



Full wwPDB EM Validation Report ⓘ

Mar 27, 2026 – 05:37 AM UTC

PDB ID : 7OPE / pdb_00007ope
EMDB ID : EMD-13017
Title : RqcH DR variant bound to 50S-peptidyl-tRNA-RqcP RQC complex (rigid body refinement)
Authors : Crowe-McAuliffe, C.; Wilson, D.N.
Deposited on : 2021-05-31
Resolution : 3.20 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

The types of validation reports are described at

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

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

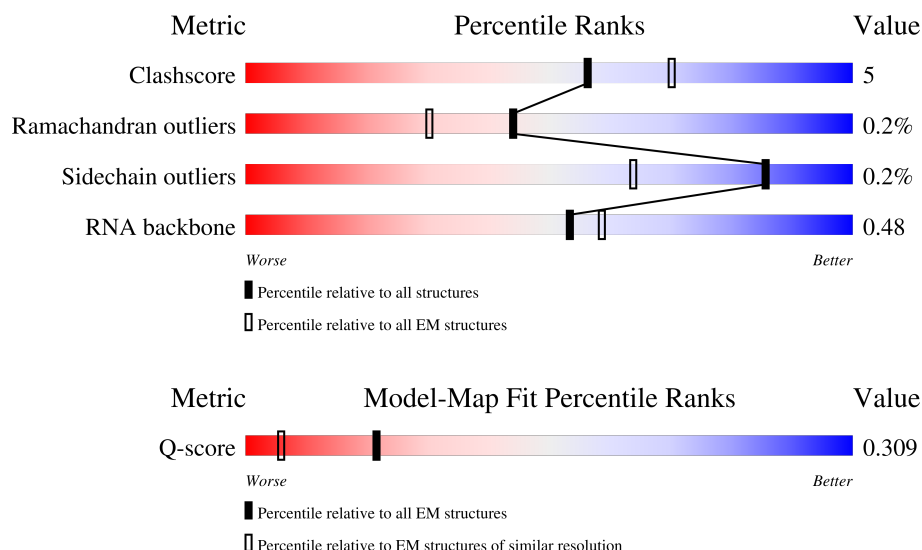
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.20 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.



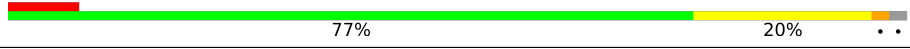
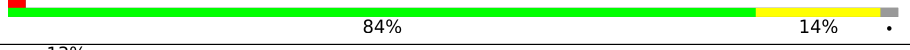
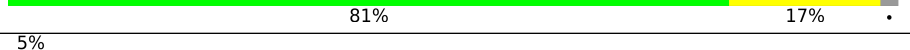
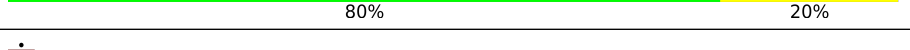
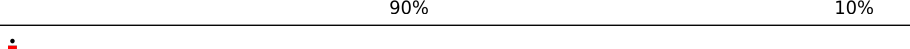
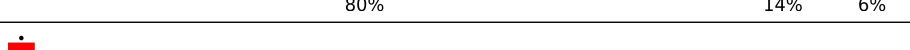
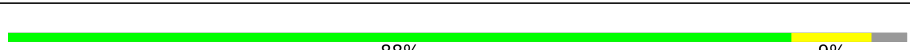
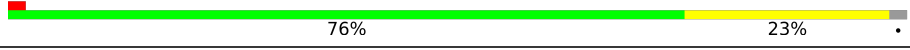
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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	A	2926	
2	B	119	
3	E	277	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	F	209	
5	G	207	
6	H	179	
7	I	179	
8	K	141	
9	L	166	
10	N	145	
11	O	122	
12	P	146	
13	Q	144	
14	R	120	
15	S	120	
16	T	115	
17	U	119	
18	V	102	
19	W	113	
20	X	95	
21	Y	103	
22	2	76	
23	a	94	
24	b	62	
25	c	66	
26	d	59	
27	f	59	
28	g	49	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	h	44	84% 16%
30	i	66	80% 17%
31	j	37	89% 11%
32	1	86	17% 92% 5%
33	0	599	50% 75% 12% 11%

2 Entry composition

There are 33 unique types of molecules in this entry. The entry contains 93862 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 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2814	Total	C	N	O	P	0	0
			60436	26962	11170	19491	2813		

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	112	Total	C	N	O	P	0	0
			2392	1068	435	778	111		

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	272	Total	C	N	O	S	0	0
			2083	1296	408	373	6		

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	206	Total	C	N	O	S	0	0
			1569	985	289	290	5		

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	205	Total	C	N	O	S	0	0
			1561	980	289	290	2		

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	H	176	Total	C	N	O	S	0	0
			1387	883	241	256	7		

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	I	175	Total	C	N	O	S	0	0
			1342	835	248	257	2		

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	K	132	Total	C	N	O	S	0	0
			974	612	172	184	6		

- Molecule 9 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L	113	Total	C	N	O	S	0	0
			886	559	152	174	1		

- Molecule 10 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	N	142	Total	C	N	O	S	0	0
			1124	710	206	203	5		

- Molecule 11 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	O	122	Total	C	N	O	S	0	0
			921	571	173	173	4		

- Molecule 12 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	P	146	Total	C	N	O	S	0	0
			1082	671	207	202	2		

- Molecule 13 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Q	135	Total	C	N	O	S	0	0
			1076	690	205	176	5		

- Molecule 14 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	R	119	Total	C	N	O	S	0	0
			954	583	186	181	4		

- Molecule 15 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	S	120	Total	C	N	O	S	0	0
			913	564	176	172	1		

- Molecule 16 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	T	115	Total	C	N	O	S	0	0
			945	600	185	159	1		

- Molecule 17 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	U	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 18 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	V	100	Total	C	N	O	0	0
			781	498	138	145		

- Molecule 19 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	W	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 20 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	X	90	Total	C	N	O	S	0	0
			725	452	134	136	3		

- Molecule 21 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Y	101	Total	C	N	O	S	0	0
			762	478	142	138	4		

- Molecule 22 is a RNA chain called tRNA-Ala-UGC.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	2	70	Total	C	N	O	P	0	0
			1496	666	271	489	70		

- Molecule 23 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	a	81	Total	C	N	O		0	0
			624	387	122	115			

- Molecule 24 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	b	58	Total	C	N	O	S	0	0
			444	275	92	75	2		

- Molecule 25 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	c	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

- Molecule 26 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	d	58	Total	C	N	O	S	0	0
			456	281	89	85	1		

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	f	53	Total	C	N	O	S	0	0
			418	258	84	69	7		

- Molecule 28 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	g	48	Total	C	N	O	S	0	0
			401	244	80	73	4		

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	h	44	Total	C	N	O	S	0	0
			368	222	89	55	2		

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	i	64	Total	C	N	O	S	0	0
			512	321	107	82	2		

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	j	37	Total	C	N	O	S	0	0
			297	186	60	46	5		

- Molecule 32 is a protein called Uncharacterized protein YabO.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	1	83	Total	C	N	O	S	0	0
			659	410	121	126	2		

- Molecule 33 is a protein called Rqc2 homolog RqcH.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	0	532	Total	C	N	O	S	0	0
			3962	2504	705	743	10		

There are 29 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	97	ALA	ASP	conflict	UNP A0A6M4JI41
0	98	ALA	ARG	conflict	UNP A0A6M4JI41
0	571	GLY	-	expression tag	UNP A0A6M4JI41
0	572	SER	-	expression tag	UNP A0A6M4JI41
0	573	GLY	-	expression tag	UNP A0A6M4JI41
0	574	GLY	-	expression tag	UNP A0A6M4JI41

Continued on next page...

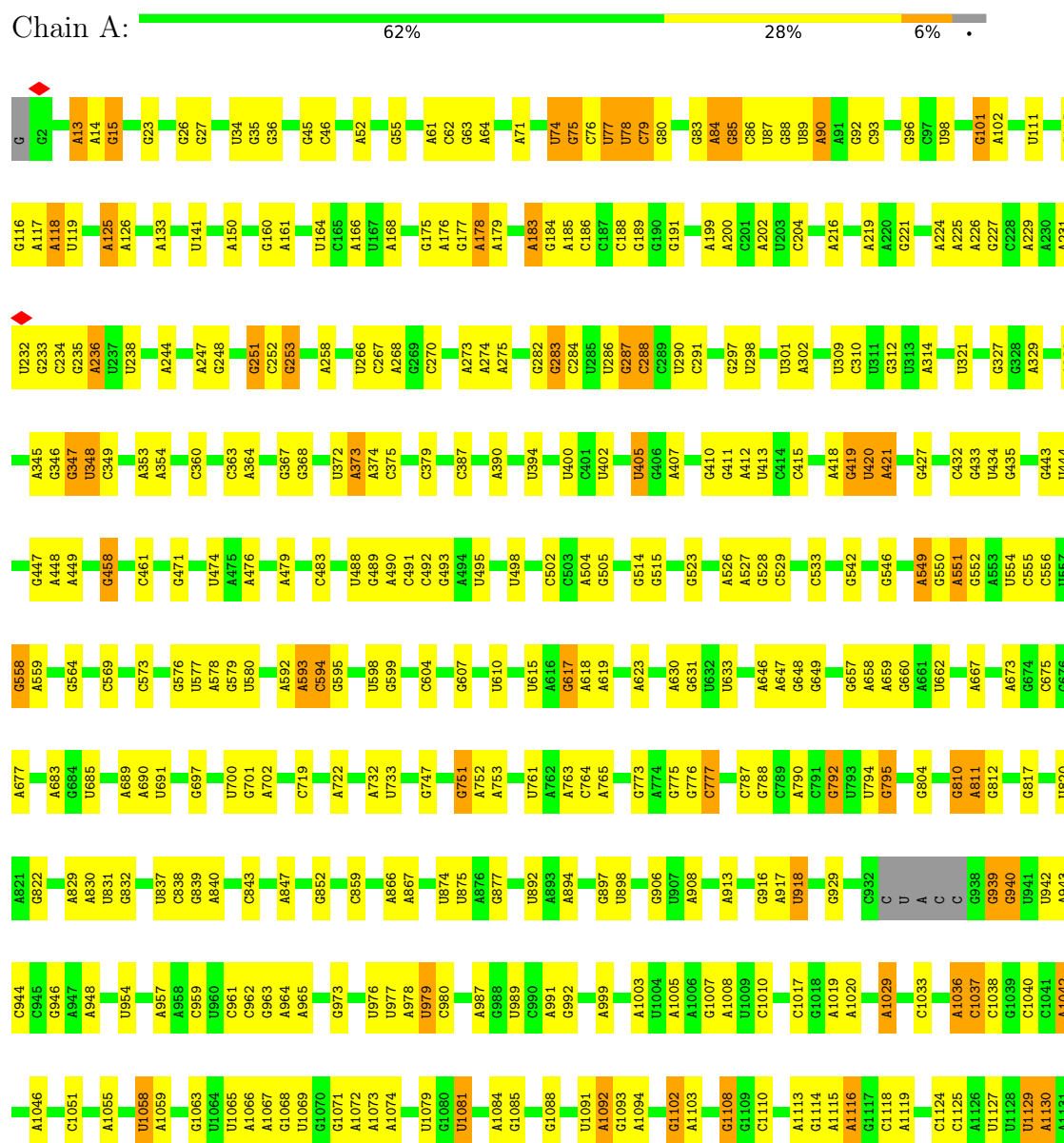
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
0	575	ASP	-	expression tag	UNP A0A6M4JI41
0	576	TYR	-	expression tag	UNP A0A6M4JI41
0	577	LYS	-	expression tag	UNP A0A6M4JI41
0	578	ASP	-	expression tag	UNP A0A6M4JI41
0	579	HIS	-	expression tag	UNP A0A6M4JI41
0	580	ASP	-	expression tag	UNP A0A6M4JI41
0	581	GLY	-	expression tag	UNP A0A6M4JI41
0	582	ASP	-	expression tag	UNP A0A6M4JI41
0	583	TYR	-	expression tag	UNP A0A6M4JI41
0	584	LYS	-	expression tag	UNP A0A6M4JI41
0	585	ASP	-	expression tag	UNP A0A6M4JI41
0	586	HIS	-	expression tag	UNP A0A6M4JI41
0	587	ASP	-	expression tag	UNP A0A6M4JI41
0	588	ILE	-	expression tag	UNP A0A6M4JI41
0	589	ASP	-	expression tag	UNP A0A6M4JI41
0	590	TYR	-	expression tag	UNP A0A6M4JI41
0	591	LYS	-	expression tag	UNP A0A6M4JI41
0	592	ASP	-	expression tag	UNP A0A6M4JI41
0	593	ASP	-	expression tag	UNP A0A6M4JI41
0	594	ASP	-	expression tag	UNP A0A6M4JI41
0	595	ASP	-	expression tag	UNP A0A6M4JI41
0	596	LYS	-	expression tag	UNP A0A6M4JI41
0	597	GLY	-	expression tag	UNP A0A6M4JI41

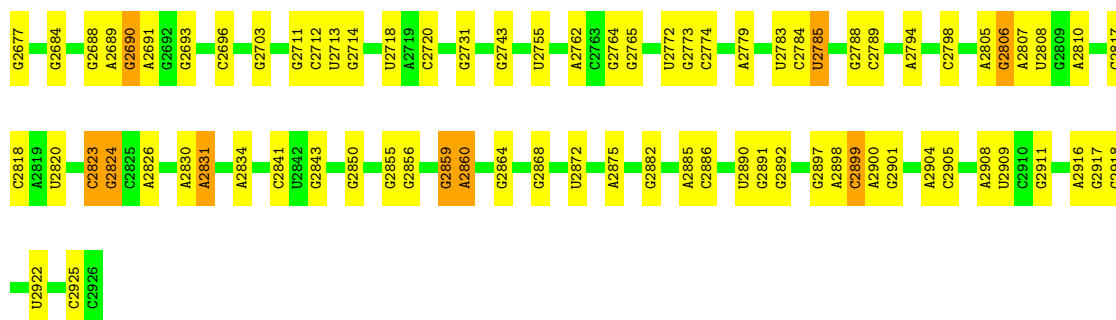
3 Residue-property plots

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: 23S rRNA

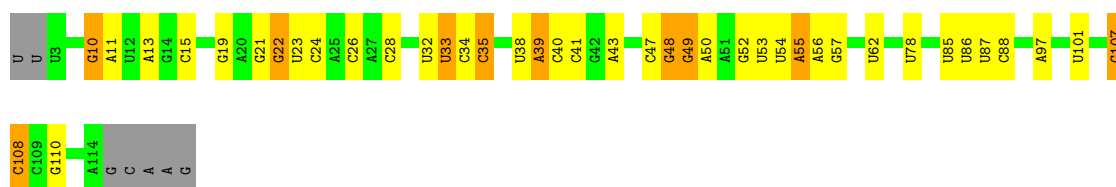


A2542	C2346	A2252	U2105	C1992	A1883	A1774	G1557	A1463	U1351	G1231	A1132
A2547	G2347	G2253	A2106	G1993	G1884	G1775	G1558	G1462	U1352	G1236	G1133
U2548	C2348	C2254	C2107	C1994	A1885	A1776	G1559	C1463	G1362	G1236	A1134
C2549	A2349	C2255	U2108	A1995	G1886	G1777	U1560	A1465	G1363	G1250	A1141
G2549	G2350	C1996	G2109	C1996	G1887	A1778	G1561	U1466	G1364	U1251	A1142
G2564	A2351	G2267	U2121	A1999	A1888	G1779	U1565	G1472	U1365	G1252	U1143
U2564	G2354	G2268	G2122	A2000	G1891	G1782	U1566	G1473	G1366	A1253	U1147
A2571	U2355	U2274	A2123	G2001	C1892	C1783	U1567	A1474	G1367	G1259	C1148
G2577	A2356	G2278	U2124	G2009	U1893	A1784	U1568	G1475	U1368	G1259	A1149
U2583	U2356	U2279	U2125	A2010	U1894	G1785	A1569	G1476	G1369	U1260	C1150
U2591	A2361	G2280	U2126	U2011	A1895	U1790	U1570	G1481	C1370	G1263	U1151
U2592	C2362	G2281	U2127	A2012	G1898	A1691	G1571	G1488	C1371	G1264	G1156
A2593	C2363	G2282	U2128	U2020	U1899	U1692	G1574	A1485	C1372	A1265	A1157
A2594	A2364	G2283	G2129	G2021	C1899	G1793	U1575	G1489	A1375	G1266	G1158
A2595	U2365	C2287	G2130	U2022	A1896	A1695	G1576	A1490	G1376	A1266	A1159
A2596	U2366	U2287	U2131	G1904	G1904	U1700	C1577	A1501	U1379	G1278	G1160
A2597	U2367	G2288	A	G1904	A1802	A1697	G	G1502	U1380	U1283	A1161
A2598	U2368	G2289	C	G1904	C1803	A1698	A	U1498	A1388	A1284	U1163
A2601	U2369	G2290	A	G1904	U1804	G1699	A	U1500	G1385	A1291	C1164
A2602	U2370	G2291	C	G1904	C1811	U1704	U	G1502	G1292	A1293	U1165
A2605	U2371	G2292	C	G1904	A1812	C1705	A	A1506	C1389	A1294	G1171
A2606	U2372	G2293	C	G1904	A1813	U1705	A	U1507	G1390	U1295	A1172
A2607	U2373	G2294	C	G1904	U1814	U1706	A	C1508	U1391	G1296	A1173
A2608	U2374	G2295	C	G1904	A1815	U1707	A	C1509	G1403	G1304	A1174
A2609	U2375	G2296	C	G1904	A1816	U1708	A	U1516	A1404	A1305	U1176
A2610	U2376	G2297	C	G1904	A1817	U1709	A	G1525	G1405	G1306	G1177
A2611	U2377	G2298	C	G1904	A1818	A1710	A	G1526	A1417	U1307	U1178
A2612	U2378	G2299	C	G1904	A1819	A1711	A	G1527	A1418	G1311	A1179
A2613	U2379	G2300	C	G1904	A1820	A1712	A	U1528	A1419	A1312	C1180
A2614	U2380	G2301	C	G1904	A1821	A1713	A	G1529	A1420	A1313	C1181
A2615	U2381	G2302	C	G1904	A1822	A1714	A	G1530	A1421	A1314	G1182
A2616	U2382	G2303	C	G1904	A1823	A1715	A	G1531	A1422	G1315	G1185
A2617	U2383	G2304	C	G1904	A1824	A1716	A	G1532	A1423	G1319	A1188
A2618	U2384	G2305	C	G1904	A1825	A1717	A	G1533	G1428	A1189	A1188
A2619	U2385	G2306	C	G1904	A1826	A1718	A	A1536	G1431	G1322	A1197
A2620	U2386	G2307	C	G1904	A1827	A1719	A	G1539	A1434	A1323	C1198
A2621	U2387	G2308	C	G1904	A1828	A1720	A	A1540	A1435	A1325	C1199
A2622	U2388	G2309	C	G1904	A1829	A1721	A	A1541	U1436	U1327	G1200
A2623	U2389	G2310	C	G1904	A1830	A1722	A	A1542	A1442	A1201	A1201
A2624	U2390	G2311	C	G1904	A1831	A1723	A	A1543	A1443	G1203	A1202
A2625	U2391	G2312	C	G1904	A1832	A1724	A	A1544	U1448	G1204	G1204
A2626	U2392	G2313	C	G1904	A1833	A1725	A	A1545	A1449	A1339	G1209
A2627	U2393	G2314	C	G1904	A1834	A1726	A	A1550	C1450	A1340	G1209
A2628	U2394	G2315	C	G1904	A1835	A1727	A	A1551	U1451	A1341	G1209
A2629	U2395	G2316	C	G1904	A1836	A1728	A	A1552	C1452	G1342	C1216
A2630	U2396	G2317	C	G1904	A1837	A1729	A	A1553	A1453	C1343	U
A2631	U2397	G2318	C	G1904	A1838	A1730	A	U	U1459	A1346	C
A2632	U2398	G2319	C	G1904	A1839	A1731	A	A1555	G1460	A1556	G1220
A2633	U2399	G2320	C	G1904	A1840	A1732	A	A1556	A1557	A1558	A1559
A2634	U2400	G2321	C	G1904	A1841	A1733	A	A1559	A1560	A1561	A1562
A2635	U2401	G2322	C	G1904	A1842	A1734	A	A1562	A1563	A1564	A1565
A2636	U2402	G2323	C	G1904	A1843	A1735	A	A1565	A1566	A1567	A1568
A2637	U2403	G2324	C	G1904	A1844	A1736	A	A1568	A1569	A1570	A1571
A2638	U2404	G2325	C	G1904	A1845	A1737	A	A1571	A1572	A1573	A1574
A2639	U2405	G2326	C	G1904	A1846	A1738	A	A1574	A1575	A1576	A1577
A2640	U2406	G2327	C	G1904	A1847	A1739	A	A1577	A1578	A1579	A1580
A2641	U2407	G2328	C	G1904	A1848	A1740	A	A1581	A1582	A1583	A1584
A2642	U2408	G2329	C	G1904	A1849	A1741	A	A1584	A1585	A1586	A1587
A2643	U2409	G2330	C	G1904	A1850	A1742	A	A1587	A1588	A1589	A1590
A2644	U2410	G2331	C	G1904	A1851	A1743	A	A1590	A1591	A1592	A1593
A2645	U2411	G2332	C	G1904	A1852	A1744	A	A1593	A1594	A1595	A1596
A2646	U2412	G2333	C	G1904	A1853	A1745	A	A1596	A1597	A1598	A1599
A2647	U2413	G2334	C	G1904	A1854	A1746	A	A1599	A1600	A1601	A1602
A2648	U2414	G2335	C	G1904	A1855	A1747	A	A1602	A1603	A1604	A1605
A2649	U2415	G2336	C	G1904	A1856	A1748	A	A1605	A1606	A1607	A1608
A2650	U2416	G2337	C	G1904	A1857	A1749	A	A1608	A1609	A1610	A1611
A2651	U2417	G2338	C	G1904	A1858	A1750	A	A1611	A1612	A1613	A1614
A2652	U2418	G2339	C	G1904	A1859	A1751	A	A1614	A1615	A1616	A1617
A2653	U2419	G2340	C	G1904	A1860	A1752	A	A1617	A1618	A1619	A1620
A2654	U2420	G2341	C	G1904	A1861	A1753	A	A1620	A1621	A1622	A1623
A2655	U2421	G2342	C	G1904	A1862	A1754	A	A1623	A1624	A1625	A1626
A2656	U2422	G2343	C	G1904	A1863	A1755	A	A1626	A1627	A1628	A1629
A2657	U2423	G2344	C	G1904	A1864	A1756	A	A1629	A1630	A1631	A1632
A2658	U2424	G2345	C	G1904	A1865	A1757	A	A1632	A1633	A1634	A1635
A2659	U2425	G2346	C	G1904	A1866	A1758	A	A1635	A1636	A1637	A1638
A2660	U2426	G2347	C	G1904	A1867	A1759	A	A1638	A1639	A1640	A1641
A2661	U2427	G2348	C	G1904	A1868	A1760	A	A1641	A1642	A1643	A1644
A2662	U2428	G2349	C	G1904	A1869	A1761	A	A1644	A1645	A1646	A1647
A2663	U2429	G2350	C	G1904	A1870	A1762	A	A1647	A1648	A1649	A1650
A2664	U2430	G2351	C	G1904	A1871	A1763	A	A1650	A1651	A1652	A1653
A2665	U2431	G2352	C	G1904	A1872	A1764	A	A1653	A1654	A1655	A1656
A2666	U2432	G2353	C	G1904	A1873	A1765	A	A1656	A1657	A1658	A1659
A2667	U2433	G2354	C	G1904	A1874	A1766	A	A1659	A1660	A1661	A1662
A2668	U2434	G2355	C	G1904	A1875	A1767	A	A1662	A1663	A1664	A1665
A2669	U2435	G2356	C	G1904	A1876	A1768	A	A1665	A1666	A1667	A1668
A2670	U2436	G2357	C	G1904	A1877	A1769	A	A1668	A1669	A1670	A1671
A2671	U2437	G2358	C	G1904	A1878	A1770	A	A1671	A1672	A1673	A1674
A2672	U2438	G2359	C	G1904	A1879	A1771	A	A1674	A1675	A1676	A1677
A2673	U2439	G2360	C	G1904	A1880	A1772	A	A1677	A1678	A1679	A1680
A2674	U2440	G2361	C	G1904	A1881	A1773	A	A1680	A1681	A1682	A1683
A2675	U2441	G2362	C	G1904	A1882	A1774	A	A1683	A1684	A1685	A1686
A2676	U2442	G2363	C	G1904	A1883	A1775	A	A1686	A1687	A1688	A1689
A2677	U2443	G2364	C	G1904	A1884	A1776	A	A1689	A1690	A1691	A1692
A2678	U2444	G2365	C	G1904	A1885	A1777	A	A1692	A1693	A1694	A1695
A2679	U2445	G2366	C	G1904	A1886	A1778	A	A1695	A1696	A1697	A1698
A2680	U2446	G2367	C	G1904	A1887	A1779	A	A1698	A1699	A1700	A1701
A2681	U2447	G2368	C	G1904	A1888	A1780	A	A1701	A1702	A1703	A1704
A2682	U2448	G2369	C	G1904	A1889	A1781	A	A1704	A1705	A1706	A1707
A2683	U2449	G2370	C	G1904	A1890	A1782	A	A1707	A1708	A1709	A1710
A2684	U2450	G2371	C	G1904	A1891	A1783	A	A1710	A1711	A1712	A1713
A2685	U2451	G2372	C	G1904	A1892	A1784	A	A1713	A1714	A1715	A1716
A2686	U2452	G2373	C	G1904	A1893	A1785	A	A1716	A1717	A1718	A1719
A2687	U2453	G2374	C	G1904	A1894	A1786	A	A1719	A1720	A1721	A1722
A2688	U2454	G2375	C	G1904	A1895	A1787	A	A1722	A1723	A1724	A1725
A2689	U2455	G2376	C	G1904	A1896	A1788	A	A1725	A1726	A1727	A1728
A2690	U2456	G2377	C	G1904	A1897	A1789	A	A1728	A1729	A1730	A1731
A2691	U2457	G2378	C	G1904	A1898	A1790	A	A1731	A1732	A1733	A1734
A2692	U2458	G2379	C	G1904	A1899	A1791	A	A1734	A1735	A1736	A1737
A2693	U2459	G2380	C	G1904	A1900	A1792	A	A1737	A1738	A1739	A1740
A2694	U2460	G2381	C	G1904	A1901	A1793	A	A1740	A1741	A1742	A1743
A2695	U2461	G2382	C	G1904	A1902	A1794	A	A1743	A1744	A1745	A1746
A2696	U2462	G2383	C	G1904	A1903	A1795	A	A1746	A1747	A1748	A1749
A2697	U2463	G2384	C	G1904	A1904	A1796	A	A1749	A17		



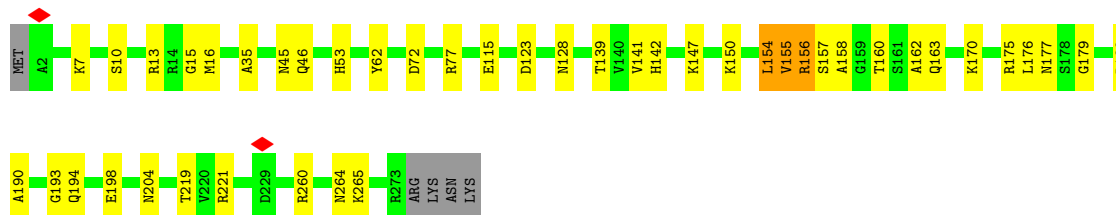
• Molecule 2: 5S rRNA

Chain B: 60% 26% 8% 6%



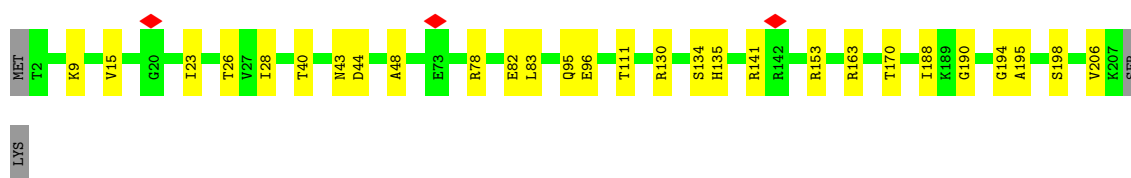
• Molecule 3: 50S ribosomal protein L2

Chain E: 82% 15% 3% 2%



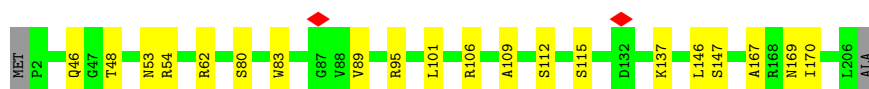
• Molecule 4: 50S ribosomal protein L3

Chain F: 85% 13% 2% 1%

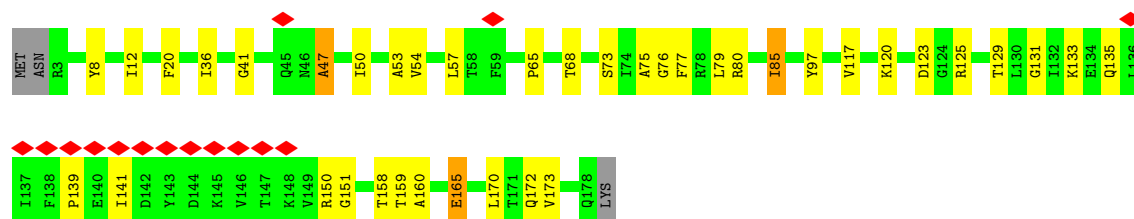
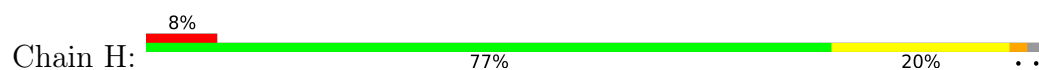


• Molecule 5: 50S ribosomal protein L4

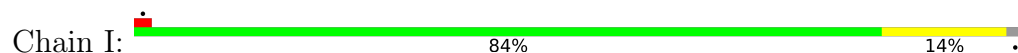
Chain G: 89% 10% 1% 0%



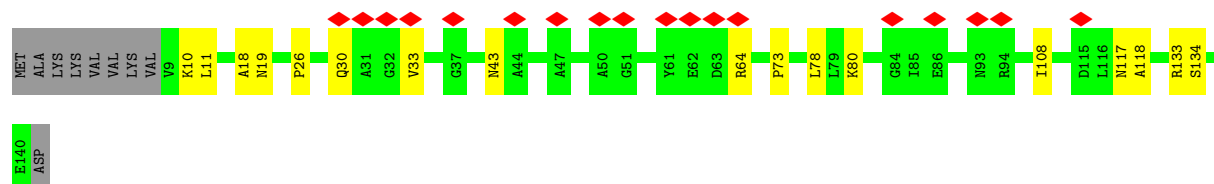
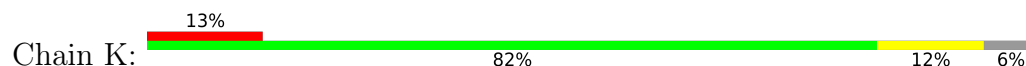
• Molecule 6: 50S ribosomal protein L5



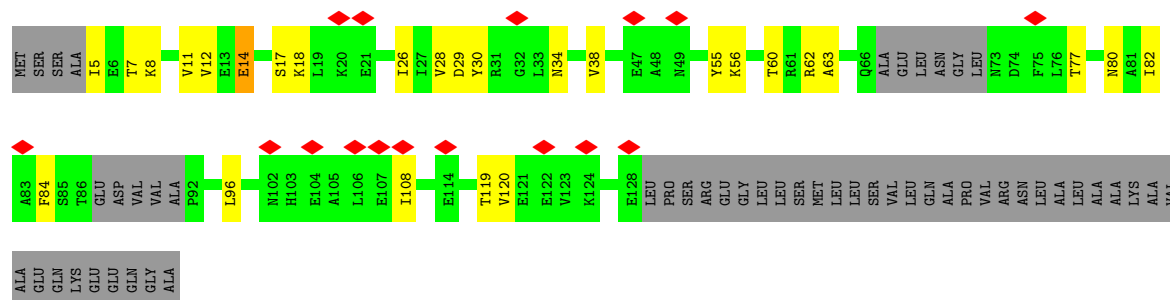
- Molecule 7: 50S ribosomal protein L6



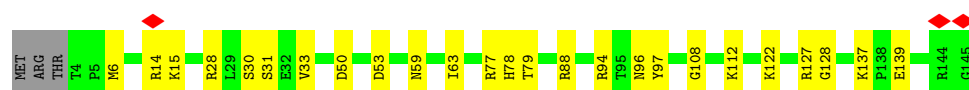
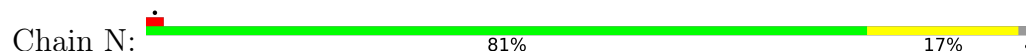
- Molecule 8: 50S ribosomal protein L11



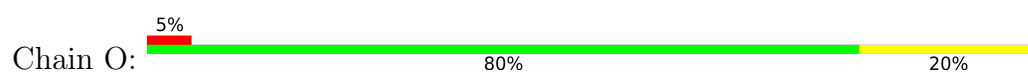
- Molecule 9: 50S ribosomal protein L10



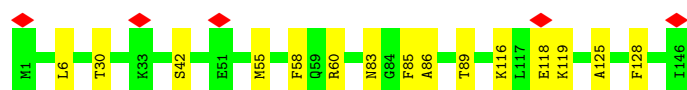
- Molecule 10: 50S ribosomal protein L13



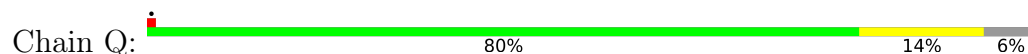
- Molecule 11: 50S ribosomal protein L14



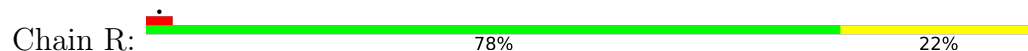
- Molecule 12: 50S ribosomal protein L15



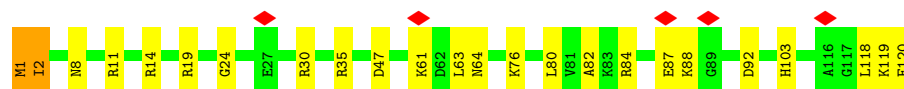
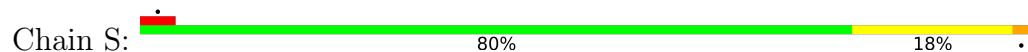
- Molecule 13: 50S ribosomal protein L16



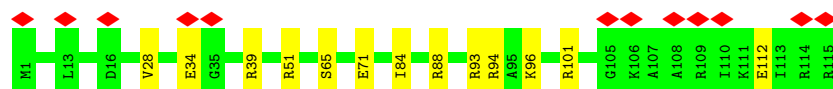
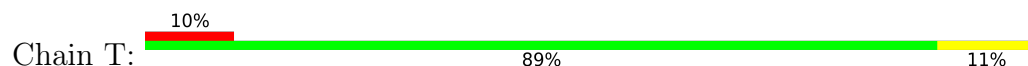
- Molecule 14: 50S ribosomal protein L17



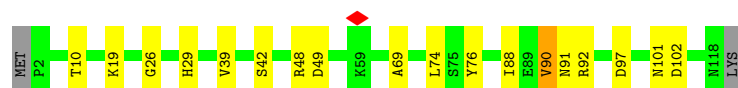
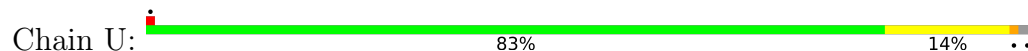
- Molecule 15: 50S ribosomal protein L18



- Molecule 16: 50S ribosomal protein L19



- Molecule 17: 50S ribosomal protein L20



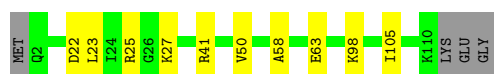
- Molecule 18: 50S ribosomal protein L21

Chain V:  88% 10%



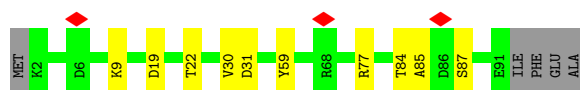
- Molecule 19: 50S ribosomal protein L22

Chain W:  88% 9%



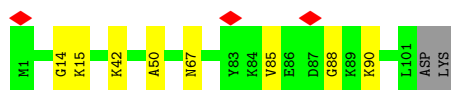
- Molecule 20: 50S ribosomal protein L23

Chain X:  84% 11% 5%



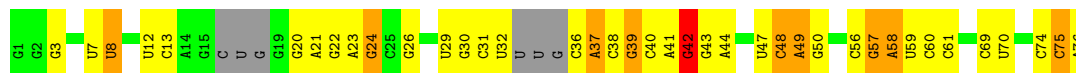
- Molecule 21: 50S ribosomal protein L24

Chain Y:  90% 8%



- Molecule 22: tRNA-Ala-UGC

Chain 2:  41% 38% 12% 8%



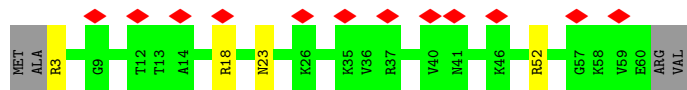
- Molecule 23: 50S ribosomal protein L27

Chain a:  72% 14% 14%



- Molecule 24: 50S ribosomal protein L28

Chain b:  19% 87% 6% 6%



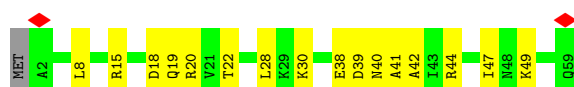
- Molecule 25: 50S ribosomal protein L29

Chain c:  76% 23%



- Molecule 26: 50S ribosomal protein L30

Chain d:  71% 27%



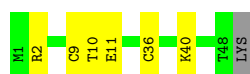
- Molecule 27: 50S ribosomal protein L32

Chain f:  68% 22% 10%



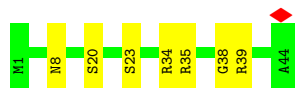
- Molecule 28: 50S ribosomal protein L33 1

Chain g:  86% 12%



- Molecule 29: 50S ribosomal protein L34

Chain h:  84% 16%



- Molecule 30: 50S ribosomal protein L35

Chain i:  80% 17%



- Molecule 31: 50S ribosomal protein L36

Chain j:  89% 11%

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	16700	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 ($e^-/\text{\AA}^2$)	34.8	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.033	Depositor
Minimum map value	-0.012	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.007	Depositor
Map size (Å)	344.4, 344.4, 344.4	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82, 0.82, 0.82	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	A	0.56	4/67693 (0.0%)	0.50	20/105598 (0.0%)
2	B	0.51	0/2675	0.65	2/4170 (0.0%)
3	E	0.69	0/2120	0.55	0/2845
4	F	0.70	0/1591	0.54	0/2132
5	G	0.67	0/1580	0.53	0/2132
6	H	1.01	2/1406 (0.1%)	1.45	4/1888 (0.2%)
7	I	0.49	0/1360	0.48	0/1832
8	K	0.26	0/988	0.47	0/1336
9	L	0.26	0/892	0.49	0/1196
10	N	0.70	0/1147	0.50	0/1542
11	O	0.64	0/928	0.57	0/1245
12	P	0.64	0/1094	0.53	0/1457
13	Q	0.67	0/1099	0.53	0/1468
14	R	0.69	1/961 (0.1%)	0.58	0/1284
15	S	0.54	0/922	0.65	2/1236 (0.2%)
16	T	0.63	0/958	0.57	0/1279
17	U	0.74	0/952	0.58	0/1266
18	V	0.69	0/792	0.53	0/1063
19	W	0.68	0/851	0.55	0/1146
20	X	0.62	0/731	0.51	0/974
21	Y	0.58	0/772	0.60	2/1032 (0.2%)
22	2	0.54	0/1669	0.89	11/2596 (0.4%)
23	a	0.70	0/632	0.57	0/839
24	b	0.45	0/448	0.54	0/596
25	c	0.54	0/531	0.59	0/707
26	d	0.64	0/458	0.56	0/613
27	f	0.64	0/425	0.52	0/563
28	g	0.60	0/406	0.54	0/540
29	h	0.74	0/371	0.51	0/483
30	i	0.67	0/519	0.50	0/680
31	j	0.70	0/300	0.50	0/393
32	1	0.82	1/662 (0.2%)	1.30	0/882
33	0	0.37	1/4031 (0.0%)	0.67	16/5456 (0.3%)
All	All	0.58	9/101964 (0.0%)	0.56	57/152469 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	15
2	B	0	4
3	E	0	1
6	H	0	1
8	K	0	1
13	Q	0	1
18	V	0	1
22	2	0	7
All	All	0	31

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	1	58	VAL	C-N	9.52	1.46	1.33
1	A	1940	U	C1'-N1	7.12	1.59	1.48
6	H	170	LEU	C-O	-6.63	1.16	1.24
1	A	1220	G	P-OP2	6.26	1.61	1.49
1	A	1220	G	P-OP1	6.25	1.61	1.49
33	0	491	PRO	CG-CD	5.70	1.70	1.50
1	A	1939	G	O3'-P	-5.69	1.52	1.61
6	H	47	ALA	C-O	-5.46	1.17	1.24
14	R	119	LEU	CA-CB	-5.10	1.44	1.53

All (57) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	0	490	ILE	C-N-CD	-16.66	56.69	125.00
1	A	1939	G	O3'-P-O5'	-12.84	84.73	104.00
1	A	1947	A	C3'-C2'-O2'	-10.61	98.69	114.60
1	A	1947	A	C2'-C3'-O3'	10.30	124.95	109.50
22	2	48	C	OP1-P-O3'	-10.09	77.72	108.00
22	2	49	A	O5'-P-OP2	-10.02	77.94	108.00
1	A	1220	G	P-O5'-C5'	-9.36	106.87	120.90
22	2	49	A	OP1-P-OP2	9.12	146.97	119.60
22	2	49	A	O5'-P-OP1	-9.01	80.96	108.00
1	A	2334	U	O4'-C1'-N1	8.18	120.47	108.20
33	0	544	PRO	N-CA-CB	8.17	110.46	103.35
22	2	48	C	OP2-P-O3'	-8.02	83.93	108.00

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	0	448	PRO	N-CA-CB	8.01	110.30	103.17
33	0	491	PRO	N-CA-CB	7.40	111.02	103.25
33	0	527	PRO	N-CA-CB	7.22	110.54	102.67
1	A	2332	G	C4'-C3'-C2'	-7.12	95.48	102.60
33	0	539	PRO	N-CA-CB	6.60	110.26	103.00
33	0	559	PRO	N-CA-CB	6.56	110.14	103.25
1	A	2343	A	C5'-C4'-C3'	-6.54	106.19	116.00
1	A	2343	A	C5'-C4'-O4'	6.50	119.56	109.80
33	0	502	PRO	N-CA-CB	6.38	109.95	103.25
1	A	2330	A	O3'-P-O5'	-6.37	94.45	104.00
1	A	2335	U	O4'-C1'-N1	6.27	117.61	108.20
1	A	1866	C	C5'-C4'-C3'	-6.14	106.80	116.00
1	A	2342	C	C2'-C3'-O3'	-5.95	104.78	113.70
1	A	2345	U	C4'-C3'-C2'	-5.86	96.74	102.60
33	0	526	VAL	C-N-CD	-5.82	101.13	125.00
22	2	26	G	C4'-C3'-C2'	-5.81	96.79	102.60
21	Y	50	ALA	CA-C-N	5.73	135.79	121.80
21	Y	50	ALA	C-N-CA	5.73	135.79	121.80
22	2	42	G	O4'-C4'-C3'	5.60	109.60	104.00
33	0	539	PRO	CA-N-CD	-5.59	104.18	112.00
33	0	491	PRO	CA-N-CD	-5.58	104.19	112.00
33	0	448	PRO	CA-N-CD	-5.58	104.19	112.00
33	0	502	PRO	CA-N-CD	-5.58	104.19	112.00
33	0	527	PRO	CA-N-CD	-5.57	104.20	112.00
33	0	544	PRO	CA-N-CD	-5.57	104.20	112.00
33	0	559	PRO	CA-N-CD	-5.57	104.20	112.00
1	A	1947	A	C4'-C3'-O3'	-5.55	101.07	109.40
2	B	55	A	C5'-C4'-C3'	-5.42	107.88	116.00
1	A	2335	U	C5'-C4'-C3'	-5.37	107.14	115.20
2	B	43	A	C4'-C3'-C2'	-5.37	97.23	102.60
22	2	24	G	C4'-C3'-C2'	-5.37	97.23	102.60
22	2	42	G	O3'-P-O5'	-5.35	95.97	104.00
6	H	20	PHE	CA-CB-CG	-5.32	108.48	113.80
1	A	2344	U	C4'-C3'-O3'	5.31	120.97	113.00
22	2	13	C	C5'-C4'-C3'	-5.31	108.04	116.00
6	H	165	GLU	N-CA-C	5.18	116.93	111.28
1	A	2334	U	N1-C1'-C2'	-5.17	106.24	114.00
1	A	2333	G	C5'-C4'-C3'	-5.16	108.25	116.00
15	S	1	MET	CA-C-N	5.10	131.14	121.97
15	S	1	MET	C-N-CA	5.10	131.14	121.97
1	A	2340	A	C4'-C3'-C2'	-5.08	97.52	102.60
6	H	53	ALA	CA-C-N	5.07	127.40	120.46

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	H	53	ALA	C-N-CA	5.07	127.40	120.46
22	2	12	U	O3'-P-O5'	-5.04	96.45	104.00
1	A	1948	A	C4'-C3'-O3'	-5.03	105.46	113.00

There are no chirality outliers.

All (31) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
22	2	23	A	Sidechain
22	2	24	G	Sidechain
22	2	39	G	Sidechain
22	2	40	C	Sidechain
22	2	41	A	Sidechain
22	2	42	G	Sidechain
22	2	57	G	Sidechain
1	A	1866	C	Sidechain
1	A	1952	U	Sidechain
1	A	1953	C	Sidechain
1	A	1955	U	Sidechain
1	A	1957	A	Sidechain
1	A	1958	G	Sidechain
1	A	2328	G	Sidechain
1	A	2331	U	Sidechain
1	A	2333	G	Sidechain
1	A	2334	U	Sidechain
1	A	2335	U	Sidechain
1	A	2336	G	Sidechain
1	A	2338	A	Sidechain
1	A	2344	U	Sidechain
1	A	2345	U	Sidechain
2	B	28	C	Sidechain
2	B	39	A	Sidechain
2	B	41	C	Sidechain
2	B	52	G	Sidechain
3	E	154	LEU	Peptide
6	H	97	TYR	Sidechain
8	K	19	ASN	Peptide
13	Q	60	ARG	Peptide
18	V	50	ASN	Peptide

5.2 Too-close contacts ⓘ

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	A	60436	0	30414	369	0
2	B	2392	0	1213	10	0
3	E	2083	0	2168	29	0
4	F	1569	0	1637	19	0
5	G	1561	0	1647	15	0
6	H	1387	0	1448	73	0
7	I	1342	0	1388	18	0
8	K	974	0	1011	14	0
9	L	886	0	920	17	0
10	N	1124	0	1162	18	0
11	O	921	0	977	21	0
12	P	1082	0	1132	11	0
13	Q	1076	0	1145	14	0
14	R	954	0	983	21	0
15	S	913	0	947	26	0
16	T	945	0	1020	9	0
17	U	940	0	1005	16	0
18	V	781	0	821	9	0
19	W	842	0	899	6	0
20	X	725	0	770	8	0
21	Y	762	0	821	6	0
22	2	1496	0	759	43	0
23	a	624	0	639	10	0
24	b	444	0	487	4	0
25	c	530	0	568	10	0
26	d	456	0	491	14	0
27	f	418	0	435	10	0
28	g	401	0	413	4	0
29	h	368	0	410	5	0
30	i	512	0	564	10	0
31	j	297	0	342	3	0
32	1	659	0	705	2	0
33	0	3962	0	3687	95	0
All	All	93862	0	63028	728	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 5.

All (728) 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:A:2340:A:C2	6:H:79:LEU:HD11	1.55	1.39
1:A:2334:U:O4	6:H:151:GLY:HA3	1.38	1.22
33:0:537:LYS:C	33:0:539:PRO:HD2	1.65	1.21
1:A:2334:U:C4	6:H:151:GLY:HA3	1.76	1.19
6:H:125:ARG:HG3	15:S:1:MET:HB2	1.27	1.14
1:A:2340:A:N3	6:H:79:LEU:HD11	1.64	1.10
22:2:44:A:OP1	33:0:286:ARG:NH2	1.86	1.08
1:A:2334:U:O4	6:H:151:GLY:CA	1.99	1.08
22:2:31:C:C2	33:0:125:ARG:CZ	2.36	1.08
1:A:2340:A:C2	6:H:79:LEU:CD1	2.38	1.05
33:0:414:ALA:HA	33:0:465:LYS:CB	1.87	1.05
33:0:523:SER:O	33:0:559:PRO:HD2	1.55	1.04
33:0:410:GLN:HB3	33:0:465:LYS:O	1.58	1.03
33:0:501:GLU:N	33:0:502:PRO:HD2	1.75	1.02
1:A:2340:A:N3	6:H:79:LEU:CD1	2.24	1.00
6:H:160:ALA:O	15:S:1:MET:HA	1.62	1.00
22:2:44:A:C5'	33:0:286:ARG:HH21	1.76	0.97
1:A:312:G:N2	1:A:405:U:C5	2.33	0.95
11:O:103:ALA:HA	11:O:122:ILE:OXT	1.66	0.95
6:H:125:ARG:HG3	15:S:1:MET:CB	1.95	0.95
1:A:2337:G:C2	6:H:77:PHE:CE1	2.56	0.94
33:0:501:GLU:H	33:0:502:PRO:HD2	1.31	0.93
33:0:413:SER:HB2	33:0:517:PHE:CB	1.99	0.93
22:2:31:C:O2	33:0:125:ARG:NH1	2.03	0.92
1:A:327:G:H1	1:A:400:U:H3	1.18	0.92
33:0:515:ALA:HB1	33:0:559:PRO:HD3	1.49	0.91
33:0:53:HIS:CD2	33:0:282:ALA:HA	2.04	0.91
6:H:159:THR:HG22	15:S:2:ILE:HG21	1.50	0.91
22:2:44:A:H5''	33:0:286:ARG:HH21	1.34	0.90
1:A:2340:A:H2	6:H:79:LEU:HD11	1.28	0.89
1:A:1152:G:HO2'	9:L:30:TYR:HH	1.16	0.89
22:2:36:C:OP1	22:2:37:A:N6	2.06	0.89
33:0:501:GLU:H	33:0:502:PRO:CD	1.86	0.88
1:A:1159:U:OP1	7:I:2:SER:OG	1.90	0.87
6:H:160:ALA:O	15:S:1:MET:CA	2.23	0.87
33:0:501:GLU:N	33:0:502:PRO:CD	2.36	0.87
1:A:2337:G:C5	6:H:77:PHE:CZ	2.65	0.84
33:0:409:GLN:CD	33:0:492:GLY:HA2	2.02	0.84
1:A:810:G:O2'	1:A:811:A:O5'	1.95	0.83
1:A:2339:A:H2	6:H:76:GLY:HA3	1.43	0.83

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:0:447:ASN:H	33:0:448:PRO:HD2	1.43	0.82
1:A:1216:C:O2	1:A:1220:G:N2	2.12	0.82
6:H:160:ALA:O	15:S:1:MET:N	2.12	0.82
1:A:2341:U:H5'	6:H:85:ILE:HD11	1.60	0.82
33:0:537:LYS:C	33:0:539:PRO:CD	2.50	0.82
1:A:1790:U:O2'	1:A:1791:A:O4'	1.98	0.80
22:2:31:C:C2	33:0:125:ARG:NH2	2.49	0.80
6:H:73:SER:HB3	22:2:56:C:C1'	2.12	0.80
1:A:2341:U:H5'	6:H:85:ILE:CD1	2.13	0.79
33:0:413:SER:CB	33:0:517:PHE:CB	2.61	0.79
6:H:73:SER:HB2	22:2:56:C:O4'	1.81	0.79
14:R:99:THR:C	14:R:120:VAL:OXT	2.26	0.78
1:A:2496:C:OP1	31:j:8:LYS:NZ	2.17	0.78
1:A:2009:G:O2'	1:A:2011:U:OP2	2.02	0.78
22:2:31:C:C2	33:0:125:ARG:NH1	2.50	0.77
1:A:1263:G:OP2	18:V:89:ARG:NH1	2.17	0.77
30:i:32:LEU:O	30:i:36:LYS:NZ	2.17	0.77
6:H:125:ARG:CG	15:S:1:MET:HB2	2.12	0.77
1:A:84:A:N6	1:A:101:G:O2'	2.18	0.77
6:H:73:SER:CB	22:2:56:C:O4'	2.32	0.77
1:A:2337:G:C6	6:H:77:PHE:CZ	2.73	0.77
1:A:2806:G:OP2	1:A:2810:A:O2'	2.02	0.77
27:f:32:SER:OG	27:f:46:CYS:SG	2.43	0.77
22:2:31:C:H1'	33:0:125:ARG:HD2	1.65	0.76
1:A:363:C:OP2	5:G:137:LYS:NZ	2.18	0.76
1:A:917:A:OP1	13:Q:6:ARG:NH2	2.18	0.76
22:2:44:A:P	33:0:286:ARG:NH2	2.59	0.76
6:H:125:ARG:CG	15:S:1:MET:CB	2.63	0.76
22:2:36:C:OP1	22:2:37:A:C6	2.39	0.76
18:V:68:ALA:O	18:V:89:ARG:NE	2.17	0.76
1:A:697:G:OP1	30:i:19:SER:OG	2.03	0.75
10:N:88:ARG:NH1	10:N:97:TYR:OH	2.19	0.75
14:R:94:ARG:NH1	14:R:120:VAL:O	2.19	0.75
1:A:364:A:N3	5:G:169:ASN:ND2	2.34	0.75
6:H:75:ALA:HB2	22:2:56:C:O2'	1.87	0.75
6:H:159:THR:HG22	15:S:2:ILE:CG2	2.15	0.75
20:X:9:LYS:O	25:c:29:ARG:NH1	2.20	0.75
1:A:840:A:OP2	1:A:2100:A:O2'	2.04	0.75
1:A:2339:A:C2	6:H:76:GLY:HA3	2.23	0.74
1:A:817:G:OP1	29:h:8:ASN:ND2	2.20	0.74
1:A:898:U:OP1	26:d:49:LYS:NZ	2.20	0.74

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:26:THR:OG1	4:F:190:GLY:O	2.06	0.74
22:2:44:A:C5'	33:0:286:ARG:NH2	2.50	0.74
33:0:538:LYS:N	33:0:539:PRO:CD	2.49	0.74
33:0:537:LYS:O	33:0:539:PRO:HD2	1.87	0.74
1:A:2127:U:O2'	1:A:2128:U:OP1	2.06	0.74
10:N:15:LYS:N	10:N:53:ASP:OD1	2.21	0.74
14:R:46:LYS:O	14:R:49:THR:OG1	2.05	0.73
1:A:1114:G:N2	1:A:1141:A:O2'	2.21	0.73
33:0:523:SER:O	33:0:559:PRO:CD	2.35	0.73
1:A:2532:A:O2'	1:A:2534:G:OP2	2.06	0.73
20:X:19:ASP:O	20:X:22:THR:OG1	2.07	0.73
13:Q:25:THR:OG1	13:Q:26:GLU:OE1	2.05	0.73
33:0:53:HIS:O	33:0:57:SER:N	2.22	0.73
1:A:458:G:OP2	1:A:2435:C:O2'	2.06	0.73
1:A:2372:U:HO2'	1:A:2402:A:HO2'	1.33	0.72
1:A:2498:A:O2'	13:Q:56:ARG:NH1	2.22	0.72
1:A:2025:C:OP1	11:O:31:LYS:NZ	2.22	0.72
1:A:2339:A:H2'	6:H:77:PHE:CE2	2.25	0.72
1:A:1542:A:O2'	1:A:1544:C:N4	2.23	0.72
33:0:53:HIS:NE2	33:0:282:ALA:HA	2.03	0.72
1:A:1695:A:HO2'	1:A:1696:G:P	2.12	0.71
1:A:1983:G:O2'	1:A:1985:U:O4	2.08	0.71
1:A:918:U:OP1	13:Q:5:LYS:N	2.22	0.71
1:A:1784:A:O2'	1:A:1785:G:OP1	2.06	0.71
1:A:1876:A:O2'	1:A:1877:A:N7	2.23	0.71
22:2:31:C:H1'	33:0:125:ARG:CD	2.20	0.71
4:F:95:GLN:NE2	4:F:96:GLU:O	2.23	0.71
33:0:538:LYS:N	33:0:539:PRO:HD2	2.06	0.71
1:A:79:C:O2'	1:A:390:A:N3	2.18	0.71
1:A:1036:A:O2'	1:A:1037:C:OP1	2.07	0.71
33:0:25:THR:OG1	33:0:38:HIS:O	2.05	0.71
14:R:19:ASP:OD1	14:R:67:ARG:NH1	2.24	0.70
1:A:282:G:O2'	1:A:283:G:O4'	2.09	0.70
1:A:1088:G:H1	1:A:1159:U:H3	1.36	0.70
22:2:31:C:N3	33:0:125:ARG:NH2	2.40	0.70
33:0:27:ILE:O	33:0:80:ARG:NH2	2.25	0.70
1:A:1259:G:OP2	17:U:19:LYS:NZ	2.18	0.70
1:A:1362:G:OP1	19:W:98:LYS:NZ	2.24	0.70
15:S:92:ASP:OD1	15:S:119:LYS:NZ	2.25	0.70
33:0:480:ARG:O	33:0:534:ARG:N	2.25	0.69
1:A:177:G:O2'	1:A:178:A:O5'	2.10	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2314:C:OP2	28:g:2:ARG:NH2	2.26	0.69
1:A:2922:U:O2'	10:N:137:LYS:NZ	2.25	0.69
1:A:419:G:N2	1:A:448:A:OP2	2.16	0.69
1:A:2595:A:N1	11:O:28:SER:OG	2.24	0.69
1:A:1828:G:OP1	3:E:260:ARG:NH1	2.26	0.69
1:A:2772:U:OP2	1:A:2784:C:N4	2.25	0.69
1:A:2294:U:OP2	1:A:2295:A:O2'	2.10	0.69
1:A:2339:A:H2'	6:H:77:PHE:HE2	1.55	0.69
12:P:85:PHE:O	12:P:119:LYS:NZ	2.17	0.69
1:A:1265:A:OP1	18:V:70:LYS:NZ	2.25	0.69
1:A:204:C:OP1	24:b:18:ARG:NH2	2.27	0.68
22:2:58:A:O2'	22:2:60:C:OP2	2.07	0.68
33:0:399:GLU:OE2	33:0:543:LYS:N	2.27	0.68
20:X:84:THR:OG1	20:X:87:SER:OG	2.05	0.68
33:0:410:GLN:HE22	33:0:467:ASN:HA	1.59	0.68
1:A:312:G:N2	1:A:405:U:C4	2.62	0.68
1:A:790:A:O2'	1:A:1704:U:OP1	2.12	0.68
1:A:1130:A:N3	1:A:1151:U:O2'	2.21	0.68
1:A:1365:U:O2'	1:A:1366:C:O4'	2.12	0.68
1:A:1315:G:OP2	1:A:1690:G:O2'	2.04	0.68
1:A:160:G:N2	1:A:168:A:OP2	2.27	0.68
1:A:2287:C:O2'	1:A:2456:C:OP2	2.11	0.67
1:A:2340:A:H2	6:H:79:LEU:CD1	1.92	0.67
7:I:57:SER:OG	7:I:59:GLN:OE1	2.04	0.67
14:R:52:LYS:NZ	14:R:94:ARG:O	2.27	0.67
1:A:515:G:N7	29:h:39:ARG:NH2	2.42	0.67
33:0:410:GLN:CB	33:0:465:LYS:O	2.41	0.67
1:A:1403:G:N2	1:A:1406:A:OP2	2.25	0.67
1:A:1094:A:OP2	1:A:1156:G:N2	2.25	0.67
22:2:3:G:H1	22:2:70:U:H3	1.43	0.67
1:A:1231:G:OP1	12:P:30:THR:OG1	2.10	0.67
1:A:719:C:OP2	12:P:42:SER:OG	2.12	0.66
3:E:72:ASP:OD2	3:E:189:ARG:NH2	2.28	0.66
33:0:410:GLN:HE22	33:0:467:ASN:CA	2.08	0.66
16:T:88:ARG:NH1	16:T:112:GLU:OE1	2.29	0.66
33:0:409:GLN:CD	33:0:492:GLY:CA	2.68	0.66
1:A:52:A:OP2	1:A:118:A:N6	2.28	0.66
1:A:1886:G:O2'	1:A:1887:G:O4'	2.03	0.66
1:A:1530:G:O2'	1:A:1531:G:OP1	2.14	0.66
1:A:2340:A:C6	6:H:41:GLY:HA3	2.30	0.66
1:A:2513:G:OP1	13:Q:45:ARG:NH1	2.30	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:13:ARG:NH1	3:E:16:MET:SD	2.69	0.65
8:K:26:PRO:O	8:K:30:GLN:NE2	2.29	0.65
1:A:1991:C:O2'	1:A:1993:G:OP2	2.14	0.65
1:A:2340:A:N3	6:H:79:LEU:HD12	2.11	0.65
1:A:1216:C:N3	1:A:1220:G:N1	2.44	0.65
1:A:2121:U:N3	1:A:2255:C:OP2	2.29	0.65
1:A:161:A:OP2	1:A:166:A:N6	2.30	0.65
1:A:1364:C:OP1	1:A:1692:U:O2'	2.15	0.65
15:S:61:LYS:O	15:S:64:ASN:ND2	2.29	0.65
10:N:78:HIS:ND1	10:N:79:THR:O	2.29	0.64
1:A:1072:A:OP2	1:A:1180:C:O2'	2.14	0.64
1:A:2341:U:C5'	6:H:85:ILE:HD11	2.26	0.64
33:0:409:GLN:CG	33:0:492:GLY:HA2	2.27	0.64
14:R:99:THR:N	14:R:120:VAL:OXT	2.31	0.64
17:U:90:VAL:O	18:V:11:GLN:NE2	2.30	0.64
1:A:604:C:O2	17:U:48:ARG:NH2	2.31	0.64
1:A:2337:G:C4	6:H:77:PHE:CZ	2.86	0.64
2:B:47:C:OP2	15:S:35:ARG:NH2	2.30	0.64
1:A:312:G:C2	1:A:405:U:C4	2.85	0.64
27:f:35:GLU:OE2	27:f:45:ALA:HB3	1.98	0.64
1:A:186:C:O2'	1:A:479:A:N3	2.25	0.64
1:A:2060:A:N3	1:A:2484:G:O2'	2.28	0.64
1:A:2307:A:OP2	23:a:20:ASN:ND2	2.31	0.64
3:E:194:GLN:NE2	3:E:198:GLU:OE1	2.31	0.64
1:A:2605:G:O2'	1:A:2608:C:OP2	2.16	0.64
1:A:867:A:N3	1:A:989:U:O2'	2.31	0.64
1:A:77:U:O2'	1:A:78:U:O5'	2.16	0.63
1:A:1291:A:OP1	17:U:10:THR:OG1	2.10	0.63
28:g:9:CYS:SG	28:g:10:THR:N	2.71	0.63
33:0:121:GLU:OE2	33:0:162:TYR:OH	2.15	0.63
6:H:54:VAL:HG13	6:H:65:PRO:HG2	1.79	0.63
10:N:59:ASN:N	10:N:128:GLY:O	2.32	0.63
1:A:2872:U:OP1	16:T:96:LYS:NZ	2.28	0.63
1:A:633:U:O3'	5:G:95:ARG:NH1	2.31	0.63
1:A:1108:G:N3	8:K:134:SER:OG	2.32	0.63
1:A:1694:G:O2'	14:R:110:ASP:OD1	2.07	0.63
1:A:2364:A:O2'	1:A:2365:A:O5'	2.14	0.63
33:0:422:ILE:HD11	33:0:466:ASN:HA	1.80	0.63
1:A:1065:U:OP1	1:A:1081:U:O2'	2.17	0.62
1:A:1313:A:O2'	1:A:1314:A:OP1	2.17	0.62
1:A:1856:U:OP2	3:E:221:ARG:NH1	2.32	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:2:44:A:H5'	33:0:286:ARG:HH21	1.61	0.62
1:A:1757:G:O2'	1:A:1758:U:O3'	2.16	0.62
2:B:21:G:O2'	2:B:22:G:O5'	2.15	0.62
1:A:1843:G:OP2	1:A:1844:A:O2'	2.13	0.62
1:A:2027:A:OP2	4:F:141:ARG:NH1	2.32	0.62
1:A:2337:G:N3	6:H:77:PHE:CE1	2.66	0.62
1:A:2334:U:C6	6:H:133:LYS:HA	2.35	0.62
1:A:2548:U:O4'	1:A:2571:A:N6	2.33	0.62
1:A:2890:U:OP2	1:A:2891:G:O2'	2.13	0.62
12:P:55:MET:O	12:P:60:ARG:NH2	2.33	0.62
4:F:9:LYS:NZ	4:F:194:GLY:O	2.20	0.62
1:A:372:U:O2'	21:Y:67:ASN:ND2	2.33	0.62
11:O:13:ASN:ND2	11:O:96:THR:OG1	2.32	0.62
1:A:2497:A:O2'	1:A:2498:A:O4'	2.17	0.61
1:A:1171:G:OP2	1:A:1172:A:O2'	2.09	0.61
1:A:1264:G:OP2	18:V:67:ARG:NH2	2.33	0.61
1:A:2864:G:O2'	14:R:45:GLU:OE1	2.14	0.61
1:A:1379:U:OP2	20:X:59:TYR:OH	2.17	0.61
1:A:1124:C:OP1	8:K:133:ARG:NH2	2.33	0.61
1:A:2841:C:O2	1:A:2908:A:O2'	2.15	0.61
6:H:80:ARG:CZ	22:2:56:C:C5	2.84	0.61
1:A:1695:A:O2'	1:A:1696:G:O5'	2.13	0.61
33:0:409:GLN:CD	33:0:492:GLY:C	2.69	0.61
1:A:2468:A:O2'	1:A:2629:A:OP1	2.13	0.61
1:A:2080:A:O2'	1:A:2643:A:N6	2.34	0.60
1:A:2337:G:C5	6:H:77:PHE:HZ	2.19	0.60
1:A:2856:G:N2	1:A:2909:U:OP2	2.34	0.60
14:R:52:LYS:NZ	14:R:98:TYR:OH	2.25	0.60
6:H:73:SER:HB3	22:2:56:C:H1'	1.83	0.60
1:A:2054:C:OP1	4:F:153:ARG:NH2	2.35	0.60
1:A:1036:A:O2'	1:A:1038:C:OP2	2.20	0.60
1:A:1325:A:O2'	1:A:1327:U:OP2	2.13	0.60
1:A:1509:C:HO2'	1:A:2731:G:HO2'	1.50	0.60
1:A:2026:A:O5'	4:F:130:ARG:NH1	2.33	0.60
6:H:80:ARG:CZ	22:2:56:C:C4	2.85	0.60
33:0:410:GLN:HE22	33:0:467:ASN:CB	2.15	0.60
1:A:1199:C:OP1	17:U:92:ARG:NH2	2.35	0.60
1:A:353:A:N3	1:A:373:A:O2'	2.31	0.60
2:B:26:C:O2	2:B:57:G:N2	2.33	0.60
17:U:39:VAL:O	17:U:42:SER:OG	2.11	0.60
22:2:31:C:C4	33:0:125:ARG:NH2	2.69	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:0:60:HIS:NE2	33:0:271:SER:O	2.34	0.59
1:A:777:C:OP1	1:A:1804:U:O2'	2.20	0.59
1:A:2341:U:C5'	6:H:85:ILE:CD1	2.79	0.59
11:O:13:ASN:OD1	11:O:96:THR:N	2.35	0.59
1:A:1811:C:O2	1:A:2637:G:O2'	2.04	0.59
1:A:2130:G:N2	1:A:2218:U:O2	2.30	0.59
1:A:2688:G:N2	1:A:2691:A:OP2	2.35	0.59
5:G:101:LEU:O	5:G:106:ARG:NH2	2.35	0.59
14:R:99:THR:CA	14:R:120:VAL:OXT	2.50	0.59
1:A:347:G:O2'	1:A:348:U:OP1	2.19	0.59
33:0:409:GLN:HG3	33:0:492:GLY:HA2	1.83	0.59
1:A:2333:G:O2'	6:H:129:THR:HG21	2.03	0.59
1:A:2684:G:O2'	1:A:2693:G:O6	2.20	0.59
1:A:2882:G:N2	1:A:2885:A:OP2	2.29	0.59
7:I:8:LEU:HD22	7:I:52:THR:HG22	1.83	0.59
1:A:546:G:N1	1:A:549:A:OP2	2.35	0.59
1:A:2333:G:O2'	6:H:129:THR:CG2	2.51	0.59
13:Q:77:LYS:NZ	13:Q:84:GLY:O	2.32	0.59
1:A:753:A:OP1	3:E:7:LYS:NZ	2.36	0.58
26:d:18:ASP:OD1	26:d:19:GLN:N	2.35	0.58
1:A:1102:G:O2'	1:A:1149:A:N6	2.36	0.58
1:A:2334:U:O4	6:H:151:GLY:C	2.46	0.58
33:0:525:SER:O	33:0:527:PRO:HD2	2.03	0.58
1:A:1820:A:N6	1:A:1857:G:O2'	2.35	0.58
26:d:8:LEU:HD21	26:d:28:LEU:HD13	1.85	0.58
33:0:418:ASP:HB3	33:0:466:ASN:CB	2.33	0.58
1:A:251:G:O2'	1:A:2461:A:OP1	2.11	0.58
11:O:87:ILE:HD13	11:O:90:ASP:O	2.04	0.58
33:0:522:ASP:C	33:0:559:PRO:HG2	2.28	0.58
1:A:1125:C:O4'	8:K:133:ARG:NH1	2.36	0.58
23:a:41:GLY:N	23:a:72:ASP:OD1	2.37	0.58
10:N:14:ARG:NH2	10:N:50:ASP:O	2.36	0.58
33:0:392:GLU:OE1	33:0:395:ARG:NH2	2.37	0.58
1:A:420:U:O2'	1:A:421:A:O5'	2.22	0.58
1:A:843:C:O3'	5:G:62:ARG:NH2	2.37	0.57
5:G:109:ALA:O	5:G:112:SER:OG	2.17	0.57
1:A:2334:U:C5	6:H:133:LYS:HA	2.39	0.57
1:A:1501:U:O2'	1:A:1502:G:N7	2.37	0.57
1:A:448:A:O2'	1:A:449:A:O4'	2.11	0.57
3:E:77:ARG:NH2	3:E:115:GLU:OE2	2.38	0.57
1:A:2106:A:OP1	1:A:2267:G:N2	2.33	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:d:39:ASP:OD1	26:d:44:ARG:NH2	2.38	0.57
1:A:1830:G:OP2	3:E:150:LYS:NZ	2.38	0.57
3:E:155:VAL:O	3:E:160:THR:OG1	2.19	0.57
9:L:29:ASP:OD1	9:L:30:TYR:N	2.38	0.57
1:A:2830:A:O2'	1:A:2831:A:OP2	2.22	0.57
1:A:1757:G:O2'	1:A:1758:U:O5'	2.23	0.56
16:T:28:VAL:HG12	16:T:84:ILE:HG22	1.87	0.56
1:A:2054:C:OP2	4:F:153:ARG:NE	2.38	0.56
1:A:83:G:N2	1:A:102:A:OP2	2.22	0.56
1:A:1010:C:O2'	1:A:2302:A:N3	2.37	0.56
1:A:2361:C:OP1	23:a:84:ARG:NH1	2.35	0.56
3:E:45:ASN:OD1	3:E:46:GLN:N	2.38	0.56
1:A:2332:G:H4'	6:H:123:ASP:HA	1.87	0.56
1:A:253:G:OP1	30:i:13:ARG:NH2	2.36	0.56
1:A:761:U:O2'	1:A:763:A:N7	2.38	0.56
1:A:1204:C:OP1	26:d:30:LYS:NZ	2.36	0.56
1:A:1127:U:O2	8:K:117:ASN:ND2	2.37	0.56
1:A:1782:G:OP1	16:T:93:ARG:NH1	2.38	0.56
1:A:75:G:OP1	25:c:44:ARG:NH2	2.39	0.55
1:A:2324:C:OP2	15:S:14:ARG:NE	2.37	0.55
14:R:99:THR:O	14:R:120:VAL:OXT	2.23	0.55
11:O:33:ALA:HB1	11:O:37:ASP:CB	2.36	0.55
33:0:410:GLN:NE2	33:0:467:ASN:HA	2.20	0.55
1:A:2038:G:OP1	19:W:41:ARG:NH1	2.40	0.55
1:A:2226:U:O2'	1:A:2227:A:O5'	2.21	0.55
1:A:675:C:O2	1:A:685:U:O2'	2.24	0.55
25:c:13:GLU:N	25:c:13:GLU:OE1	2.39	0.55
1:A:623:A:O2'	1:A:2048:U:OP1	2.24	0.55
1:A:2712:C:O2	11:O:76:TYR:OH	2.24	0.55
1:A:1883:A:O2'	1:A:1884:G:OP1	2.23	0.55
12:P:83:ASN:O	12:P:119:LYS:NZ	2.24	0.55
33:0:409:GLN:NE2	33:0:492:GLY:HA2	2.21	0.55
1:A:897:G:O2'	26:d:22:THR:HG22	2.07	0.55
1:A:2406:A:O2'	15:S:120:PHE:OXT	2.24	0.55
1:A:1058:U:O4	10:N:31:SER:OG	2.24	0.54
12:P:116:LYS:NZ	12:P:118:GLU:OE2	2.41	0.54
1:A:1177:G:O2'	1:A:2054:C:O2'	2.15	0.54
7:I:89:GLU:OE1	7:I:89:GLU:N	2.40	0.54
33:0:410:GLN:OE1	33:0:467:ASN:N	2.40	0.54
1:A:339:A:O3'	21:Y:90:LYS:NZ	2.41	0.54
9:L:5:ILE:N	9:L:8:LYS:HZ3	2.05	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:593:A:O2'	1:A:594:C:O5'	2.26	0.54
1:A:2859:G:O2'	1:A:2860:A:O5'	2.24	0.54
25:c:6:ILE:O	25:c:60:ARG:NH2	2.41	0.54
33:0:409:GLN:OE1	33:0:492:GLY:C	2.50	0.54
1:A:2108:U:O2'	24:b:23:ASN:OD1	2.23	0.54
1:A:2386:U:OP1	23:a:28:ARG:NH1	2.41	0.54
3:E:142:HIS:ND1	3:E:193:GLY:O	2.40	0.54
6:H:158:THR:HG22	6:H:160:ALA:H	1.73	0.54
1:A:116:G:OP2	1:A:118:A:O2'	2.26	0.54
1:A:1110:C:OP1	8:K:80:LYS:NZ	2.41	0.54
3:E:154:LEU:O	3:E:156:ARG:N	2.41	0.54
22:2:44:A:H5'	33:0:286:ARG:NH2	2.20	0.54
31:j:14:CYS:SG	31:j:32:HIS:ND1	2.81	0.54
1:A:373:A:N1	21:Y:15:LYS:NZ	2.56	0.53
33:0:185:LEU:HD11	33:0:192:LEU:HD13	1.91	0.53
6:H:75:ALA:CB	22:2:56:C:O2'	2.57	0.53
11:O:22:ILE:HD11	11:O:42:THR:HG23	1.89	0.53
1:A:1981:A:OP1	11:O:44:LYS:NZ	2.31	0.53
4:F:43:ASN:OD1	4:F:44:ASP:N	2.41	0.53
1:A:490:A:OP1	5:G:46:GLN:N	2.42	0.53
7:I:158:TYR:O	7:I:172:ARG:NH1	2.39	0.53
26:d:15:ARG:O	26:d:20:ARG:NH2	2.41	0.53
10:N:30:SER:HA	10:N:33:VAL:HG22	1.91	0.53
11:O:120:GLU:OE1	16:T:65:SER:OG	2.25	0.53
15:S:24:GLY:O	15:S:47:ASP:N	2.42	0.53
1:A:1498:U:O2'	1:A:1499:A:N7	2.42	0.53
1:A:2364:A:HO2'	1:A:2365:A:P	2.32	0.53
5:G:80:SER:HG	5:G:83:TRP:CD1	2.26	0.53
13:Q:30:GLY:O	13:Q:134:ARG:NH2	2.41	0.53
10:N:50:ASP:OD1	10:N:122:LYS:NZ	2.42	0.53
13:Q:42:ILE:HD12	13:Q:97:VAL:HG21	1.92	0.52
8:K:10:LYS:C	8:K:11:LEU:HD12	2.34	0.52
1:A:287:G:N3	1:A:288:C:N4	2.58	0.52
1:A:488:U:O2	5:G:46:GLN:NE2	2.41	0.52
1:A:2233:C:OP1	3:E:147:LYS:NZ	2.42	0.52
1:A:2898:A:O2'	1:A:2899:C:OP1	2.28	0.52
27:f:30:CYS:N	27:f:35:GLU:O	2.39	0.52
1:A:111:U:OP1	25:c:58:ARG:NH2	2.42	0.52
1:A:236:A:H61	1:A:476:A:H61	1.57	0.52
1:A:898:U:O2	26:d:42:ALA:HB1	2.09	0.52
1:A:1033:C:O2'	1:A:1046:A:N3	2.35	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:K:117:ASN:OD1	8:K:118:ALA:N	2.42	0.52
1:A:1113:A:OP1	33:0:384:LYS:NZ	2.43	0.52
1:A:419:G:O2'	1:A:447:G:O6	2.24	0.52
15:S:30:ARG:NH2	15:S:47:ASP:OD1	2.43	0.52
22:2:31:C:H1'	33:0:125:ARG:NE	2.25	0.52
1:A:274:A:O2'	1:A:415:C:O2'	2.15	0.52
1:A:2344:U:O2'	6:H:125:ARG:HG2	2.10	0.52
1:A:2390:A:OP2	30:i:24:ARG:NH2	2.38	0.52
1:A:792:G:O2'	1:A:795:G:O2'	2.16	0.51
6:H:159:THR:HA	15:S:2:ILE:HG22	1.91	0.51
1:A:274:A:HO2'	1:A:415:C:HO2'	1.45	0.51
7:I:108:VAL:HG13	7:I:109:GLY:H	1.76	0.51
1:A:2104:U:OP2	1:A:2267:G:O2'	2.16	0.51
1:A:2522:U:O2'	13:Q:80:GLU:OE2	2.19	0.51
1:A:2404:G:N2	1:A:2407:A:OP2	2.31	0.51
11:O:48:PRO:O	11:O:50:GLY:N	2.43	0.51
15:S:87:GLU:OE2	15:S:88:LYS:NZ	2.43	0.51
30:i:40:GLN:O	30:i:44:LEU:HD13	2.11	0.51
14:R:8:ARG:O	14:R:13:ARG:NH2	2.43	0.51
1:A:2048:U:OP2	27:f:6:ARG:NH2	2.44	0.51
1:A:2334:U:O4	6:H:151:GLY:N	2.44	0.51
1:A:2850:G:O6	4:F:163:ARG:NH1	2.44	0.51
33:0:447:ASN:H	33:0:448:PRO:CD	2.19	0.51
1:A:52:A:OP2	1:A:116:G:N1	2.43	0.51
1:A:2688:G:P	7:I:159:LYS:HZ1	2.33	0.51
33:0:523:SER:N	33:0:559:PRO:HG2	2.26	0.51
1:A:1452:C:H2'	1:A:1453:A:C8	2.46	0.51
1:A:1129:U:N3	1:A:1132:A:OP2	2.41	0.50
1:A:1993:G:O2'	1:A:1996:C:OP2	2.18	0.50
1:A:2337:G:C4	6:H:77:PHE:CE1	2.99	0.50
15:S:19:ARG:NH1	15:S:47:ASP:OD2	2.43	0.50
1:A:1460:G:O2'	1:A:1631:A:N6	2.44	0.50
1:A:1970:C:N4	1:A:1994:C:O4'	2.45	0.50
1:A:2384:C:O4'	23:a:44:ILE:HD11	2.11	0.50
22:2:31:C:N1	33:0:125:ARG:CZ	2.73	0.50
7:I:59:GLN:OE1	7:I:62:HIS:ND1	2.44	0.50
1:A:2278:U:N3	1:A:2282:G:OP2	2.41	0.50
1:A:2279:G:N2	1:A:2305:G:OP1	2.45	0.50
26:d:18:ASP:O	26:d:22:THR:HG23	2.12	0.50
1:A:1008:A:HO2'	1:A:2525:C:HO2'	1.60	0.50
33:0:128:ASN:OD1	33:0:129:ILE:N	2.45	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:L:7:THR:O	9:L:11:VAL:HG23	2.12	0.50
9:L:77:THR:O	9:L:80:ASN:ND2	2.44	0.50
1:A:1956:A:H2'	1:A:1957:A:C8	2.46	0.50
7:I:8:LEU:CD2	7:I:52:THR:HG22	2.42	0.50
9:L:56:LYS:O	9:L:60:THR:OG1	2.18	0.50
23:a:23:ASP:OD1	23:a:24:SER:N	2.45	0.49
33:0:94:ALA:HB2	33:0:101:ILE:HD11	1.94	0.49
15:S:8:ASN:OD1	15:S:11:ARG:NH2	2.45	0.49
3:E:53:HIS:CE1	3:E:219:THR:HG23	2.48	0.49
33:0:409:GLN:NE2	33:0:493:SER:N	2.59	0.49
1:A:347:G:HO2'	1:A:348:U:P	2.35	0.49
1:A:1831:A:H2	1:A:1844:A:H62	1.61	0.49
3:E:176:LEU:O	3:E:179:GLY:N	2.40	0.49
17:U:90:VAL:HG12	18:V:39:LEU:HD13	1.94	0.49
33:0:9:TYR:O	33:0:12:THR:OG1	2.27	0.49
1:A:2922:U:O3'	10:N:137:LYS:NZ	2.46	0.49
1:A:1189:A:OP1	10:N:28:ARG:NH1	2.43	0.49
8:K:33:VAL:HG12	8:K:64:ARG:HG2	1.94	0.49
1:A:1263:G:N2	1:A:1266:A:OP2	2.38	0.49
1:A:1462:G:O2'	1:A:1633:G:O2'	2.28	0.49
33:0:53:HIS:CD2	33:0:282:ALA:CA	2.89	0.49
1:A:1158:G:O2'	1:A:1159:U:O5'	2.31	0.49
27:f:33:CYS:N	27:f:46:CYS:SG	2.86	0.49
1:A:630:A:H5'	5:G:89:VAL:HG21	1.93	0.48
1:A:1734:A:OP2	1:A:1743:A:N6	2.32	0.48
10:N:63:ILE:O	10:N:94:ARG:NH2	2.46	0.48
25:c:59:GLU:HA	25:c:62:ILE:HG22	1.94	0.48
3:E:123:ASP:OD1	3:E:128:ASN:ND2	2.45	0.48
1:A:45:G:H21	1:A:183:A:H61	1.61	0.48
1:A:85:G:N1	1:A:98:U:C2	2.82	0.48
1:A:514:G:OP2	29:h:34:ARG:NH2	2.46	0.48
1:A:776:G:OP1	3:E:10:SER:OG	2.32	0.48
1:A:1339:A:H4'	1:A:1340:A:H5'	1.95	0.48
28:g:36:CYS:O	28:g:40:LYS:N	2.46	0.48
33:0:410:GLN:NE2	33:0:467:ASN:CA	2.74	0.48
1:A:2320:U:O2'	1:A:2403:C:O2	2.30	0.48
1:A:2340:A:H2	6:H:79:LEU:CG	2.25	0.48
1:A:13:A:O2'	1:A:15:G:N7	2.45	0.48
1:A:1759:U:H3	1:A:1774:A:H62	1.61	0.48
2:B:10:G:OP2	23:a:79:ARG:NH1	2.47	0.48
29:h:20:SER:O	29:h:23:SER:OG	2.20	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:0:406:GLN:NE2	33:0:492:GLY:O	2.32	0.48
33:0:522:ASP:CA	33:0:559:PRO:HG2	2.43	0.48
1:A:1074:A:N3	1:A:2515:G:O2'	2.42	0.48
12:P:125:ALA:HB3	12:P:128:PHE:HE1	1.79	0.48
1:A:1853:G:OP2	3:E:53:HIS:ND1	2.46	0.48
3:E:141:VAL:CG1	3:E:190:ALA:HB1	2.44	0.48
1:A:527:A:O2'	21:Y:42:LYS:O	2.32	0.48
1:A:2688:G:O2'	1:A:2690:G:N7	2.35	0.48
5:G:112:SER:O	5:G:115:SER:OG	2.23	0.48
8:K:18:ALA:HB3	8:K:43:ASN:ND2	2.28	0.48
1:A:965:A:N3	2:B:78:U:O2'	2.46	0.47
3:E:15:GLY:O	3:E:204:ASN:ND2	2.46	0.47
33:0:133:ASP:OD1	33:0:134:ALA:N	2.47	0.47
1:A:1516:A:N7	1:A:1569:A:N1	2.62	0.47
26:d:44:ARG:HD3	26:d:47:ILE:HD11	1.96	0.47
1:A:64:A:H61	1:A:90:A:H61	1.62	0.47
1:A:1475:G:HO2'	1:A:1476:C:H6	1.60	0.47
1:A:27:G:N2	1:A:558:G:O2'	2.47	0.47
1:A:1371:G:N7	1:A:1654:A:O2'	2.45	0.47
15:S:63:LEU:O	15:S:76:LYS:NZ	2.37	0.47
17:U:90:VAL:HG23	17:U:91:ASN:H	1.79	0.47
1:A:722:A:N3	1:A:2472:C:O2'	2.43	0.47
1:A:906:G:O2'	1:A:963:G:O6	2.30	0.47
7:I:64:ALA:O	7:I:68:THR:HG23	2.15	0.47
1:A:461:C:O2	1:A:1893:U:O2'	2.30	0.47
1:A:1305:A:O3'	27:f:16:ARG:NH2	2.47	0.47
1:A:1417:A:O2'	1:A:1418:U:OP2	2.25	0.47
1:A:1574:G:N1	1:A:1592:A:OP2	2.43	0.47
1:A:2335:U:H2'	1:A:2336:G:C4	2.49	0.47
6:H:135:GLN:HG2	6:H:141:ILE:HG21	1.96	0.47
10:N:108:GLY:O	10:N:112:LYS:NZ	2.48	0.47
16:T:34:GLU:OE2	16:T:39:ARG:NH2	2.48	0.47
1:A:248:G:N7	30:i:8:ARG:NH2	2.63	0.47
1:A:1846:G:OP2	3:E:156:ARG:NH2	2.44	0.47
1:A:2593:A:OP1	1:A:2677:G:O2'	2.29	0.47
9:L:14:GLU:O	9:L:17:SER:OG	2.21	0.47
30:i:4:MET:HE1	30:i:60:GLN:HE21	1.80	0.47
1:A:1365:U:HO2'	1:A:1366:C:H6	1.62	0.47
1:A:1092:A:N3	9:L:62:ARG:NH1	2.63	0.47
1:A:1252:G:O2'	1:A:1253:A:OP2	2.33	0.47
1:A:1972:U:O2'	1:A:1973:U:OP2	2.26	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:R:18:ARG:O	14:R:21:THR:OG1	2.30	0.47
1:A:1403:G:OP1	24:b:3:ARG:NH1	2.48	0.46
1:A:1645:C:OP1	20:X:77:ARG:NH1	2.48	0.46
32:1:67:THR:O	32:1:67:THR:HG23	2.16	0.46
1:A:1055:A:N3	1:A:1199:C:O2'	2.41	0.46
1:A:2340:A:C2	6:H:77:PHE:HB3	2.51	0.46
1:A:74:U:OP1	25:c:47:ARG:NH2	2.48	0.46
1:A:2823:C:O2'	1:A:2824:G:O4'	2.25	0.46
17:U:97:ASP:OD1	17:U:101:ASN:ND2	2.49	0.46
26:d:8:LEU:CD2	26:d:28:LEU:HD13	2.45	0.46
1:A:312:G:C2	1:A:405:U:O4	2.68	0.46
19:W:58:ALA:O	19:W:63:GLU:N	2.48	0.46
1:A:2063:U:HO2'	1:A:2064:G:P	2.39	0.46
1:A:2334:U:C4	6:H:151:GLY:CA	2.66	0.46
11:O:113:LYS:O	11:O:117:LEU:HD23	2.16	0.46
17:U:102:ASP:OD2	18:V:2:TYR:OH	2.28	0.46
22:2:44:A:H5''	33:0:286:ARG:NH2	2.17	0.46
1:A:1698:G:O6	14:R:7:GLY:N	2.44	0.46
11:O:87:ILE:HD13	11:O:90:ASP:H	1.81	0.46
21:Y:85:VAL:HG13	21:Y:88:GLY:O	2.15	0.46
33:0:240:ILE:HG23	33:0:240:ILE:O	2.16	0.46
1:A:523:G:N1	1:A:526:A:OP2	2.45	0.46
1:A:2334:U:OP2	6:H:131:GLY:N	2.49	0.46
4:F:15:VAL:O	4:F:23:ILE:N	2.49	0.46
14:R:17:LEU:O	14:R:21:THR:HG23	2.15	0.46
33:0:21:GLY:N	33:0:88:ILE:O	2.44	0.46
8:K:78:LEU:HD13	8:K:108:ILE:HG23	1.98	0.46
17:U:88:ILE:HG22	17:U:88:ILE:O	2.15	0.46
1:A:273:A:OP2	1:A:297:G:N2	2.42	0.45
1:A:2080:A:N6	1:A:2643:A:O2'	2.45	0.45
4:F:111:THR:OG1	4:F:170:THR:HG22	2.16	0.45
6:H:80:ARG:NE	22:2:56:C:C4	2.84	0.45
9:L:34:ASN:O	9:L:38:VAL:HG23	2.16	0.45
14:R:102:MET:HE2	14:R:116:ILE:HD11	1.98	0.45
33:0:246:VAL:O	33:0:246:VAL:HG13	2.16	0.45
9:L:82:ILE:HD12	9:L:84:PHE:CE2	2.51	0.45
12:P:86:ALA:O	12:P:89:THR:HG22	2.16	0.45
22:2:56:C:H2'	22:2:57:G:O4'	2.17	0.45
1:A:610:U:OP1	18:V:81:ASN:ND2	2.47	0.45
8:K:73:PRO:CG	8:K:78:LEU:HD21	2.46	0.45
1:A:732:A:O2'	1:A:820:U:O4	2.29	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:2:7:U:H3'	22:2:8:U:H5'	1.98	0.45
22:2:42:G:O3'	33:0:32:LYS:NZ	2.50	0.45
1:A:287:G:H21	1:A:288:C:H42	1.63	0.45
1:A:1542:A:N3	1:A:1625:C:O2'	2.49	0.45
1:A:2274:U:O2'	1:A:2465:G:OP2	2.21	0.45
4:F:28:ILE:HD12	4:F:188:ILE:HD12	1.99	0.45
1:A:1485:A:H2	1:A:1600:G:H21	1.65	0.45
1:A:2703:G:H4'	11:O:30:ARG:HE	1.81	0.45
4:F:40:THR:OG1	4:F:43:ASN:OD1	2.31	0.45
4:F:195:ALA:O	4:F:198:SER:OG	2.27	0.45
6:H:12:ILE:HD11	6:H:173:VAL:HG12	1.98	0.45
19:W:50:VAL:HG13	19:W:105:ILE:HD12	1.98	0.45
22:2:43:G:P	33:0:32:LYS:HZ2	2.39	0.45
33:0:348:VAL:O	33:0:359:ILE:N	2.41	0.45
1:A:447:G:O6	24:b:52:ARG:NH1	2.49	0.45
1:A:747:G:O2'	1:A:1677:A:N3	2.39	0.45
1:A:1895:A:N6	1:A:1904:G:O2'	2.49	0.45
3:E:162:ALA:HB1	3:E:175:ARG:O	2.17	0.45
19:W:22:ASP:OD1	19:W:25:ARG:NH1	2.46	0.45
25:c:9:LEU:HD23	25:c:11:THR:H	1.81	0.45
1:A:64:A:H61	1:A:90:A:N6	2.14	0.45
1:A:2341:U:H5'	6:H:85:ILE:HD12	1.94	0.45
6:H:125:ARG:HG3	15:S:1:MET:CG	2.44	0.45
26:d:19:GLN:O	26:d:22:THR:OG1	2.30	0.45
1:A:1040:C:O2'	1:A:1042:A:OP1	2.24	0.45
1:A:2053:C:O2'	1:A:2054:C:O5'	2.34	0.45
4:F:48:ALA:HB1	4:F:83:LEU:O	2.17	0.45
8:K:73:PRO:HG2	8:K:78:LEU:HD21	1.99	0.45
23:a:77:PHE:CD1	23:a:87:VAL:HG12	2.52	0.45
1:A:569:C:O2	1:A:598:U:O2'	2.34	0.44
4:F:206:VAL:O	4:F:206:VAL:HG13	2.16	0.44
9:L:28:VAL:HG12	9:L:108:ILE:HA	1.98	0.44
11:O:24:VAL:HG11	11:O:33:ALA:HB2	1.99	0.44
26:d:40:ASN:OD1	26:d:41:ALA:N	2.50	0.44
33:0:171:ILE:N	33:0:199:HIS:O	2.50	0.44
28:g:11:GLU:OE1	28:g:11:GLU:N	2.48	0.44
1:A:1733:U:O2'	1:A:1745:A:N7	2.43	0.44
1:A:2063:U:O2'	1:A:2064:G:O5'	2.33	0.44
1:A:2785:U:OP2	31:j:19:ARG:NH2	2.45	0.44
1:A:2252:A:OP1	3:E:170:LYS:NZ	2.45	0.44
1:A:2344:U:H4'	1:A:2345:U:OP1	2.17	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:Q:44:ASN:OD1	13:Q:45:ARG:N	2.50	0.44
33:O:525:SER:O	33:O:527:PRO:CD	2.64	0.44
1:A:1968:U:OP1	1:A:2633:U:O2'	2.33	0.44
3:E:35:ALA:O	3:E:62:TYR:N	2.51	0.44
4:F:134:SER:OG	4:F:135:HIS:N	2.50	0.44
7:I:166:GLU:OE1	7:I:166:GLU:N	2.42	0.44
22:2:47:U:O2'	22:2:50:G:OP1	2.33	0.44
1:A:1849:U:OP1	3:E:177:ASN:ND2	2.50	0.44
1:A:2344:U:H2'	1:A:2345:U:C6	2.52	0.44
22:2:38:C:H2'	22:2:39:G:C8	2.52	0.44
1:A:1699:A:N6	1:A:2035:C:O4'	2.48	0.44
1:A:2664:U:O2'	4:F:82:GLU:OE1	2.27	0.44
1:A:1306:G:O2'	1:A:2041:G:O6	2.33	0.44
9:L:108:ILE:HG22	9:L:108:ILE:O	2.18	0.44
25:c:42:ARG:O	25:c:46:VAL:HG23	2.18	0.44
33:O:7:PHE:HA	33:O:254:LEU:HD11	1.99	0.44
7:I:108:VAL:HG13	7:I:109:GLY:N	2.32	0.44
13:Q:72:LYS:O	13:Q:94:VAL:N	2.48	0.44
1:A:492:C:H2'	1:A:493:G:O4'	2.18	0.43
1:A:617:G:N2	1:A:2060:A:OP1	2.48	0.43
1:A:751:G:H2'	1:A:773:G:H22	1.82	0.43
1:A:2817:C:O2'	1:A:2834:A:N3	2.45	0.43
18:V:36:GLU:OE1	18:V:36:GLU:N	2.51	0.43
19:W:23:LEU:O	19:W:27:LYS:NZ	2.45	0.43
1:A:1163:U:H2'	1:A:1164:C:C6	2.53	0.43
1:A:2630:C:H5''	22:2:75:C:OP1	2.17	0.43
17:U:88:ILE:O	17:U:90:VAL:N	2.51	0.43
33:O:362:PRO:C	33:O:363:LEU:HD12	2.43	0.43
1:A:894:A:H62	1:A:979:U:H3	1.67	0.43
1:A:1783:C:OP1	16:T:94:ARG:NE	2.51	0.43
1:A:2394:G:N7	30:i:39:LYS:NZ	2.54	0.43
2:B:107:G:HO2'	2:B:108:C:H6	1.65	0.43
22:2:31:C:O2	33:O:125:ARG:CZ	2.50	0.43
1:A:1158:G:HO2'	1:A:1159:U:P	2.40	0.43
1:A:85:G:C6	1:A:98:U:N3	2.86	0.43
16:T:71:GLU:OE1	16:T:101:ARG:NH1	2.51	0.43
32:1:28:ILE:HD12	32:1:28:ILE:C	2.42	0.43
14:R:26:ILE:O	14:R:82:LYS:NZ	2.51	0.43
12:P:125:ALA:HB3	12:P:128:PHE:CE1	2.54	0.43
14:R:85:SER:OG	14:R:86:ASP:N	2.52	0.43
22:2:57:G:C2'	22:2:58:A:H5'	2.48	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:157:SER:OG	3:E:158:ALA:N	2.52	0.43
10:N:96:ASN:O	10:N:127:ARG:NH2	2.47	0.43
33:0:242:ASN:HB3	33:0:266:ARG:HG2	2.00	0.43
1:A:2670:A:OP1	10:N:77:ARG:NH1	2.48	0.43
23:a:80:PHE:N	23:a:84:ARG:O	2.46	0.43
25:c:24:GLU:O	25:c:28:LEU:HD23	2.18	0.43
1:A:657:G:O2'	1:A:660:G:O6	2.37	0.42
22:2:69:C:H2'	22:2:70:U:C6	2.54	0.42
1:A:273:A:OP2	1:A:297:G:N1	2.49	0.42
1:A:1464:A:H2	1:A:1627:A:H62	1.67	0.42
1:A:2316:A:O2'	1:A:2317:A:O5'	2.34	0.42
3:E:264:ASN:OD1	3:E:265:LYS:N	2.51	0.42
1:A:354:A:OP1	21:Y:14:GLY:N	2.52	0.42
1:A:1058:U:O2	10:N:28:ARG:NH1	2.52	0.42
7:I:55:ARG:NH2	7:I:58:ASP:OD1	2.51	0.42
1:A:2337:G:C6	6:H:77:PHE:CE2	3.07	0.42
6:H:125:ARG:O	15:S:1:MET:HB2	2.20	0.42
33:0:409:GLN:HE22	33:0:493:SER:N	2.18	0.42
1:A:1304:G:OP1	27:f:16:ARG:NH2	2.51	0.42
1:A:2337:G:N3	6:H:77:PHE:HE1	2.14	0.42
7:I:38:PHE:CE2	7:I:73:LEU:HD21	2.55	0.42
10:N:6:MET:SD	10:N:6:MET:N	2.93	0.42
15:S:82:ALA:HA	15:S:118:LEU:HD11	2.02	0.42
1:A:1159:U:O2'	1:A:1160:G:OP2	2.30	0.42
1:A:2089:A:O2'	1:A:2090:G:OP2	2.37	0.42
11:O:24:VAL:CG1	11:O:33:ALA:HB2	2.49	0.42
1:A:268:A:N1	1:A:474:U:O2'	2.50	0.42
1:A:1283:U:O2'	12:P:6:LEU:O	2.35	0.42
6:H:73:SER:CB	22:2:56:C:C1'	2.87	0.42
9:L:17:SER:HG	9:L:18:LYS:H	1.68	0.42
13:Q:28:HIS:O	13:Q:134:ARG:NH2	2.53	0.42
20:X:30:VAL:HG12	20:X:31:ASP:N	2.35	0.42
1:A:1046:A:OP2	1:A:1200:G:N1	2.44	0.41
1:A:1765:G:N2	1:A:1768:A:OP2	2.52	0.41
9:L:55:TYR:CE2	9:L:82:ILE:HD11	2.55	0.41
11:O:34:ASN:O	11:O:62:ILE:HG21	2.20	0.41
11:O:105:GLU:OE1	11:O:105:GLU:N	2.52	0.41
33:0:335:ASN:ND2	33:0:348:VAL:HG13	2.35	0.41
1:A:489:G:N3	5:G:48:THR:OG1	2.52	0.41
1:A:2783:U:O2'	1:A:2785:U:OP2	2.32	0.41
6:H:36:ILE:CG2	6:H:57:LEU:HD11	2.50	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2343:A:H2'	1:A:2344:U:C6	2.55	0.41
5:G:167:ALA:HA	5:G:170:ILE:HD13	2.02	0.41
1:A:115:C:O2'	1:A:125:A:N3	2.40	0.41
1:A:1452:C:H2'	1:A:1453:A:H8	1.84	0.41
1:A:2577:G:O2'	11:O:4:GLN:NE2	2.50	0.41
2:B:48:G:HO2'	2:B:49:G:P	2.42	0.41
17:U:26:GLY:O	17:U:29:HIS:ND1	2.53	0.41
20:X:84:THR:OG1	20:X:85:ALA:O	2.38	0.41
22:2:37:A:H2'	22:2:38:C:C6	2.56	0.41
1:A:247:A:OP2	30:i:8:ARG:NH2	2.46	0.41
1:A:1017:C:O2'	1:A:1029:A:N3	2.49	0.41
1:A:2341:U:H4'	6:H:68:THR:OG1	2.21	0.41
1:A:580:U:O2'	17:U:49:ASP:OD2	2.27	0.41
1:A:939:G:O2'	1:A:940:G:O5'	2.38	0.41
1:A:1322:G:N1	1:A:1325:A:OP2	2.54	0.41
6:H:47:ALA:O	6:H:50:ILE:HG22	2.20	0.41
13:Q:12:GLU:O	13:Q:87:LYS:NZ	2.54	0.41
17:U:69:ALA:O	17:U:74:LEU:N	2.48	0.41
33:0:515:ALA:HB1	33:0:559:PRO:CD	2.35	0.41
1:A:221:G:H22	1:A:238:U:H4'	1.86	0.41
1:A:1887:G:HO2'	1:A:1888:A:P	2.41	0.41
1:A:2233:C:OP2	3:E:150:LYS:NZ	2.53	0.41
1:A:2529:U:O2'	1:A:2533:U:OP1	2.34	0.41
33:0:350:ASN:OD1	33:0:351:TYR:N	2.54	0.41
1:A:1366:C:O2'	14:R:108:ARG:NH1	2.45	0.41
1:A:1965:A:OP2	1:A:1991:C:N4	2.47	0.41
2:B:11:A:N7	23:a:82:ARG:NH1	2.69	0.41
6:H:12:ILE:HG12	6:H:172:GLN:HB3	2.03	0.41
17:U:76:TYR:HH	17:U:92:ARG:HE	1.69	0.41
1:A:551:A:O2'	1:A:552:G:O5'	2.38	0.41
1:A:1116:A:O2'	1:A:1143:U:O3'	2.39	0.41
1:A:2875:A:OP2	1:A:2891:G:N1	2.49	0.41
2:B:33:U:O2'	2:B:34:C:O4'	2.38	0.41
2:B:35:C:O2	15:S:103:HIS:NE2	2.44	0.41
6:H:139:PRO:C	6:H:141:ILE:H	2.28	0.41
7:I:163:ILE:HD12	7:I:163:ILE:H	1.86	0.41
9:L:12:VAL:HG23	9:L:63:ALA:HB2	2.03	0.41
14:R:86:ASP:O	14:R:89:THR:OG1	2.34	0.41
26:d:38:GLU:N	26:d:38:GLU:OE1	2.53	0.41
33:0:46:GLN:N	33:0:46:GLN:OE1	2.53	0.41
33:0:139:ILE:HD13	33:0:156:VAL:O	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:O:522:ASP:HA	33:O:559:PRO:HG2	2.03	0.41
1:A:283:G:O6	1:A:287:G:N2	2.53	0.41
1:A:775:G:H3'	1:A:776:G:H5'	2.03	0.41
1:A:2774:C:H42	1:A:2788:G:H1	1.69	0.41
5:G:53:ASN:OD1	5:G:54:ARG:N	2.52	0.41
27:f:28:THR:O	27:f:37:LYS:N	2.54	0.41
3:E:139:THR:N	3:E:163:GLN:OE1	2.54	0.40
7:I:81:SER:OG	7:I:82:LYS:N	2.54	0.40
12:P:58:PHE:O	30:i:13:ARG:NE	2.54	0.40
27:f:30:CYS:O	27:f:34:GLY:N	2.44	0.40
29:h:35:ARG:O	29:h:38:GLY:N	2.54	0.40
5:G:146:LEU:O	5:G:147:SER:OG	2.33	0.40
10:N:139:GLU:OE1	10:N:139:GLU:N	2.55	0.40
27:f:18:THR:OG1	27:f:19:HIS:N	2.55	0.40
33:O:350:ASN:ND2	33:O:355:GLU:OE2	2.54	0.40
1:A:1164:C:H2'	1:A:1165:U:O4'	2.21	0.40
1:A:1691:A:O2'	1:A:1692:U:OP2	2.24	0.40
1:A:2713:U:OP2	16:T:51:ARG:NH1	2.54	0.40
7:I:51:LEU:HD13	7:I:52:THR:N	2.36	0.40
7:I:102:ASN:OD1	7:I:103:LYS:N	2.55	0.40
8:K:33:VAL:HG12	8:K:64:ARG:CG	2.52	0.40
9:L:26:ILE:HG21	9:L:96:LEU:HD13	2.03	0.40
11:O:103:ALA:HB1	11:O:105:GLU:OE1	2.20	0.40
13:Q:26:GLU:OE1	13:Q:26:GLU:N	2.55	0.40
14:R:85:SER:O	14:R:89:THR:HG23	2.22	0.40
15:S:80:LEU:HD21	15:S:84:ARG:CZ	2.51	0.40
1:A:1542:A:HO2'	1:A:1544:C:N4	2.19	0.40
1:A:1759:U:O2'	1:A:1760:A:O5'	2.40	0.40
9:L:119:THR:HG22	9:L:120:VAL:N	2.36	0.40
20:X:30:VAL:HG12	20:X:31:ASP:OD1	2.22	0.40
1:A:2855:G:OP1	4:F:78:ARG:NH2	2.55	0.40
6:H:8:TYR:HA	6:H:12:ILE:HD12	2.01	0.40

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	
3	E	270/277 (98%)	256 (95%)	12 (4%)	2 (1%)	18	52
4	F	204/209 (98%)	187 (92%)	17 (8%)	0	100	100
5	G	203/207 (98%)	184 (91%)	19 (9%)	0	100	100
6	H	174/179 (97%)	166 (95%)	8 (5%)	0	100	100
7	I	173/179 (97%)	153 (88%)	20 (12%)	0	100	100
8	K	130/141 (92%)	115 (88%)	15 (12%)	0	100	100
9	L	107/166 (64%)	106 (99%)	1 (1%)	0	100	100
10	N	140/145 (97%)	127 (91%)	13 (9%)	0	100	100
11	O	120/122 (98%)	105 (88%)	15 (12%)	0	100	100
12	P	144/146 (99%)	136 (94%)	8 (6%)	0	100	100
13	Q	133/144 (92%)	117 (88%)	16 (12%)	0	100	100
14	R	117/120 (98%)	106 (91%)	11 (9%)	0	100	100
15	S	118/120 (98%)	105 (89%)	12 (10%)	1 (1%)	16	50
16	T	113/115 (98%)	105 (93%)	8 (7%)	0	100	100
17	U	115/119 (97%)	106 (92%)	8 (7%)	1 (1%)	14	47
18	V	98/102 (96%)	80 (82%)	18 (18%)	0	100	100
19	W	107/113 (95%)	94 (88%)	13 (12%)	0	100	100
20	X	88/95 (93%)	83 (94%)	5 (6%)	0	100	100
21	Y	99/103 (96%)	84 (85%)	15 (15%)	0	100	100
23	a	79/94 (84%)	71 (90%)	8 (10%)	0	100	100
24	b	56/62 (90%)	50 (89%)	6 (11%)	0	100	100
25	c	63/66 (96%)	61 (97%)	2 (3%)	0	100	100
26	d	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
27	f	51/59 (86%)	47 (92%)	4 (8%)	0	100	100
28	g	46/49 (94%)	41 (89%)	5 (11%)	0	100	100
29	h	42/44 (96%)	41 (98%)	1 (2%)	0	100	100
30	i	62/66 (94%)	59 (95%)	3 (5%)	0	100	100
31	j	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
32	1	81/86 (94%)	79 (98%)	2 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	0	518/599 (86%)	476 (92%)	39 (8%)	3 (1%)	21	56
All	All	3742/4023 (93%)	3428 (92%)	307 (8%)	7 (0%)	44	73

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	E	156	ARG
15	S	2	ILE
33	0	491	PRO
3	E	155	VAL
33	0	447	ASN
33	0	538	LYS
17	U	90	VAL

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	
3	E	220/225 (98%)	220 (100%)	0	100	100
4	F	167/170 (98%)	167 (100%)	0	100	100
5	G	169/170 (99%)	169 (100%)	0	100	100
6	H	151/154 (98%)	146 (97%)	5 (3%)	33	65
7	I	148/151 (98%)	148 (100%)	0	100	100
8	K	102/110 (93%)	102 (100%)	0	100	100
9	L	98/138 (71%)	97 (99%)	1 (1%)	68	80
10	N	120/123 (98%)	120 (100%)	0	100	100
11	O	101/101 (100%)	101 (100%)	0	100	100
12	P	110/110 (100%)	110 (100%)	0	100	100
13	Q	109/116 (94%)	109 (100%)	0	100	100
14	R	99/100 (99%)	99 (100%)	0	100	100
15	S	93/93 (100%)	93 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	T	100/100 (100%)	100 (100%)	0	100	100
17	U	96/98 (98%)	96 (100%)	0	100	100
18	V	83/84 (99%)	83 (100%)	0	100	100
19	W	90/93 (97%)	90 (100%)	0	100	100
20	X	81/85 (95%)	81 (100%)	0	100	100
21	Y	85/87 (98%)	85 (100%)	0	100	100
23	a	63/74 (85%)	63 (100%)	0	100	100
24	b	47/50 (94%)	47 (100%)	0	100	100
25	c	56/57 (98%)	56 (100%)	0	100	100
26	d	52/53 (98%)	52 (100%)	0	100	100
27	f	47/53 (89%)	47 (100%)	0	100	100
28	g	46/47 (98%)	46 (100%)	0	100	100
29	h	39/39 (100%)	39 (100%)	0	100	100
30	i	54/56 (96%)	54 (100%)	0	100	100
31	j	35/35 (100%)	35 (100%)	0	100	100
32	1	73/75 (97%)	72 (99%)	1 (1%)	59	77
33	0	374/527 (71%)	374 (100%)	0	100	100
All	All	3108/3374 (92%)	3101 (100%)	7 (0%)	85	89

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	H	85	ILE
6	H	117	VAL
6	H	120	LYS
6	H	150	ARG
6	H	165	GLU
9	L	14	GLU
32	1	63	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
5	G	10	ASN
6	H	178	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
13	Q	13	HIS
17	U	38	GLN
17	U	101	ASN
19	W	37	ASN
19	W	97	ASN
21	Y	2	HIS
21	Y	53	GLN
21	Y	67	ASN
25	c	16	GLN
33	0	259	HIS
33	0	326	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2808/2926 (95%)	667 (23%)	61 (2%)
2	B	111/119 (93%)	30 (27%)	3 (2%)
22	2	67/76 (88%)	15 (22%)	3 (4%)
All	All	2986/3121 (95%)	712 (23%)	67 (2%)

All (712) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	13	A
1	A	14	A
1	A	15	G
1	A	23	G
1	A	26	G
1	A	34	U
1	A	35	G
1	A	36	G
1	A	46	C
1	A	55	G
1	A	61	A
1	A	62	C
1	A	63	G
1	A	71	A
1	A	74	U
1	A	75	G
1	A	76	C
1	A	77	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	78	U
1	A	79	C
1	A	80	G
1	A	84	A
1	A	85	G
1	A	86	C
1	A	87	U
1	A	89	U
1	A	90	A
1	A	92	G
1	A	93	C
1	A	96	G
1	A	101	G
1	A	117	A
1	A	118	A
1	A	119	U
1	A	125	A
1	A	126	A
1	A	133	A
1	A	141	U
1	A	150	A
1	A	164	U
1	A	175	G
1	A	176	A
1	A	178	A
1	A	179	A
1	A	183	A
1	A	184	G
1	A	185	A
1	A	188	C
1	A	189	G
1	A	191	G
1	A	199	A
1	A	200	A
1	A	202	A
1	A	216	A
1	A	219	A
1	A	224	A
1	A	225	A
1	A	226	A
1	A	227	G
1	A	229	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	231	A
1	A	232	U
1	A	233	G
1	A	234	C
1	A	235	G
1	A	236	A
1	A	244	A
1	A	251	G
1	A	252	C
1	A	253	G
1	A	258	A
1	A	266	U
1	A	267	C
1	A	270	C
1	A	275	A
1	A	283	G
1	A	284	C
1	A	286	U
1	A	287	G
1	A	288	C
1	A	290	U
1	A	291	C
1	A	298	U
1	A	301	U
1	A	302	A
1	A	309	U
1	A	310	C
1	A	314	A
1	A	321	U
1	A	329	A
1	A	345	A
1	A	346	G
1	A	348	U
1	A	349	C
1	A	360	C
1	A	367	G
1	A	368	G
1	A	373	A
1	A	374	A
1	A	375	C
1	A	379	C
1	A	387	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	394	U
1	A	402	U
1	A	405	U
1	A	407	A
1	A	410	G
1	A	411	G
1	A	412	A
1	A	413	U
1	A	418	A
1	A	419	G
1	A	420	U
1	A	421	A
1	A	427	G
1	A	432	C
1	A	433	G
1	A	434	U
1	A	435	G
1	A	444	U
1	A	458	G
1	A	471	G
1	A	483	C
1	A	491	C
1	A	495	U
1	A	498	U
1	A	502	C
1	A	504	A
1	A	505	G
1	A	528	G
1	A	529	C
1	A	533	C
1	A	542	G
1	A	550	G
1	A	551	A
1	A	554	U
1	A	555	C
1	A	556	C
1	A	559	A
1	A	564	G
1	A	573	C
1	A	576	G
1	A	577	U
1	A	578	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	579	G
1	A	592	A
1	A	593	A
1	A	594	C
1	A	595	G
1	A	599	G
1	A	607	G
1	A	615	U
1	A	617	G
1	A	618	A
1	A	619	A
1	A	631	G
1	A	646	A
1	A	647	A
1	A	648	G
1	A	649	G
1	A	658	A
1	A	659	A
1	A	662	U
1	A	667	A
1	A	673	A
1	A	677	A
1	A	683	A
1	A	690	A
1	A	691	U
1	A	700	U
1	A	701	G
1	A	702	A
1	A	733	U
1	A	752	A
1	A	764	C
1	A	765	A
1	A	777	C
1	A	787	C
1	A	788	G
1	A	792	G
1	A	794	U
1	A	795	G
1	A	804	G
1	A	810	G
1	A	811	A
1	A	812	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	822	G
1	A	829	A
1	A	830	A
1	A	831	U
1	A	832	G
1	A	837	U
1	A	838	C
1	A	839	G
1	A	847	A
1	A	852	G
1	A	859	C
1	A	866	A
1	A	874	U
1	A	875	U
1	A	877	G
1	A	892	U
1	A	908	A
1	A	913	A
1	A	916	G
1	A	918	U
1	A	929	G
1	A	939	G
1	A	940	G
1	A	942	U
1	A	943	A
1	A	944	C
1	A	946	G
1	A	948	A
1	A	954	U
1	A	957	A
1	A	959	C
1	A	961	C
1	A	962	C
1	A	964	A
1	A	973	G
1	A	977	U
1	A	978	A
1	A	979	U
1	A	980	C
1	A	987	A
1	A	991	A
1	A	992	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	999	A
1	A	1003	A
1	A	1005	A
1	A	1007	G
1	A	1019	A
1	A	1020	A
1	A	1029	A
1	A	1036	A
1	A	1037	C
1	A	1042	A
1	A	1051	C
1	A	1058	U
1	A	1059	A
1	A	1063	G
1	A	1067	A
1	A	1068	G
1	A	1069	U
1	A	1071	G
1	A	1073	A
1	A	1079	U
1	A	1081	U
1	A	1084	A
1	A	1085	G
1	A	1091	U
1	A	1092	A
1	A	1093	G
1	A	1102	G
1	A	1103	A
1	A	1108	G
1	A	1115	A
1	A	1116	A
1	A	1118	C
1	A	1119	A
1	A	1129	U
1	A	1130	A
1	A	1133	G
1	A	1134	A
1	A	1143	U
1	A	1147	U
1	A	1156	G
1	A	1157	A
1	A	1158	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1159	U
1	A	1160	G
1	A	1161	A
1	A	1162	C
1	A	1163	U
1	A	1173	A
1	A	1174	A
1	A	1175	A
1	A	1176	U
1	A	1177	G
1	A	1179	A
1	A	1181	C
1	A	1182	G
1	A	1185	G
1	A	1188	A
1	A	1189	A
1	A	1197	A
1	A	1201	A
1	A	1203	G
1	A	1209	G
1	A	1236	G
1	A	1251	U
1	A	1252	G
1	A	1259	G
1	A	1260	A
1	A	1278	G
1	A	1284	A
1	A	1293	A
1	A	1295	U
1	A	1296	G
1	A	1305	A
1	A	1306	G
1	A	1307	U
1	A	1311	G
1	A	1312	A
1	A	1313	A
1	A	1314	A
1	A	1315	G
1	A	1319	G
1	A	1323	A
1	A	1333	C
1	A	1339	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1340	A
1	A	1341	U
1	A	1343	C
1	A	1346	A
1	A	1351	U
1	A	1352	U
1	A	1363	G
1	A	1364	C
1	A	1365	U
1	A	1366	C
1	A	1368	U
1	A	1370	C
1	A	1371	G
1	A	1372	C
1	A	1375	A
1	A	1376	G
1	A	1380	U
1	A	1384	C
1	A	1385	G
1	A	1388	A
1	A	1389	C
1	A	1391	U
1	A	1404	A
1	A	1417	A
1	A	1418	U
1	A	1424	A
1	A	1425	C
1	A	1426	A
1	A	1427	G
1	A	1428	G
1	A	1431	G
1	A	1434	A
1	A	1435	U
1	A	1436	U
1	A	1442	A
1	A	1448	U
1	A	1449	C
1	A	1451	U
1	A	1459	U
1	A	1460	G
1	A	1465	A
1	A	1466	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1472	G
1	A	1473	A
1	A	1474	C
1	A	1476	C
1	A	1481	G
1	A	1489	U
1	A	1490	A
1	A	1499	A
1	A	1500	U
1	A	1501	U
1	A	1502	G
1	A	1506	A
1	A	1507	U
1	A	1508	C
1	A	1516	A
1	A	1525	G
1	A	1526	G
1	A	1527	C
1	A	1528	U
1	A	1529	G
1	A	1530	G
1	A	1531	G
1	A	1532	A
1	A	1533	A
1	A	1536	A
1	A	1539	C
1	A	1540	A
1	A	1542	A
1	A	1543	U
1	A	1545	C
1	A	1550	C
1	A	1551	C
1	A	1553	A
1	A	1556	A
1	A	1558	G
1	A	1559	C
1	A	1560	U
1	A	1561	G
1	A	1566	G
1	A	1568	G
1	A	1569	A
1	A	1570	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1571	G
1	A	1576	G
1	A	1577	C
1	A	1595	U
1	A	1602	U
1	A	1608	A
1	A	1614	A
1	A	1615	A
1	A	1617	A
1	A	1626	U
1	A	1632	G
1	A	1652	C
1	A	1653	A
1	A	1655	A
1	A	1661	A
1	A	1672	A
1	A	1684	U
1	A	1685	A
1	A	1692	U
1	A	1693	C
1	A	1696	G
1	A	1697	A
1	A	1699	A
1	A	1700	A
1	A	1705	C
1	A	1708	U
1	A	1710	A
1	A	1712	G
1	A	1713	A
1	A	1719	G
1	A	1738	U
1	A	1743	A
1	A	1745	A
1	A	1748	G
1	A	1757	G
1	A	1758	U
1	A	1759	U
1	A	1760	A
1	A	1761	G
1	A	1762	G
1	A	1766	C
1	A	1767	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1768	A
1	A	1771	C
1	A	1776	A
1	A	1778	A
1	A	1779	G
1	A	1782	G
1	A	1785	G
1	A	1793	G
1	A	1802	A
1	A	1811	C
1	A	1812	A
1	A	1814	A
1	A	1820	A
1	A	1829	C
1	A	1830	G
1	A	1839	A
1	A	1841	G
1	A	1845	A
1	A	1846	G
1	A	1864	G
1	A	1865	C
1	A	1867	C
1	A	1872	C
1	A	1877	A
1	A	1882	A
1	A	1883	A
1	A	1884	G
1	A	1885	A
1	A	1887	G
1	A	1891	G
1	A	1898	G
1	A	1899	U
1	A	1904	G
1	A	1935	G
1	A	1948	A
1	A	1958	G
1	A	1959	G
1	A	1960	U
1	A	1967	A
1	A	1968	U
1	A	1969	U
1	A	1972	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1973	U
1	A	1984	U
1	A	1989	A
1	A	1993	G
1	A	1996	C
1	A	1999	A
1	A	2000	A
1	A	2001	G
1	A	2020	U
1	A	2022	U
1	A	2025	C
1	A	2026	A
1	A	2049	A
1	A	2051	U
1	A	2052	A
1	A	2054	C
1	A	2060	A
1	A	2061	G
1	A	2062	A
1	A	2064	G
1	A	2072	C
1	A	2078	A
1	A	2081	G
1	A	2084	C
1	A	2085	G
1	A	2089	A
1	A	2090	G
1	A	2098	G
1	A	2109	G
1	A	2121	U
1	A	2123	A
1	A	2125	U
1	A	2128	U
1	A	2129	G
1	A	2219	G
1	A	2227	A
1	A	2228	A
1	A	2232	G
1	A	2233	C
1	A	2240	U
1	A	2245	G
1	A	2246	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	2249	G
1	A	2252	A
1	A	2254	A
1	A	2255	C
1	A	2267	G
1	A	2268	G
1	A	2280	G
1	A	2296	A
1	A	2308	G
1	A	2312	C
1	A	2315	A
1	A	2316	A
1	A	2317	A
1	A	2323	C
1	A	2325	U
1	A	2331	U
1	A	2333	G
1	A	2334	U
1	A	2335	U
1	A	2336	G
1	A	2338	A
1	A	2339	A
1	A	2340	A
1	A	2341	U
1	A	2343	A
1	A	2345	U
1	A	2347	G
1	A	2348	C
1	A	2349	A
1	A	2350	G
1	A	2351	A
1	A	2354	G
1	A	2356	A
1	A	2363	C
1	A	2364	A
1	A	2374	G
1	A	2376	C
1	A	2379	C
1	A	2390	A
1	A	2401	G
1	A	2412	G
1	A	2414	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	2415	U
1	A	2417	A
1	A	2420	G
1	A	2421	A
1	A	2425	G
1	A	2430	U
1	A	2431	U
1	A	2435	C
1	A	2451	C
1	A	2452	U
1	A	2453	C
1	A	2454	A
1	A	2455	A
1	A	2458	G
1	A	2459	A
1	A	2460	U
1	A	2464	A
1	A	2468	A
1	A	2469	C
1	A	2470	C
1	A	2474	G
1	A	2476	G
1	A	2477	A
1	A	2488	A
1	A	2505	A
1	A	2507	A
1	A	2509	C
1	A	2511	A
1	A	2520	U
1	A	2523	G
1	A	2527	C
1	A	2531	G
1	A	2532	A
1	A	2533	U
1	A	2534	G
1	A	2542	A
1	A	2547	A
1	A	2548	U
1	A	2549	C
1	A	2564	G
1	A	2583	U
1	A	2591	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	2595	A
1	A	2596	G
1	A	2598	G
1	A	2601	A
1	A	2602	C
1	A	2607	G
1	A	2611	G
1	A	2613	U
1	A	2631	A
1	A	2632	G
1	A	2638	U
1	A	2639	C
1	A	2642	U
1	A	2644	U
1	A	2652	G
1	A	2659	G
1	A	2665	U
1	A	2674	G
1	A	2689	A
1	A	2690	G
1	A	2696	C
1	A	2711	G
1	A	2714	G
1	A	2718	U
1	A	2720	C
1	A	2743	G
1	A	2755	U
1	A	2762	A
1	A	2764	G
1	A	2765	G
1	A	2773	G
1	A	2779	A
1	A	2785	U
1	A	2789	C
1	A	2794	A
1	A	2798	C
1	A	2806	G
1	A	2807	A
1	A	2808	U
1	A	2818	C
1	A	2820	U
1	A	2823	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	2824	G
1	A	2826	A
1	A	2831	A
1	A	2843	G
1	A	2859	G
1	A	2860	A
1	A	2868	G
1	A	2886	C
1	A	2892	G
1	A	2897	G
1	A	2899	C
1	A	2900	A
1	A	2901	G
1	A	2905	C
1	A	2911	G
1	A	2916	A
1	A	2917	G
1	A	2918	G
1	A	2925	C
2	B	10	G
2	B	13	A
2	B	15	C
2	B	19	G
2	B	22	G
2	B	23	U
2	B	24	C
2	B	32	U
2	B	33	U
2	B	35	C
2	B	38	U
2	B	39	A
2	B	40	C
2	B	48	G
2	B	49	G
2	B	50	A
2	B	53	U
2	B	54	U
2	B	55	A
2	B	56	A
2	B	62	U
2	B	85	U
2	B	86	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	87	U
2	B	88	C
2	B	97	A
2	B	101	U
2	B	107	G
2	B	108	C
2	B	110	G
22	2	8	U
22	2	20	G
22	2	21	A
22	2	22	G
22	2	29	U
22	2	30	G
22	2	32	U
22	2	37	A
22	2	48	C
22	2	49	A
22	2	58	A
22	2	59	U
22	2	61	C
22	2	75	C
22	2	76	A

All (67) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	88	G
1	A	92	G
1	A	175	G
1	A	224	A
1	A	252	C
1	A	347	G
1	A	411	G
1	A	443	G
1	A	528	G
1	A	549	A
1	A	554	U
1	A	558	G
1	A	631	G
1	A	689	A
1	A	751	G
1	A	831	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	976	U
1	A	1036	A
1	A	1066	A
1	A	1172	A
1	A	1250	G
1	A	1294	A
1	A	1305	A
1	A	1313	A
1	A	1339	A
1	A	1351	U
1	A	1435	U
1	A	1448	U
1	A	1507	U
1	A	1525	G
1	A	1530	G
1	A	1565	U
1	A	1567	U
1	A	1570	U
1	A	1631	A
1	A	1671	G
1	A	1691	A
1	A	1758	U
1	A	1784	A
1	A	1813	A
1	A	1828	G
1	A	1882	A
1	A	1883	A
1	A	1886	G
1	A	1947	A
1	A	2127	U
1	A	2254	A
1	A	2295	A
1	A	2316	A
1	A	2335	U
1	A	2336	G
1	A	2338	A
1	A	2344	U
1	A	2420	G
1	A	2452	U
1	A	2454	A
1	A	2468	A
1	A	2510	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	2631	A
1	A	2805	A
1	A	2904	A
2	B	48	G
2	B	49	G
2	B	55	A
22	2	48	C
22	2	58	A
22	2	74	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](#)

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 [i](#)

There are no chain breaks in this entry.

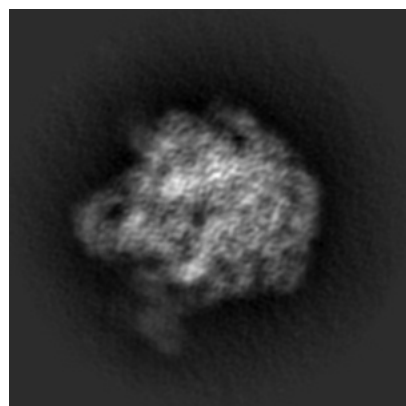
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13017. These allow visual inspection of the internal detail of the map and identification of artifacts.

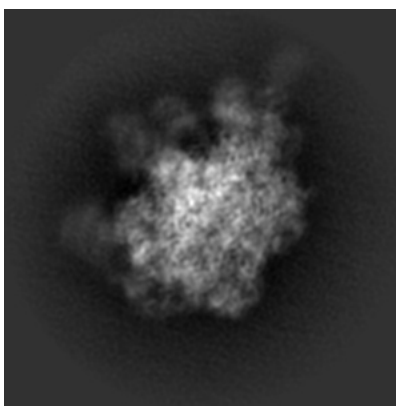
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

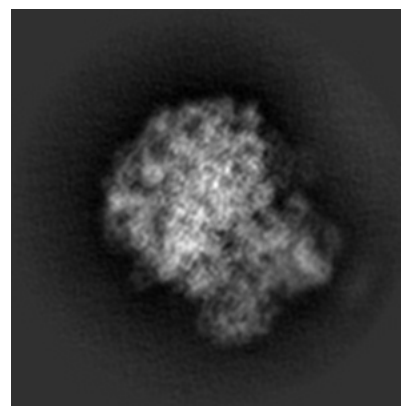
6.1.1 Primary map



X

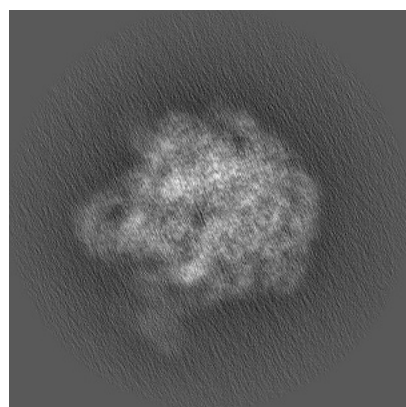


Y

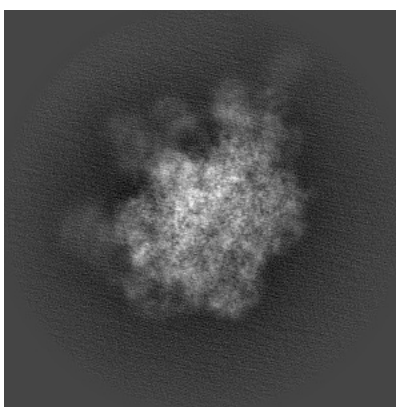


Z

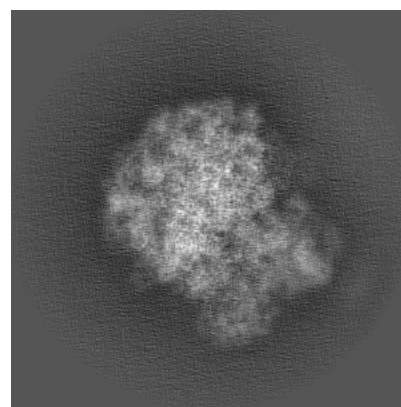
6.1.2 Raw map



X



Y

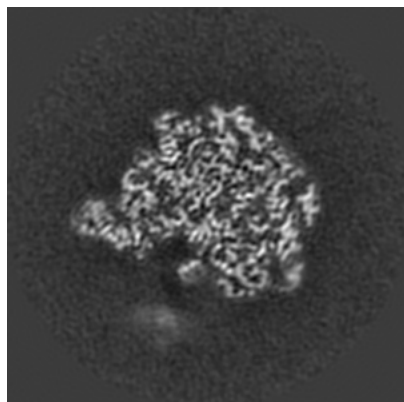


Z

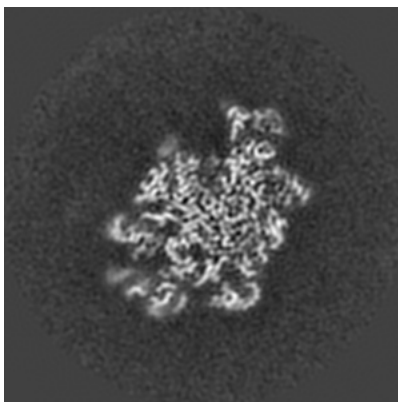
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

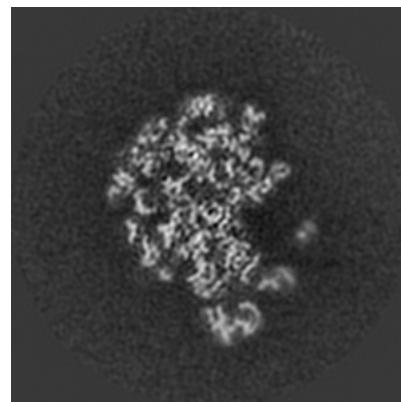
6.2.1 Primary map



X Index: 210

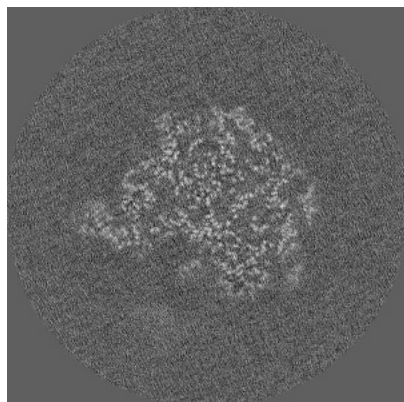


Y Index: 210

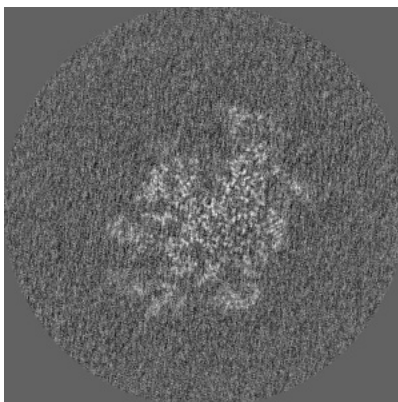


Z Index: 210

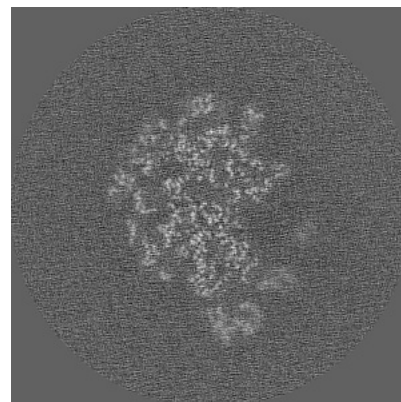
6.2.2 Raw map



X Index: 210



Y Index: 210

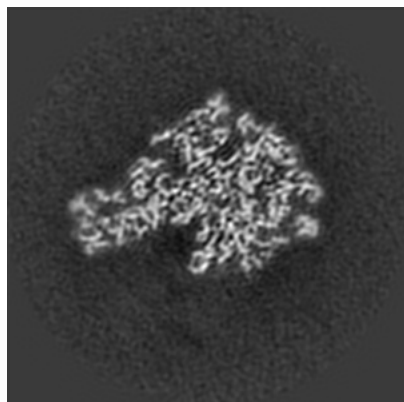


Z Index: 210

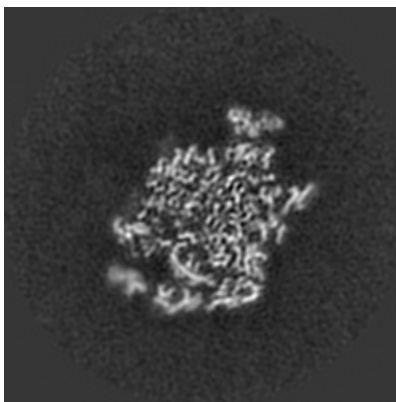
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

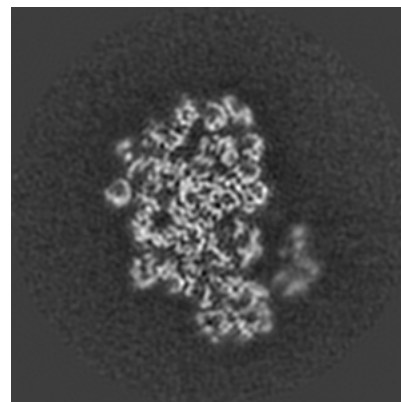
6.3.1 Primary map



X Index: 227

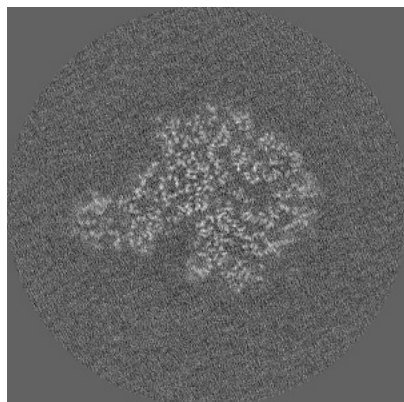


Y Index: 217

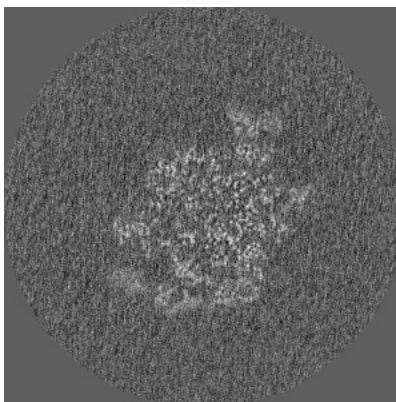


Z Index: 191

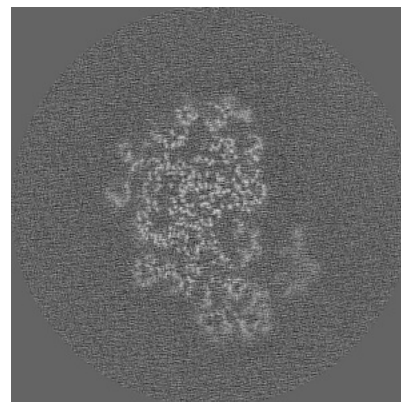
6.3.2 Raw map



X Index: 219



Y Index: 216

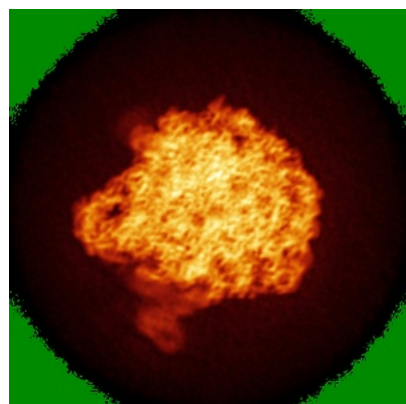


Z Index: 190

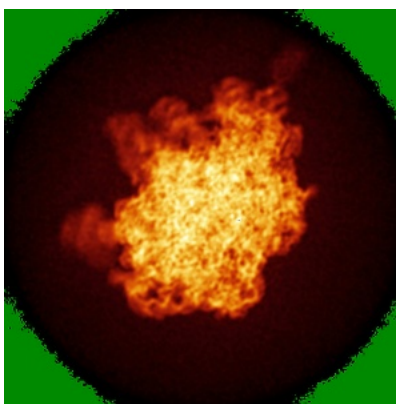
The images above show the largest variance slices of the map in three orthogonal directions.

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

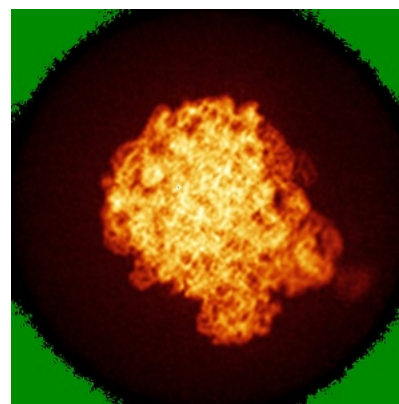
6.4.1 Primary map



X

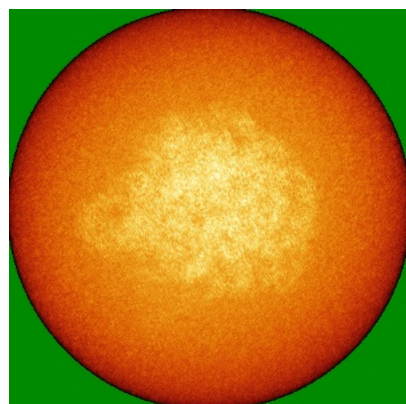


Y

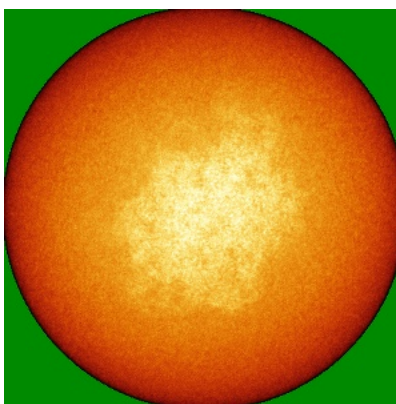


Z

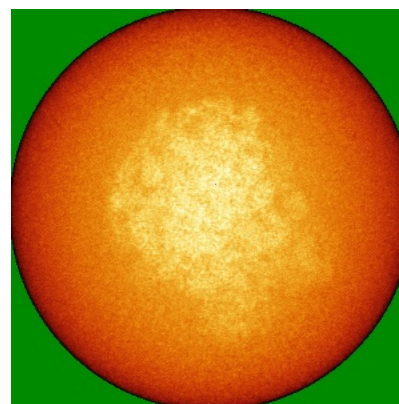
6.4.2 Raw map



X



Y

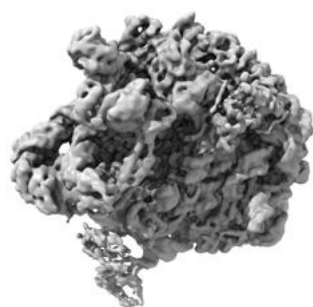


Z

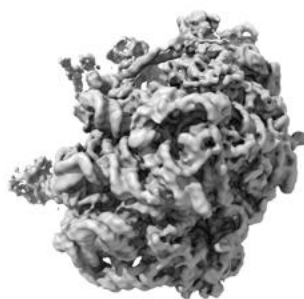
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



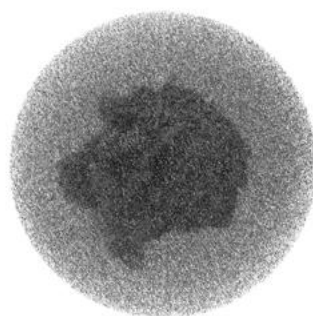
Y



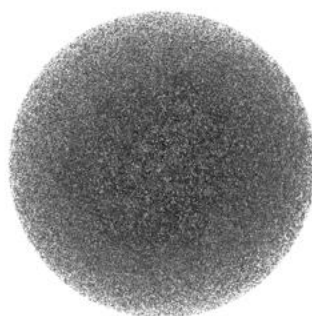
Z

The images above show the 3D surface view of the map at the recommended contour level 0.007. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

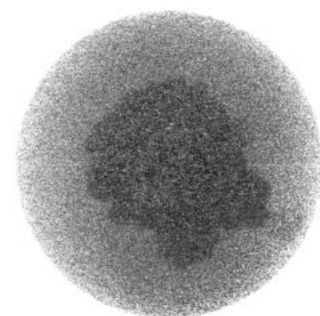
6.5.2 Raw map



X



Y



Z

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.

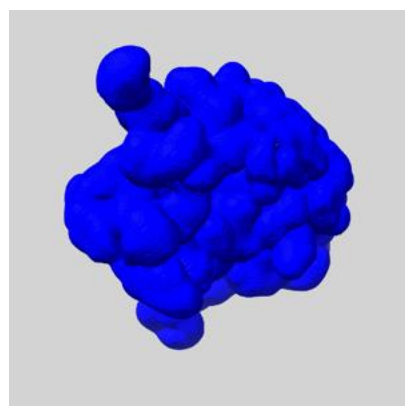
6.6 Mask visualisation [i](#)

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

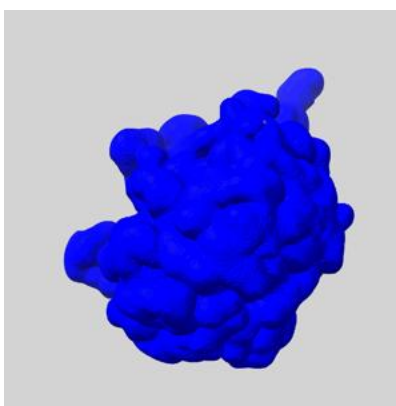
A mask typically either:

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

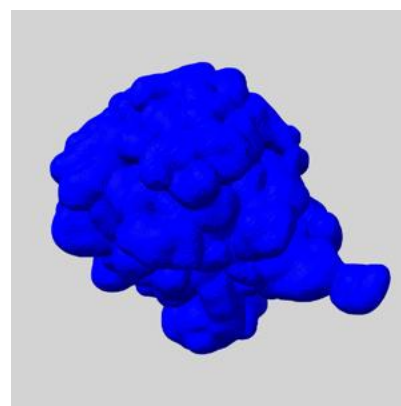
6.6.1 emd_13017_msk_1.map [i](#)



X



Y

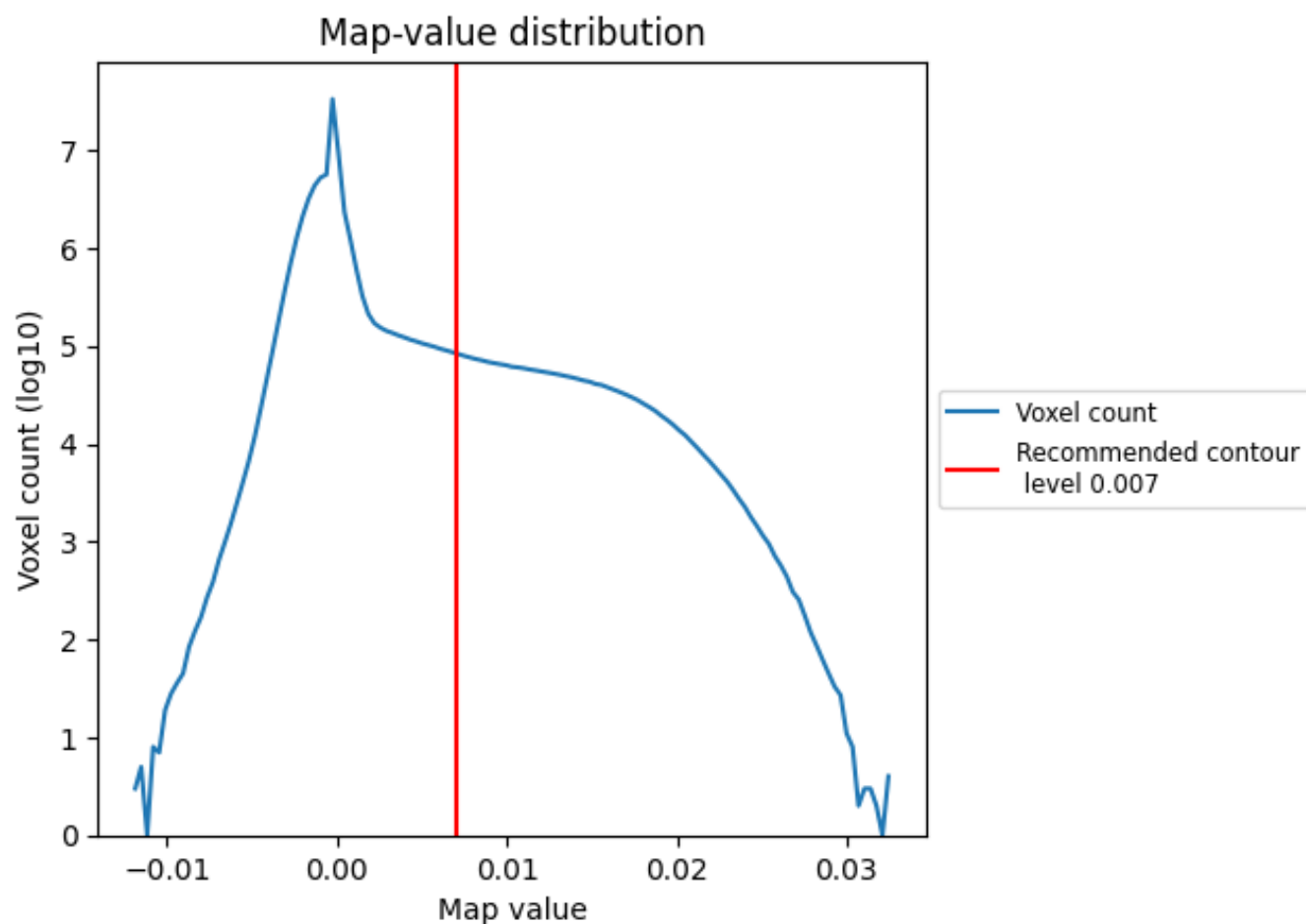


Z

7 Map analysis [i](#)

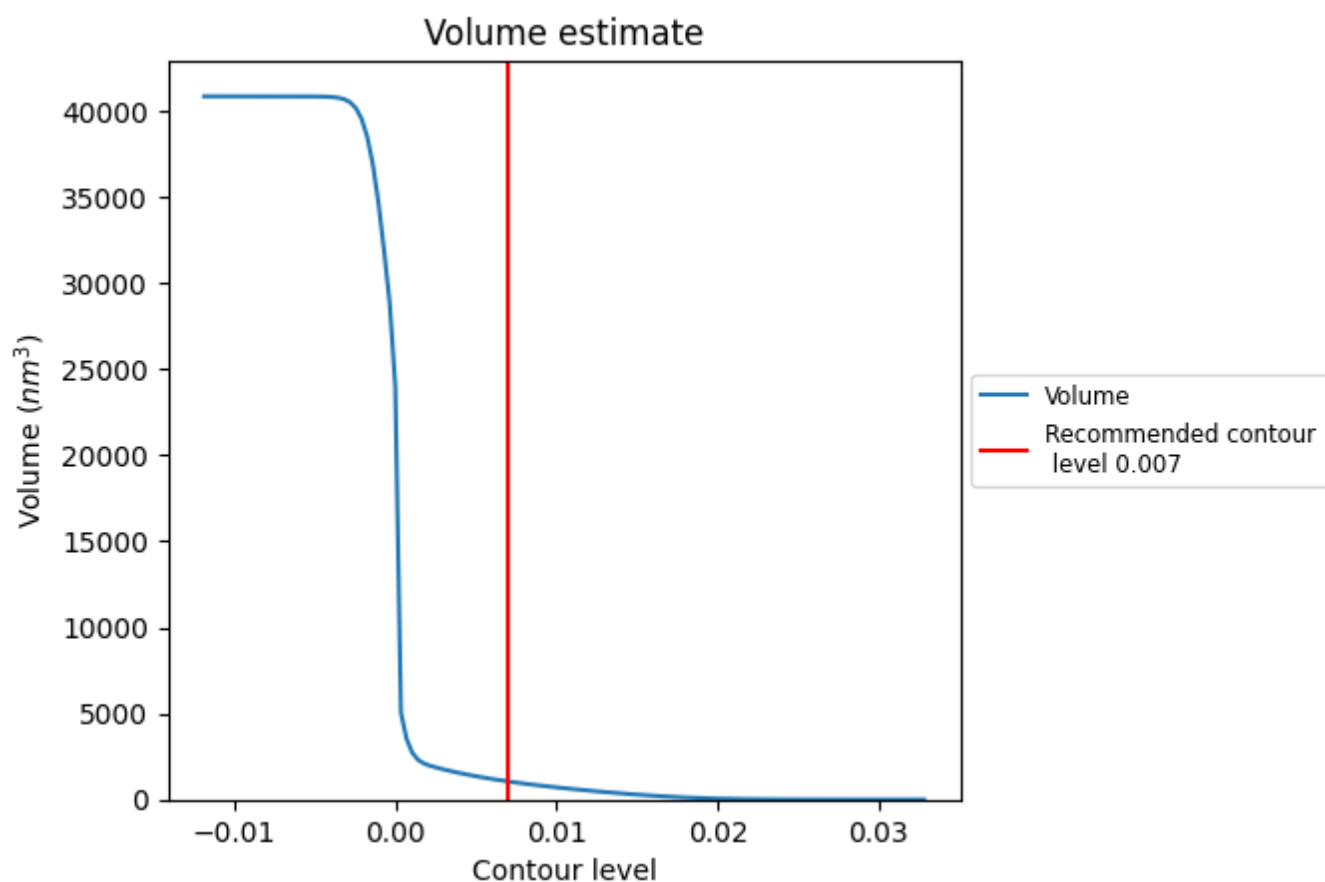
This section contains the results of statistical analysis of the map.

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.

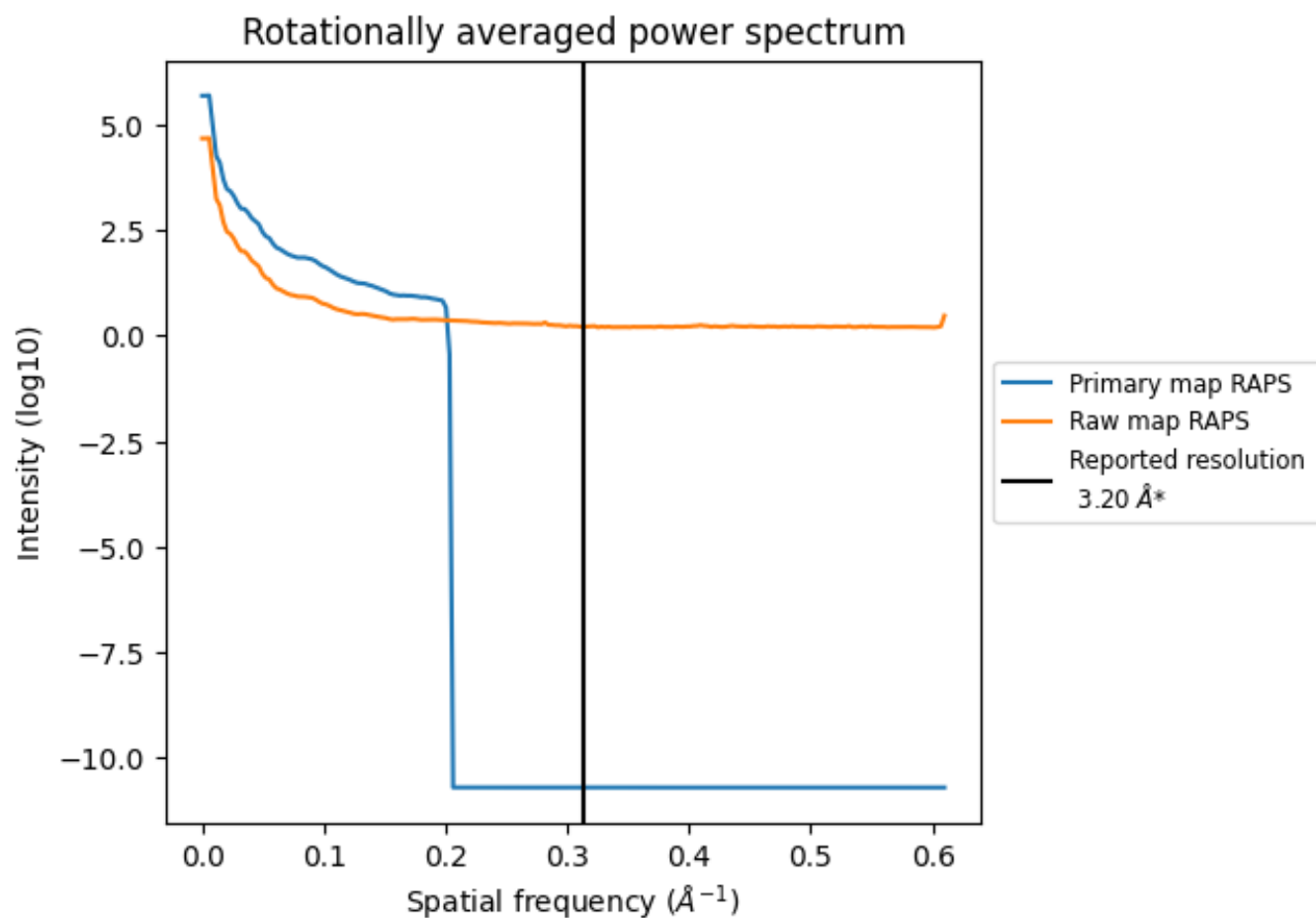
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1052 nm^3 ; this corresponds to an approximate mass of 950 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 ⓘ

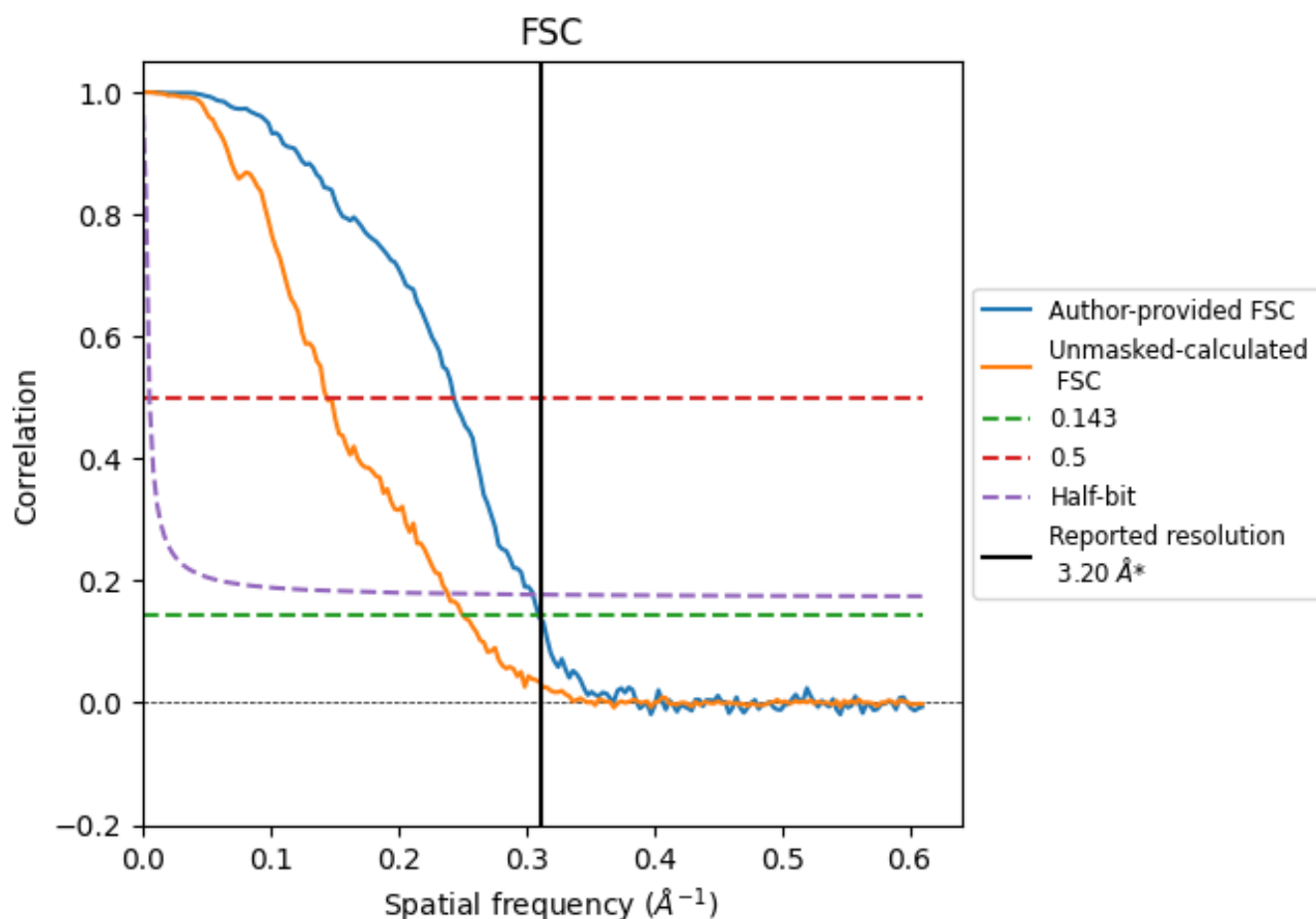


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

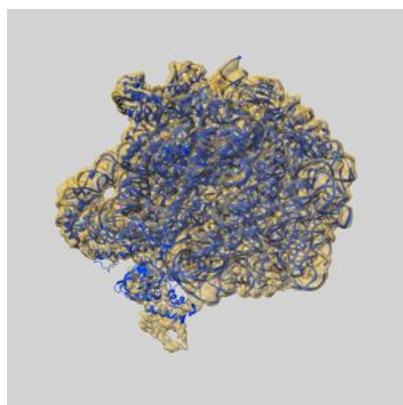
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.23	4.11	3.27
Unmasked-calculated*	3.99	6.93	4.19

*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 3.99 differs from the reported value 3.2 by more than 10 %

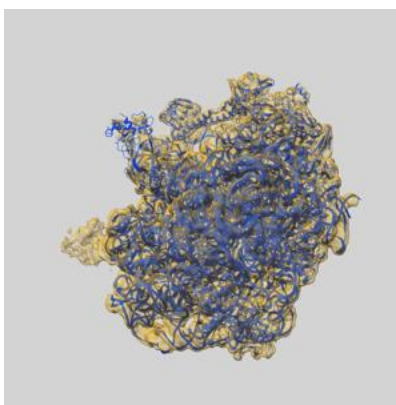
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13017 and PDB model 7OPE. Per-residue inclusion information can be found in section 3 on page 11.

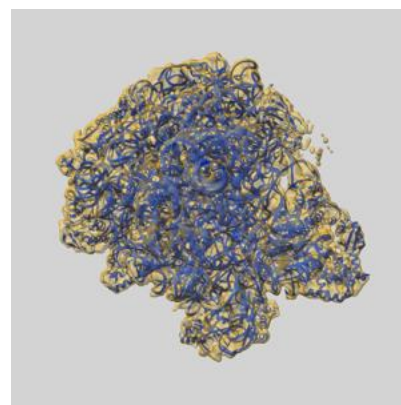
9.1 Map-model overlay [i](#)



X



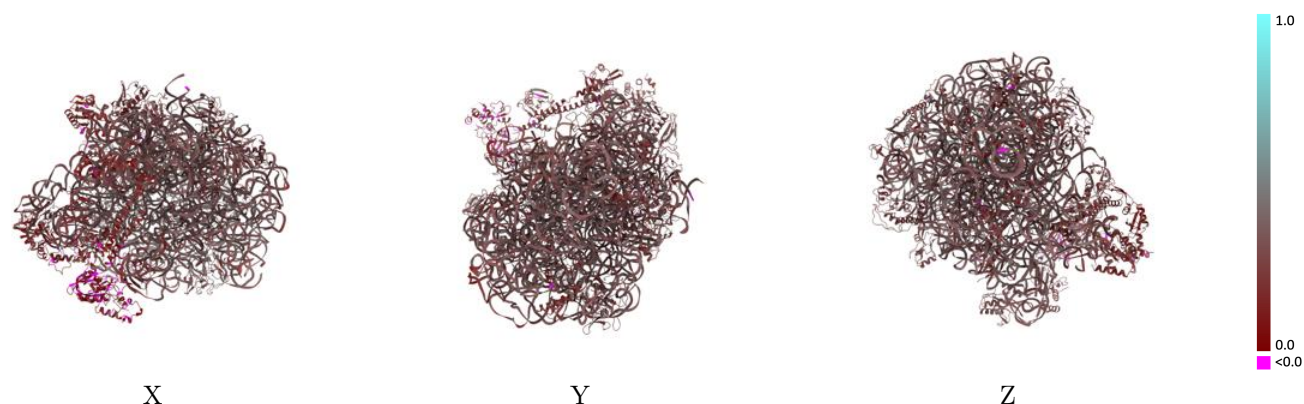
Y



Z

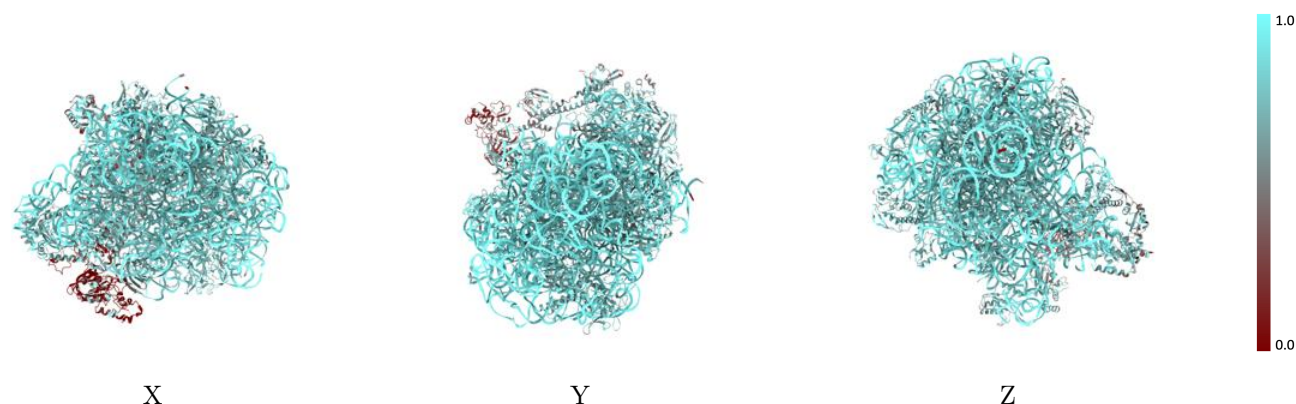
The images above show the 3D surface view of the map at the recommended contour level 0.007 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



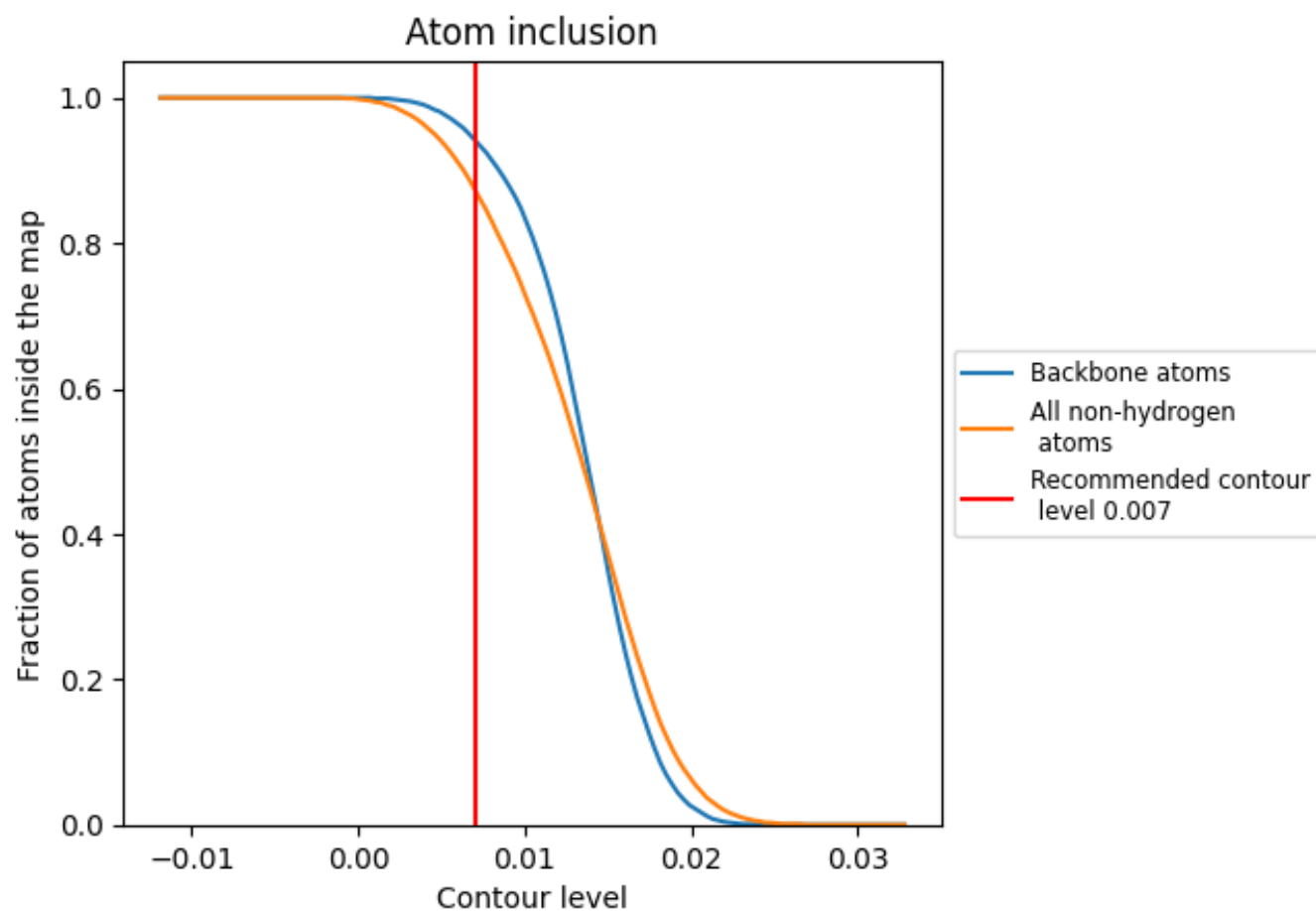
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.007).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 87% 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 (0.007) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8740	 0.3090
0	 0.3380	 0.1470
1	 0.5730	 0.2490
2	 0.9180	 0.3030
A	 0.9630	 0.3310
B	 0.9770	 0.3290
E	 0.7650	 0.2990
F	 0.7350	 0.2990
G	 0.7550	 0.2890
H	 0.6420	 0.2020
I	 0.7560	 0.2910
K	 0.6790	 0.1940
L	 0.6440	 0.2150
N	 0.7420	 0.2950
O	 0.7020	 0.2860
P	 0.7450	 0.2870
Q	 0.7620	 0.3130
R	 0.7240	 0.2620
S	 0.7470	 0.2640
T	 0.6880	 0.2960
U	 0.7630	 0.2580
V	 0.7900	 0.3270
W	 0.7630	 0.3020
X	 0.7440	 0.3020
Y	 0.7590	 0.3050
a	 0.7530	 0.2880
b	 0.5440	 0.2640
c	 0.7410	 0.2410
d	 0.7470	 0.2760
f	 0.7800	 0.3020
g	 0.7910	 0.2860
h	 0.7510	 0.2770
i	 0.7460	 0.3070
j	 0.7530	 0.2990

