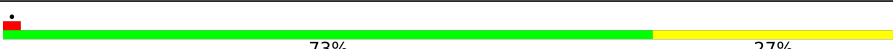
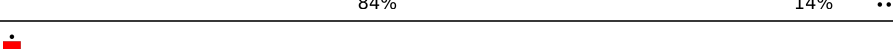
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7587 (3.50 - 4.50)

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	2	1870	44%39%7%9%
2	B	295	6% 45%29%26%
3	C	264	63%18%19%

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Mol	Chain	Length	Quality of chain
4	D	221	
5	E	281	
6	F	263	
7	G	204	
8	H	249	
9	I	432	
10	J	208	
11	K	194	
12	L	149	
13	M	158	
14	N	132	
15	O	151	
16	P	168	
17	Q	145	
18	R	172	
19	S	135	
20	T	152	
21	U	145	
22	V	119	
23	W	83	
24	X	130	
25	Y	143	
26	Z	131	
27	a	124	
28	b	101	

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Mol	Chain	Length	Quality of chain
29	c	84	
30	d	69	
31	e	56	
32	f	133	
33	g	188	
34	h	317	
35	n	25	
36	z	400	

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 78761 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 RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1697	Total	C	N	O	P	0	0
			36227	16170	6504	11857	1696		

- Molecule 2 is a protein called uS2 (SA).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	114	THR	ALA	conflict	UNP G1TLT8

- Molecule 3 is a protein called eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 4 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	221	Total	C	N	O	S	0	0
			1716	1111	295	301	9		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	73	MET	VAL	conflict	UNP G1TUT9
D	101	SER	ALA	conflict	UNP G1TUT9
D	119	GLY	ALA	conflict	UNP G1TUT9
D	194	ARG	HIS	conflict	UNP G1TUT9

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Chain	Residue	Modelled	Actual	Comment	Reference
D	215	MET	LEU	conflict	UNP G1TUT9
D	227	ARG	TRP	conflict	UNP G1TUT9
D	228	GLY	SER	conflict	UNP G1TUT9

- Molecule 5 is a protein called uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 6 is a protein called eS4 (S4 X isoform).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	25	GLY	SER	conflict	UNP G1TK17
F	51	ARG	LYS	conflict	UNP G1TK17
F	78	THR	ALA	conflict	UNP G1TK17
F	156	VAL	MET	conflict	UNP G1TK17

- Molecule 7 is a protein called uS7.

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

- Molecule 8 is a protein called eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 9 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 10 is a protein called eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 11 is a protein called uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 12 is a protein called eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 13 is a protein called uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	151	Total	C	N	O	S	0	0
			1233	785	231	211	6		

- Molecule 14 is a protein called eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 15 is a protein called uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 16 is a protein called uS11.

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

- Molecule 17 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	115	Total	C	N	O	S	0	0
			956	610	176	163	7		

- Molecule 18 is a protein called uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 19 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 20 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 21 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

- Molecule 22 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 23 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
W	3	ASN	SER	conflict	UNP G1TM82
W	4	ASP	ASN	conflict	UNP G1TM82
W	33	GLN	PRO	conflict	UNP G1TM82
W	50	PHE	SER	conflict	UNP G1TM82
W	75	ALA	SER	conflict	UNP G1TM82
W	76	ASP	HIS	conflict	UNP G1TM82
W	81	LYS	GLN	conflict	UNP G1TM82

- Molecule 24 is a protein called uS8.

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

- Molecule 25 is a protein called uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 26 is a protein called eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 27 is a protein called eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	77	Total	C	N	O	S	0	0
			614	393	114	106	1		

- Molecule 28 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	28	ARG	CYS	conflict	UNP G1TFE8
b	56	ALA	VAL	conflict	UNP G1TFE8

- Molecule 29 is a protein called eS27.

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

- Molecule 30 is a protein called eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	67	Total	C	N	O	S	0	0
			530	321	108	99	2		

- Molecule 31 is a protein called uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 32 is a protein called eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	57	Total	C	N	O	S	0	0
			457	282	101	73	1		

- Molecule 33 is a protein called eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 34 is a protein called Receptor for Activated C Kinase 1 (RACK1).

Mol	Chain	Residues	Atoms					AltConf	Trace
34	h	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 35 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	n	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 36 is a RNA chain called HCV IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	z	162	Total	C	N	O	P	0	0
			3465	1542	621	1140	162		

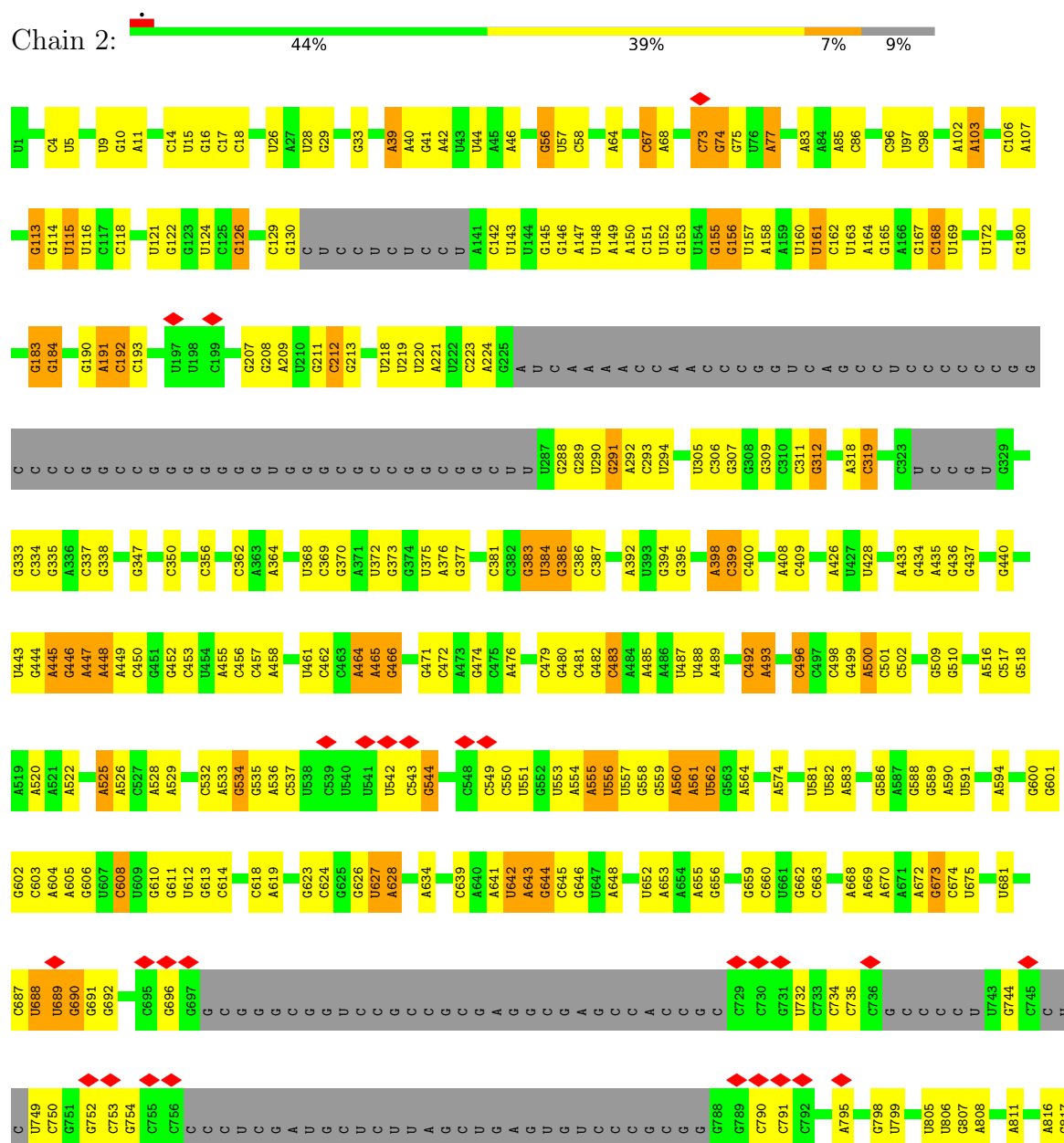
- Molecule 37 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
37	b	1	Total	Zn	0
			1	1	
37	g	1	Total	Zn	0
			1	1	

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 18S rRNA



U1840	C	A1679	A1537	G1451	A1386	U1306	U1239	A1080	A980	G895	A818
C1841	C	G1680	C1538	A1451	A1387	U1307	A1240	U1081	A981	G896	G819
G1842	A	C1618	C1542	A1455	A1388	U1308	A1241	A1082	G988	U898	U820
U1843	G	A1694	U1543	G1456	U1392	C1309	U1242	A1083	A983	G901	G821
A1844		A1695	G1544	U1457	G1393	U1310	U1243	C1085	A990	A904	U822
G1846		A1699	C1547	G1458	G1394	C1311	G1244		G991	A905	A825
G1847		C1700	U1549	G1459	G1395	G1312	G1245		A992	G905	A830
G1849		G1701	U1550	U1462	A1396	U1314	A1251	U1088	A996	U906	A830
A1850		C1702	G1551	U1463	A1397	U1315	C1252	C1091	A997	G907	C834
A1851		C1703	U1552	G1466	G1398	G1318	A1253	C1094	A998	G908	C
C1852		G1704	G1553		U1400		G1254	G999	G999	G910	A
C1853		C1705	C1554	C1472	A1401		G1255	C1095	C1000	A913	G
U1854		G1706	U1555	A1473	A1402	U1323	G1256	G1096	A1001	U914	C
G1855		G1780	U1556	A1474	A1403	G1324	A1257	C1097	U1002	G915	C
G1856		A1781	A1556	A1475	C1403	U1327	A1258	C1098	U1003	A916	
G1857		G1782	C1557	U1476	U1404	G1327	A1259	G1099	U1004	U917	G841
G1858		A1711	U1558	A1477	A1405		C1262	C1103	G1005	U918	
C1783		A1712	C1559	U1478	G1406	G1330	U1263	G1104	C1006	G845	U844
A1860		G1784	U1560	U1479	U1407	G1331	A1264	U1109	A1007	G846	G845
A1861		C1785	G1561	A1480	A1408	A1332	A1265	C1109	A1008	A920	G846
G1862		U1786	C1562	U1481	U1409		A1266	G1110	A1009	G921	A847
A1863		G1787	G1563	G1490	C1415	U1340	G1268	U1111	G1010	A922	C851
A1864		A1718	C1564	G1491	C1416	C1341	G1269	U1112	A1011	G824	G852
U1864		A1719	C1565	C1417	C1417	U1342	C1272	U1113	A1012	G925	
C1865		U1720	U1566	C	C		C1273	U1114	U1013	G928	G859
		G1722	G1567	C	C	U1348	C1274	C1118	U1017	G929	A861
G1796		U1726	U1568	A1486	C1412	G1348	G1275	G1121	U1018	C930	U862
U1797		G1727	C1569	A1487	G1413	G1349	A1276	C1124	C1019	G933	U863
C1798		U1728	U1570	G1488	A1414	U1350	C1277	G1125	A1020		A864
G1799		A1650	C1571	U1489	A1415	U1351	C1278	G1126	A1023	U940	U866
G1805		U1729	U1572	G1490	C1416	G1352	C1279	U1130	A1030	C941	G867
A1806		U1730	C1573	G1491	C1417	A1353	G1280	G1135	A1031	G942	G868
C1807		A1731	U1574	C1492	C1417	G1354	G1281	C1136	G1032	U943	A869
U1808		G1736	C1575	A1493	C	G1355	A1282	C1137	U944	U870	U871
A1809		G1737	U1576	U1494	G1424	C1356	C1283	U1138	U945	A872	A872
U1810		U1740	C1577	G1495	G1425	U1357	A1284	C1139	U1045	G873	G873
C1811		C1743	U1578	U1496	G1426	U1358	G1285	G1140	U1046	A874	A874
A1813		G1744	A1586	G1497	C1427	U1359	C1286		G1047	C876	C876
G1814		G1748	U1587	A1498	U1427	G1360	U1287	A1144	G1048	C877	C877
			C1589	A1506	C	U1361	U1288	A1145	A1055	C879	C879
A1822		C1751	U1590	G1507	C	G1362	U1289	C1146		G961	U882
A1823		G1754	G1597	G1507	A1438	G1363	G1290	U1147	U1061	A862	U885
A1824		C1755	G1598	G1521	A1439	G1365	A1293	A1148	U1064	A863	U885
A1825		U1756	U1601	G1526	U1442	G1366	G1294	A1149	C1065	A864	A886
U1827		C1756	U1602	C1527	C	U1371	A1295	G1151	G1065	U965	
C1828		G1757	G1603	G1528	A1443	G1375	U1296	U1152	A1070	G971	U889
G1829		U1758	U1604	U1531	C1443	A1376	U1297	C1153	A1071	G975	U890
U1830		G1759	G1605	G1532	U1447	U1377	G1298	U1154	G1071	U892	U891
A1831		G1760	U1606	C1533	G1447	A1378	U1299	U1155	G1076	U893	G894
A1834		U1761	U1607	C1534	G1448	U1379	A1301	U1156			
A1835		C	U1608	U1535	G1449	C1380	G1302				
G1836		G	G1612	G1536	G1450	A1381	C1303				
G1837		C	G1613			A1382	U1304				
U1838						A1383	C1305				
U1839											

Chain B:

6%

45%

29%

26%

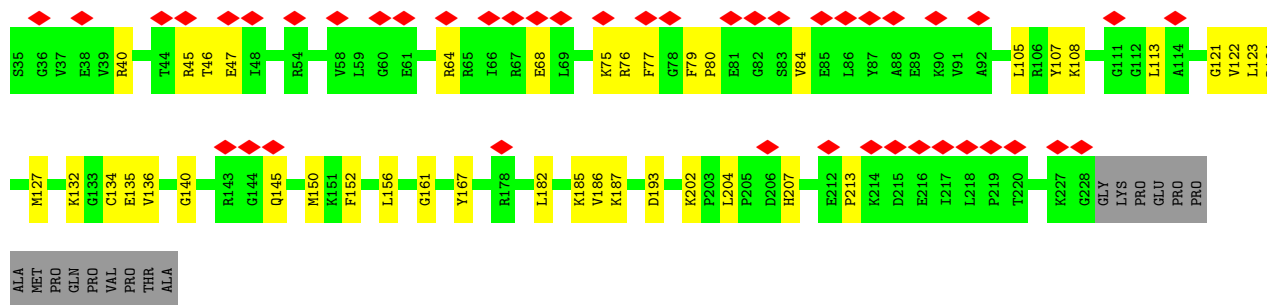
Position	Conserved Amino Acids (bits)
1	Met (0.25), Ser (0.15), Thr (0.10), Val (0.05)
2	Ser (0.25), Thr (0.15), Val (0.10), Ile (0.05)
3	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)
4	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)
5	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)
6	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)
7	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)
8	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)
9	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)
10	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)
11	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)
12	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)
13	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)
14	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)
15	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)
16	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)
17	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)
18	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)
19	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)
20	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)
21	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)
22	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)
23	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)
24	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)
25	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)
26	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)
27	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)
28	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)
29	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)
30	Val (0.25), Ile (0.15), Thr (0.10), Ser (0.05)

Chain C:

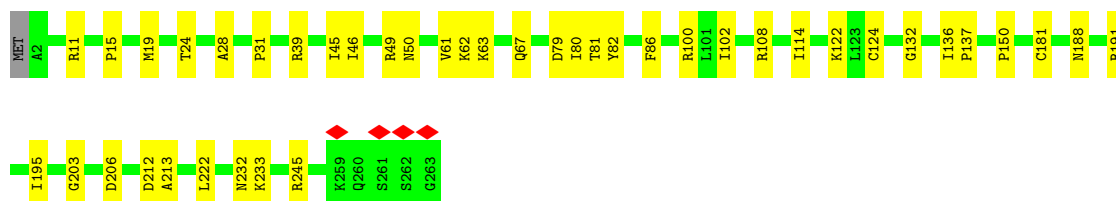
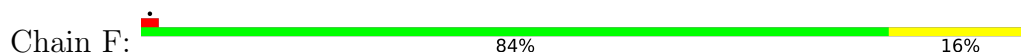
Position	Amino Acid	Information Content (bits)
1	SER	0.15
2	SER	0.15
3	GLY	0.15
4	LYS	0.15
5	ALA	0.15
6	THR	0.15
7	GLY	0.15
8	ASP	0.15
9	GLU	0.15
10	GLU	0.15
11	THR	0.15
12	GLY	0.15
13	ALA	0.15
14	LYS	0.15
15	LYS	0.15
16	VAL	0.15
17	GLU	0.15
18	GLU	0.15
19	ARG	0.15
20	ALA	0.15
21	ALA	0.15
22	ASP	0.15
23	GLY	0.15
24	TYR	0.15
25	GLU	0.15
26	PRO	0.15
27	PRO	0.15
28	VAL	0.15
29	GLN	0.15
30	GLU	0.15
31	SER	0.15
32	VAL	0.15
33	MET	0.15
34	ALA	0.15
35	VAL	0.15
36	GLY	0.15
37	LYS	0.15
38	ASN	0.15
39	ARG	0.15
40	LEU	0.15
41	THR	0.15
42	LYS	0.15
43	GLY	0.15
44	LYS	0.15
45	GLY	0.15
46	LYS	0.15
47	ALA	0.15
48	LYS	0.15
49	LYS	0.15
50	LYS	0.15
51	V21	0.15
52	V22	0.15
53	S26	0.15
54	K27	0.15
55	K28	0.15
56	V33	0.15
57	K34	0.15
58	A35	0.15
59	I44	0.15
60	I48	0.15
61	V49	0.15
62	T50	0.15
63	T55	0.15
64	L62	0.15
65	R65	0.15
66	E68	0.15
67	L71	0.15
68	E78	0.15
69	V79	0.15
70	R82	0.15
71	K83	0.15
72	F84	0.15
73	T88	0.15
74	C96	0.15
75	L97	0.15
76	T98	0.15
77	M103	0.15
78	L104	0.15
79	L105	0.15
80	A123	0.15
81	H124	0.15
82	K128	0.15
83	G132	0.15
84	C139	0.15
85	V140	0.15
86	K144	0.15
87	M147	0.15
88	I150	0.15
89	T153	0.15
90	S154	0.15
91	Y155	0.15
92	A156	0.15
93	Q157	0.15
94	I164	0.15
95	R165	0.15
96	M168	0.15
97	H169	0.15
98	E170	0.15
99	I171	0.15
100	M172	0.15
101	T173	0.15
102	L181	0.15
103	V184	0.15
104	L188	0.15
105	I189	0.15
106	P190	0.15
107	D191	0.15
108	Q202	0.15
109	H208	0.15
110	D209	0.15
111	R213	0.15
112	M217	0.15
113	K220	0.15
114	G233	0.15
115	GLY	0.15
116	GLY	0.15
117	SER	0.15

Chain D:

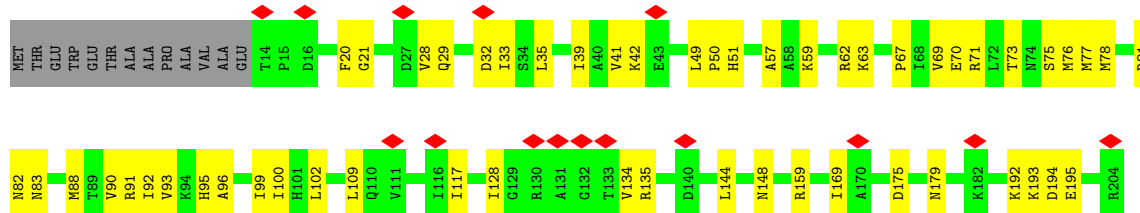
Chain E:



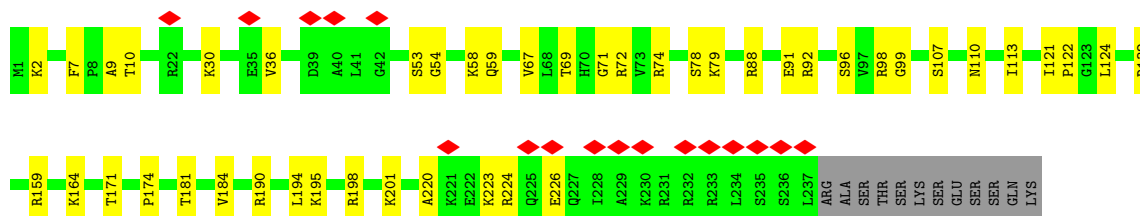
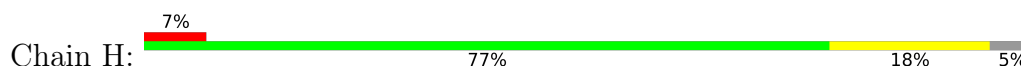
• Molecule 6: eS4 (S4 X isoform)



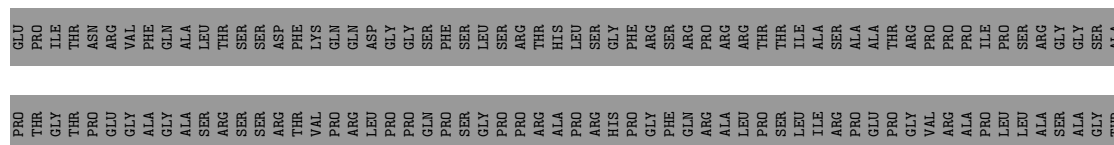
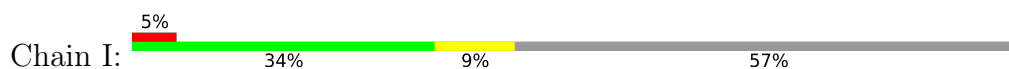
• Molecule 7: uS7

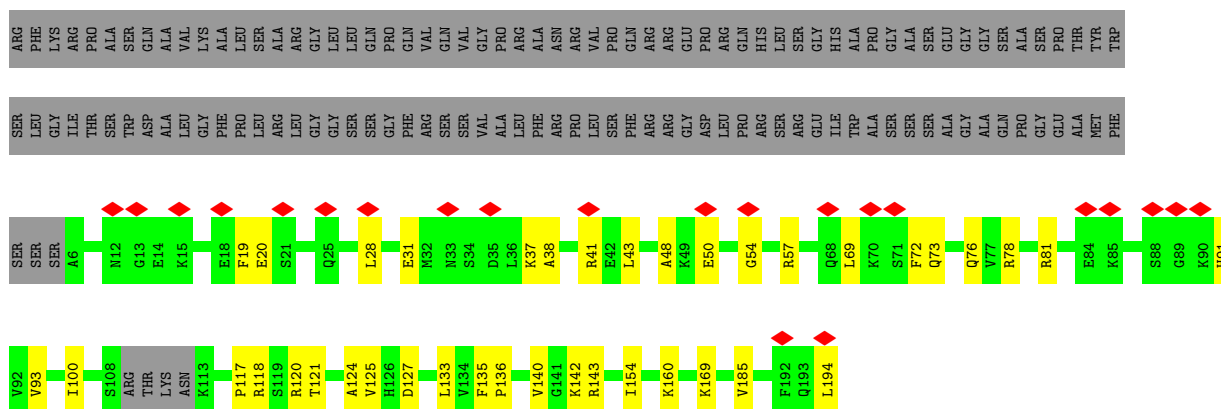


• Molecule 8: eS6

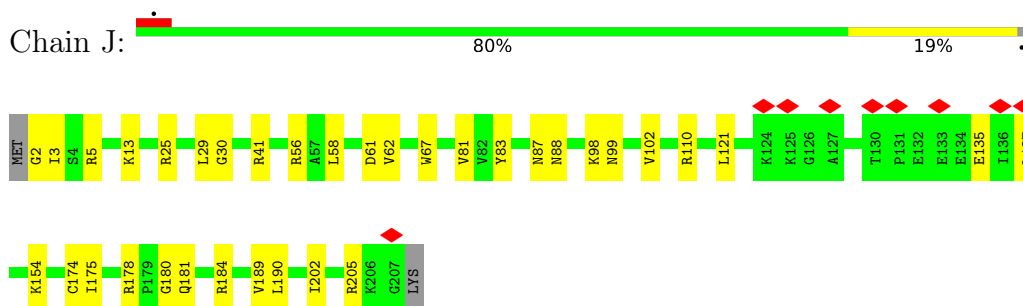


• Molecule 9: eS7

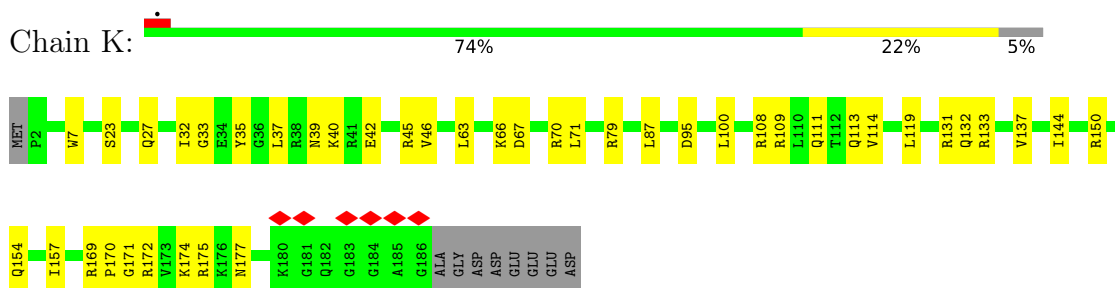




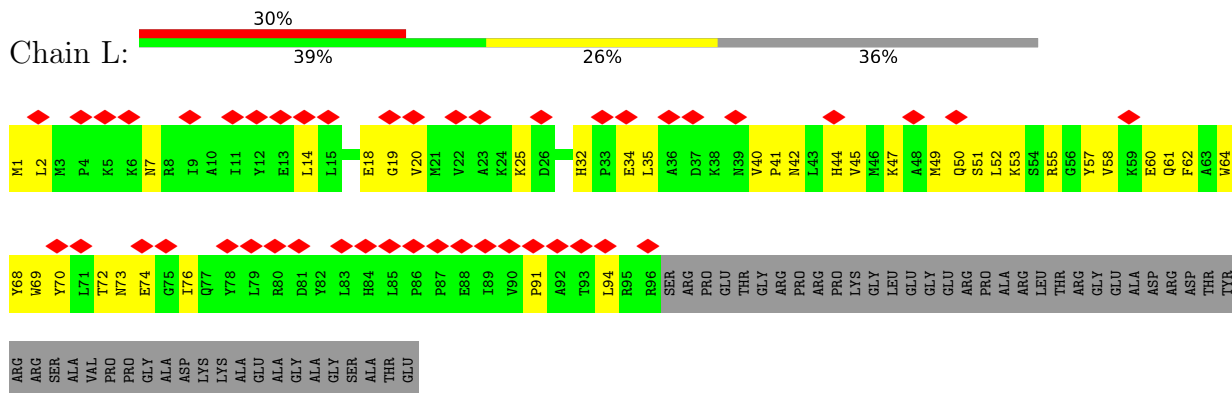
• Molecule 10: eS8



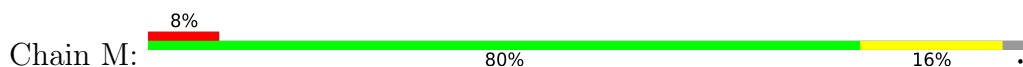
• Molecule 11: uS4

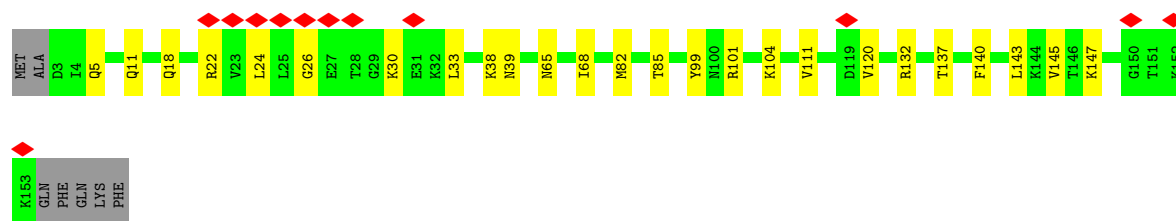


• Molecule 12: eS10



• Molecule 13: uS17

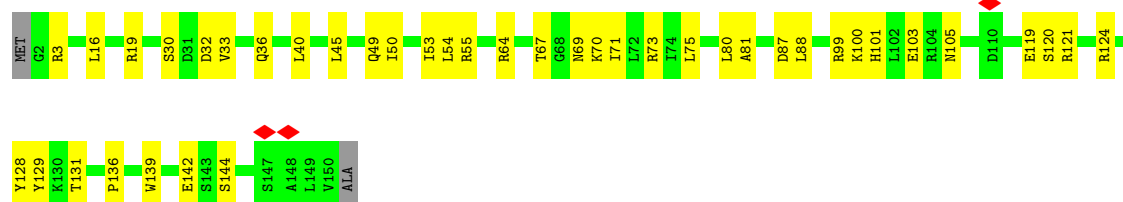




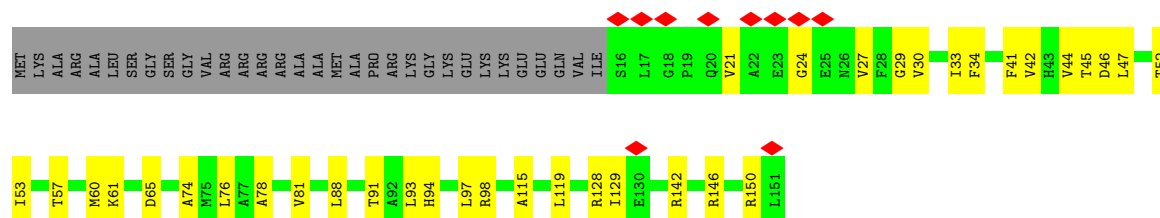
• Molecule 14: eS12



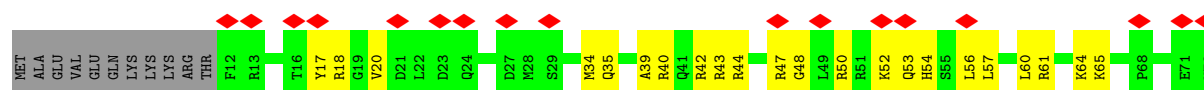
• Molecule 15: uS15

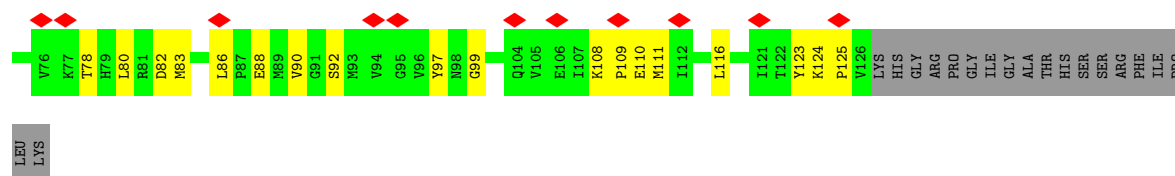


• Molecule 16: uS11

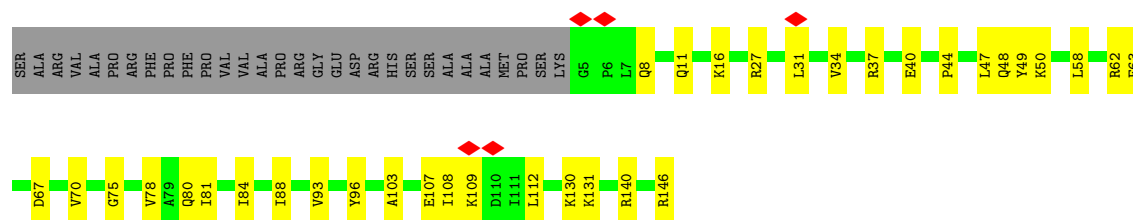


• Molecule 17: uS19

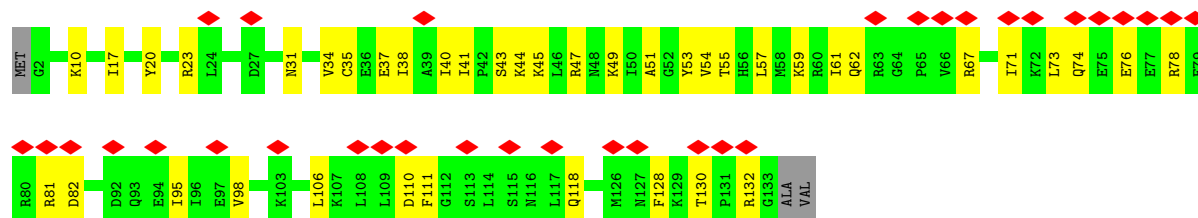




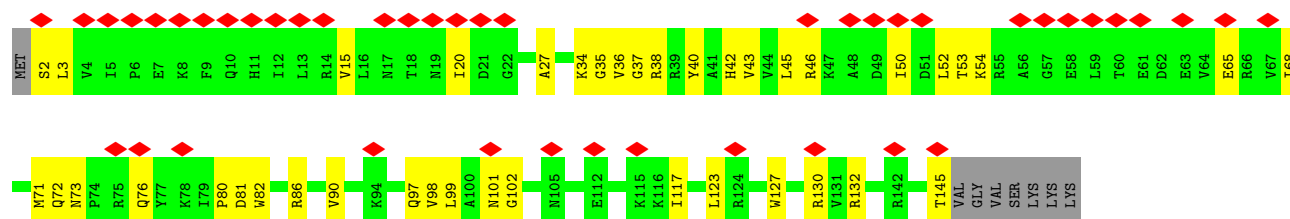
• Molecule 18: uS9



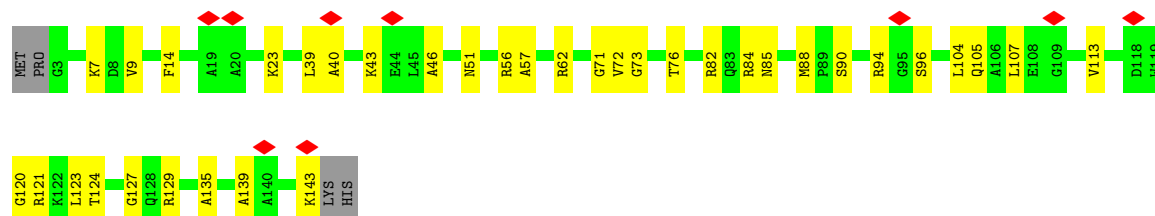
• Molecule 19: eS17



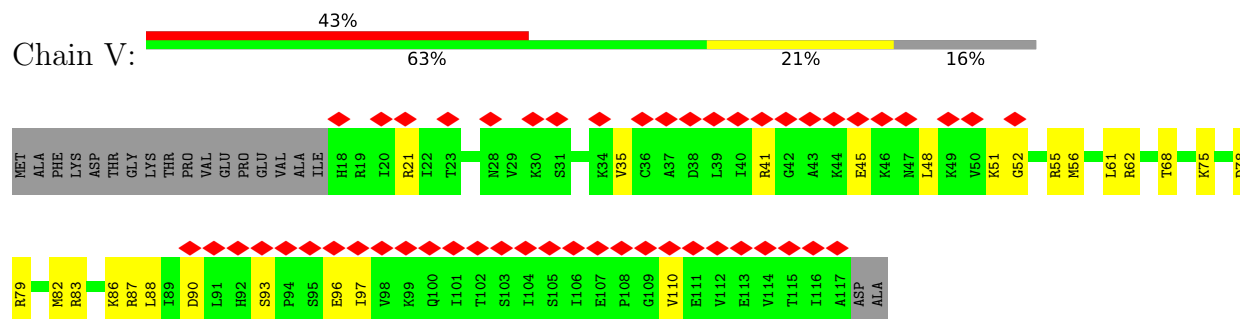
• Molecule 20: uS13



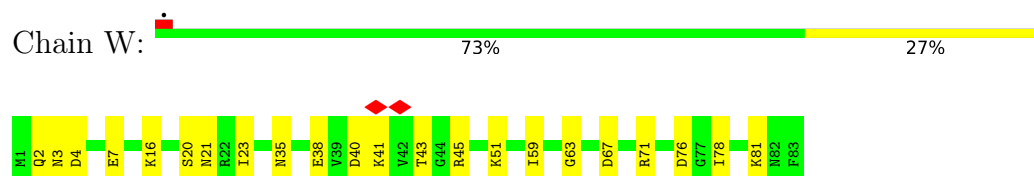
• Molecule 21: eS19



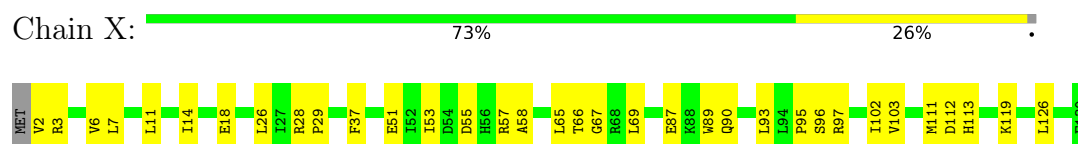
- Molecule 22: uS10



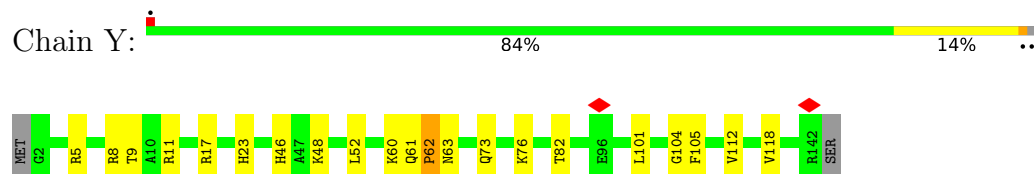
- Molecule 23: eS21



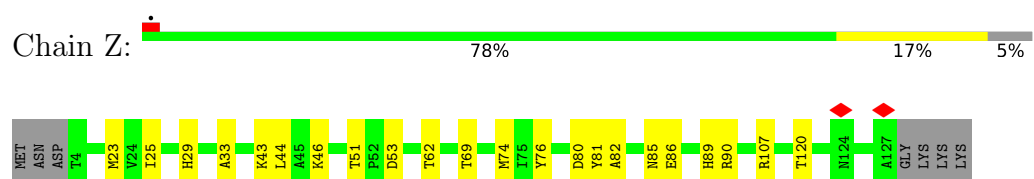
- Molecule 24: uS8



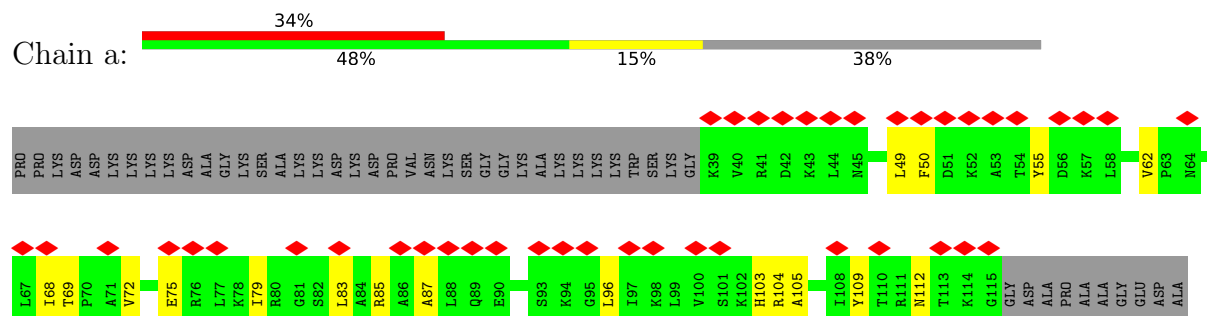
- Molecule 25: uS12



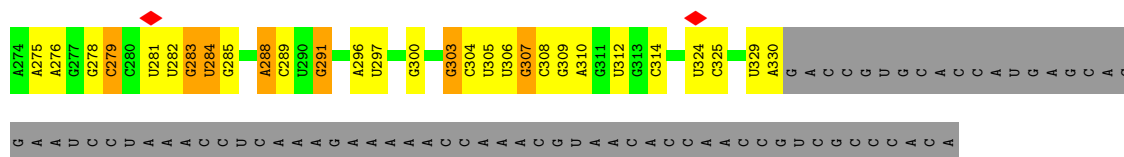
- Molecule 26: eS24



- Molecule 27: eS25



GLU	ASP	HIS	HIS	ALA	ARG	GLY	ILE	PRO	PRO	ASP	ASN	GLN	ARG	LEU	ILE	PHE	ALA	GLY	LYS	GLN	LEU	GLU	ASP	GLY	ARG	THR	THR	LEU	SER	ASP	TYR	ASN	ILE	GLN	LYS	GLU	SER	THR	LEU	HIS	LEU	VAL	LEU	ARG	LEU	ARG	GLY	GLY	ALA	LYS	LYS	ARG	LYS	LYS	K83	S84	S85	T86	T87	C89
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	144252	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	70.9	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	52000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.085	Depositor
Minimum map value	-0.037	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.0125	Depositor
Map size (Å)	380.0, 380.0, 380.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.95, 0.95, 0.95	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	2	0.08	0/40506	0.22	0/63123
2	B	0.11	0/1747	0.32	0/2374
3	C	0.10	0/1756	0.30	0/2350
4	D	0.10	0/1753	0.28	0/2369
5	E	0.14	0/1796	0.35	0/2417
6	F	0.11	0/2118	0.30	0/2849
7	G	0.11	0/1531	0.33	0/2059
8	H	0.11	0/1946	0.28	0/2590
9	I	0.10	0/1510	0.28	0/2022
10	J	0.13	0/1715	0.32	0/2287
11	K	0.10	0/1550	0.28	0/2069
12	L	0.12	0/834	0.34	0/1125
13	M	0.09	0/1254	0.28	0/1677
14	N	0.09	0/918	0.27	0/1233
15	O	0.10	0/1226	0.27	0/1649
16	P	0.12	0/1029	0.32	0/1380
17	Q	0.13	0/974	0.39	0/1301
18	R	0.11	0/1146	0.28	0/1534
19	S	0.12	0/1082	0.34	0/1452
20	T	0.11	0/1208	0.33	0/1618
21	U	0.10	0/1115	0.26	0/1493
22	V	0.09	0/805	0.25	0/1081
23	W	0.10	0/643	0.30	0/860
24	X	0.12	0/1051	0.34	0/1406
25	Y	0.13	0/1116	0.37	1/1490 (0.1%)
26	Z	0.10	0/1028	0.30	0/1366
27	a	0.12	0/620	0.32	0/831
28	b	0.10	0/828	0.26	0/1109
29	c	0.11	0/665	0.32	0/891
30	d	0.12	0/532	0.32	0/712
31	e	0.10	0/470	0.27	0/623
32	f	0.11	0/462	0.32	0/607

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	g	0.06	0/567	0.19	0/753
34	h	0.10	0/2493	0.29	0/3394
35	n	0.08	0/240	0.24	0/305
36	z	0.08	0/3871	0.20	0/6034
All	All	0.10	0/84105	0.26	1/122433 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	Y	62	PRO	CA-N-CD	-6.14	103.40	112.00

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	2	36227	0	18299	591	0
2	B	1710	0	1708	60	0
3	C	1729	0	1803	34	0
4	D	1716	0	1806	39	0
5	E	1768	0	1866	40	0
6	F	2076	0	2177	25	0
7	G	1509	0	1563	46	0
8	H	1923	0	2089	31	0
9	I	1488	0	1582	25	0
10	J	1686	0	1772	28	0
11	K	1525	0	1640	36	0
12	L	810	0	836	30	0
13	M	1233	0	1310	20	0
14	N	908	0	939	16	0
15	O	1202	0	1289	27	0
16	P	1016	0	1039	26	0
17	Q	956	0	1002	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	R	1128	0	1195	26	0
19	S	1068	0	1121	30	0
20	T	1190	0	1249	33	0
21	U	1097	0	1130	30	0
22	V	795	0	862	16	0
23	W	636	0	637	17	0
24	X	1034	0	1080	27	0
25	Y	1098	0	1167	22	0
26	Z	1011	0	1083	16	0
27	a	614	0	678	13	0
28	b	814	0	863	19	0
29	c	651	0	672	9	0
30	d	530	0	561	7	0
31	e	459	0	452	14	0
32	f	457	0	502	13	0
33	g	555	0	563	13	0
34	h	2436	0	2393	67	0
35	n	239	0	289	5	0
36	z	3465	0	1751	42	0
37	b	1	0	0	0	0
37	g	1	0	0	0	0
All	All	78761	0	60968	1305	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 10.

The worst 5 of 1305 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)
1:2:318:A:C2	1:2:333:G:N1	2.21	1.07
1:2:1743:G:H21	1:2:1791:A:H62	1.08	0.98
1:2:1743:G:N2	1:2:1791:A:H62	1.65	0.93
1:2:1048:G:H21	1:2:1070:A:H62	1.17	0.91
1:2:318:A:H2	1:2:333:G:N1	1.66	0.89

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	
2	B	215/295 (73%)	198 (92%)	17 (8%)	0	100	100
3	C	211/264 (80%)	201 (95%)	10 (5%)	0	100	100
4	D	219/221 (99%)	212 (97%)	7 (3%)	0	100	100
5	E	226/281 (80%)	219 (97%)	7 (3%)	0	100	100
6	F	260/263 (99%)	243 (94%)	17 (6%)	0	100	100
7	G	189/204 (93%)	176 (93%)	13 (7%)	0	100	100
8	H	235/249 (94%)	233 (99%)	2 (1%)	0	100	100
9	I	181/432 (42%)	172 (95%)	9 (5%)	0	100	100
10	J	204/208 (98%)	192 (94%)	12 (6%)	0	100	100
11	K	183/194 (94%)	179 (98%)	4 (2%)	0	100	100
12	L	94/149 (63%)	89 (95%)	5 (5%)	0	100	100
13	M	149/158 (94%)	136 (91%)	13 (9%)	0	100	100
14	N	115/132 (87%)	107 (93%)	8 (7%)	0	100	100
15	O	147/151 (97%)	142 (97%)	5 (3%)	0	100	100
16	P	134/168 (80%)	130 (97%)	4 (3%)	0	100	100
17	Q	113/145 (78%)	103 (91%)	10 (9%)	0	100	100
18	R	140/172 (81%)	133 (95%)	7 (5%)	0	100	100
19	S	130/135 (96%)	119 (92%)	11 (8%)	0	100	100
20	T	142/152 (93%)	135 (95%)	7 (5%)	0	100	100
21	U	139/145 (96%)	134 (96%)	5 (4%)	0	100	100
22	V	98/119 (82%)	95 (97%)	3 (3%)	0	100	100
23	W	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
24	X	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
25	Y	139/143 (97%)	134 (96%)	5 (4%)	0	100	100
26	Z	122/131 (93%)	120 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	a	75/124 (60%)	72 (96%)	3 (4%)	0	100	100
28	b	99/101 (98%)	96 (97%)	3 (3%)	0	100	100
29	c	81/84 (96%)	75 (93%)	6 (7%)	0	100	100
30	d	65/69 (94%)	61 (94%)	4 (6%)	0	100	100
31	e	53/56 (95%)	49 (92%)	4 (8%)	0	100	100
32	f	55/133 (41%)	51 (93%)	4 (7%)	0	100	100
33	g	66/188 (35%)	66 (100%)	0	0	100	100
34	h	311/317 (98%)	297 (96%)	14 (4%)	0	100	100
35	n	23/25 (92%)	23 (100%)	0	0	100	100
All	All	4821/5821 (83%)	4592 (95%)	229 (5%)	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	
2	B	180/245 (74%)	180 (100%)	0	100	100
3	C	194/231 (84%)	194 (100%)	0	100	100
4	D	187/187 (100%)	187 (100%)	0	100	100
5	E	190/232 (82%)	190 (100%)	0	100	100
6	F	224/225 (100%)	224 (100%)	0	100	100
7	G	161/170 (95%)	161 (100%)	0	100	100
8	H	207/218 (95%)	207 (100%)	0	100	100
9	I	165/360 (46%)	165 (100%)	0	100	100
10	J	178/180 (99%)	178 (100%)	0	100	100
11	K	161/168 (96%)	161 (100%)	0	100	100
12	L	87/125 (70%)	87 (100%)	0	100	100
13	M	136/142 (96%)	136 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	N	99/108 (92%)	99 (100%)	0	100	100
15	O	130/131 (99%)	130 (100%)	0	100	100
16	P	106/130 (82%)	106 (100%)	0	100	100
17	Q	105/130 (81%)	105 (100%)	0	100	100
18	R	117/140 (84%)	117 (100%)	0	100	100
19	S	119/121 (98%)	119 (100%)	0	100	100
20	T	125/132 (95%)	125 (100%)	0	100	100
21	U	111/116 (96%)	111 (100%)	0	100	100
22	V	92/107 (86%)	92 (100%)	0	100	100
23	W	67/67 (100%)	67 (100%)	0	100	100
24	X	112/113 (99%)	112 (100%)	0	100	100
25	Y	113/115 (98%)	113 (100%)	0	100	100
26	Z	107/113 (95%)	107 (100%)	0	100	100
27	a	68/102 (67%)	68 (100%)	0	100	100
28	b	88/88 (100%)	88 (100%)	0	100	100
29	c	75/76 (99%)	75 (100%)	0	100	100
30	d	60/62 (97%)	60 (100%)	0	100	100
31	e	48/49 (98%)	48 (100%)	0	100	100
32	f	47/106 (44%)	47 (100%)	0	100	100
33	g	61/154 (40%)	61 (100%)	0	100	100
34	h	272/275 (99%)	272 (100%)	0	100	100
35	n	24/24 (100%)	24 (100%)	0	100	100
All	All	4216/4942 (85%)	4216 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
30	d	7	GLN
31	e	10	HIS
34	h	14	HIS
12	L	42	ASN
12	L	7	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1685/1870 (90%)	354 (21%)	10 (0%)
36	z	160/400 (40%)	42 (26%)	0
All	All	1845/2270 (81%)	396 (21%)	10 (0%)

5 of 396 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	4	C
1	2	5	U
1	2	9	U
1	2	10	G
1	2	11	A

5 of 10 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	1137	U
1	2	1664	A
1	2	1676	U
1	2	561	A
1	2	627	U

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

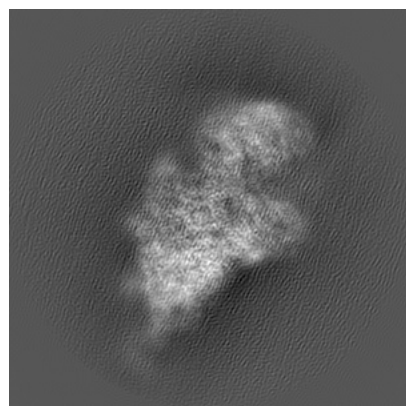
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25534. These allow visual inspection of the internal detail of the map and identification of artifacts.

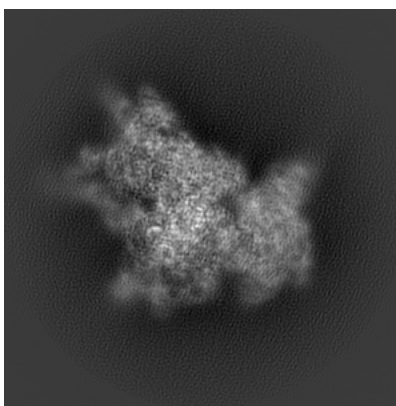
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

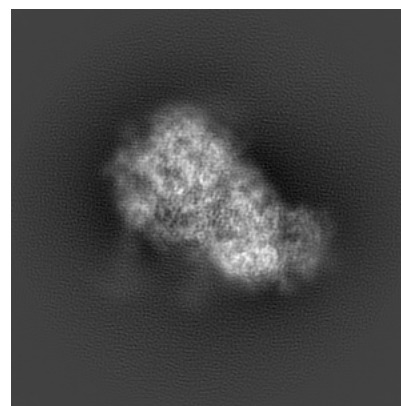
6.1.1 Primary map



X

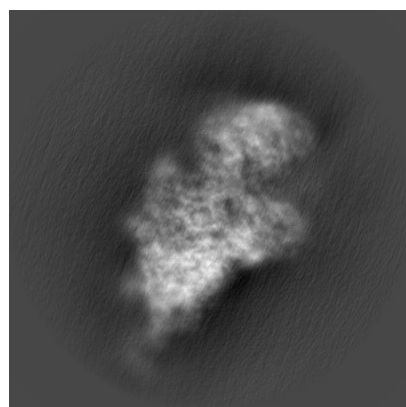


Y

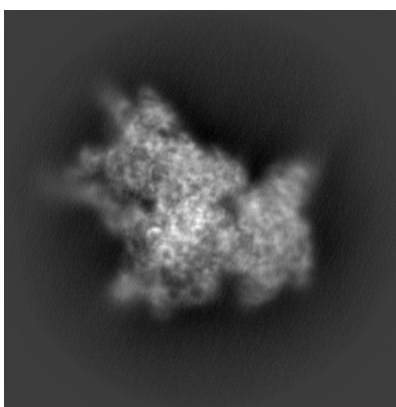


Z

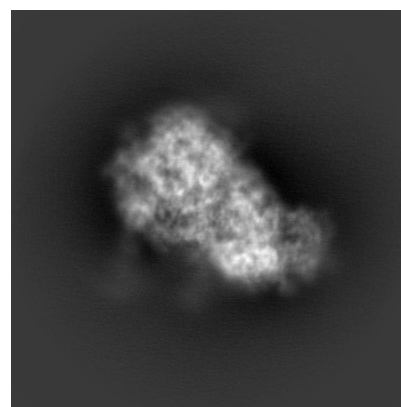
6.1.2 Raw map



X



Y

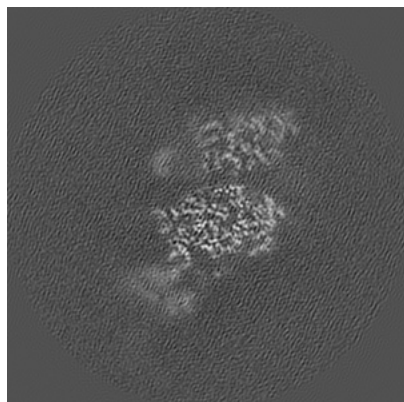


Z

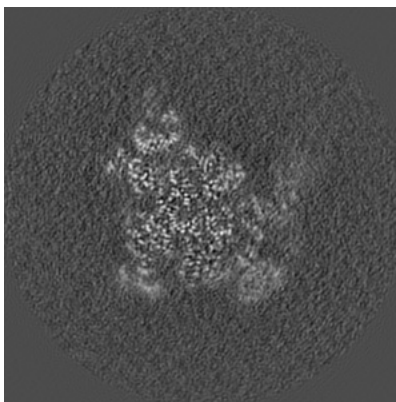
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

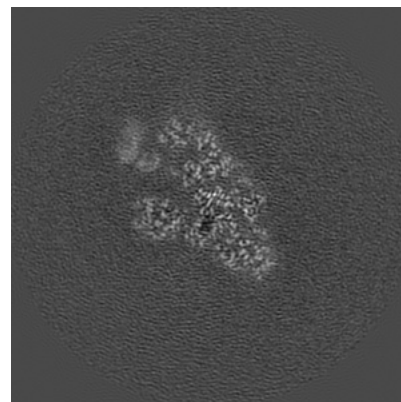
6.2.1 Primary map



X Index: 200

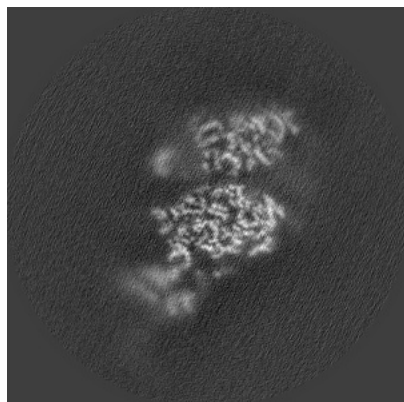


Y Index: 200

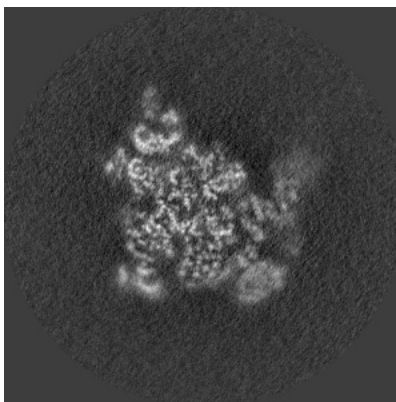


Z Index: 200

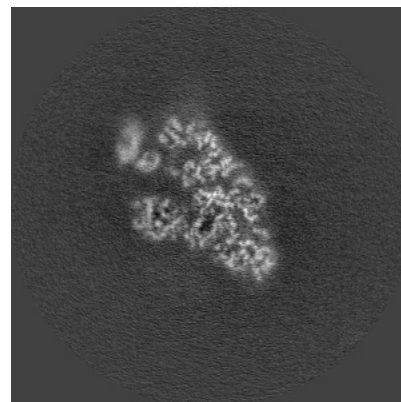
6.2.2 Raw map



X Index: 200



Y Index: 200

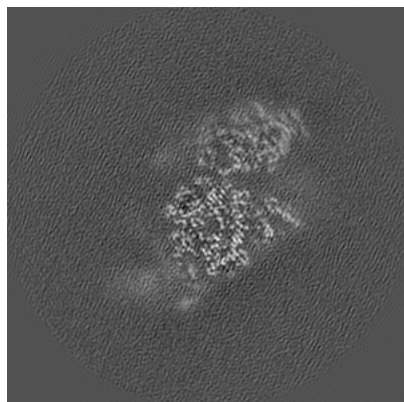


Z Index: 200

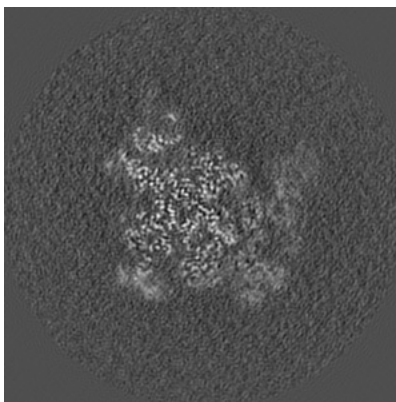
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

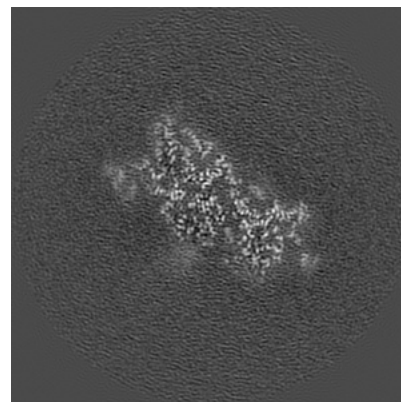
6.3.1 Primary map



X Index: 190

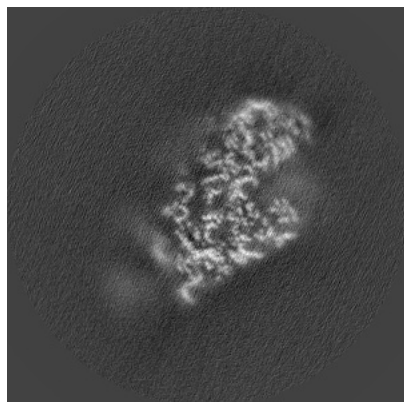


Y Index: 202

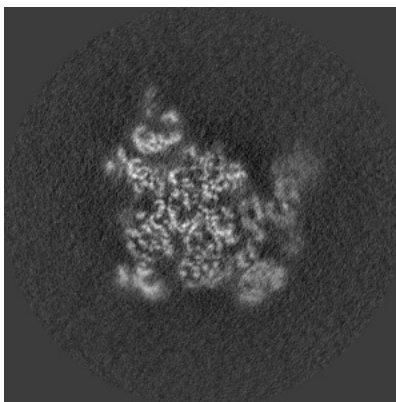


Z Index: 166

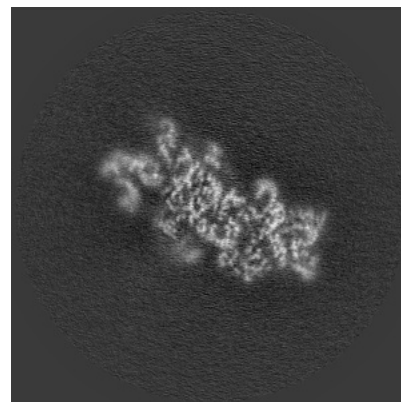
6.3.2 Raw map



X Index: 180



Y Index: 201

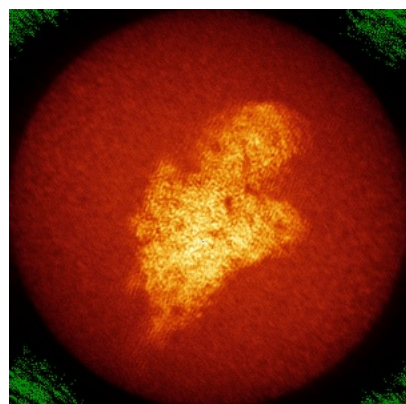


Z Index: 155

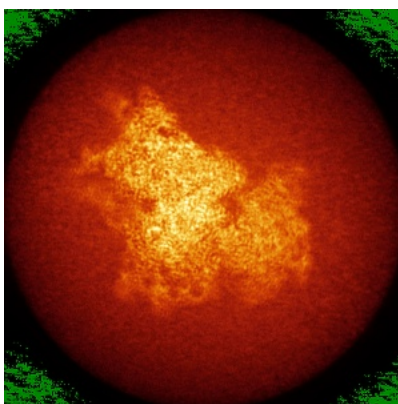
The images above show the largest variance slices of the map in three orthogonal directions.

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

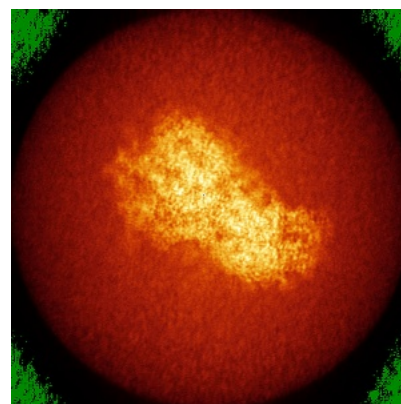
6.4.1 Primary map



X

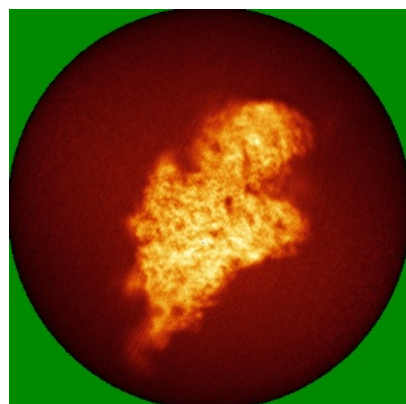


Y

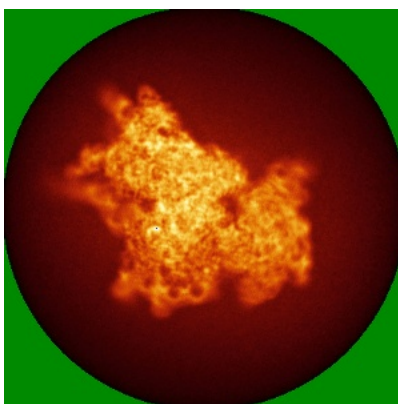


Z

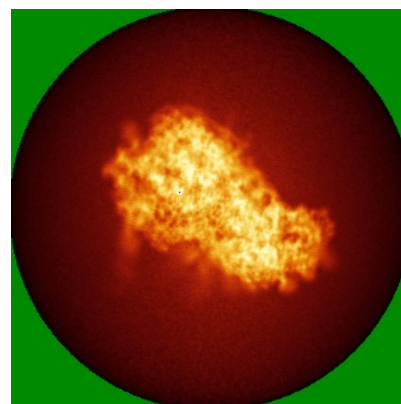
6.4.2 Raw map



X



Y

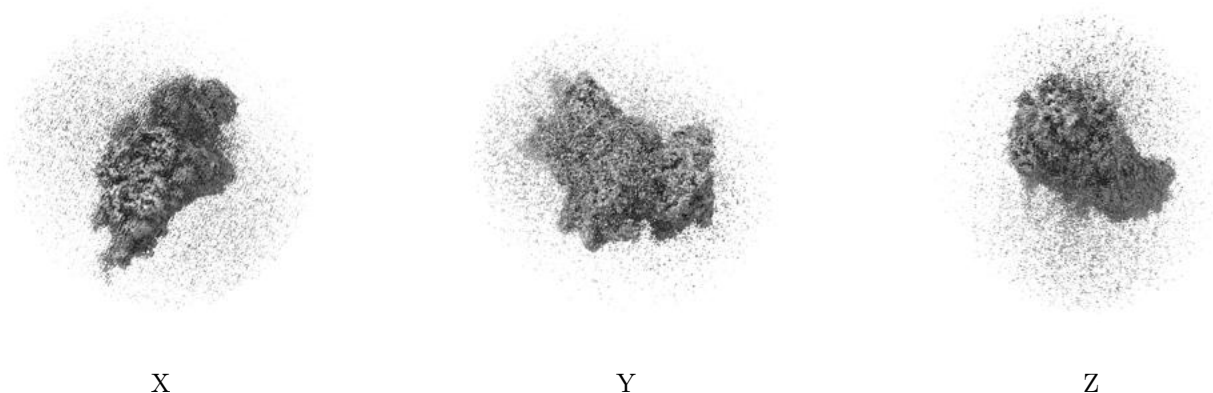


Z

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.

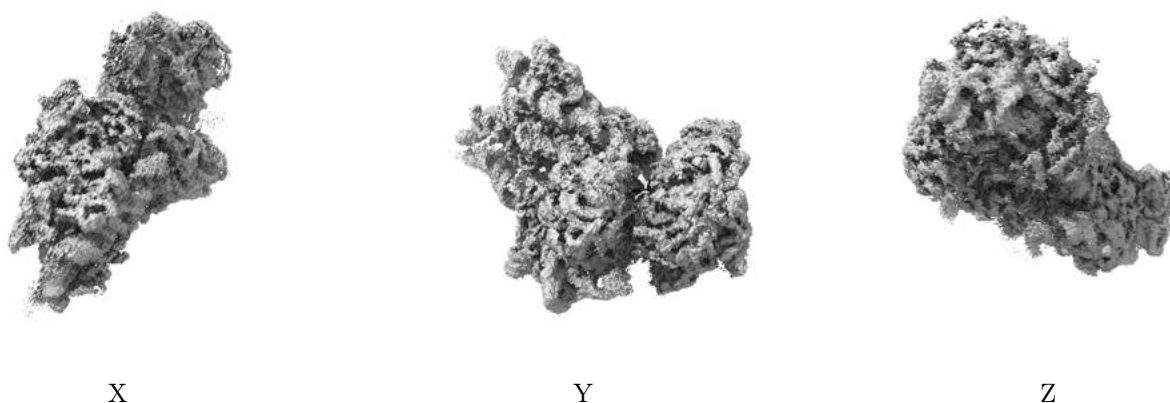
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0125. 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.

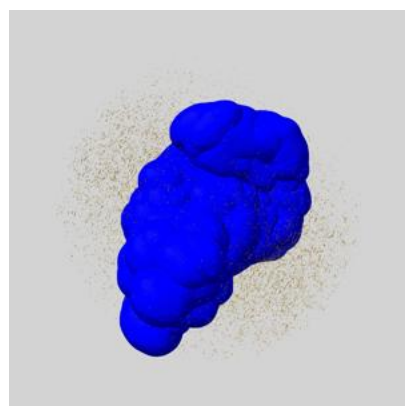
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

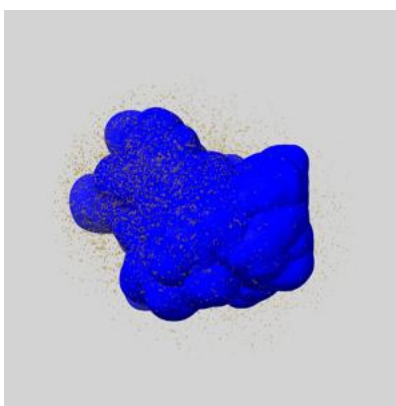
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

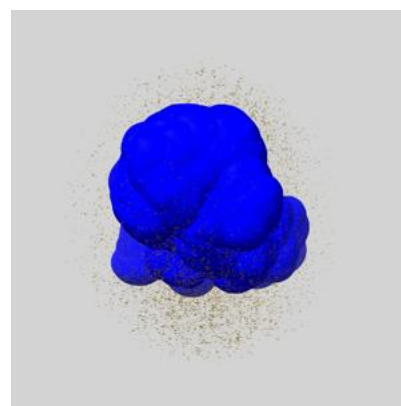
6.6.1 emd_25534_msk_1.map [i](#)



X



Y

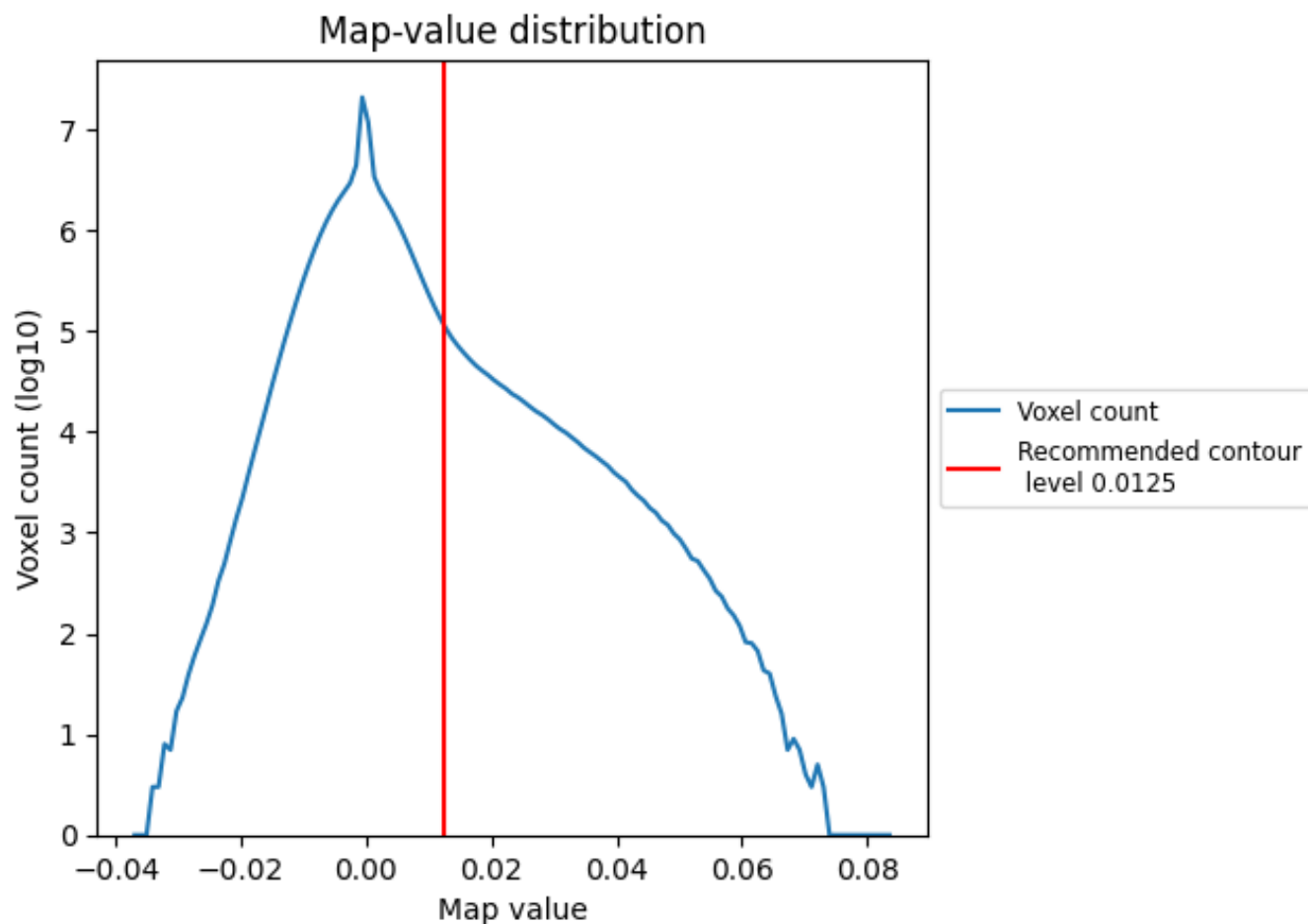


Z

7 Map analysis [i](#)

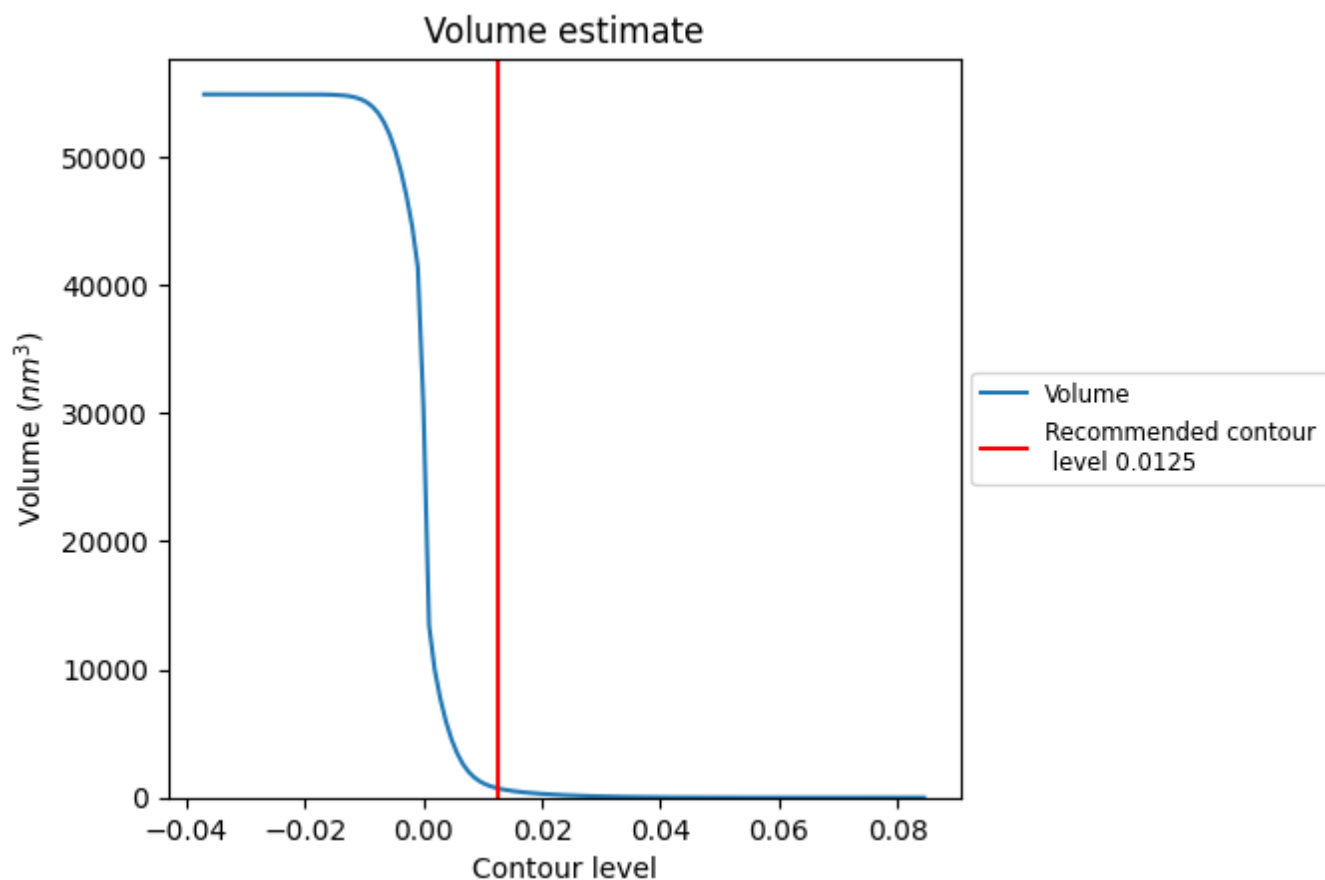
This section contains the results of statistical analysis of the map.

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.

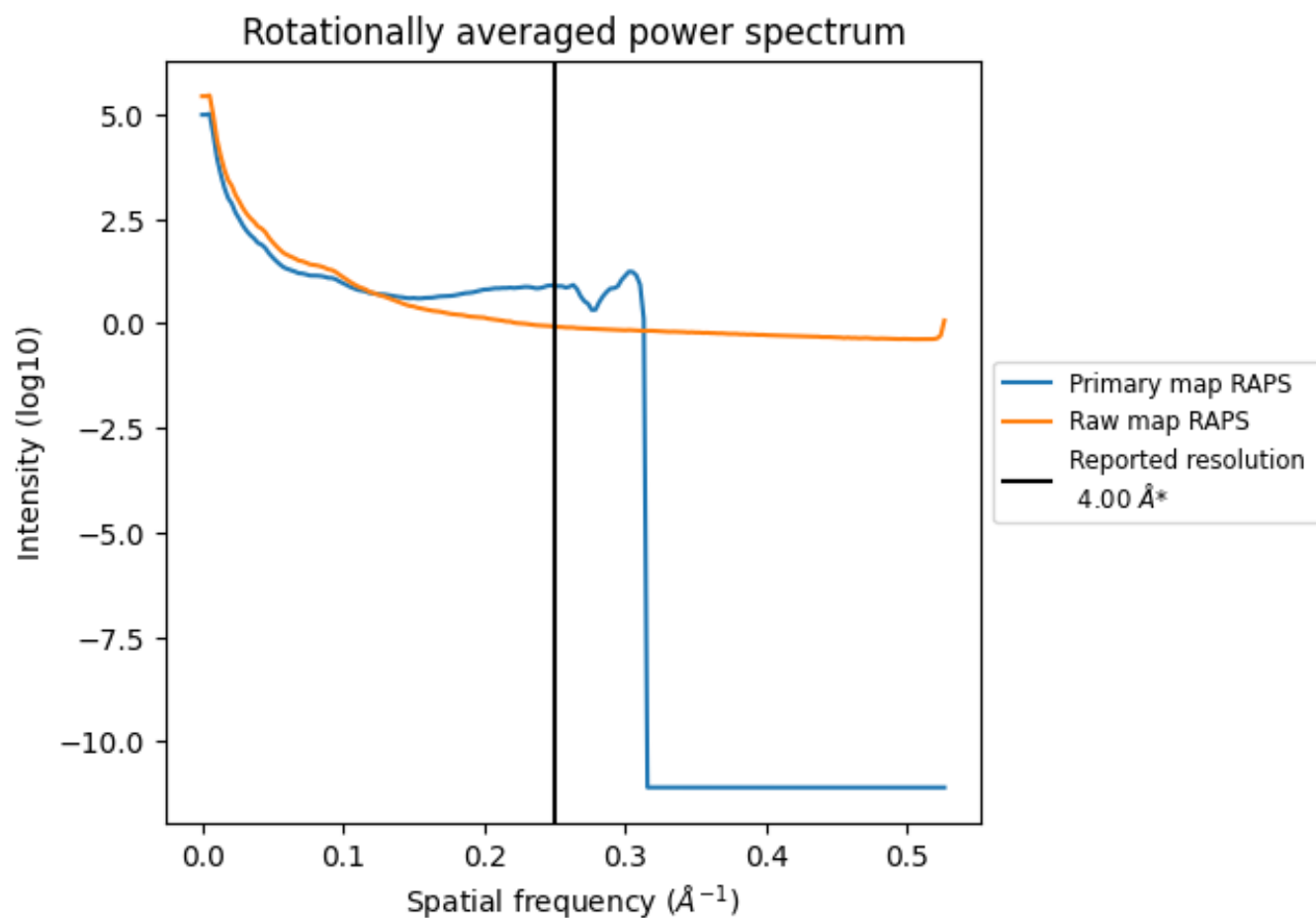
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 732 nm³; this corresponds to an approximate mass of 662 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 ⓘ

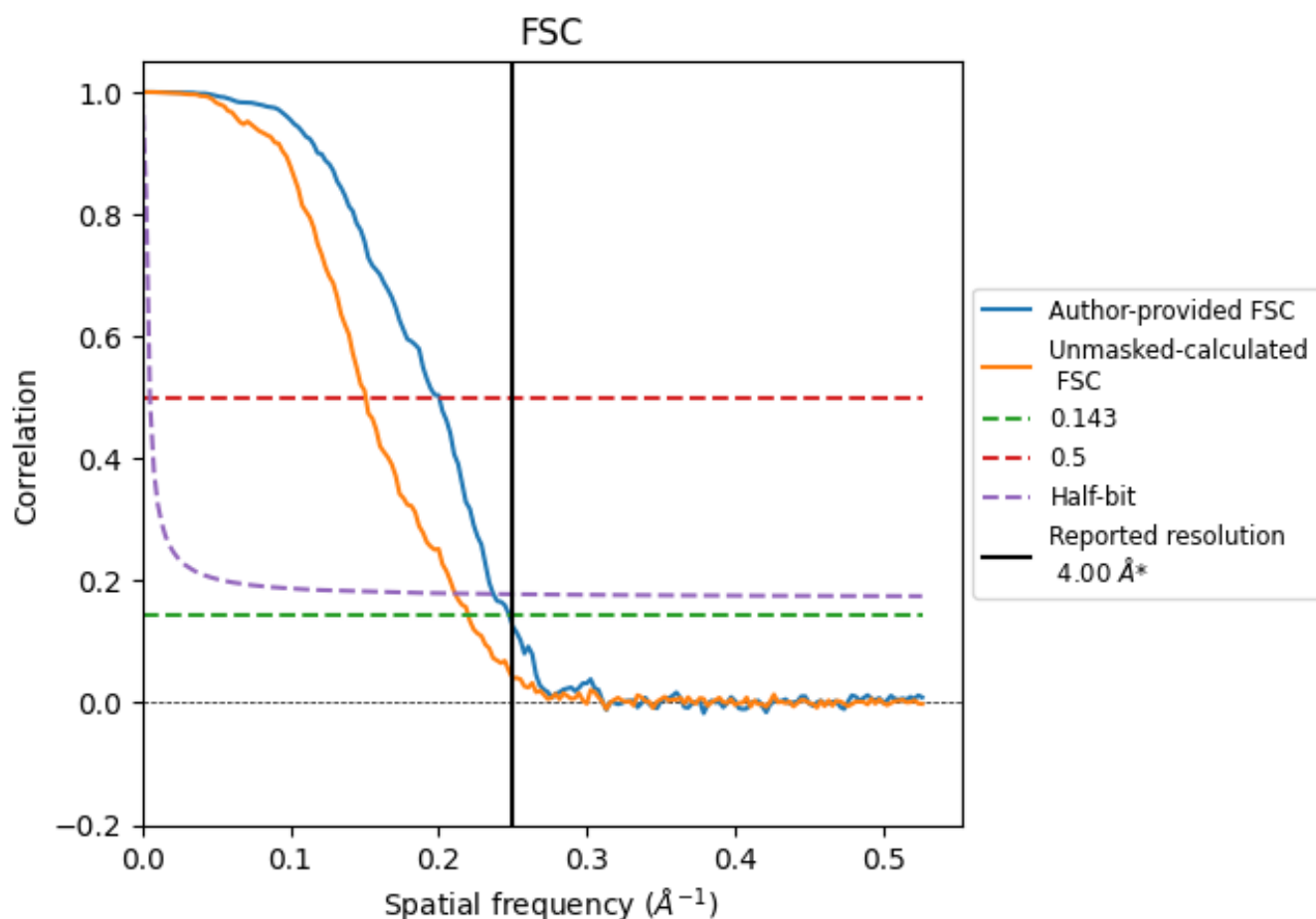


*Reported resolution corresponds to spatial frequency of 0.250 Å⁻¹

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 0.250 Å⁻¹

8.2 Resolution estimates [i](#)

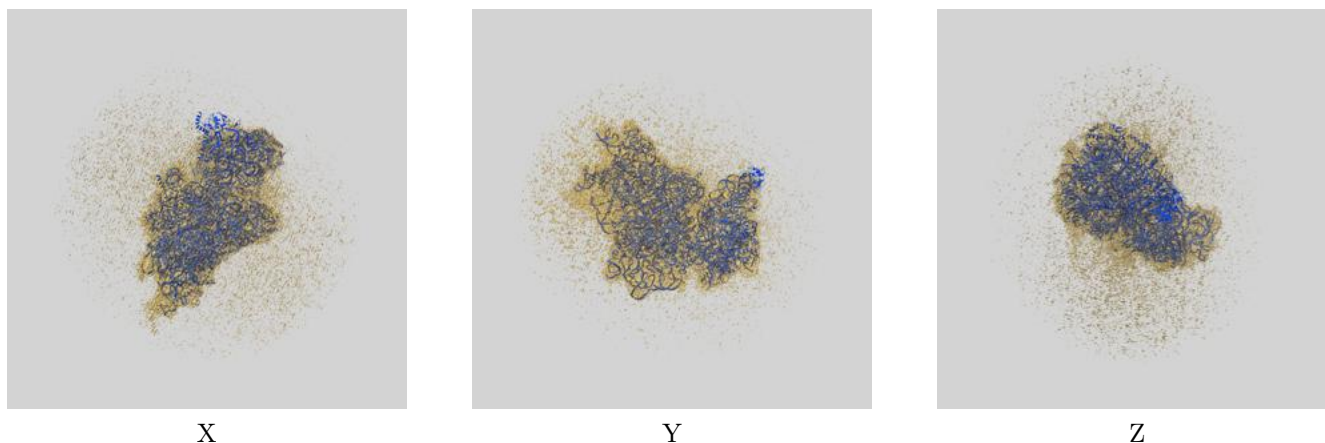
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	4.04	4.99	4.22
Unmasked-calculated*	4.55	6.63	4.74

*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 4.55 differs from the reported value 4.0 by more than 10 %

9 Map-model fit [i](#)

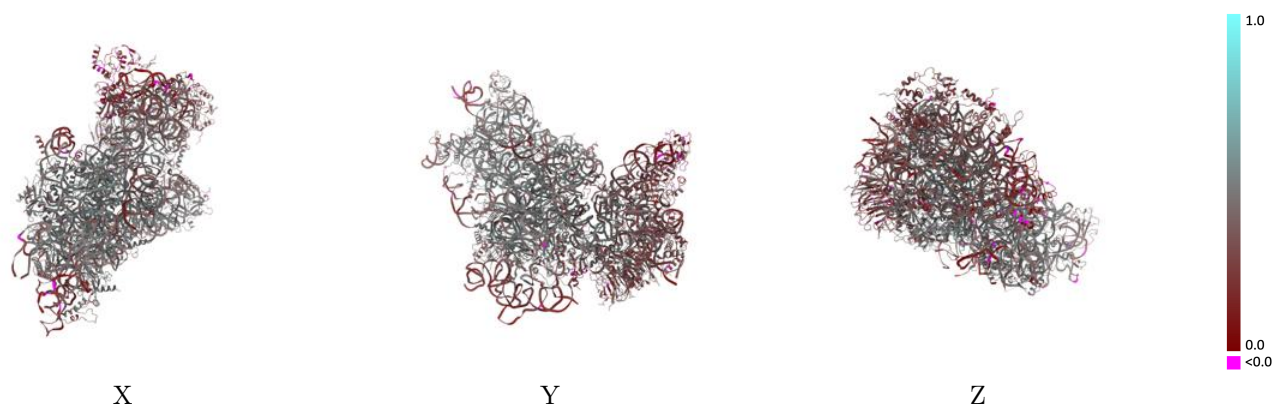
This section contains information regarding the fit between EMDB map EMD-25534 and PDB model 7SYN. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



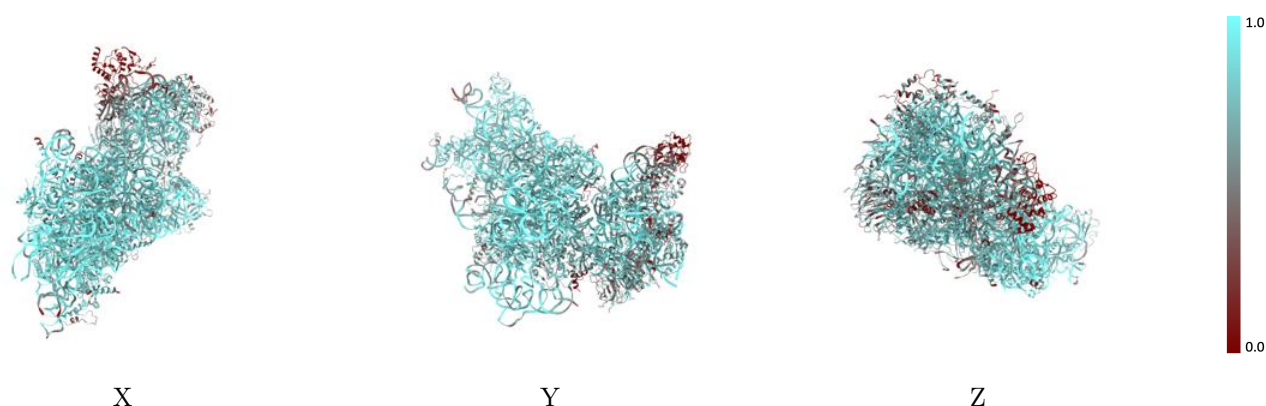
The images above show the 3D surface view of the map at the recommended contour level 0.0125 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



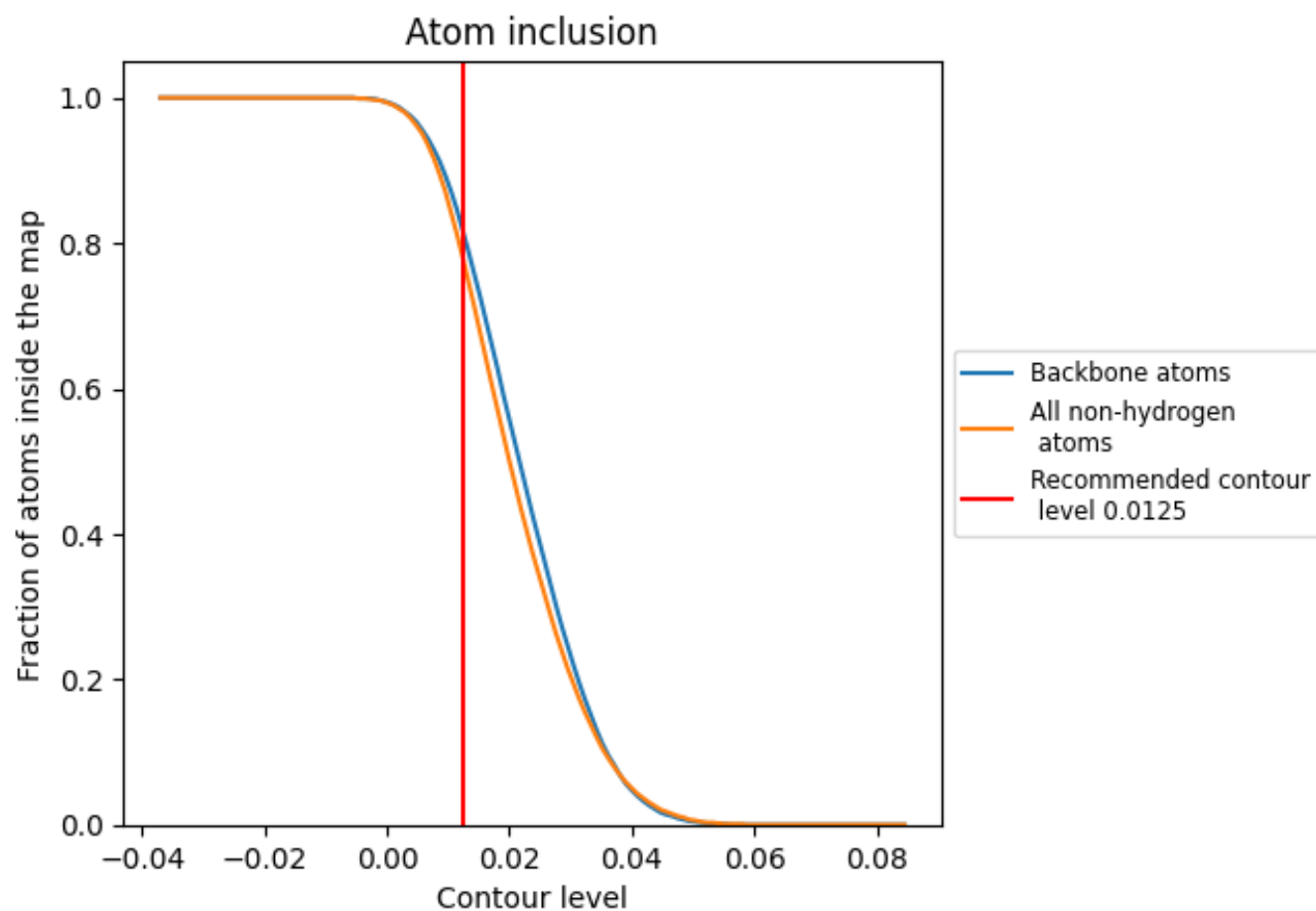
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0125).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 78% 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 (0.0125) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7760	 0.3950
2	 0.8700	 0.4010
B	 0.7340	 0.4260
C	 0.8050	 0.4390
D	 0.7830	 0.4650
E	 0.5650	 0.3600
F	 0.8560	 0.4930
G	 0.7030	 0.3870
H	 0.7730	 0.4030
I	 0.6840	 0.4110
J	 0.8080	 0.4580
K	 0.8380	 0.4720
L	 0.4440	 0.2890
M	 0.7950	 0.4900
N	 0.0270	 0.1870
O	 0.8290	 0.4730
P	 0.7960	 0.4330
Q	 0.5450	 0.2730
R	 0.7410	 0.4060
S	 0.5810	 0.3540
T	 0.5260	 0.3040
U	 0.7230	 0.3440
V	 0.4110	 0.3350
W	 0.7990	 0.4640
X	 0.8280	 0.4970
Y	 0.8170	 0.4780
Z	 0.8720	 0.4630
a	 0.4170	 0.3000
b	 0.8060	 0.4780
c	 0.7590	 0.4490
d	 0.5980	 0.4020
e	 0.6870	 0.4010
f	 0.5230	 0.3160
g	 0.0650	 0.1960
h	 0.5770	 0.3160



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Chain	Atom inclusion	Q-score
n	 0.7800	 0.4770
z	 0.7640	 0.2520