



Full wwPDB EM Validation Report ⓘ

Aug 5, 2026 – 11:16 AM EDT

PDB ID : 9OJM / pdb_00009ojm
EMDB ID : EMD-70544
Title : Human mitochondrial 28S PIC with tRNA and mtIF2
Authors : Kober, D.L.; Wang, J.
Deposited on : 2025-05-08
Resolution : 2.50 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.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

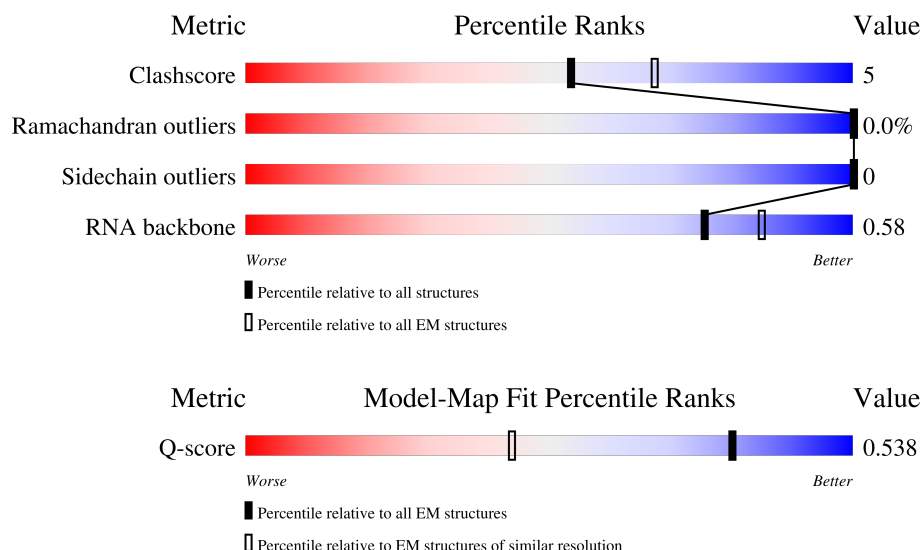
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.50 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.



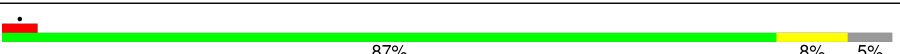
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7115 (2.00 - 3.00)

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	0	215	
2	1	278	
3	2	118	

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Mol	Chain	Length	Quality of chain
4	3	71	
5	4	616	
6	5	71	
7	6	4	
8	7	571	
9	A	955	
10	B	225	
11	C	132	
12	D	343	
13	E	122	
14	F	208	
15	G	344	
16	H	140	
17	I	137	
18	J	108	
19	K	101	
20	L	174	
21	M	119	
22	N	110	
23	O	193	
24	P	97	
25	Q	87	
26	R	295	
27	S	135	
28	T	168	

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Mol	Chain	Length	Quality of chain
29	U	176	
30	V	379	
31	W	100	
32	X	352	
33	Y	149	
34	Z	100	

2 Entry composition

There are 42 unique types of molecules in this entry. The entry contains 74356 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Small ribosomal subunit protein mS34.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	215	Total	C	N	O	S	0	0
			1787	1130	339	313	5		

- Molecule 2 is a protein called Small ribosomal subunit protein mS35.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	278	Total	C	N	O	S	0	0
			2256	1430	386	429	11		

- Molecule 3 is a protein called Coiled-coil-helix-coiled-coil-helix domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	118	Total	C	N	O	S	0	0
			935	579	182	166	8		

- Molecule 4 is a protein called Small ribosomal subunit protein mS38.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	71	Total	C	N	O	S	0	0
			629	403	135	90	1		

- Molecule 5 is a protein called Small ribosomal subunit protein mS39.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	592	Total	C	N	O	S	0	0
			4795	3070	812	885	28		

- Molecule 6 is a RNA chain called RNA (71-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	71	Total	C	N	O	P	0	0
			1498	673	264	491	70		

- Molecule 7 is a RNA chain called mRNA (5'-R(P*AP*UP*GP*U)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	4	Total	C	N	O	P	0	0
			86	38	14	30	4		

- Molecule 8 is a protein called Translation initiation factor IF-2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	571	Total	C	N	O	S	0	0
			4147	2592	741	802	12		

- Molecule 9 is a RNA chain called 12S mitochondrial RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	955	Total	C	N	O	P	0	0
			20282	9098	3652	6577	955		

- Molecule 10 is a protein called Small ribosomal subunit protein uS2m.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	225	Total	C	N	O	S	0	0
			1828	1164	331	323	10		

- Molecule 11 is a protein called 28S ribosomal protein S24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	132	Total	C	N	O	S	0	0
			1083	699	195	185	4		

- Molecule 12 is a protein called 28S ribosomal protein S5, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	D	343	Total	C	N	O	S	0	0
			2731	1713	518	487	13		

- Molecule 13 is a protein called 28S ribosomal protein S6, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	E	122	Total	C	N	O	S	0	0
			972	614	177	177	4		

- Molecule 14 is a protein called 28S ribosomal protein S7, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	208	Total	C	N	O	S	0	0
			1725	1104	312	298	11		

- Molecule 15 is a protein called Small ribosomal subunit protein uS9m.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	G	327	Total	C	N	O	S	0	0
			2688	1710	477	487	14		

- Molecule 16 is a protein called Small ribosomal subunit protein uS10m.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	H	140	Total	C	N	O	S	0	0
			1152	745	194	210	3		

- Molecule 17 is a protein called Small ribosomal subunit protein uS11m.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I	137	Total	C	N	O	S	0	0
			1019	641	193	181	4		

- Molecule 18 is a protein called 28S ribosomal protein S12, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	108	Total	C	N	O	S	0	0
			839	521	169	143	6		

- Molecule 19 is a protein called 28S ribosomal protein S14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K	101	Total	C	N	O	S	0	0
			862	537	179	141	5		

- Molecule 20 is a protein called Small ribosomal subunit protein uS15m.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	174	Total	C	N	O	S	0	0
			1453	925	270	251	7		

- Molecule 21 is a protein called Small ribosomal subunit protein bS16m.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	M	119	Total	C	N	O	S	0	0
			942	594	185	157	6		

- Molecule 22 is a protein called Small ribosomal subunit protein uS17m.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	N	110	Total	C	N	O	S	0	0
			868	562	156	147	3		

- Molecule 23 is a protein called 28S ribosomal protein S18b, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	O	193	Total	C	N	O	S	0	0
			1592	1014	294	277	7		

- Molecule 24 is a protein called 28S ribosomal protein S18c, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	P	97	Total	C	N	O	S	0	0
			781	501	134	138	8		

- Molecule 25 is a protein called 28S ribosomal protein S21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Q	87	Total	C	N	O	S	0	0
			744	460	150	126	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	50	ARG	CYS	variant	UNP P82921

- Molecule 26 is a protein called Small ribosomal subunit protein mS22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	R	295	Total	C	N	O	S	0	0
			2409	1533	413	455	8		

- Molecule 27 is a protein called 28S ribosomal protein S23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	S	135	Total	C	N	O	S	0	0
			1111	716	198	196	1		

- Molecule 28 is a protein called Small ribosomal subunit protein mS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	T	168	Total	C	N	O	S	0	0
			1371	877	239	244	11		

- Molecule 29 is a protein called Small ribosomal subunit protein mS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	U	176	Total	C	N	O	S	0	0
			1488	916	301	267	4		

- Molecule 30 is a protein called Small ribosomal subunit protein mS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	V	362	Total	C	N	O	S	0	0
			2969	1904	495	558	12		

- Molecule 31 is a protein called Small ribosomal subunit protein bS1m.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	W	100	Total	C	N	O	S	0	0
			789	498	141	146	4		

- Molecule 32 is a protein called Small ribosomal subunit protein mS29.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	X	352	Total	C	N	O	S	0	0
			2849	1822	499	517	11		

- Molecule 33 is a protein called 28S ribosomal protein S27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Y	149	Total	C	N	O	S	0	0
			1246	801	207	234	4		

- Molecule 34 is a protein called Small ribosomal subunit protein mS33.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Z	100	Total	C	N	O	S	0	0
			839	534	153	148	4		

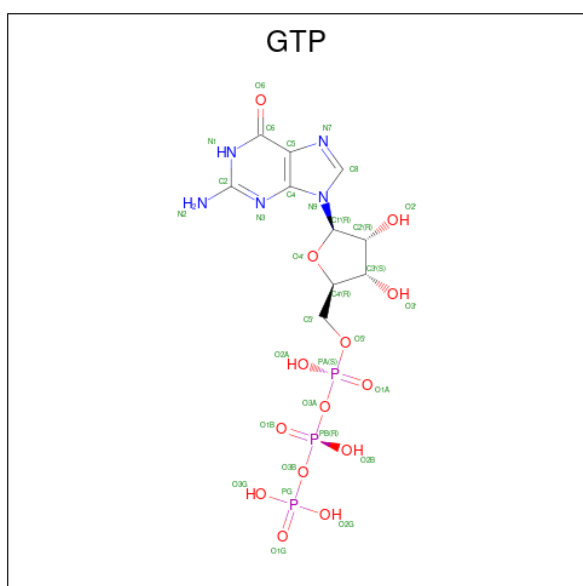
- Molecule 35 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
35	3	1	Total	Mg	0
			1	1	
35	7	1	Total	Mg	0
			1	1	
35	A	68	Total	Mg	0
			68	68	
35	B	1	Total	Mg	0
			1	1	
35	X	1	Total	Mg	0
			1	1	

- Molecule 36 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
36	7	1	Total	K	0
			1	1	
36	A	19	Total	K	0
			19	19	

- Molecule 37 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).

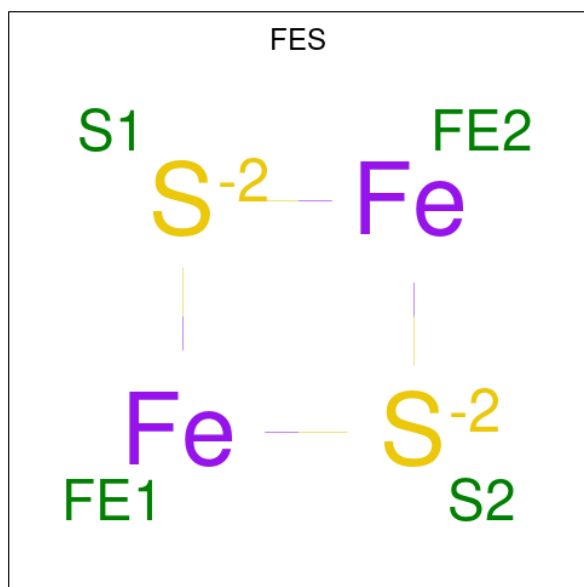


Mol	Chain	Residues	Atoms					AltConf
37	7	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 38 is ZINC ION (CCD ID: ZN) (formula: Zn).

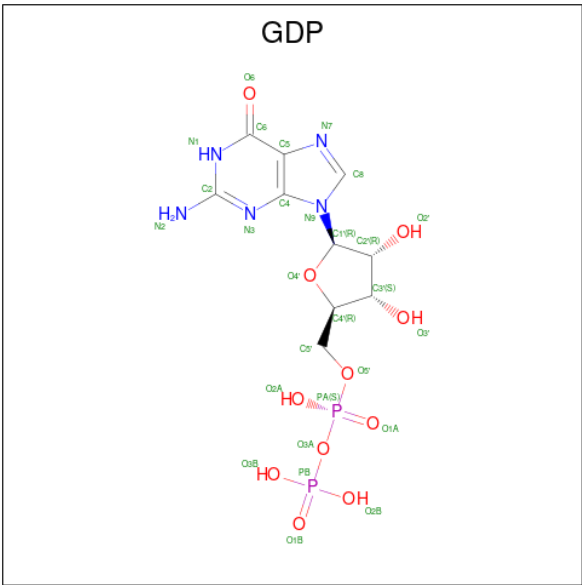
Mol	Chain	Residues	Atoms		AltConf
38	O	1	Total	Zn	0
			1	1	

- Molecule 39 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe₂S₂).



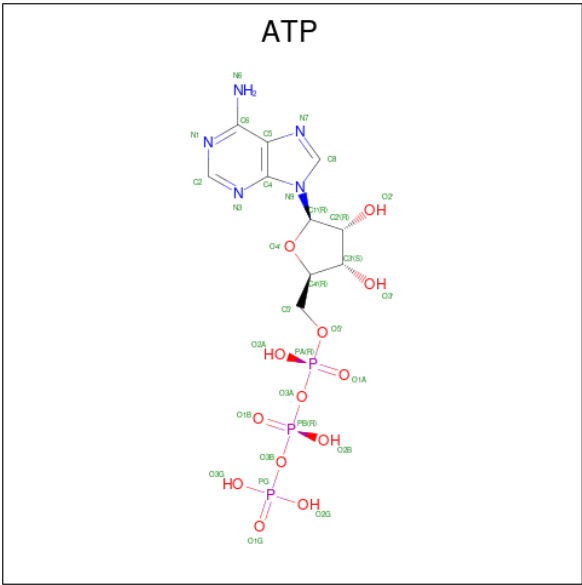
Mol	Chain	Residues	Atoms			AltConf
39	P	1	Total	Fe	S	0
			4	2	2	
39	T	1	Total	Fe	S	0
			4	2	2	

- Molecule 40 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



Mol	Chain	Residues	Atoms					AltConf
40	X	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 41 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
41	X	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 42 is water.

Mol	Chain	Residues	Atoms		AltConf
42	0	2	Total 2	O 2	0
42	1	21	Total 21	O 21	0
42	2	14	Total 14	O 14	0
42	3	10	Total 10	O 10	0
42	4	14	Total 14	O 14	0
42	5	29	Total 29	O 29	0
42	6	6	Total 6	O 6	0
42	7	14	Total 14	O 14	0
42	A	791	Total 791	O 791	0
42	B	48	Total 48	O 48	0
42	C	14	Total 14	O 14	0
42	D	47	Total 47	O 47	0
42	E	13	Total 13	O 13	0
42	F	22	Total 22	O 22	0
42	G	53	Total 53	O 53	0
42	H	23	Total 23	O 23	0
42	I	22	Total 22	O 22	0
42	J	12	Total 12	O 12	0
42	K	17	Total 17	O 17	0
42	L	30	Total 30	O 30	0
42	M	7	Total 7	O 7	0
42	N	11	Total 11	O 11	0

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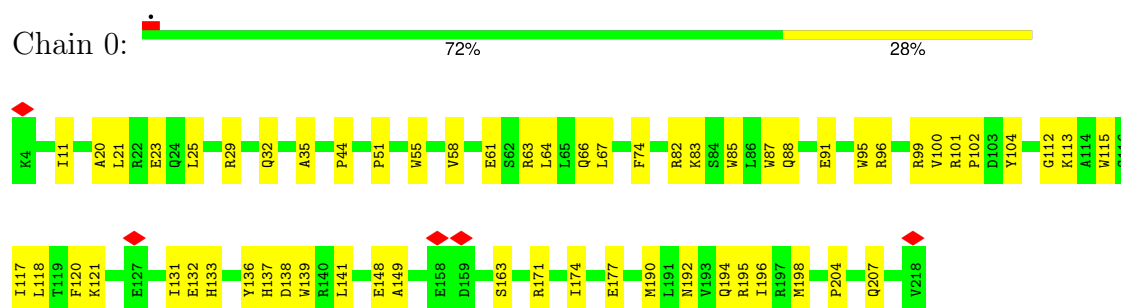
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Mol	Chain	Residues	Atoms		AltConf
42	O	37	Total 37	O 37	0
42	P	13	Total 13	O 13	0
42	Q	20	Total 20	O 20	0
42	R	12	Total 12	O 12	0
42	S	16	Total 16	O 16	0
42	T	13	Total 13	O 13	0
42	U	15	Total 15	O 15	0
42	W	15	Total 15	O 15	0
42	X	12	Total 12	O 12	0
42	Y	13	Total 13	O 13	0
42	Z	13	Total 13	O 13	0

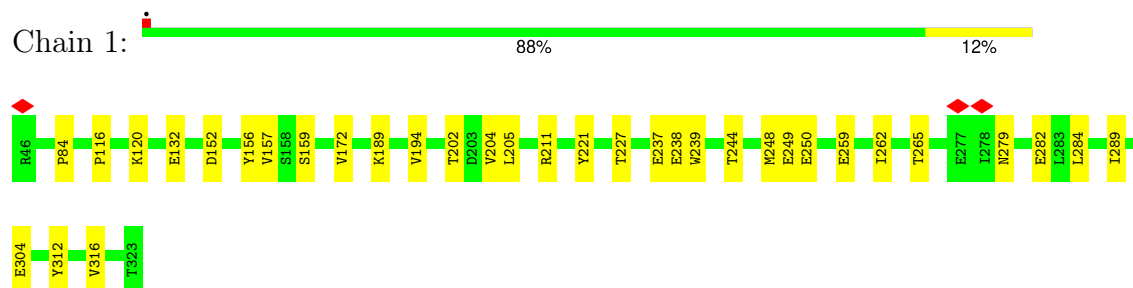
3 Residue-property plots

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.

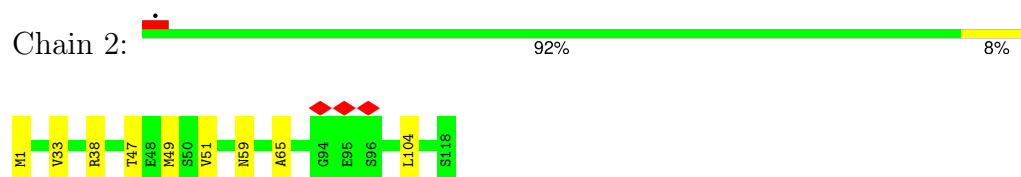
- Molecule 1: Small ribosomal subunit protein mS34



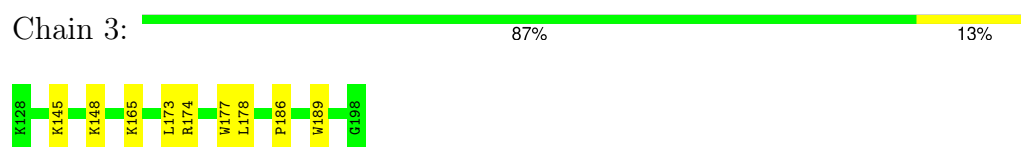
- Molecule 2: Small ribosomal subunit protein mS35



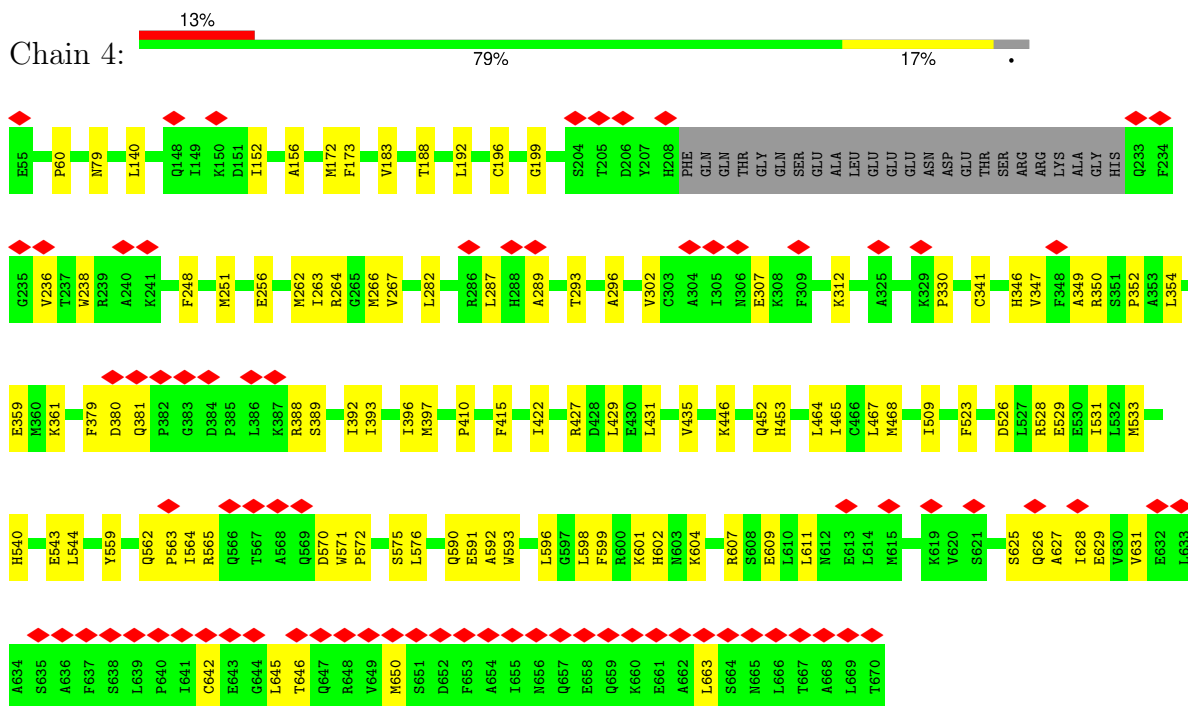
- Molecule 3: Coiled-coil-helix-coiled-coil-helix domain-containing protein 1



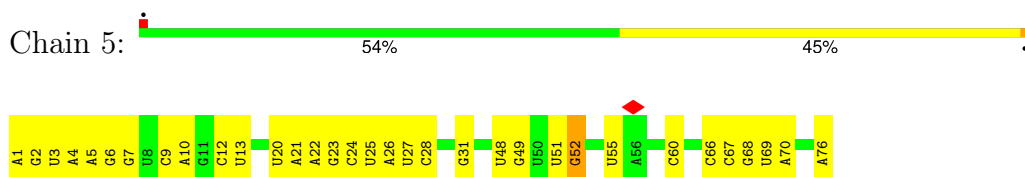
- Molecule 4: Small ribosomal subunit protein mS38



- Molecule 5: Small ribosomal subunit protein mS39



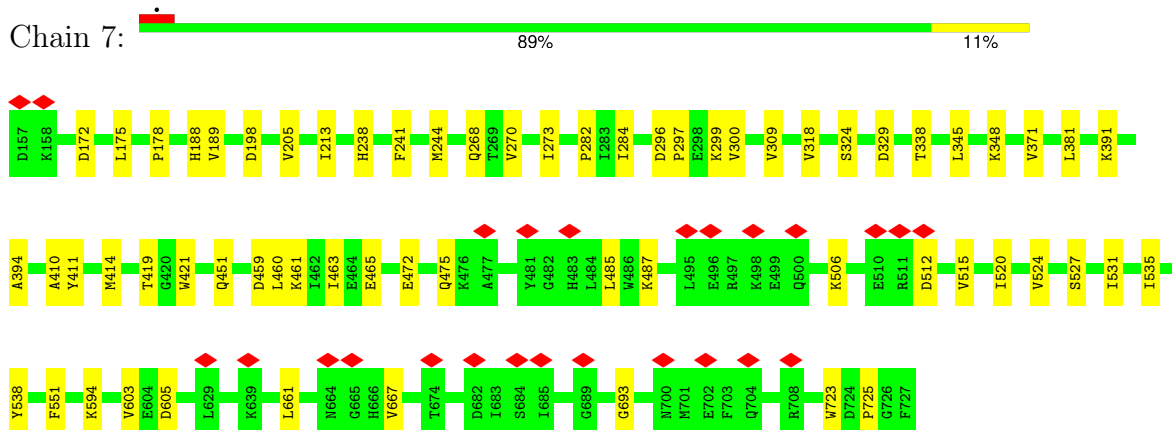
- Molecule 6: RNA (71-MER)



- Molecule 7: mRNA (5'-R(P*AP*UP*GP*U)-3')



- Molecule 8: Translation initiation factor IF-2, mitochondrial



Chain A: 68% 30%

The visualization displays the sequence of Chain A, with residues grouped into blocks. The color coding indicates the residue's environment: green for buried, yellow for interface, and red for exposed. The secondary structure is overlaid on the sequence, showing the spatial arrangement of the chain. The progress bar at the top shows the chain's progress from 68% (green/yellow) to 30% (red).

Residue blocks (from top to bottom):

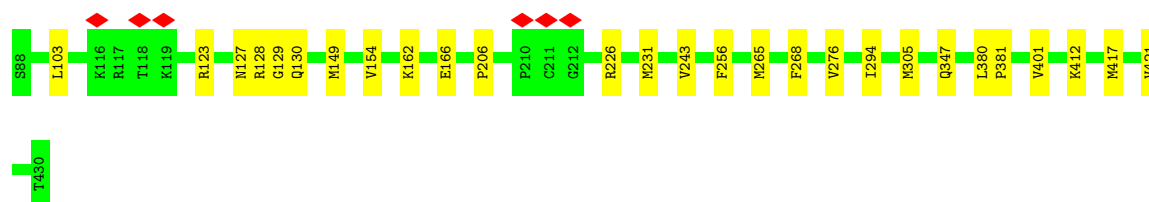
- Block 1: C1537 to C1539, U1542 to U1546, C1557 to C1562, U1568 to U1571, C1577 to C1582, U1580 to U1584, C1589 to C1590, G1594 to G1595, A1599, C1602
- Block 2: U1407 to U1430, G1438 to G1444, C1429 to C1430, U1455 to U1456, A1470 to A1471, G1472 to G1473, C1486 to C1488, U1489 to U1490, C1494 to C1494, G1497 to G1498, U1499 to U1500, U1504 to U1505, U1506 to U1507, C1508 to C1508, U1509 to U1510, C1511 to C1511, A1519 to A1521, U1522 to U1523, A1524 to A1525, U1526 to U1527, A1528 to A1529, C1533 to C1533
- Block 3: U1267 to U1275, C1273 to C1274, G1275 to G1275, U1283 to U1283, U1284 to U1284, G1285 to G1285, C1290 to C1290, U1291 to U1291, A1300 to A1300, U1308 to U1308, A1317 to A1317, A1318 to A1318, G1326 to G1326, C1330 to C1330, U1334 to U1334, G1335 to G1335, A1343 to A1343, G1348 to G1348, U1349 to U1349, A1356 to A1356, A1365 to A1365, C1366 to C1366, U1367 to U1367, U1370 to U1370, U1371 to U1371, C1372 to C1372, U1373 to U1373, A1374 to A1374, C1375 to C1375, G1376 to G1376, C1377 to C1377, U1378 to U1378, A1382 to A1382, U1526 to U1526, A1527 to A1527, A1528 to A1528, A1529 to A1529, C1533 to C1533
- Block 4: U1014 to U1015, A1019 to A1019, U1021 to U1021, A1025 to A1025, A1026 to A1026, G1027 to G1027, U1033 to U1033, U1034 to U1034, C1038 to C1038, U1043 to U1043, U1044 to U1044, G1045 to G1045, A1049 to A1049, G1057 to G1057, C1065 to C1065, A1068 to A1068, A1080 to A1080, U1081 to U1081, A1082 to A1082, U1089 to U1089, A1090 to A1090, C1098 to C1098, A1103 to A1103, C1104 to C1104, A1105 to A1105, C1106 to C1106, U1107 to U1107, C1108 to C1108, A1109 to A1109, C1236 to C1236, U1114 to U1114, U1115 to U1115, A1116 to A1116, A1117 to A1117, U1246 to U1246, G1247 to G1247, C1248 to C1248, U1249 to U1249, A1121 to A1121, U1132 to U1132, C1133 to C1133, A1148 to A1148, C1261 to C1261, C1405 to C1405, U1406 to U1406
- Block 5: C897 to C897, C904 to C904, U911 to U911, U912 to U912, A919 to A919, A923 to A923, A929 to A929, G930 to G930, A938 to A938, A939 to A939, A942 to A942, G943 to G943, U944 to U944, G945 to G945, A952 to A952, U953 to U953, C954 to C954, A955 to A955, C958 to C958, C959 to C959, C960 to C960, U961 to U961, C962 to C962, A967 to A967, A970 to A970, A971 to A971, G972 to G972, C973 to C973, U974 to U974, A977 to A977, C981 to C981, A982 to A982, C983 to C983, U992 to U992, A995 to A995, A996 to A996, C1001 to C1001, C1002 to C1002, A1003 to A1003, G1004 to G1004, C1011 to C1011, A1012 to A1012, A1014 to A1014, A1015 to A1015, A1016 to A1016, A1017 to A1017, A1018 to A1018, A1019 to A1019, A1020 to A1020, A1021 to A1021, A1022 to A1022, A1023 to A1023, A1024 to A1024, A1025 to A1025, A1026 to A1026, A1027 to A1027, A1028 to A1028, A1029 to A1029, A1030 to A1030, A1031 to A1031, A1032 to A1032, A1033 to A1033, A1034 to A1034, A1035 to A1035, A1036 to A1036, A1037 to A1037, A1038 to A1038, A1039 to A1039, A1040 to A1040, A1041 to A1041, A1042 to A1042, A1043 to A1043, A1044 to A1044, A1045 to A1045, A1046 to A1046, A1047 to A1047, A1048 to A1048, A1049 to A1049, A1050 to A1050, A1051 to A1051, A1052 to A1052, A1053 to A1053, A1054 to A1054, A1055 to A1055, A1056 to A1056, A1057 to A1057, A1058 to A1058, A1059 to A1059, A1060 to A1060, A1061 to A1061, A1062 to A1062, A1063 to A1063, A1064 to A1064, A1065 to A1065, A1066 to A1066, A1067 to A1067, A1068 to A1068, A1069 to A1069, A1070 to A1070, A1071 to A1071, A1072 to A1072, A1073 to A1073, A1074 to A1074, A1075 to A1075, A1076 to A1076, A1077 to A1077, A1078 to A1078, A1079 to A1079, A1080 to A1080, A1081 to A1081, A1082 to A1082, A1083 to A1083, A1084 to A1084, A1085 to A1085, A1086 to A1086, A1087 to A1087, A1088 to A1088, A1089 to A1089, A1090 to A1090, A1091 to A1091, A1092 to A1092, A1093 to A1093, A1094 to A1094, A1095 to A1095, A1096 to A1096, A1097 to A1097, A1098 to A1098, A1099 to A1099, A1100 to A1100, A1101 to A1101, A1102 to A1102, A1103 to A1103, A1104 to A1104, A1105 to A1105, A1106 to A1106, A1107 to A1107, A1108 to A1108, A1109 to A1109, A1110 to A1110, A1111 to A1111, A1112 to A1112, A1113 to A1113, A1114 to A1114, A1115 to A1115, A1116 to A1116, A1117 to A1117, A1118 to A1118, A1119 to A1119, A1120 to A1120, A1121 to A1121, A1122 to A1122, A1123 to A1123, A1124 to A1124, A1125 to A1125, A1126 to A1126, A1127 to A1127, A1128 to A1128, A1129 to A1129, A1130 to A1130, A1131 to A1131, A1132 to A1132, A1133 to A1133, A1134 to A1134, A1135 to A1135, A1136 to A1136, A1137 to A1137, A1138 to A1138, A1139 to A1139, A1140 to A1140, A1141 to A1141, A1142 to A1142, A1143 to A1143, A1144 to A1144, A1145 to A1145, A1146 to A1146, A1147 to A1147, A1148 to A1148, A1149 to A1149, A1150 to A1150, A1151 to A1151, A1152 to A1152, A1153 to A1153, A1154 to A1154, A1155 to A1155, A1156 to A1156, A1157 to A1157, A1158 to A1158, A1159 to A1159, A1160 to A1160, A1161 to A1161, A1162 to A1162, A1163 to A1163, A1164 to A1164, A1165 to A1165, A1166 to A1166, A1167 to A1167, A1168 to A1168, A1169 to A116

Chain B:

Chain C: 89% 11%

Label	Color
K36	Green
T52	Yellow
A53	Yellow
F59	Green
H60	Yellow
M96	Green
W97	Green
G98	Yellow
A105	Yellow
L108	Yellow
V109	Yellow
L110	Yellow
K111	Yellow
R112	Yellow
E118	Yellow
I119	Green
C120	Yellow
A121	Yellow
V122	Yellow
K161	Yellow
L167	Green

Chain D: 92% 8%



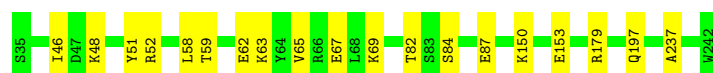
- Molecule 13: 28S ribosomal protein S6, mitochondrial

Chain E: 91% 9%



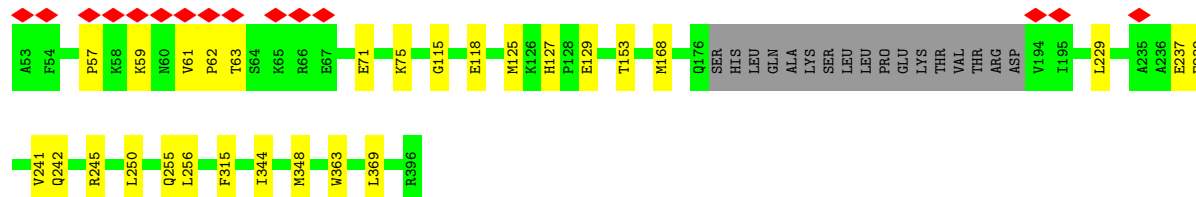
- Molecule 14: 28S ribosomal protein S7, mitochondrial

Chain F: 91% 9%



- Molecule 15: Small ribosomal subunit protein uS9m

Chain G: 87% 8% 5%



- Molecule 16: Small ribosomal subunit protein uS10m

Chain H: 86% 14%



- Molecule 17: Small ribosomal subunit protein uS11m

Chain I: 89% 11%



- Molecule 18: 28S ribosomal protein S12, mitochondrial

Chain J: 92% 8%



- Molecule 19: 28S ribosomal protein S14, mitochondrial

Chain K: 89% 11%



- Molecule 20: Small ribosomal subunit protein uS15m

Chain L: 87% 13%



- Molecule 21: Small ribosomal subunit protein bS16m

Chain M: 88% 12%



- Molecule 22: Small ribosomal subunit protein uS17m

Chain N: 96% 4%



- Molecule 23: 28S ribosomal protein S18b, mitochondrial

Chain O: 88% 12%



- Molecule 24: 28S ribosomal protein S18c, mitochondrial

Chain P: 90% 10%



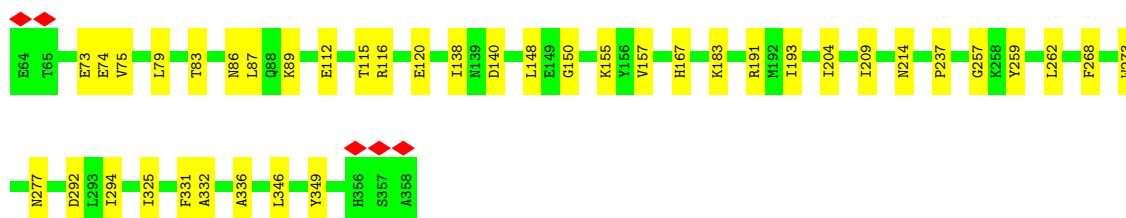
- Molecule 25: 28S ribosomal protein S21, mitochondrial

Chain Q:  92% 8%



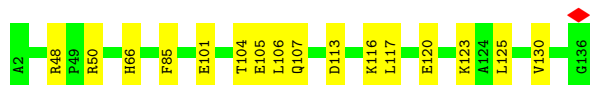
- Molecule 26: Small ribosomal subunit protein mS22

Chain R:  86% 14%



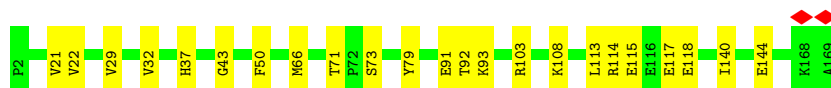
- Molecule 27: 28S ribosomal protein S23, mitochondrial

Chain S:  88% 12%



- Molecule 28: Small ribosomal subunit protein mS25

Chain T:  86% 14%



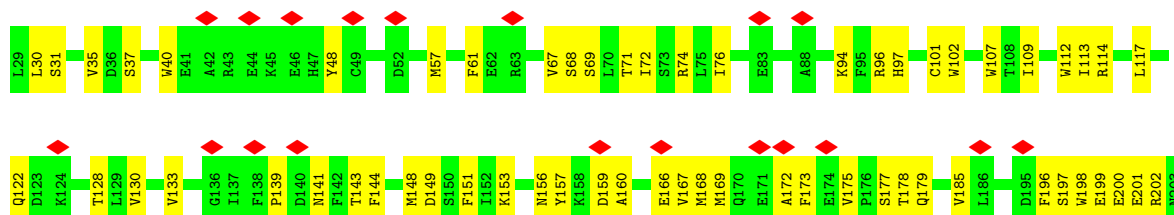
- Molecule 29: Small ribosomal subunit protein mS26

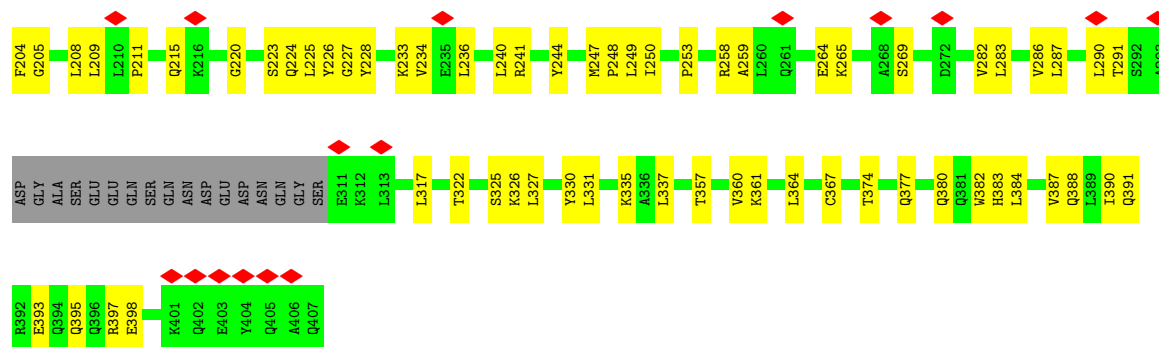
Chain U:  89% 11%



- Molecule 30: Small ribosomal subunit protein mS27

Chain V:  9% 63% 32%





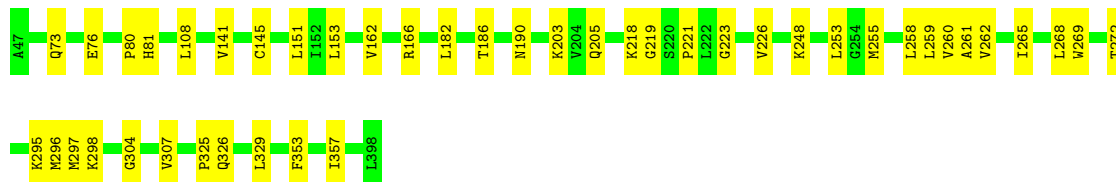
- Molecule 31: Small ribosomal subunit protein bS1m

Chain W: 87% 12%



- Molecule 32: Small ribosomal subunit protein mS29

Chain X: 88% 13%



- Molecule 33: 28S ribosomal protein S27, mitochondrial

Chain Y: 14% 91% 9%



- Molecule 34: Small ribosomal subunit protein mS33

Chain Z: 88% 12%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	107666	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.391	Depositor
Minimum map value	-0.122	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.028	Depositor
Map size (Å)	495.59998, 495.59998, 495.59998	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.826, 0.826, 0.826	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GDP, 5MU, K, MA6, B8T, ATP, ZN, 5MC, MG, FES, GTP

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	0	0.18	0/1834	0.36	0/2484
2	1	0.19	0/2304	0.30	0/3117
3	2	0.36	1/949 (0.1%)	0.37	0/1268
4	3	0.23	0/640	0.40	0/844
5	4	0.16	0/4904	0.33	0/6636
6	5	0.18	0/1673	0.27	0/2602
7	6	0.73	1/95 (1.1%)	0.25	0/144
8	7	0.16	0/4207	0.33	0/5704
9	A	0.29	0/22562	0.28	0/35124
10	B	0.25	0/1871	0.35	0/2531
11	C	0.25	0/1113	0.32	0/1505
12	D	0.24	0/2783	0.31	0/3724
13	E	0.23	0/989	0.33	0/1335
14	F	0.22	0/1767	0.35	0/2373
15	G	0.22	0/2746	0.30	0/3681
16	H	0.25	0/1178	0.35	0/1598
17	I	0.32	0/1039	0.40	0/1400
18	J	0.24	0/855	0.33	0/1148
19	K	0.27	0/880	0.31	0/1182
20	L	0.22	0/1477	0.28	0/1974
21	M	0.24	0/963	0.38	0/1295
22	N	0.24	0/886	0.31	0/1199
23	O	0.21	0/1648	0.32	0/2243
24	P	0.25	0/798	0.32	0/1070
25	Q	0.39	1/756 (0.1%)	0.33	0/1005
26	R	0.18	0/2456	0.29	0/3317
27	S	0.26	0/1138	0.40	0/1533
28	T	0.23	0/1402	0.36	0/1883
29	U	0.18	0/1510	0.32	0/2025
30	V	0.16	0/3030	0.39	0/4093
31	W	0.24	0/801	0.36	0/1079
32	X	0.19	0/2921	0.32	0/3954

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Y	0.20	0/1280	0.32	0/1725
34	Z	0.22	0/857	0.33	0/1141
All	All	0.24	3/76312 (0.0%)	0.32	0/107936

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	2	1	MET	C-N	8.36	1.45	1.33
25	Q	1	MET	C-N	7.48	1.44	1.33
7	6	1	A	OP3-P	6.50	1.61	1.48

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	0	1787	0	1796	49	0
2	1	2256	0	2288	24	0
3	2	935	0	970	6	0
4	3	629	0	702	8	0
5	4	4795	0	4796	84	0
6	5	1498	0	766	26	0
7	6	86	0	43	0	0
8	7	4147	0	3941	34	0
9	A	20282	0	10297	152	0
10	B	1828	0	1815	15	0
11	C	1083	0	1088	9	0
12	D	2731	0	2804	20	0
13	E	972	0	1000	10	0
14	F	1725	0	1769	18	0
15	G	2688	0	2687	22	0
16	H	1152	0	1183	14	0
17	I	1019	0	1059	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	J	839	0	887	6	0
19	K	862	0	885	9	0
20	L	1453	0	1540	14	0
21	M	942	0	965	11	0
22	N	868	0	928	3	0
23	O	1592	0	1557	23	0
24	P	781	0	806	10	0
25	Q	744	0	755	5	0
26	R	2409	0	2428	28	0
27	S	1111	0	1115	12	0
28	T	1371	0	1393	15	0
29	U	1488	0	1499	18	0
30	V	2969	0	2961	89	0
31	W	789	0	802	10	0
32	X	2849	0	2843	25	0
33	Y	1246	0	1197	15	0
34	Z	839	0	858	10	0
35	3	1	0	0	0	0
35	7	1	0	0	0	0
35	A	68	0	0	0	0
35	B	1	0	0	0	0
35	X	1	0	0	0	0
36	7	1	0	0	0	0
36	A	19	0	0	0	0
37	7	32	0	12	0	0
38	O	1	0	0	0	0
39	P	4	0	0	0	0
39	T	4	0	0	0	0
40	X	28	0	12	0	0
41	X	31	0	12	0	0
42	0	2	0	0	0	0
42	1	21	0	0	0	0
42	2	14	0	0	0	0
42	3	10	0	0	0	0
42	4	14	0	0	0	0
42	5	29	0	0	0	0
42	6	6	0	0	0	0
42	7	14	0	0	0	0
42	A	791	0	0	0	0
42	B	48	0	0	0	0
42	C	14	0	0	0	0
42	D	47	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	E	13	0	0	0	0
42	F	22	0	0	0	0
42	G	53	0	0	0	0
42	H	23	0	0	0	0
42	I	22	0	0	0	0
42	J	12	0	0	0	0
42	K	17	0	0	0	0
42	L	30	0	0	0	0
42	M	7	0	0	0	0
42	N	11	0	0	0	0
42	O	37	0	0	0	0
42	P	13	0	0	0	0
42	Q	20	0	0	0	0
42	R	12	0	0	0	0
42	S	16	0	0	0	0
42	T	13	0	0	0	0
42	U	15	0	0	0	0
42	W	15	0	0	0	0
42	X	12	0	0	0	0
42	Y	13	0	0	0	0
42	Z	13	0	0	0	0
All	All	74356	0	62459	699	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 (699) 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)
6:5:5:A:N6	6:5:68:G:H1	1.48	1.10
32:X:108:LEU:HD23	32:X:141:VAL:HG21	1.59	0.83
27:S:106:LEU:HB3	27:S:117:LEU:HD11	1.61	0.82
30:V:240:LEU:HG	30:V:244:TYR:HE1	1.46	0.80
1:0:91:GLU:HG3	1:0:121:LYS:HA	1.60	0.80
5:4:528:ARG:HD2	5:4:559:TYR:HE1	1.46	0.79
9:A:1236:C:H5''	19:K:33:ARG:HE	1.47	0.79
6:5:5:A:N1	6:5:68:G:N2	2.29	0.78
6:5:67:C:H2'	6:5:68:G:H8	1.47	0.77
5:4:602:HIS:CE1	5:4:604:LYS:HZ3	2.05	0.75
5:4:509:ILE:HG23	5:4:531:ILE:HD11	1.68	0.74
9:A:1523:A:H5''	30:V:68:SER:HB2	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:4:393:ILE:HA	5:4:396:ILE:HG12	1.71	0.73
6:5:67:C:H2'	6:5:68:G:C8	2.24	0.72
12:D:130:GLN:HB3	34:Z:72:ARG:HH12	1.52	0.72
28:T:22:VAL:HG21	28:T:113:LEU:HD21	1.71	0.72
12:D:149:MET:HE1	12:D:154:VAL:HG22	1.72	0.71
1:0:100:VAL:HG12	1:0:102:PRO:HD3	1.72	0.71
5:4:392:ILE:HG13	5:4:393:ILE:HD12	1.73	0.71
9:A:1382:A:H5''	32:X:166:ARG:HH21	1.55	0.71
2:1:189:LYS:HG3	34:Z:11:MET:HE1	1.71	0.70
2:1:227:THR:HA	16:H:184:ILE:HD11	1.71	0.70
6:5:76:A:H1'	8:7:693:GLY:HA3	1.74	0.70
23:O:208:PRO:HG2	23:O:213:LEU:HD11	1.74	0.70
15:G:344:ILE:HG22	15:G:348:MET:HE2	1.73	0.70
2:1:84:PRO:HD2	15:G:125:MET:HE3	1.74	0.69
9:A:1201:A:H2'	9:A:1202:G:C8	2.28	0.69
19:K:61:THR:HG21	34:Z:27:ASN:HD21	1.58	0.69
30:V:236:LEU:HD22	30:V:290:LEU:HD22	1.74	0.69
31:W:109:GLU:CD	31:W:110:ASN:H	2.00	0.69
5:4:156:ALA:HB3	5:4:172:MET:HE1	1.74	0.69
25:Q:67:GLU:HG3	31:W:154:LEU:HB2	1.75	0.68
13:E:92:ASN:HB2	24:P:117:MET:HE3	1.76	0.67
1:0:85:TRP:HH2	1:0:95:TRP:HE1	1.43	0.67
32:X:81:HIS:CD2	32:X:190:ASN:HB3	2.30	0.67
30:V:179:GLN:OE1	30:V:215:GLN:NE2	2.27	0.66
24:P:139:ARG:NH1	24:P:141:ARG:HB2	2.10	0.66
30:V:247:MET:HE1	30:V:249:LEU:HD12	1.78	0.66
30:V:291:THR:HG22	30:V:327:LEU:HD21	1.78	0.66
26:R:83:THR:HG22	26:R:268:PHE:HB3	1.78	0.66
30:V:141:ASN:HA	30:V:144:PHE:HD2	1.60	0.65
21:M:63:GLU:HG2	26:R:155:LYS:HE2	1.79	0.65
28:T:21:VAL:HG22	28:T:103:ARG:HB2	1.78	0.65
5:4:598:LEU:HA	5:4:601:LYS:HD2	1.79	0.64
8:7:381:LEU:HB3	8:7:410:ALA:HB3	1.79	0.64
5:4:248:PHE:HA	5:4:251:MET:HE1	1.79	0.64
31:W:139:ARG:HG3	31:W:139:ARG:HH11	1.61	0.64
9:A:1201:A:H2'	9:A:1202:G:H8	1.63	0.64
9:A:845:A:H4'	29:U:60:TYR:CE2	2.34	0.63
30:V:109:ILE:HG21	30:V:139:PRO:HA	1.80	0.63
8:7:371:VAL:HG22	8:7:419:THR:HG22	1.81	0.63
5:4:576:LEU:HB3	5:4:599:PHE:HE1	1.63	0.63
8:7:524:VAL:HG23	8:7:527:SER:H	1.64	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:29:ARG:H	1:0:32:GLN:NE2	1.97	0.63
16:H:104:ILE:HG21	16:H:145:LEU:HD23	1.80	0.63
9:A:961:U:H4'	9:A:962:C:H5''	1.80	0.63
9:A:1025:A:H2'	9:A:1026:A:C8	2.34	0.62
18:J:62:VAL:HA	18:J:83:VAL:HG12	1.81	0.62
21:M:111:ARG:HG3	23:O:236:PRO:HD3	1.81	0.62
9:A:663:A:H2'	9:A:664:G:C8	2.34	0.62
32:X:262:VAL:HG21	32:X:265:ILE:HD13	1.81	0.62
6:5:5:A:H61	6:5:68:G:H1	0.72	0.61
30:V:151:PHE:CE2	30:V:159:ASP:HB2	2.34	0.61
30:V:151:PHE:CE2	30:V:156:ASN:HB3	2.34	0.61
5:4:446:LYS:HG2	33:Y:292:GLN:NE2	2.14	0.61
9:A:1440:G:H2'	9:A:1441:A:C8	2.36	0.61
5:4:570:ASP:HA	5:4:602:HIS:HE1	1.66	0.61
30:V:68:SER:HB3	30:V:71:THR:HG22	1.81	0.61
23:O:235:MET:HG2	26:R:150:GLY:HA3	1.82	0.61
9:A:1068:A:H5''	17:I:190:LYS:HD3	1.82	0.60
9:A:852:A:H3'	9:A:853:C:H6	1.65	0.60
9:A:1119:U:P	27:S:48:ARG:HH22	2.24	0.60
16:H:76:LEU:HG	16:H:148:LEU:HD21	1.84	0.60
6:5:69:U:H2'	6:5:70:A:H8	1.68	0.59
30:V:167:VAL:HG13	30:V:172:ALA:HB3	1.83	0.59
8:7:282:PRO:HG2	8:7:345:LEU:HD11	1.82	0.59
10:B:162:CYS:HB3	10:B:254:GLN:HG3	1.85	0.59
1:0:87:TRP:CD1	23:O:218:ARG:HH12	2.21	0.59
26:R:294:ILE:HG13	26:R:349:TYR:CE2	2.38	0.58
9:A:738:A:H2'	9:A:740:G:C4	2.37	0.58
9:A:740:G:H2'	9:A:741:A:H8	1.68	0.58
8:7:309:VAL:HG13	8:7:318:VAL:HG21	1.85	0.58
30:V:96:ARG:HH21	30:V:133:VAL:HA	1.68	0.58
30:V:233:LYS:HB2	30:V:286:VAL:HG21	1.86	0.58
2:1:211:ARG:HD3	2:1:221:TYR:CE2	2.38	0.58
30:V:199:GLU:HA	30:V:202:ARG:HE	1.69	0.58
8:7:411:TYR:HB2	8:7:414:MET:HE3	1.86	0.58
4:3:174:ARG:HG3	4:3:178:LEU:HD13	1.84	0.57
5:4:397:MET:HE1	5:4:415:PHE:HZ	1.69	0.57
27:S:48:ARG:HH21	27:S:50:ARG:NH2	2.02	0.57
17:I:96:GLN:HE21	17:I:109:PHE:HZ	1.52	0.57
9:A:734:C:P	9:A:735:A:H5''	2.44	0.57
23:O:213:LEU:HB3	23:O:217:ARG:HH12	1.69	0.57
28:T:71:THR:HG22	28:T:73:SER:H	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1236:C:H5''	19:K:33:ARG:NE	2.18	0.57
5:4:263:ILE:HD11	5:4:293:THR:HG23	1.86	0.57
9:A:777:G:H5''	22:N:21:LYS:HB3	1.86	0.57
9:A:1545:U:H2'	9:A:1546:A:C8	2.39	0.57
32:X:80:PRO:HG2	32:X:81:HIS:HD2	1.69	0.57
24:P:139:ARG:HH12	24:P:141:ARG:HB2	1.70	0.57
30:V:265:LYS:O	30:V:269:SER:HB3	2.05	0.57
30:V:387:VAL:HA	30:V:390:ILE:HD12	1.87	0.57
5:4:410:PRO:HA	33:Y:289:VAL:HG11	1.87	0.56
16:H:76:LEU:HD22	16:H:174:LYS:HG2	1.86	0.56
1:0:95:TRP:CE3	1:0:131:ILE:HG12	2.40	0.56
28:T:29:VAL:HB	28:T:79:TYR:HB2	1.87	0.56
5:4:528:ARG:HD2	5:4:559:TYR:CE1	2.35	0.56
5:4:607:ARG:HD2	5:4:609:GLU:HG2	1.87	0.56
26:R:209:ILE:HD12	26:R:214:ASN:HB3	1.87	0.56
9:A:1269:U:H4'	9:A:1270:U:H3'	1.88	0.55
1:0:174:ILE:O	1:0:177:GLU:HG3	2.06	0.55
16:H:135:GLU:HB3	19:K:126:ALA:HB2	1.87	0.55
5:4:346:HIS:C	5:4:350:ARG:HE	2.14	0.55
1:0:113:LYS:HE3	1:0:115:TRP:HH2	1.70	0.55
9:A:1578:A:H2'	9:A:1579:C:C6	2.41	0.55
27:S:120:GLU:HA	27:S:123:LYS:HZ2	1.72	0.55
5:4:152:ILE:HA	5:4:172:MET:HE3	1.87	0.55
10:B:62:ILE:HG22	10:B:63:LEU:HD22	1.89	0.55
23:O:192:THR:HG23	23:O:197:ASP:HB2	1.89	0.55
24:P:52:ILE:HD13	27:S:66:HIS:CE1	2.42	0.55
30:V:96:ARG:HD2	30:V:101:CYS:SG	2.47	0.55
9:A:1589:C:H2'	9:A:1590:A:C8	2.42	0.55
11:C:52:THR:HG23	11:C:161:LYS:HE3	1.87	0.55
1:0:132:GLU:HA	1:0:207:GLN:HE21	1.72	0.54
4:3:148:LYS:HG3	9:A:1154:A:C2	2.42	0.54
30:V:40:TRP:CZ3	30:V:114:ARG:HB3	2.42	0.54
5:4:199:GLY:HA2	5:4:238:TRP:HZ3	1.70	0.54
9:A:977:A:H1'	17:I:182:PRO:HB3	1.88	0.54
1:0:99:ARG:HD3	9:A:1526:U:H2'	1.90	0.54
10:B:172:ARG:O	10:B:175:MET:HG2	2.07	0.54
16:H:146:GLU:HG2	16:H:147:HIS:CD2	2.42	0.54
6:5:22:A:H2'	6:5:23:G:H8	1.73	0.54
30:V:202:ARG:HG2	30:V:234:VAL:HG11	1.90	0.54
11:C:111:LYS:HB2	11:C:118:GLU:HB2	1.90	0.54
15:G:315:PHE:CD2	15:G:369:LEU:HD21	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:4:361:LYS:NZ	33:Y:251:PHE:HB3	2.23	0.54
6:5:4:A:H2'	6:5:5:A:C8	2.43	0.54
12:D:103:LEU:HD11	12:D:123:ARG:HB2	1.90	0.54
24:P:77:VAL:HG13	24:P:120:MET:HG3	1.90	0.54
10:B:61:LYS:NZ	10:B:271:TYR:HB2	2.23	0.54
10:B:167:HIS:CE1	15:G:153:THR:HA	2.43	0.54
26:R:325:ILE:HG23	26:R:346:LEU:HD21	1.90	0.54
1:0:58:VAL:HG23	1:0:137:HIS:HD1	1.72	0.53
6:5:1:A:H2'	6:5:2:G:H8	1.73	0.53
23:O:177:PHE:CE1	26:R:237:PRO:HG2	2.43	0.53
28:T:114:ARG:HA	28:T:117:GLU:HG2	1.90	0.53
32:X:258:LEU:O	32:X:304:GLY:HA3	2.09	0.53
19:K:54:ILE:HG21	19:K:75:ILE:HB	1.91	0.53
5:4:350:ARG:HH22	5:4:381:GLN:HB2	1.73	0.53
5:4:393:ILE:HG22	5:4:431:LEU:HD11	1.89	0.53
9:A:845:A:H2'	9:A:846:A:C8	2.44	0.53
9:A:732:A:H2'	9:A:733:U:C6	2.44	0.53
11:C:98:GLY:HA3	34:Z:71:TYR:CE1	2.44	0.53
9:A:871:A:H4'	9:A:872:G:H5'	1.89	0.53
19:K:120:LEU:HB3	19:K:123:ILE:HD12	1.91	0.53
3:2:33:VAL:HG21	3:2:104:LEU:HD23	1.91	0.53
9:A:821:U:H2'	9:A:822:G:H8	1.74	0.53
30:V:322:THR:HG23	30:V:325:SER:H	1.73	0.53
8:7:506:LYS:HG2	9:A:1494:C:H5'	1.90	0.52
5:4:262:MET:HE3	5:4:266:MET:HE3	1.91	0.52
30:V:113:ILE:HG21	30:V:143:THR:HG23	1.91	0.52
34:Z:95:LYS:HE3	34:Z:98:GLU:OE1	2.09	0.52
9:A:929:A:H1'	12:D:421:VAL:HG22	1.91	0.52
9:A:1267:U:H2'	9:A:1268:C:C6	2.44	0.52
5:4:256:GLU:HG2	5:4:287:LEU:HB3	1.90	0.52
8:7:297:PRO:HA	8:7:300:VAL:HG22	1.92	0.52
5:4:380:ASP:HB3	5:4:422:ILE:HD11	1.91	0.52
23:O:150:LEU:O	23:O:154:ILE:HG12	2.09	0.52
23:O:208:PRO:HB3	29:U:54:PHE:HD1	1.75	0.52
9:A:1258:A:N7	9:A:1330:C:H5'	2.25	0.52
15:G:61:VAL:HG23	15:G:63:THR:HB	1.92	0.52
1:0:118:LEU:HD21	1:0:120:PHE:HB2	1.92	0.52
25:Q:72:ILE:O	25:Q:76:MET:HG2	2.10	0.52
26:R:140:ASP:HB3	26:R:183:LYS:HD2	1.92	0.52
29:U:129:ARG:O	29:U:132:GLU:HG3	2.10	0.52
10:B:262:GLU:O	10:B:266:GLN:HG3	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1014:A:H4'	17:I:184:ASN:HB3	1.91	0.51
23:O:213:LEU:HB3	23:O:217:ARG:NH1	2.25	0.51
29:U:80:ARG:HA	29:U:83:HIS:NE2	2.25	0.51
14:F:82:THR:HG23	15:G:315:PHE:HB2	1.92	0.51
4:3:189:TRP:CE2	20:L:209:LEU:HD12	2.46	0.51
5:4:307:GLU:HG2	5:4:312:LYS:HE3	1.91	0.51
8:7:531:ILE:O	8:7:535:ILE:HG12	2.10	0.51
12:D:294:ILE:HB	12:D:305:MET:HE3	1.93	0.51
3:2:59:ASN:HD22	3:2:65:ALA:HB1	1.75	0.51
9:A:1265:C:H4'	16:H:122:GLN:HG2	1.92	0.51
16:H:118:PHE:HE1	16:H:136:MET:HE2	1.75	0.51
27:S:101:GLU:O	27:S:104:THR:HG22	2.11	0.51
30:V:76:ILE:HD12	30:V:112:TRP:HB2	1.93	0.51
30:V:149:ASP:O	30:V:153:LYS:HG2	2.11	0.51
2:1:159:SER:HB2	11:C:112:ARG:HB3	1.93	0.51
6:5:1:A:H2'	6:5:2:G:C8	2.44	0.50
6:5:22:A:H2'	6:5:23:G:C8	2.45	0.50
5:4:140:LEU:HD21	33:Y:309:LYS:HE3	1.93	0.50
8:7:213:ILE:HD11	8:7:238:HIS:HB2	1.94	0.50
29:U:80:ARG:HA	29:U:83:HIS:CD2	2.47	0.50
30:V:384:LEU:O	30:V:387:VAL:HG22	2.10	0.50
1:0:101:ARG:NH1	9:A:1528:A:H4'	2.26	0.50
12:D:380:LEU:HD12	12:D:381:PRO:HD2	1.93	0.50
13:E:71:PRO:HD3	20:L:97:MET:HE1	1.93	0.50
14:F:65:VAL:O	14:F:69:LYS:HG3	2.10	0.50
26:R:74:GLU:HG2	26:R:75:VAL:N	2.27	0.50
5:4:464:LEU:HD12	5:4:468:MET:HE2	1.94	0.50
20:L:163:ARG:HA	20:L:166:MET:HE2	1.92	0.50
9:A:853:C:H2'	9:A:854:U:C6	2.46	0.50
1:0:132:GLU:HB3	1:0:207:GLN:HB2	1.94	0.50
4:3:177:TRP:CD1	4:3:178:LEU:HD12	2.47	0.50
5:4:593:TRP:CZ2	5:4:626:GLN:HB3	2.47	0.50
5:4:628:ILE:HA	5:4:631:VAL:HG22	1.94	0.50
9:A:672:A:H2'	9:A:673:U:C6	2.46	0.50
9:A:738:A:H5''	9:A:740:G:N7	2.26	0.50
24:P:49:ASP:HA	31:W:85:ARG:HH11	1.77	0.50
30:V:141:ASN:ND2	30:V:175:VAL:HG12	2.27	0.50
30:V:374:THR:HA	30:V:377:GLN:CD	2.37	0.50
5:4:79:ASN:HB3	16:H:50:LEU:HD22	1.93	0.49
5:4:236:VAL:HG12	5:4:238:TRP:H	1.76	0.49
9:A:1470:A:H2'	9:A:1471:A:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:S:113:ASP:HB3	27:S:116:LYS:HE2	1.94	0.49
9:A:1003:A:H2'	9:A:1004:G:C8	2.47	0.49
9:A:1376:C:H4'	9:A:1377:C:H5'	1.94	0.49
30:V:200:GLU:O	30:V:204:PHE:HD2	1.95	0.49
1:O:192:ASN:HD21	1:O:194:GLN:HG3	1.77	0.49
31:W:114:ILE:HG21	31:W:142:LEU:HD11	1.93	0.49
9:A:1132:U:H2'	9:A:1133:C:C6	2.47	0.49
1:O:101:ARG:CZ	9:A:1528:A:H4'	2.42	0.49
12:D:401:VAL:HG21	28:T:50:PHE:CE1	2.48	0.49
4:3:173:LEU:HB3	20:L:209:LEU:HD13	1.93	0.49
19:K:34:MET:HE3	19:K:95:SER:HB2	1.94	0.49
30:V:168:MET:HE1	30:V:169:MET:HE2	1.94	0.49
30:V:377:GLN:HA	30:V:380:GLN:CD	2.37	0.49
1:O:96:ARG:HB3	1:O:117:ILE:HG22	1.95	0.49
9:A:1003:A:H2'	9:A:1004:G:H8	1.78	0.49
11:C:96:MET:HB2	11:C:108:LEU:HD11	1.95	0.49
26:R:332:ALA:HA	26:R:336:ALA:HB3	1.95	0.49
30:V:31:SER:O	30:V:35:VAL:HG23	2.13	0.49
30:V:241:ARG:HA	30:V:244:TYR:CZ	2.48	0.49
12:D:380:LEU:HD13	26:R:87:LEU:HB3	1.94	0.49
2:1:157:VAL:HG13	33:Y:315:ILE:HG13	1.93	0.49
20:L:136:ILE:O	20:L:140:GLU:HG3	2.13	0.49
30:V:197:SER:O	30:V:201:GLU:HG3	2.12	0.49
1:O:51:PRO:HG3	9:A:705:C:H5'	1.95	0.48
30:V:388:GLN:HA	30:V:391:GLN:CD	2.38	0.48
9:A:733:U:H2'	9:A:734:C:C6	2.48	0.48
26:R:191:ARG:HG3	26:R:204:ILE:HG23	1.95	0.48
5:4:611:LEU:HD13	5:4:645:LEU:HD22	1.94	0.48
9:A:911:U:H2'	9:A:912:U:C6	2.49	0.48
30:V:393:GLU:HG3	30:V:397:ARG:HH21	1.77	0.48
9:A:696:U:H2'	9:A:697:G:C8	2.49	0.48
9:A:970:A:H2'	9:A:971:A:C8	2.47	0.48
13:E:26:ILE:HG23	13:E:36:VAL:HG21	1.93	0.48
14:F:84:SER:HB3	14:F:87:GLU:HG2	1.94	0.48
21:M:101:PRO:HB3	29:U:59:ARG:HB3	1.94	0.48
28:T:115:GLU:O	28:T:118:GLU:HG3	2.13	0.48
9:A:1545:U:H2'	9:A:1546:A:H8	1.78	0.48
13:E:23:LYS:O	13:E:27:GLU:HG3	2.14	0.48
23:O:105:CYS:HB2	23:O:142:VAL:HA	1.94	0.48
30:V:264:GLU:HG2	30:V:337:LEU:HD21	1.94	0.48
30:V:198:TRP:O	30:V:202:ARG:HG3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:152:ASP:HB2	2:1:172:VAL:HB	1.96	0.48
5:4:389:SER:HA	5:4:392:ILE:HG12	1.94	0.48
9:A:872:G:H2'	9:A:873:G:C8	2.48	0.48
2:1:237:GLU:CD	2:1:239:TRP:HE1	2.21	0.48
5:4:431:LEU:O	5:4:435:VAL:HG23	2.14	0.48
9:A:1057:G:H4'	9:A:1578:A:H4'	1.96	0.48
14:F:46:ILE:HD12	15:G:315:PHE:HZ	1.78	0.48
27:S:85:PHE:HB2	31:W:100:VAL:HG12	1.96	0.48
28:T:43:GLY:HA3	28:T:93:LYS:O	2.14	0.48
5:4:361:LYS:HZ3	33:Y:251:PHE:HB3	1.77	0.48
5:4:427:ARG:HB3	5:4:468:MET:HE3	1.94	0.48
29:U:125:ARG:O	29:U:128:GLU:HG3	2.14	0.48
30:V:30:LEU:HD12	30:V:149:ASP:HB2	1.96	0.48
1:0:61:GLU:HB2	1:0:137:HIS:O	2.14	0.48
6:5:68:G:H2'	6:5:69:U:H6	1.79	0.48
6:5:69:U:H2'	6:5:70:A:C8	2.48	0.48
9:A:1470:A:H2'	9:A:1471:A:H8	1.79	0.48
8:7:188:HIS:CE1	8:7:268:GLN:HG2	2.49	0.47
8:7:520:ILE:O	8:7:551:PHE:HA	2.14	0.47
30:V:226:TYR:HE1	30:V:282:VAL:HG21	1.79	0.47
9:A:1275:A:H2	9:A:1300:A:H62	1.61	0.47
5:4:238:TRP:CZ2	5:4:266:MET:HE1	2.49	0.47
5:4:238:TRP:CE2	5:4:266:MET:HE1	2.49	0.47
8:7:485:LEU:HG	8:7:487:LYS:H	1.78	0.47
9:A:1308:U:H4'	15:G:118:GLU:HG2	1.96	0.47
9:A:1558:A:H3'	9:A:1559:G:H8	1.80	0.47
18:J:35:GLN:HG2	18:J:38:ARG:HH22	1.80	0.47
23:O:123:LEU:HB3	23:O:154:ILE:HD13	1.96	0.47
27:S:106:LEU:CB	27:S:117:LEU:HD11	2.39	0.47
28:T:91:GLU:HG2	28:T:92:THR:HG23	1.97	0.47
29:U:71:ARG:O	29:U:75:VAL:HG23	2.14	0.47
32:X:153:LEU:HB3	32:X:260:VAL:HG12	1.96	0.47
1:0:198:MET:SD	29:U:65:GLN:HB2	2.54	0.47
5:4:267:VAL:HG21	5:4:296:ALA:HB1	1.96	0.47
14:F:58:LEU:HB2	14:F:63:LYS:NZ	2.30	0.47
23:O:216:LEU:HD11	29:U:53:PHE:HB3	1.96	0.47
30:V:383:HIS:O	30:V:387:VAL:HG13	2.15	0.47
32:X:145:CYS:SG	32:X:259:LEU:HD22	2.54	0.47
9:A:745:A:C4	9:A:746:A:C8	3.03	0.47
5:4:354:LEU:HD11	33:Y:250:ILE:HB	1.95	0.47
5:4:429:LEU:HD11	5:4:465:ILE:HD13	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:4:572:PRO:HG2	5:4:575:SER:OG	2.15	0.47
8:7:472:GLU:O	8:7:475:GLN:HG3	2.15	0.47
9:A:715:G:H2'	9:A:716:U:C6	2.49	0.47
9:A:852:A:H3'	9:A:853:C:C6	2.47	0.47
9:A:944:U:H2'	9:A:945:G:C8	2.50	0.47
12:D:162:LYS:O	12:D:166:GLU:HG3	2.15	0.47
14:F:59:THR:O	14:F:63:LYS:HG2	2.14	0.47
1:0:171:ARG:HD3	23:O:199:TRP:HZ2	1.79	0.47
1:0:192:ASN:HB3	1:0:195:ARG:HH12	1.80	0.47
1:0:118:LEU:HD11	1:0:204:PRO:HG2	1.95	0.47
9:A:681:U:H2'	9:A:682:A:H8	1.80	0.47
2:1:132:GLU:O	5:4:60:PRO:HG3	2.15	0.47
3:2:59:ASN:HD22	3:2:65:ALA:CB	2.28	0.47
13:E:92:ASN:CB	24:P:117:MET:HE3	2.45	0.47
32:X:223:GLY:HA2	32:X:226:VAL:HG22	1.96	0.47
6:5:6:G:H2'	6:5:7:G:C8	2.50	0.46
9:A:731:A:H2'	9:A:732:A:H8	1.80	0.46
9:A:1200:G:C2	9:A:1201:A:C8	3.03	0.46
9:A:1440:G:H2'	9:A:1441:A:H8	1.77	0.46
9:A:1577:U:H2'	9:A:1578:A:C8	2.50	0.46
20:L:115:ILE:HG21	20:L:181:ILE:HD13	1.96	0.46
30:V:220:GLY:O	30:V:224:GLN:HG3	2.15	0.46
5:4:592:ALA:O	5:4:596:LEU:HG	2.14	0.46
9:A:1033:U:H2'	9:A:1034:U:C6	2.50	0.46
9:A:1488:5MC:H2'	9:A:1489:G:C8	2.51	0.46
12:D:127:ASN:OD1	34:Z:72:ARG:HD3	2.15	0.46
30:V:208:LEU:HD11	30:V:223:SER:HB2	1.97	0.46
33:Y:386:ILE:HD12	33:Y:386:ILE:H	1.80	0.46
2:1:202:THR:O	2:1:204:VAL:HG23	2.15	0.46
10:B:146:SER:O	10:B:168:THR:HA	2.15	0.46
14:F:58:LEU:HB2	14:F:63:LYS:HZ2	1.80	0.46
30:V:112:TRP:HE1	30:V:128:THR:HG21	1.80	0.46
30:V:395:GLN:HA	30:V:398:GLU:HG2	1.98	0.46
5:4:346:HIS:HB3	5:4:350:ARG:HH21	1.80	0.46
5:4:523:PHE:HB3	5:4:562:GLN:HE22	1.81	0.46
6:5:66:C:H2'	6:5:67:C:C6	2.50	0.46
14:F:63:LYS:O	14:F:67:GLU:OE1	2.33	0.46
30:V:236:LEU:HD13	30:V:290:LEU:HD13	1.97	0.46
1:0:136:TYR:CZ	9:A:705:C:H2'	2.51	0.46
30:V:240:LEU:HG	30:V:244:TYR:CE1	2.38	0.46
30:V:374:THR:HA	30:V:377:GLN:OE1	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:35:ALA:O	1:0:44:PRO:HD2	2.16	0.46
1:0:74:PHE:HD1	30:V:102:TRP:HD1	1.63	0.46
8:7:270:VAL:O	8:7:273:ILE:HG22	2.15	0.46
9:A:838:U:H2'	9:A:839:A:H8	1.81	0.46
23:O:123:LEU:HB3	23:O:154:ILE:CD1	2.46	0.46
29:U:58:GLU:O	29:U:61:GLN:HG2	2.16	0.46
30:V:48:TYR:HE2	30:V:74:ARG:HD2	1.81	0.46
5:4:289:ALA:HB1	5:4:293:THR:HG21	1.97	0.46
9:A:732:A:H2'	9:A:733:U:H6	1.81	0.46
9:A:659:U:OP1	12:D:226:ARG:HD3	2.15	0.46
9:A:821:U:H2'	9:A:822:G:C8	2.51	0.46
16:H:182:GLU:HA	16:H:185:LYS:NZ	2.31	0.46
26:R:262:LEU:O	26:R:268:PHE:HB2	2.16	0.46
30:V:287:LEU:HD21	30:V:331:LEU:HB2	1.98	0.46
32:X:325:PRO:O	32:X:329:LEU:HB2	2.15	0.46
9:A:1317:A:H3'	9:A:1318:A:H8	1.81	0.46
9:A:1504:U:H2'	9:A:1505:A:C8	2.51	0.46
8:7:198:ASP:OD1	8:7:205:VAL:HG22	2.16	0.45
9:A:1190:C:H2'	9:A:1191:C:H6	1.82	0.45
14:F:48:LYS:O	14:F:52:ARG:HG2	2.15	0.45
15:G:229:LEU:HD21	15:G:241:VAL:HG11	1.98	0.45
9:A:1508:C:H2'	9:A:1509:U:H6	1.81	0.45
5:4:590:GLN:HG2	5:4:591:GLU:N	2.30	0.45
9:A:839:A:H2'	9:A:840:A:H8	1.81	0.45
9:A:1557:A:OP1	18:J:72:LYS:HG2	2.15	0.45
20:L:98:ALA:HB1	20:L:102:GLU:HG3	1.97	0.45
30:V:57:MET:HE3	30:V:67:VAL:HG11	1.98	0.45
30:V:107:TRP:HB3	30:V:382:TRP:CD2	2.52	0.45
31:W:139:ARG:HG3	31:W:139:ARG:NH1	2.29	0.45
1:0:11:ILE:HB	9:A:806:C:C2	2.51	0.45
5:4:350:ARG:HH12	5:4:388:ARG:HH21	1.64	0.45
9:A:981:C:H2'	9:A:982:A:H8	1.81	0.45
9:A:1020:C:C5	9:A:1021:U:C4	3.04	0.45
12:D:256:PHE:HZ	12:D:347:GLN:HG2	1.81	0.45
17:I:60:PHE:CE2	25:Q:15:GLN:HB2	2.52	0.45
1:0:132:GLU:OE1	1:0:133:HIS:ND1	2.47	0.45
8:7:459:ASP:O	8:7:463:ILE:HD12	2.16	0.45
12:D:243:VAL:HG11	12:D:268:PHE:HD1	1.81	0.45
30:V:40:TRP:CE3	30:V:114:ARG:HB3	2.52	0.45
30:V:199:GLU:HA	30:V:202:ARG:NE	2.32	0.45
9:A:733:U:H2'	9:A:734:C:H6	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:D:412:LYS:HG3	12:D:417:MET:HB2	1.98	0.45
19:K:50:GLU:O	19:K:54:ILE:HG12	2.17	0.45
27:S:101:GLU:O	27:S:105:GLU:OE1	2.35	0.45
1:O:82:ARG:HB2	1:O:139:TRP:CZ3	2.52	0.45
5:4:446:LYS:HG2	33:Y:292:GLN:HE22	1.78	0.45
8:7:603:VAL:HG11	8:7:725:PRO:HG3	1.98	0.45
9:A:740:G:H2'	9:A:741:A:C8	2.51	0.45
30:V:247:MET:HG2	30:V:248:PRO:HD2	1.98	0.45
5:4:627:ALA:O	5:4:631:VAL:HG13	2.17	0.45
8:7:188:HIS:CD2	8:7:189:VAL:H	2.34	0.45
9:A:1561:C:H2'	9:A:1562:G:O4'	2.16	0.45
15:G:238:GLU:O	15:G:242:GLN:HG2	2.17	0.45
23:O:208:PRO:HB3	29:U:54:PHE:CD1	2.52	0.45
32:X:205:GLN:HA	32:X:218:LYS:HG3	1.98	0.45
9:A:764:A:H4'	9:A:765:C:O4'	2.17	0.45
9:A:853:C:H2'	9:A:854:U:H6	1.82	0.45
9:A:1528:A:H2'	9:A:1529:A:C8	2.52	0.45
10:B:193:ILE:O	10:B:219:THR:HA	2.17	0.45
18:J:51:PRO:HG3	18:J:122:LYS:HB3	1.98	0.45
1:O:102:PRO:HA	1:O:112:GLY:HA3	1.98	0.45
2:1:262:ILE:HA	2:1:265:THR:HG22	1.98	0.45
5:4:359:GLU:HG3	33:Y:256:LEU:HD12	1.98	0.45
8:7:172:ASP:HB3	8:7:175:LEU:HG	1.99	0.45
12:D:128:ARG:HG3	12:D:129:GLY:N	2.32	0.45
14:F:153:GLU:HB3	14:F:179:ARG:CG	2.47	0.45
30:V:48:TYR:CE2	30:V:74:ARG:HD2	2.52	0.45
30:V:117:LEU:HD23	30:V:122:GLN:HG2	1.99	0.45
9:A:1116:A:P	10:B:100:ARG:HH22	2.40	0.44
23:O:218:ARG:HD3	30:V:317:LEU:HA	1.99	0.44
26:R:112:GLU:HA	26:R:115:THR:HG22	2.00	0.44
30:V:37:SER:HB2	30:V:40:TRP:HE3	1.82	0.44
30:V:326:LYS:HE3	30:V:330:TYR:OH	2.17	0.44
5:4:563:PRO:HA	5:4:565:ARG:CZ	2.47	0.44
5:4:593:TRP:CH2	5:4:626:GLN:HB3	2.52	0.44
6:5:27:U:H2'	6:5:28:C:H6	1.82	0.44
34:Z:9:PHE:CZ	34:Z:13:ARG:HD2	2.51	0.44
1:O:21:LEU:O	1:O:25:LEU:HG	2.17	0.44
1:O:61:GLU:HB2	1:O:137:HIS:C	2.42	0.44
9:A:740:G:N3	9:A:741:A:C8	2.85	0.44
9:A:1407:U:H2'	9:A:1408:A:C8	2.52	0.44
9:A:1510:U:H2'	9:A:1511:C:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1527:A:H2'	9:A:1528:A:O4'	2.17	0.44
17:I:129:GLN:HE21	17:I:167:MET:CE	2.30	0.44
26:R:204:ILE:HD12	28:T:144:GLU:HG2	1.98	0.44
5:4:350:ARG:HB3	5:4:379:PHE:HE2	1.83	0.44
9:A:1429:C:H4'	9:A:1430:A:H5'	1.98	0.44
9:A:1499:U:H2'	9:A:1500:C:H6	1.82	0.44
17:I:129:GLN:HE21	17:I:167:MET:HE3	1.82	0.44
20:L:112:MET:O	20:L:116:VAL:HG22	2.17	0.44
30:V:130:VAL:HA	30:V:166:GLU:OE2	2.18	0.44
6:5:27:U:H2'	6:5:28:C:C6	2.53	0.44
15:G:127:HIS:ND1	15:G:129:GLU:HG3	2.33	0.44
23:O:177:PHE:HE1	26:R:237:PRO:HG2	1.81	0.44
30:V:225:LEU:HD11	30:V:283:LEU:HD22	1.98	0.44
5:4:262:MET:O	5:4:266:MET:HG2	2.18	0.44
5:4:625:SER:O	5:4:629:GLU:HG3	2.17	0.44
9:A:862:A:H2'	9:A:863:C:C6	2.53	0.44
9:A:1114:U:H2'	9:A:1115:U:C6	2.53	0.44
12:D:231:MET:HE2	12:D:231:MET:HB2	1.85	0.44
12:D:243:VAL:HG11	12:D:268:PHE:CD1	2.53	0.44
15:G:71:GLU:O	15:G:75:LYS:HG2	2.17	0.44
30:V:148:MET:SD	30:V:185:VAL:HG21	2.58	0.44
33:Y:347:ILE:CD1	33:Y:392:ILE:HG21	2.47	0.44
5:4:529:GLU:O	5:4:533:MET:HG2	2.18	0.44
5:4:570:ASP:HA	5:4:602:HIS:CE1	2.48	0.44
8:7:661:LEU:O	8:7:667:VAL:HA	2.17	0.44
9:A:771:A:H2'	9:A:772:A:C8	2.52	0.44
9:A:1499:U:H2'	9:A:1500:C:C6	2.53	0.44
12:D:206:PRO:HG2	12:D:276:VAL:HG11	1.99	0.44
20:L:175:TYR:HB2	22:N:89:GLY:HA3	2.00	0.44
26:R:257:GLY:HA2	26:R:259:TYR:CE2	2.52	0.44
1:0:63:ARG:HB2	1:0:66:GLN:HB2	1.99	0.44
5:4:302:VAL:HG21	5:4:341:CYS:SG	2.57	0.44
22:N:8:VAL:HB	22:N:68:ALA:HB1	2.00	0.44
30:V:228:TYR:HB3	30:V:259:ALA:HB2	2.00	0.44
30:V:331:LEU:HD11	30:V:335:LYS:HE3	1.98	0.44
5:4:650:MET:HE2	5:4:650:MET:HB2	1.90	0.44
13:E:37:ARG:HG3	29:U:167:PHE:CE1	2.53	0.44
17:I:140:LYS:HD2	17:I:169:GLY:HA3	1.99	0.44
21:M:21:LEU:HD23	21:M:32:TYR:CG	2.53	0.44
26:R:167:HIS:HB3	26:R:193:ILE:HD13	1.99	0.44
30:V:96:ARG:NH2	30:V:133:VAL:HA	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:X:261:ALA:HA	32:X:307:VAL:O	2.17	0.44
1:0:58:VAL:HG23	1:0:137:HIS:ND1	2.32	0.43
3:2:49:MET:HE1	14:F:237:ALA:CB	2.48	0.43
5:4:467:LEU:HG	5:4:468:MET:SD	2.58	0.43
5:4:562:GLN:HG3	5:4:564:ILE:H	1.81	0.43
1:0:67:LEU:HD23	1:0:141:LEU:HB3	2.00	0.43
3:2:38:ARG:HG2	9:A:1183:U:OP1	2.18	0.43
9:A:832:U:H2'	9:A:833:A:C8	2.52	0.43
9:A:1002:C:H2'	9:A:1003:A:H8	1.83	0.43
9:A:1370:U:C2	9:A:1371:U:C5	3.06	0.43
9:A:1507:A:H2'	9:A:1508:C:H6	1.82	0.43
30:V:287:LEU:O	30:V:291:THR:HG23	2.19	0.43
31:W:108:VAL:O	31:W:109:GLU:HG3	2.19	0.43
8:7:594:LYS:HD3	8:7:605:ASP:OD2	2.17	0.43
9:A:995:A:H2'	9:A:996:A:C8	2.54	0.43
9:A:1471:A:H2'	9:A:1472:G:C8	2.53	0.43
27:S:104:THR:O	27:S:107:GLN:HB2	2.18	0.43
27:S:125:LEU:HD12	27:S:130:VAL:HG21	2.00	0.43
30:V:157:TYR:HA	30:V:160:ALA:HB3	2.00	0.43
2:1:244:THR:O	2:1:248:MET:HG2	2.18	0.43
5:4:173:PHE:HE1	5:4:183:VAL:HG21	1.84	0.43
9:A:1239:C:H2'	9:A:1240:A:C8	2.54	0.43
10:B:220:VAL:HG22	10:B:234:TYR:HB2	2.00	0.43
20:L:147:ARG:HG3	20:L:148:LYS:HD3	1.99	0.43
32:X:203:LYS:NZ	32:X:221:PRO:HG3	2.33	0.43
2:1:238:GLU:HG2	2:1:239:TRP:N	2.32	0.43
5:4:429:LEU:HD22	5:4:468:MET:O	2.18	0.43
9:A:845:A:H5'	29:U:64:ARG:HH22	1.84	0.43
20:L:167:LEU:HD11	20:L:187:ILE:HG21	2.00	0.43
1:0:83:LYS:HB3	1:0:138:ASP:OD1	2.19	0.43
5:4:282:LEU:HD21	5:4:289:ALA:HB2	2.00	0.43
6:5:23:G:H2'	6:5:24:C:C6	2.54	0.43
9:A:758:U:O4	9:A:1159:A:HI'	2.19	0.43
9:A:952:A:H2'	9:A:953:U:C6	2.53	0.43
14:F:82:THR:O	14:F:87:GLU:HG3	2.18	0.43
18:J:114:ARG:HA	18:J:122:LYS:HA	2.00	0.43
20:L:73:LEU:HD23	20:L:95:LEU:HD23	2.00	0.43
23:O:55:PRO:HB3	23:O:114:HIS:HB2	2.00	0.43
30:V:173:PHE:CD1	30:V:211:PRO:HB3	2.53	0.43
2:1:259:GLU:HA	2:1:262:ILE:HG22	2.01	0.43
8:7:538:TYR:HA	8:7:723:TRP:CD1	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1544:A:H2'	9:A:1545:U:C6	2.54	0.43
15:G:241:VAL:O	15:G:245:ARG:HG2	2.18	0.43
1:0:171:ARG:HA	1:0:174:ILE:HG12	2.00	0.43
5:4:330:PRO:HD2	33:Y:262:MET:HE1	2.01	0.43
11:C:96:MET:HE3	11:C:96:MET:HB3	1.90	0.43
30:V:388:GLN:HG3	30:V:391:GLN:HE22	1.84	0.43
32:X:162:VAL:HB	32:X:272:THR:HG22	2.01	0.43
32:X:248:LYS:HB2	32:X:296:MET:SD	2.59	0.43
2:1:156:TYR:CD2	16:H:171:GLU:HG2	2.54	0.43
5:4:452:GLN:HE21	5:4:453:HIS:CE1	2.36	0.43
5:4:642:CYS:HA	5:4:645:LEU:HG	2.00	0.43
9:A:747:A:H2'	9:A:748:G:H8	1.84	0.43
10:B:142:ILE:O	10:B:164:GLU:HB3	2.19	0.43
4:3:145:LYS:NZ	9:A:1583:MA6:H5''	2.34	0.43
8:7:284:ILE:HD12	8:7:338:THR:HG22	2.00	0.43
9:A:1365:A:H4'	9:A:1389:G:H4'	2.01	0.43
17:I:100:VAL:HG12	17:I:106:PRO:HA	2.01	0.43
30:V:322:THR:O	30:V:326:LYS:HG2	2.17	0.43
31:W:120:PHE:HB3	31:W:164:GLU:HA	2.01	0.43
9:A:982:A:H2'	9:A:983:C:H6	1.82	0.42
9:A:1497:C:H2'	9:A:1498:C:H6	1.84	0.42
30:V:205:GLY:O	30:V:209:LEU:HD23	2.19	0.42
31:W:104:ILE:HG21	31:W:107:ILE:HD11	2.01	0.42
32:X:268:LEU:HB2	32:X:269:TRP:CE3	2.54	0.42
32:X:295:LYS:O	32:X:298:LYS:HG2	2.19	0.42
33:Y:285:GLN:O	33:Y:289:VAL:HG13	2.19	0.42
10:B:61:LYS:HZ1	10:B:271:TYR:HB2	1.84	0.42
14:F:153:GLU:HB3	14:F:179:ARG:HG2	2.01	0.42
28:T:114:ARG:O	28:T:117:GLU:HG2	2.19	0.42
1:0:64:LEU:HB2	1:0:139:TRP:CD1	2.55	0.42
9:A:741:A:C6	9:A:742:U:C4	3.07	0.42
9:A:1577:U:H2'	9:A:1578:A:H8	1.84	0.42
13:E:37:ARG:HD2	13:E:69:TYR:HE1	1.83	0.42
14:F:62:GLU:HA	14:F:65:VAL:HG22	2.02	0.42
3:2:47:THR:O	3:2:51:VAL:HG23	2.18	0.42
5:4:350:ARG:HH12	5:4:388:ARG:NH2	2.17	0.42
12:D:265:MET:SD	15:G:57:PRO:HD2	2.58	0.42
28:T:22:VAL:HG23	28:T:108:LYS:HB2	2.02	0.42
30:V:357:THR:HG22	30:V:361:LYS:NZ	2.34	0.42
2:1:279:ASN:CG	2:1:282:GLU:HB2	2.45	0.42
4:3:186:PRO:HB3	20:L:216:GLU:HG3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1246:U:C5	34:Z:96:LYS:HD2	2.54	0.42
21:M:19:ILE:HG22	21:M:36:ALA:HB2	2.02	0.42
24:P:124:TYR:HB3	25:Q:9:ALA:HB2	2.00	0.42
26:R:79:LEU:O	26:R:83:THR:HG23	2.20	0.42
26:R:86:ASN:OD1	26:R:89:LYS:HB3	2.20	0.42
26:R:331:PHE:CE2	26:R:336:ALA:HB2	2.53	0.42
32:X:353:PHE:O	32:X:357:ILE:HD12	2.19	0.42
1:O:113:LYS:HE3	1:O:115:TRP:CH2	2.53	0.42
9:A:1181:G:H2'	9:A:1182:C:C6	2.55	0.42
11:C:58:ALA:HB3	11:C:60:HIS:CE1	2.55	0.42
21:M:63:GLU:OE1	26:R:157:VAL:HG21	2.19	0.42
32:X:203:LYS:HD2	32:X:219:GLY:O	2.18	0.42
2:1:249:GLU:HG2	2:1:250:GLU:N	2.33	0.42
2:1:279:ASN:OD1	2:1:282:GLU:HB2	2.19	0.42
9:A:738:A:H2'	9:A:740:G:C5	2.55	0.42
30:V:357:THR:HA	30:V:360:VAL:HG12	2.02	0.42
32:X:182:LEU:O	32:X:186:THR:HG23	2.19	0.42
9:A:715:G:H2'	9:A:716:U:H6	1.84	0.42
9:A:1455:U:H2'	9:A:1456:U:C6	2.55	0.42
30:V:200:GLU:O	30:V:204:PHE:CD2	2.73	0.42
5:4:571:TRP:O	5:4:604:LYS:HE2	2.19	0.42
8:7:178:PRO:HA	8:7:348:LYS:HG2	2.02	0.42
8:7:296:ASP:HB3	8:7:299:LYS:HB3	2.02	0.42
9:A:1542:U:H2'	9:A:1543:U:C6	2.55	0.42
23:O:95:ILE:CD1	23:O:100:VAL:HG22	2.50	0.42
23:O:184:VAL:O	26:R:138:ILE:HD13	2.20	0.42
1:O:88:GLN:HA	23:O:215:ARG:HD3	2.02	0.42
9:A:955:A:OP2	28:T:37:HIS:HE1	2.03	0.42
9:A:1581:G:H2'	9:A:1583:MA6:OP2	2.20	0.42
12:D:128:ARG:HG3	12:D:129:GLY:H	1.85	0.42
34:Z:26:THR:HB	34:Z:31:MET:HE3	2.02	0.42
30:V:175:VAL:HG13	30:V:178:THR:H	1.85	0.41
30:V:250:ILE:HG21	30:V:258:ARG:HH12	1.85	0.41
32:X:73:GLN:HA	32:X:76:GLU:HG2	2.02	0.41
5:4:540:HIS:CG	5:4:544:LEU:HD23	2.55	0.41
6:5:51:U:H2'	6:5:52:G:O4'	2.20	0.41
9:A:1373:U:H2'	9:A:1374:A:H8	1.86	0.41
9:A:1506:U:H2'	9:A:1507:A:C8	2.54	0.41
30:V:240:LEU:HD22	30:V:253:PRO:HG3	2.02	0.41
4:3:165:LYS:HE3	9:A:1148:A:P	2.60	0.41
9:A:1012:A:H2'	9:A:1013:A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1044:U:H2'	9:A:1045:G:O4'	2.21	0.41
9:A:1239:C:H2'	9:A:1240:A:H8	1.85	0.41
14:F:51:TYR:HB3	15:G:363:TRP:CD2	2.54	0.41
17:I:129:GLN:NE2	17:I:133:ILE:HD11	2.35	0.41
1:O:163:SER:HB3	1:O:190:MET:HB3	2.00	0.41
9:A:799:A:H2'	9:A:800:C:C6	2.55	0.41
14:F:197:GLN:O	14:F:197:GLN:HG2	2.19	0.41
1:O:192:ASN:HB3	1:O:195:ARG:NH1	2.36	0.41
6:5:23:G:H2'	6:5:24:C:H6	1.84	0.41
9:A:812:A:H2'	9:A:813:A:C8	2.56	0.41
24:P:52:ILE:HD11	24:P:54:MET:HE2	2.01	0.41
30:V:177:SER:HB2	30:V:367:CYS:HB3	2.03	0.41
1:O:20:ALA:O	1:O:23:GLU:HG3	2.20	0.41
2:1:116:PRO:O	2:1:120:LYS:HG3	2.21	0.41
2:1:284:LEU:HA	2:1:289:ILE:HG13	2.01	0.41
6:5:2:G:H2'	6:5:3:U:C6	2.55	0.41
8:7:460:LEU:HB2	18:J:136:GLN:HG3	2.01	0.41
9:A:832:U:H2'	9:A:833:A:H8	1.83	0.41
9:A:1506:U:H2'	9:A:1507:A:H8	1.86	0.41
14:F:82:THR:HG23	15:G:315:PHE:CD1	2.56	0.41
30:V:61:PHE:CZ	30:V:94:LYS:HB3	2.56	0.41
32:X:253:LEU:HB2	32:X:255:MET:HE1	2.01	0.41
5:4:347:VAL:HA	5:4:350:ARG:CG	2.50	0.41
9:A:973:C:O2'	9:A:974:U:H5'	2.21	0.41
9:A:1334:G:H2'	9:A:1335:U:O4'	2.21	0.41
21:M:99:LEU:HD23	26:R:148:LEU:HD21	2.03	0.41
23:O:205:TRP:HZ2	29:U:51:ALA:HB1	1.86	0.41
30:V:69:SER:HA	30:V:72:ILE:HG22	2.02	0.41
32:X:151:LEU:HD12	32:X:151:LEU:HA	1.80	0.41
5:4:349:ALA:C	5:4:352:PRO:HD2	2.46	0.41
8:7:512:ASP:HB3	8:7:515:VAL:HG23	2.02	0.41
9:A:700:A:H4'	9:A:701:G:O5'	2.20	0.41
9:A:746:A:C4	9:A:747:A:C8	3.09	0.41
15:G:250:LEU:HD23	15:G:250:LEU:H	1.85	0.41
15:G:315:PHE:CE2	15:G:369:LEU:HD21	2.56	0.41
30:V:196:PHE:HB3	30:V:201:GLU:HG2	2.03	0.41
30:V:226:TYR:CE1	30:V:282:VAL:HG11	2.55	0.41
33:Y:286:LEU:O	33:Y:289:VAL:HG22	2.21	0.41
2:1:194:VAL:HG11	2:1:205:LEU:HD11	2.03	0.41
5:4:188:THR:O	5:4:192:LEU:HG	2.20	0.41
5:4:256:GLU:HG3	5:4:287:LEU:HD22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:4:646:THR:HG23	5:4:663:LEU:HD22	2.03	0.41
8:7:461:LYS:O	8:7:465:GLU:HG2	2.21	0.41
9:A:854:U:H2'	9:A:855:A:C8	2.56	0.41
9:A:1348:G:H2'	9:A:1349:U:C6	2.56	0.41
9:A:1372:C:H2'	9:A:1373:U:H6	1.86	0.41
13:E:37:ARG:HD2	13:E:69:TYR:CE1	2.55	0.41
13:E:108:ILE:HD11	24:P:100:CYS:HB3	2.02	0.41
14:F:150:LYS:HA	14:F:153:GLU:HG3	2.03	0.41
16:H:185:LYS:HE2	16:H:185:LYS:HB2	1.79	0.41
17:I:181:ILE:HD11	25:Q:39:ILE:HD11	2.03	0.41
20:L:207:LYS:O	20:L:211:ILE:HG12	2.21	0.41
21:M:55:ASP:HB2	28:T:140:ILE:HD13	2.02	0.41
30:V:209:LEU:CD2	30:V:227:GLY:HA3	2.50	0.41
5:4:526:ASP:O	5:4:529:GLU:HG3	2.21	0.41
6:5:12:C:H2'	6:5:13:U:H6	1.86	0.41
6:5:68:G:H2'	6:5:69:U:C6	2.56	0.41
8:7:324:SER:HB3	8:7:329:ASP:HB3	2.03	0.41
9:A:862:A:H2'	9:A:863:C:H6	1.86	0.41
9:A:896:A:H2'	9:A:897:C:C6	2.55	0.41
9:A:1089:U:H2'	9:A:1090:A:H8	1.85	0.41
10:B:193:ILE:HB	10:B:219:THR:HG22	2.02	0.41
11:C:105:ALA:HB3	11:C:122:VAL:HG12	2.03	0.41
30:V:74:ARG:HH22	30:V:390:ILE:HD11	1.85	0.41
30:V:360:VAL:O	30:V:364:LEU:HB2	2.21	0.41
32:X:265:ILE:HG12	32:X:297:MET:HE2	2.03	0.41
1:0:104:TYR:HB2	30:V:97:HIS:O	2.21	0.40
5:4:264:ARG:NH2	33:Y:278:TRP:HB3	2.35	0.40
5:4:543:GLU:HG2	5:4:544:LEU:N	2.35	0.40
6:5:12:C:H2'	6:5:13:U:C6	2.56	0.40
6:5:25:U:C2	6:5:26:A:C8	3.09	0.40
8:7:391:LYS:HE2	8:7:451:GLN:OE1	2.20	0.40
9:A:1173:C:H2'	9:A:1174:U:C6	2.56	0.40
11:C:109:VAL:HB	11:C:120:CYS:HB2	2.02	0.40
15:G:115:GLY:HA3	16:H:84:ASP:OD1	2.22	0.40
19:K:54:ILE:O	19:K:58:ARG:HG3	2.21	0.40
26:R:273:TRP:NE1	26:R:277:ASN:HD21	2.18	0.40
26:R:292:ASP:OD2	26:R:349:TYR:HE1	2.04	0.40
28:T:32:VAL:HB	28:T:66:MET:HG3	2.03	0.40
1:0:55:TRP:HA	1:0:58:VAL:HG12	2.02	0.40
1:0:198:MET:HE1	29:U:61:GLN:HA	2.02	0.40
2:1:304:GLU:OE1	32:X:326:GLN:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:4:393:ILE:HD13	5:4:422:ILE:HG21	2.04	0.40
9:A:955:A:O4'	9:A:1042:U:H1'	2.21	0.40
9:A:1489:G:H2'	9:A:1490:U:H6	1.87	0.40
30:V:199:GLU:HB2	30:V:202:ARG:HH21	1.85	0.40
1:0:58:VAL:CG2	1:0:137:HIS:HD1	2.34	0.40
2:1:239:TRP:CG	34:Z:10:ARG:HE	2.39	0.40
5:4:388:ARG:O	5:4:392:ILE:HG12	2.22	0.40
8:7:241:PHE:HB3	8:7:244:MET:HB3	2.02	0.40
10:B:189:LEU:HD23	10:B:189:LEU:HA	1.94	0.40
10:B:229:PRO:HA	10:B:232:ILE:HD12	2.02	0.40
15:G:59:LYS:HE2	15:G:62:PRO:HA	2.04	0.40
16:H:78:VAL:HG22	16:H:172:VAL:HG23	2.04	0.40
21:M:54:TYR:CD1	21:M:66:VAL:HG22	2.56	0.40
21:M:78:GLY:O	29:U:75:VAL:HG22	2.21	0.40
21:M:83:LEU:HD12	21:M:88:GLU:HG3	2.03	0.40
26:R:73:GLU:HG2	26:R:74:GLU:N	2.37	0.40
26:R:116:ARG:O	26:R:120:GLU:HG2	2.21	0.40
1:0:148:GLU:HG2	1:0:149:ALA:N	2.36	0.40
8:7:394:ALA:HB2	8:7:421:TRP:CD2	2.56	0.40
9:A:1190:C:H2'	9:A:1191:C:C6	2.57	0.40
9:A:1372:C:H2'	9:A:1373:U:C6	2.56	0.40
15:G:168:MET:HE2	15:G:237:GLU:HG3	2.02	0.40
17:I:122:LYS:HB2	17:I:122:LYS:HE3	1.87	0.40
30:V:74:ARG:HA	30:V:74:ARG:HD3	1.89	0.40
1:0:196:ILE:HG13	1:0:196:ILE:O	2.21	0.40
2:1:312:TYR:O	2:1:316:VAL:HG23	2.22	0.40
5:4:196:CYS:SG	5:4:262:MET:HA	2.61	0.40
9:A:731:A:H2'	9:A:732:A:C8	2.56	0.40
13:E:118:TYR:HB3	13:E:123:ARG:NH2	2.37	0.40
15:G:255:GLN:HG3	15:G:256:LEU:O	2.21	0.40
29:U:97:LYS:O	29:U:101:GLU:HG2	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	213/215 (99%)	209 (98%)	4 (2%)	0	100	100
2	1	276/278 (99%)	270 (98%)	6 (2%)	0	100	100
3	2	116/118 (98%)	112 (97%)	4 (3%)	0	100	100
4	3	69/71 (97%)	68 (99%)	1 (1%)	0	100	100
5	4	588/616 (96%)	573 (97%)	15 (3%)	0	100	100
8	7	569/571 (100%)	554 (97%)	15 (3%)	0	100	100
10	B	223/225 (99%)	220 (99%)	3 (1%)	0	100	100
11	C	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
12	D	341/343 (99%)	331 (97%)	10 (3%)	0	100	100
13	E	120/122 (98%)	119 (99%)	1 (1%)	0	100	100
14	F	206/208 (99%)	201 (98%)	5 (2%)	0	100	100
15	G	323/344 (94%)	316 (98%)	7 (2%)	0	100	100
16	H	138/140 (99%)	134 (97%)	3 (2%)	1 (1%)	18	34
17	I	135/137 (98%)	130 (96%)	5 (4%)	0	100	100
18	J	106/108 (98%)	105 (99%)	1 (1%)	0	100	100
19	K	99/101 (98%)	98 (99%)	1 (1%)	0	100	100
20	L	172/174 (99%)	170 (99%)	2 (1%)	0	100	100
21	M	117/119 (98%)	115 (98%)	2 (2%)	0	100	100
22	N	108/110 (98%)	106 (98%)	2 (2%)	0	100	100
23	O	191/193 (99%)	188 (98%)	3 (2%)	0	100	100
24	P	95/97 (98%)	94 (99%)	1 (1%)	0	100	100
25	Q	85/87 (98%)	84 (99%)	1 (1%)	0	100	100
26	R	293/295 (99%)	285 (97%)	8 (3%)	0	100	100
27	S	133/135 (98%)	133 (100%)	0	0	100	100
28	T	166/168 (99%)	166 (100%)	0	0	100	100
29	U	174/176 (99%)	172 (99%)	2 (1%)	0	100	100
30	V	358/379 (94%)	349 (98%)	9 (2%)	0	100	100
31	W	98/100 (98%)	97 (99%)	0	1 (1%)	12	24
32	X	350/352 (99%)	345 (99%)	5 (1%)	0	100	100
33	Y	147/149 (99%)	140 (95%)	7 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	Z	98/100 (98%)	98 (100%)	0	0	100	100
All	All	6237/6363 (98%)	6109 (98%)	126 (2%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	H	126	ILE
31	W	109	GLU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	188/188 (100%)	188 (100%)	0	100	100
2	1	256/256 (100%)	256 (100%)	0	100	100
3	2	100/101 (99%)	100 (100%)	0	100	100
4	3	65/65 (100%)	65 (100%)	0	100	100
5	4	529/549 (96%)	529 (100%)	0	100	100
8	7	396/481 (82%)	396 (100%)	0	100	100
10	B	198/198 (100%)	198 (100%)	0	100	100
11	C	115/115 (100%)	115 (100%)	0	100	100
12	D	286/286 (100%)	286 (100%)	0	100	100
13	E	104/104 (100%)	104 (100%)	0	100	100
14	F	185/185 (100%)	185 (100%)	0	100	100
15	G	285/301 (95%)	285 (100%)	0	100	100
16	H	130/130 (100%)	130 (100%)	0	100	100
17	I	105/105 (100%)	105 (100%)	0	100	100
18	J	93/93 (100%)	93 (100%)	0	100	100
19	K	91/91 (100%)	91 (100%)	0	100	100
20	L	158/158 (100%)	158 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	M	97/97 (100%)	97 (100%)	0	100	100
22	N	96/96 (100%)	96 (100%)	0	100	100
23	O	174/174 (100%)	174 (100%)	0	100	100
24	P	88/88 (100%)	88 (100%)	0	100	100
25	Q	78/79 (99%)	78 (100%)	0	100	100
26	R	264/264 (100%)	264 (100%)	0	100	100
27	S	116/116 (100%)	116 (100%)	0	100	100
28	T	153/153 (100%)	153 (100%)	0	100	100
29	U	152/152 (100%)	152 (100%)	0	100	100
30	V	325/339 (96%)	325 (100%)	0	100	100
31	W	87/87 (100%)	87 (100%)	0	100	100
32	X	311/311 (100%)	311 (100%)	0	100	100
33	Y	137/137 (100%)	137 (100%)	0	100	100
34	Z	90/90 (100%)	90 (100%)	0	100	100
All	All	5452/5589 (98%)	5452 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (38) such sidechains are listed below:

Mol	Chain	Res	Type
1	0	192	ASN
1	0	207	GLN
5	4	148	GLN
5	4	189	ASN
5	4	269	HIS
5	4	346	HIS
5	4	373	HIS
5	4	452	GLN
5	4	504	ASN
5	4	562	GLN
5	4	602	HIS
8	7	274	GLN
12	D	341	ASN
14	F	122	GLN
17	I	96	GLN
17	I	129	GLN

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Mol	Chain	Res	Type
19	K	28	HIS
20	L	169	ASN
22	N	44	ASN
26	R	108	GLN
26	R	278	ASN
26	R	305	HIS
27	S	66	HIS
27	S	91	ASN
28	T	54	GLN
30	V	38	HIS
30	V	383	HIS
31	W	121	HIS
32	X	81	HIS
32	X	291	HIS
32	X	302	HIS
32	X	394	HIS
33	Y	285	GLN
33	Y	292	GLN
33	Y	337	HIS
34	Z	27	ASN
34	Z	56	HIS
34	Z	63	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
6	5	70/71 (98%)	10 (14%)	0
7	6	3/4 (75%)	1 (33%)	0
9	A	954/955 (99%)	121 (12%)	0
All	All	1027/1030 (99%)	132 (12%)	0

All (132) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	5	9	C
6	5	10	A
6	5	20	U
6	5	21	A
6	5	31	G
6	5	48	U
6	5	49	G

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Mol	Chain	Res	Type
6	5	52	G
6	5	55	U
6	5	60	C
7	6	4	U
9	A	651	A
9	A	680	U
9	A	688	A
9	A	704	U
9	A	718	A
9	A	721	U
9	A	722	C
9	A	737	C
9	A	738	A
9	A	739	C
9	A	753	A
9	A	760	A
9	A	761	A
9	A	766	G
9	A	773	U
9	A	791	G
9	A	796	G
9	A	830	U
9	A	832	U
9	A	835	C
9	A	851	A
9	A	860	A
9	A	868	C
9	A	871	A
9	A	889	G
9	A	890	C
9	A	904	C
9	A	919	A
9	A	923	A
9	A	938	A
9	A	939	A
9	A	942	A
9	A	954	C
9	A	958	C
9	A	960	C
9	A	961	U
9	A	962	C
9	A	967	A

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Mol	Chain	Res	Type
9	A	992	U
9	A	1001	C
9	A	1002	C
9	A	1011	C
9	A	1015	A
9	A	1019	A
9	A	1042	U
9	A	1049	A
9	A	1065	C
9	A	1080	A
9	A	1081	U
9	A	1082	A
9	A	1098	C
9	A	1103	A
9	A	1105	C
9	A	1106	C
9	A	1107	U
9	A	1109	A
9	A	1117	A
9	A	1121	A
9	A	1151	C
9	A	1154	A
9	A	1160	A
9	A	1167	A
9	A	1179	G
9	A	1188	A
9	A	1189	U
9	A	1190	C
9	A	1193	U
9	A	1197	G
9	A	1206	G
9	A	1209	C
9	A	1215	U
9	A	1220	A
9	A	1223	C
9	A	1225	C
9	A	1229	U
9	A	1247	G
9	A	1248	C
9	A	1250	C
9	A	1251	A
9	A	1261	C

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Mol	Chain	Res	Type
9	A	1271	C
9	A	1273	G
9	A	1283	A
9	A	1284	U
9	A	1285	G
9	A	1290	C
9	A	1291	U
9	A	1326	A
9	A	1327	G
9	A	1330	C
9	A	1343	A
9	A	1356	A
9	A	1367	A
9	A	1376	C
9	A	1378	C
9	A	1390	A
9	A	1405	C
9	A	1420	U
9	A	1422	G
9	A	1430	A
9	A	1438	G
9	A	1447	G
9	A	1519	A
9	A	1520	U
9	A	1522	U
9	A	1525	C
9	A	1526	U
9	A	1527	A
9	A	1533	C
9	A	1537	C
9	A	1538	G
9	A	1539	C
9	A	1557	A
9	A	1558	A
9	A	1568	U
9	A	1571	U
9	A	1582	G
9	A	1584	MA6
9	A	1594	G
9	A	1595	G
9	A	1599	A

There are no RNA pucker outliers to report.

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

5 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	5MC	A	1488	9	19,22,23	4.24	8 (42%)	26,32,35	0.95	1 (3%)
9	B8T	A	1486	35,9	19,22,23	3.08	8 (42%)	25,31,34	0.86	1 (4%)
9	MA6	A	1584	9	23,26,27	1.44	6 (26%)	33,38,41	2.80	14 (42%)
9	5MU	A	1076	9	19,22,23	0.55	0	27,32,35	0.59	0
9	MA6	A	1583	9	23,26,27	1.43	5 (21%)	33,38,41	2.78	14 (42%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	5MC	A	1488	9	-	0/7/25/26	0/2/2/2
9	B8T	A	1486	35,9	-	1/7/27/28	0/2/2/2
9	MA6	A	1584	9	-	1/11/29/30	0/3/3/3
9	5MU	A	1076	9	-	0/7/25/26	0/2/2/2
9	MA6	A	1583	9	-	0/11/29/30	0/3/3/3

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	1488	5MC	C6-C5	9.62	1.50	1.34
9	A	1488	5MC	C5-C4	7.99	1.50	1.44
9	A	1488	5MC	C4-N3	7.38	1.45	1.34
9	A	1486	B8T	C4-N3	6.81	1.44	1.32
9	A	1488	5MC	C2-N3	6.69	1.49	1.36
9	A	1486	B8T	C2-N3	6.08	1.48	1.36
9	A	1486	B8T	C6-C5	5.89	1.48	1.35
9	A	1488	5MC	C4-N4	5.53	1.48	1.34
9	A	1488	5MC	C6-N1	5.39	1.47	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	1486	B8T	C4-N4	4.15	1.44	1.36
9	A	1488	5MC	C2-N1	4.06	1.48	1.40
9	A	1486	B8T	C2-N1	3.87	1.48	1.40
9	A	1584	MA6	C5-C4	-3.59	1.32	1.39
9	A	1583	MA6	C5-C4	-3.52	1.32	1.39
9	A	1486	B8T	C5-C4	3.37	1.48	1.41
9	A	1486	B8T	O2-C2	-3.06	1.18	1.23
9	A	1486	B8T	C6-N1	2.88	1.44	1.38
9	A	1584	MA6	C6-N6	2.87	1.44	1.36
9	A	1583	MA6	C6-N6	2.83	1.44	1.36
9	A	1488	5MC	O2-C2	-2.72	1.18	1.23
9	A	1584	MA6	C5-N7	-2.64	1.34	1.39
9	A	1583	MA6	C5-N7	-2.53	1.34	1.39
9	A	1583	MA6	C8-N9	-2.51	1.33	1.37
9	A	1584	MA6	C8-N9	-2.47	1.33	1.37
9	A	1583	MA6	C4-N9	-2.33	1.32	1.37
9	A	1584	MA6	C4-N9	-2.22	1.33	1.37
9	A	1584	MA6	C5-C6	-2.01	1.36	1.41

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	1583	MA6	N1-C6-N6	-8.00	107.11	116.86
9	A	1584	MA6	N1-C6-N6	-8.00	107.11	116.86
9	A	1583	MA6	N1-C2-N3	-5.89	119.67	128.58
9	A	1584	MA6	N1-C2-N3	-5.72	119.92	128.58
9	A	1583	MA6	C5-C6-N6	4.93	133.14	125.33
9	A	1584	MA6	C5-C6-N6	4.91	133.11	125.33
9	A	1583	MA6	N9-C8-N7	-4.60	107.41	113.94
9	A	1584	MA6	C1'-N9-C8	-4.42	117.28	127.09
9	A	1584	MA6	N9-C8-N7	-4.40	107.69	113.94
9	A	1584	MA6	C5-C4-N3	-4.28	120.83	126.72
9	A	1583	MA6	C1'-N9-C8	-4.27	117.62	127.09
9	A	1583	MA6	C5-C4-N3	-4.02	121.18	126.72
9	A	1583	MA6	C2-N1-C6	3.68	120.83	111.83
9	A	1584	MA6	C2-N1-C6	3.53	120.45	111.83
9	A	1584	MA6	C4-C5-C6	3.35	119.37	115.91
9	A	1584	MA6	C4-N9-C1'	3.24	134.20	126.63
9	A	1584	MA6	C2-N3-C4	3.20	119.66	111.83
9	A	1583	MA6	C2-N3-C4	3.16	119.55	111.83
9	A	1583	MA6	C4-N9-C8	3.08	108.97	105.74
9	A	1583	MA6	C4-C5-C6	3.02	119.03	115.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	1583	MA6	C4-N9-C1'	2.90	133.41	126.63
9	A	1488	5MC	C5-C6-N1	-2.89	120.18	123.31
9	A	1583	MA6	C5-N7-C8	2.87	107.96	103.45
9	A	1584	MA6	C5-N7-C8	2.84	107.92	103.45
9	A	1584	MA6	C4-N9-C8	2.62	108.48	105.74
9	A	1584	MA6	N3-C4-N9	2.41	131.27	127.17
9	A	1583	MA6	N3-C4-N9	2.37	131.19	127.17
9	A	1486	B8T	C6-C5-C4	2.33	119.81	117.00
9	A	1584	MA6	C4-C5-N7	-2.26	108.00	110.58
9	A	1583	MA6	C4-C5-N7	-2.22	108.04	110.58

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	A	1584	MA6	C4'-C5'-O5'-P
9	A	1486	B8T	O4'-C4'-C5'-O5'

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	1488	5MC	1	0
9	A	1583	MA6	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 98 ligands modelled in this entry, 93 are monoatomic - leaving 5 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
39	FES	P	201	24,13	0,4,4	-	-	-		
40	GDP	X	401	-	29,30,30	3.83	16 (55%)	45,47,47	1.74	10 (22%)
37	GTP	7	803	35	33,34,34	0.95	1 (3%)	50,54,54	1.60	9 (18%)
39	FES	T	201	28,21	0,4,4	-	-	-		
41	ATP	X	403	35	32,33,33	0.56	1 (3%)	48,52,52	0.33	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
39	FES	P	201	24,13	-	-	0/1/1/1
40	GDP	X	401	-	-	1/16/32/32	0/3/3/3
37	GTP	7	803	35	-	5/22/38/38	0/3/3/3
39	FES	T	201	28,21	-	-	0/1/1/1
41	ATP	X	403	35	-	4/22/38/38	0/3/3/3

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
40	X	401	GDP	C2'-C3'	-10.92	1.23	1.53
40	X	401	GDP	C4-N3	6.61	1.49	1.34
40	X	401	GDP	O4'-C4'	-6.43	1.30	1.45
40	X	401	GDP	C2-N3	5.49	1.46	1.33
40	X	401	GDP	C1'-N9	-5.44	1.32	1.47
40	X	401	GDP	C3'-C4'	5.39	1.66	1.53
40	X	401	GDP	PA-O3A	5.35	1.65	1.59
40	X	401	GDP	C2-N2	4.82	1.45	1.34
40	X	401	GDP	O4'-C1'	3.95	1.51	1.42
40	X	401	GDP	O2'-C2'	3.05	1.50	1.43
40	X	401	GDP	C5-N7	-2.98	1.33	1.39
40	X	401	GDP	C2-N1	2.69	1.44	1.37
40	X	401	GDP	O6-C6	-2.62	1.18	1.23
40	X	401	GDP	C5-C6	2.46	1.53	1.44
40	X	401	GDP	C6-N1	2.34	1.43	1.38
40	X	401	GDP	C2'-C1'	2.29	1.60	1.53
37	7	803	GTP	C2-N3	2.12	1.38	1.33
41	X	403	ATP	PB-O3B	-2.10	1.57	1.59

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
40	X	401	GDP	C5-C4-N3	-5.30	119.95	128.39
37	7	803	GTP	C5-C4-N3	-5.09	120.30	128.39
40	X	401	GDP	C2-N3-C4	4.58	120.19	112.30
37	7	803	GTP	C2-N3-C4	4.51	120.07	112.30
37	7	803	GTP	N9-C4-N3	3.33	132.62	125.95
40	X	401	GDP	C2-N1-C6	-3.18	119.34	125.11
40	X	401	GDP	N9-C4-N3	3.15	132.25	125.95
37	7	803	GTP	C2-N1-C6	-2.92	119.82	125.11
40	X	401	GDP	N9-C8-N7	-2.90	108.01	113.40
40	X	401	GDP	C5-C6-N1	2.73	120.21	113.25
37	7	803	GTP	N9-C8-N7	-2.56	108.65	113.40
40	X	401	GDP	O6-C6-C5	-2.53	119.85	126.53
37	7	803	GTP	C8-N7-C5	2.49	108.70	104.26
37	7	803	GTP	C5-C6-N1	2.43	119.44	113.25
37	7	803	GTP	O6-C6-C5	-2.42	120.15	126.53
40	X	401	GDP	C8-N7-C5	2.15	108.08	104.26
37	7	803	GTP	C3'-C2'-C1'	2.11	105.46	101.46
40	X	401	GDP	C1'-N9-C4	-2.10	120.30	126.49
40	X	401	GDP	C3'-C2'-C1'	2.04	105.32	101.46

There are no chirality outliers.

All (10) torsion outliers are listed below:

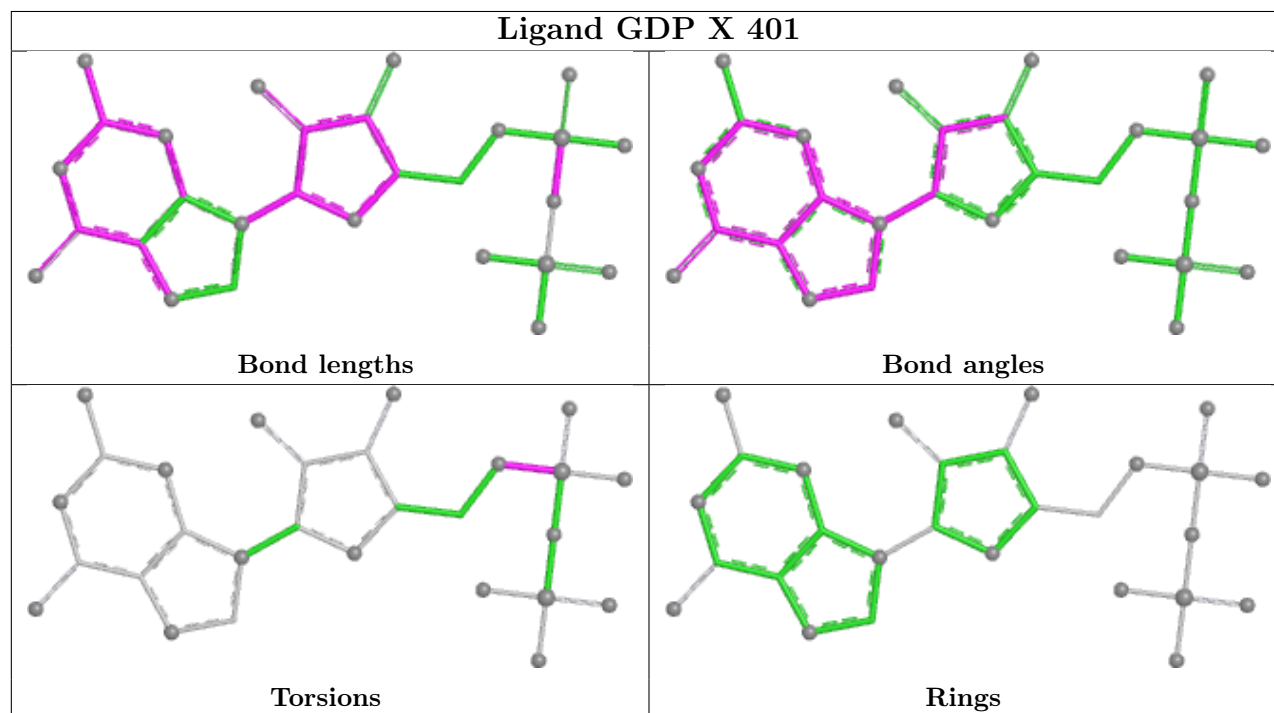
Mol	Chain	Res	Type	Atoms
37	7	803	GTP	PA-O3A-PB-O3B
41	X	403	ATP	PB-O3B-PG-O3G
37	7	803	GTP	PG-O3B-PB-O2B
41	X	403	ATP	PA-O3A-PB-O1B
40	X	401	GDP	C5'-O5'-PA-O1A
37	7	803	GTP	O4'-C4'-C5'-O5'
37	7	803	GTP	PA-O3A-PB-O2B
37	7	803	GTP	C3'-C4'-C5'-O5'
41	X	403	ATP	PG-O3B-PB-O2B
41	X	403	ATP	PA-O3A-PB-O2B

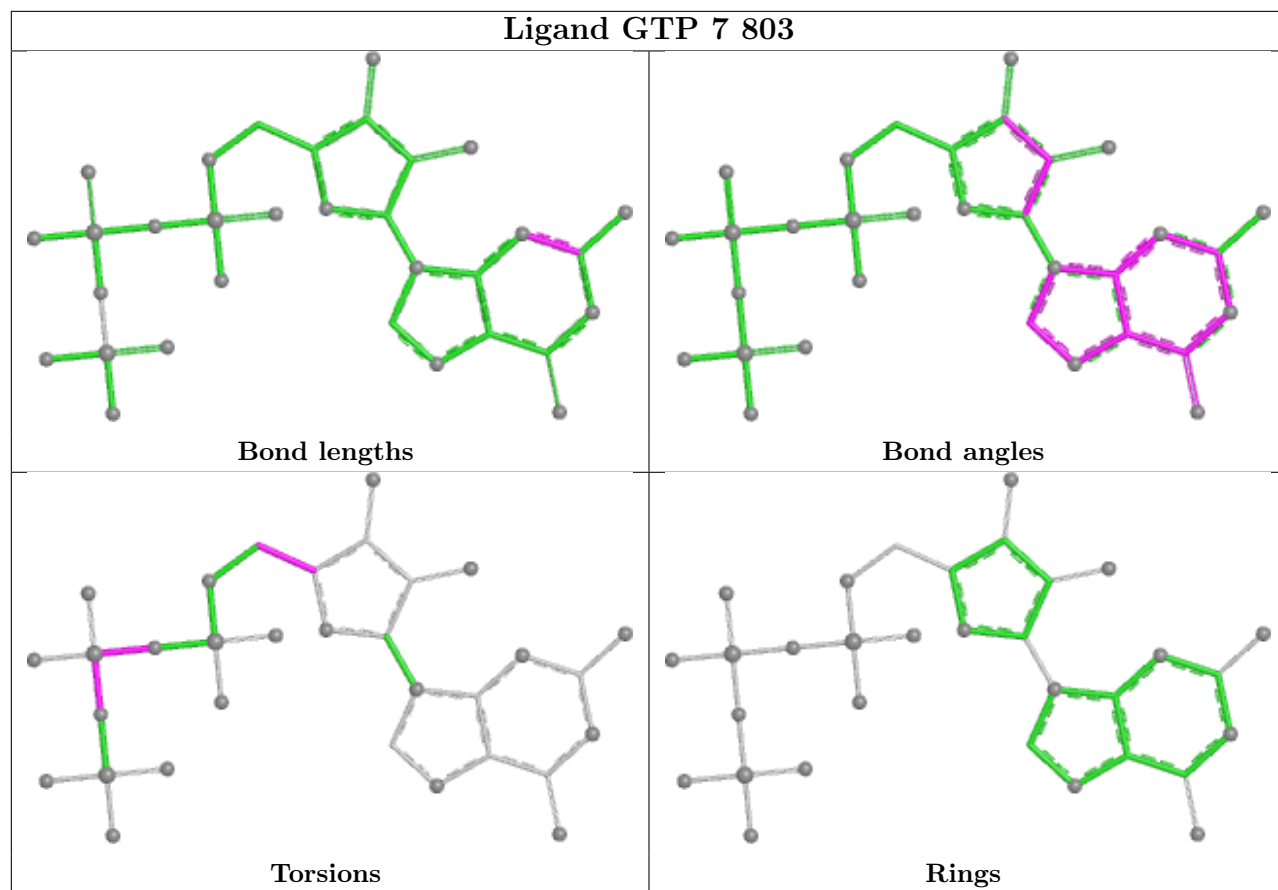
There are no ring outliers.

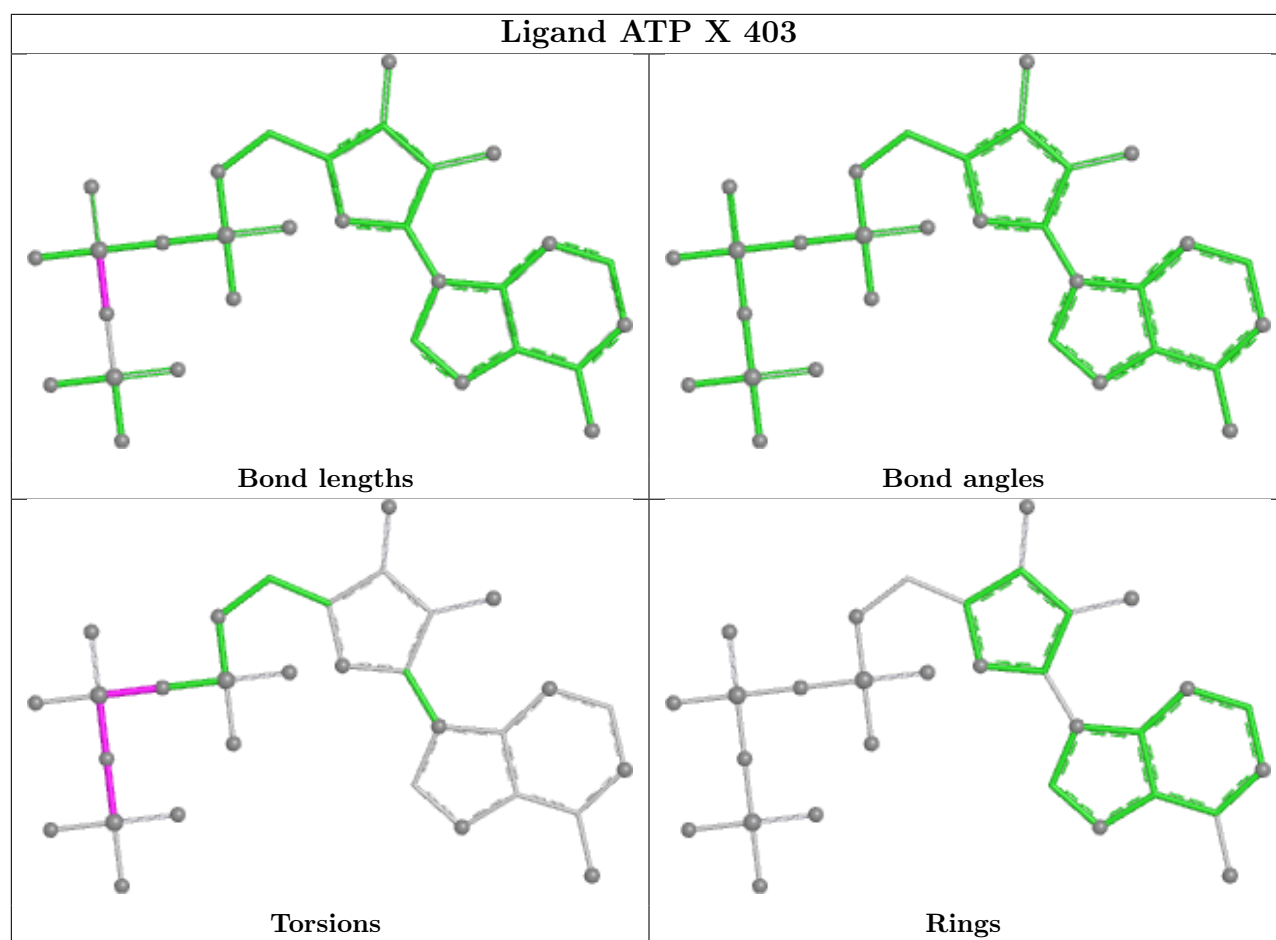
No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.

Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

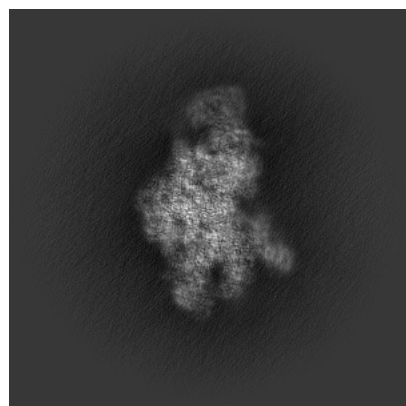
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-70544. These allow visual inspection of the internal detail of the map and identification of artifacts.

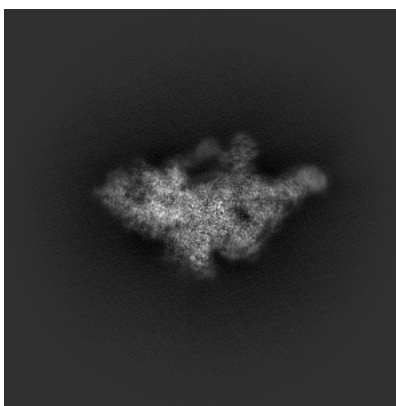
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

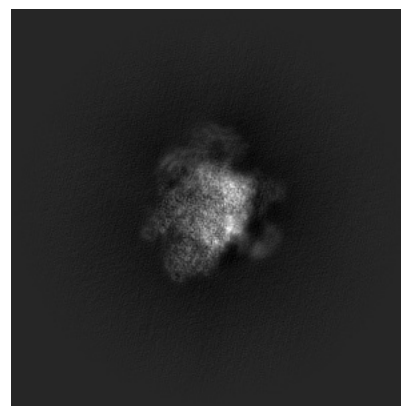
6.1.1 Primary map



X

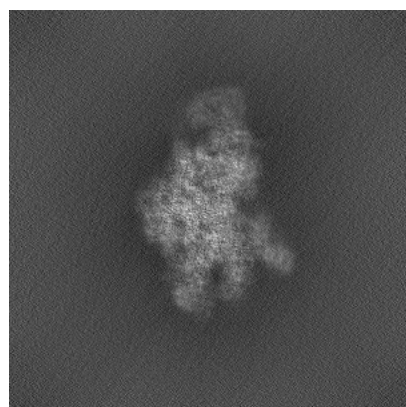


Y

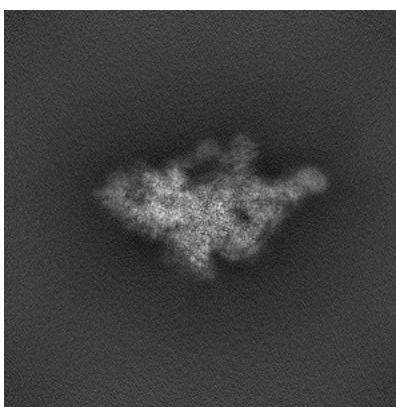


Z

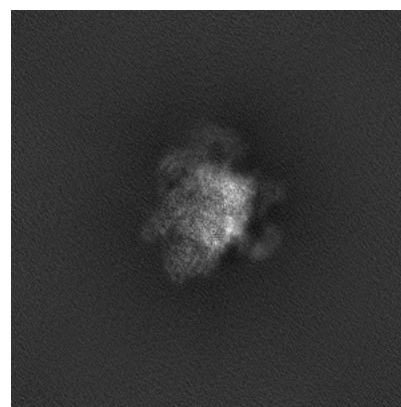
6.1.2 Raw map



X



Y

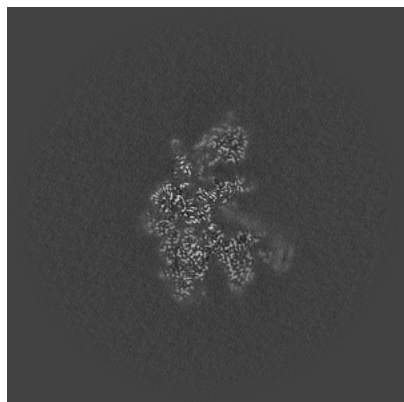


Z

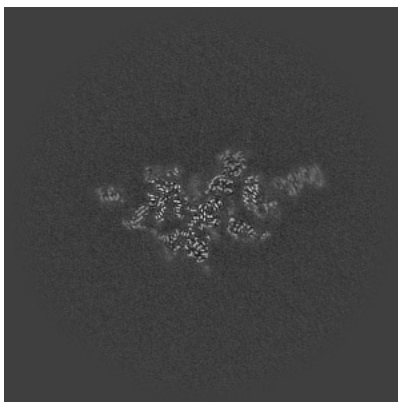
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

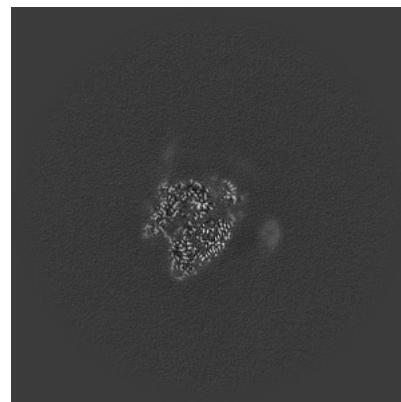
6.2.1 Primary map



X Index: 300

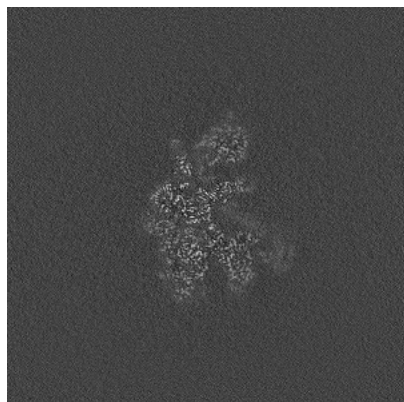


Y Index: 300

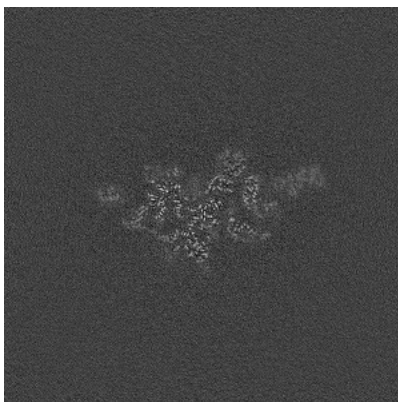


Z Index: 300

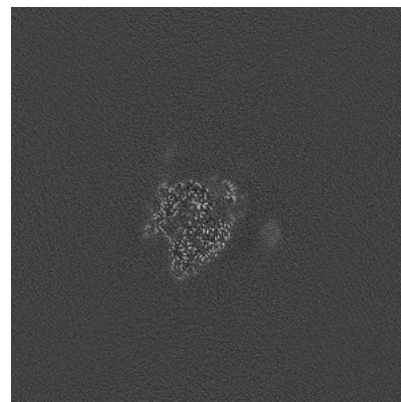
6.2.2 Raw map



X Index: 300



Y Index: 300

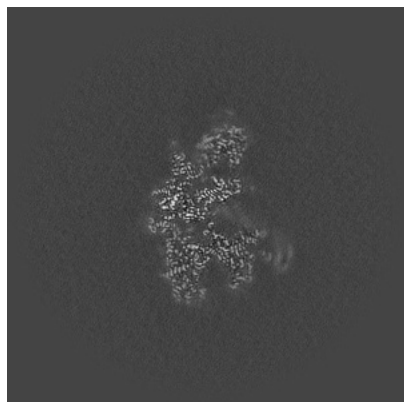


Z Index: 300

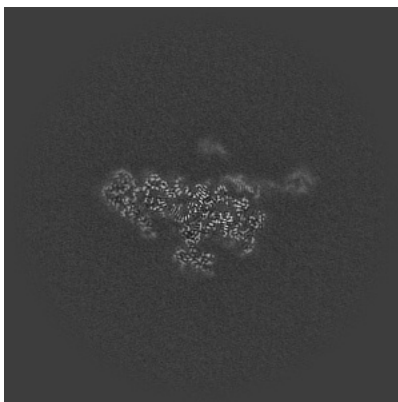
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

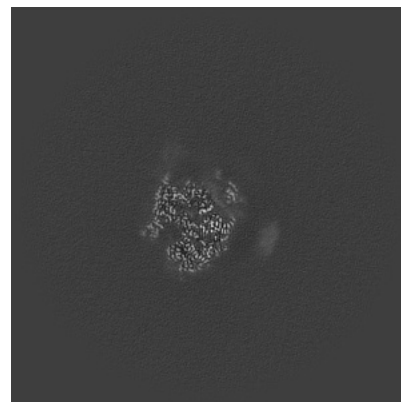
6.3.1 Primary map



X Index: 303

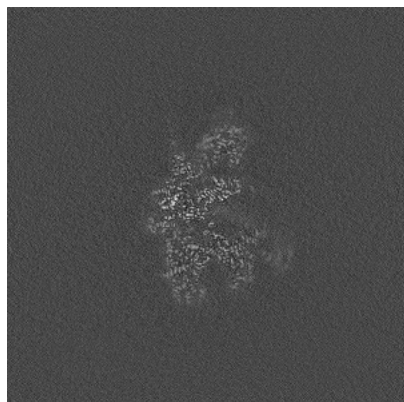


Y Index: 273

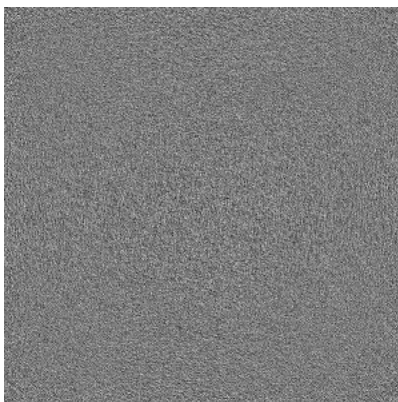


Z Index: 294

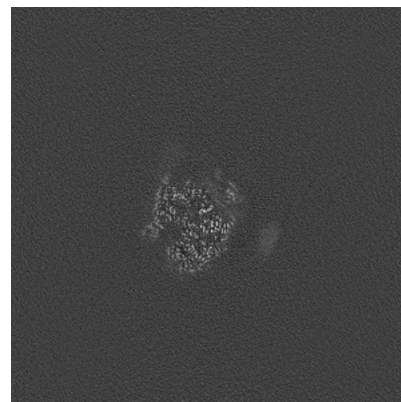
6.3.2 Raw map



X Index: 303



Y Index: 0

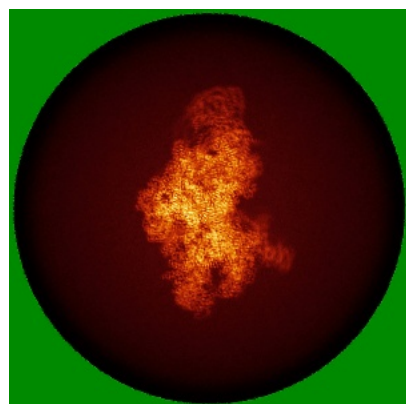


Z Index: 294

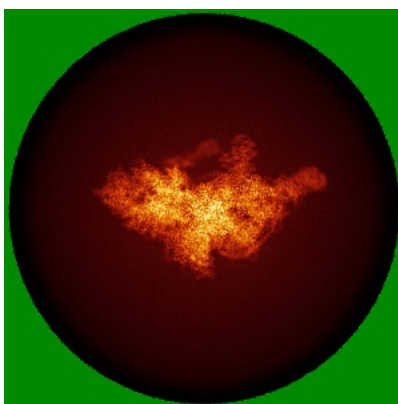
The images above show the largest variance slices of the map in three orthogonal directions.

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

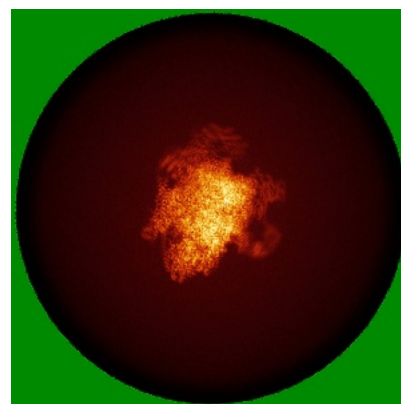
6.4.1 Primary map



X

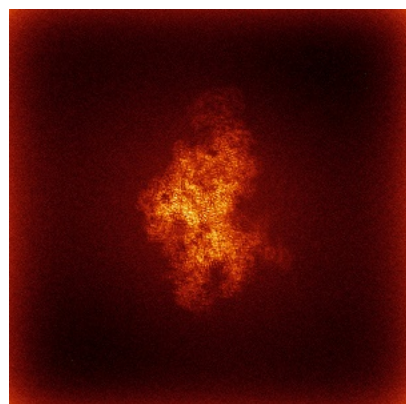


Y

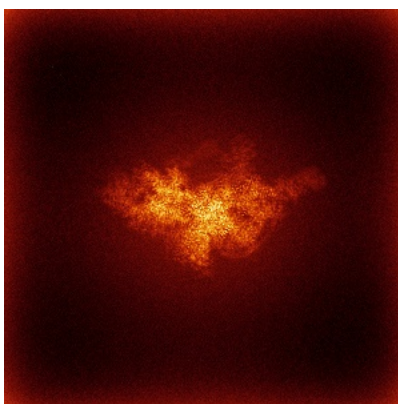


Z

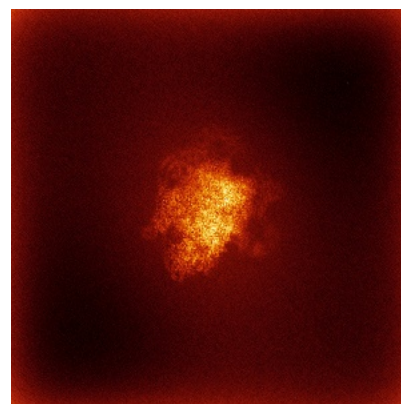
6.4.2 Raw map



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



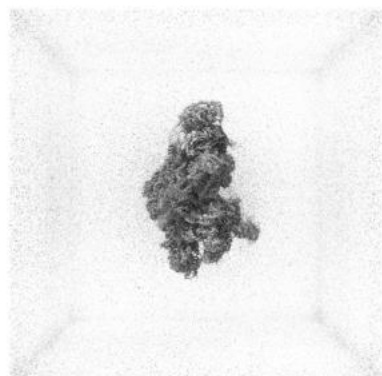
Y



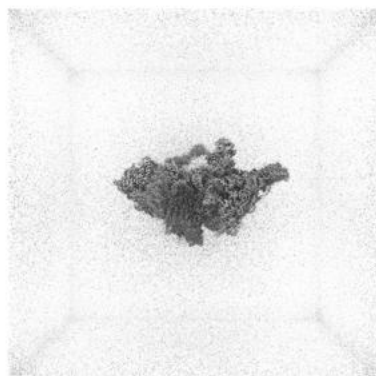
Z

The images above show the 3D surface view of the map at the recommended contour level 0.028. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

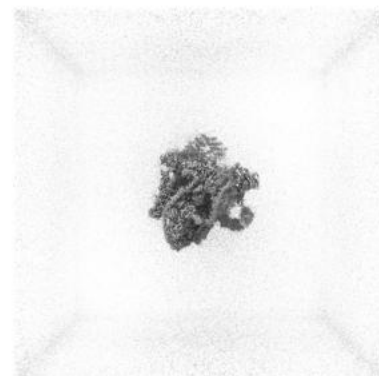
6.5.2 Raw map



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.

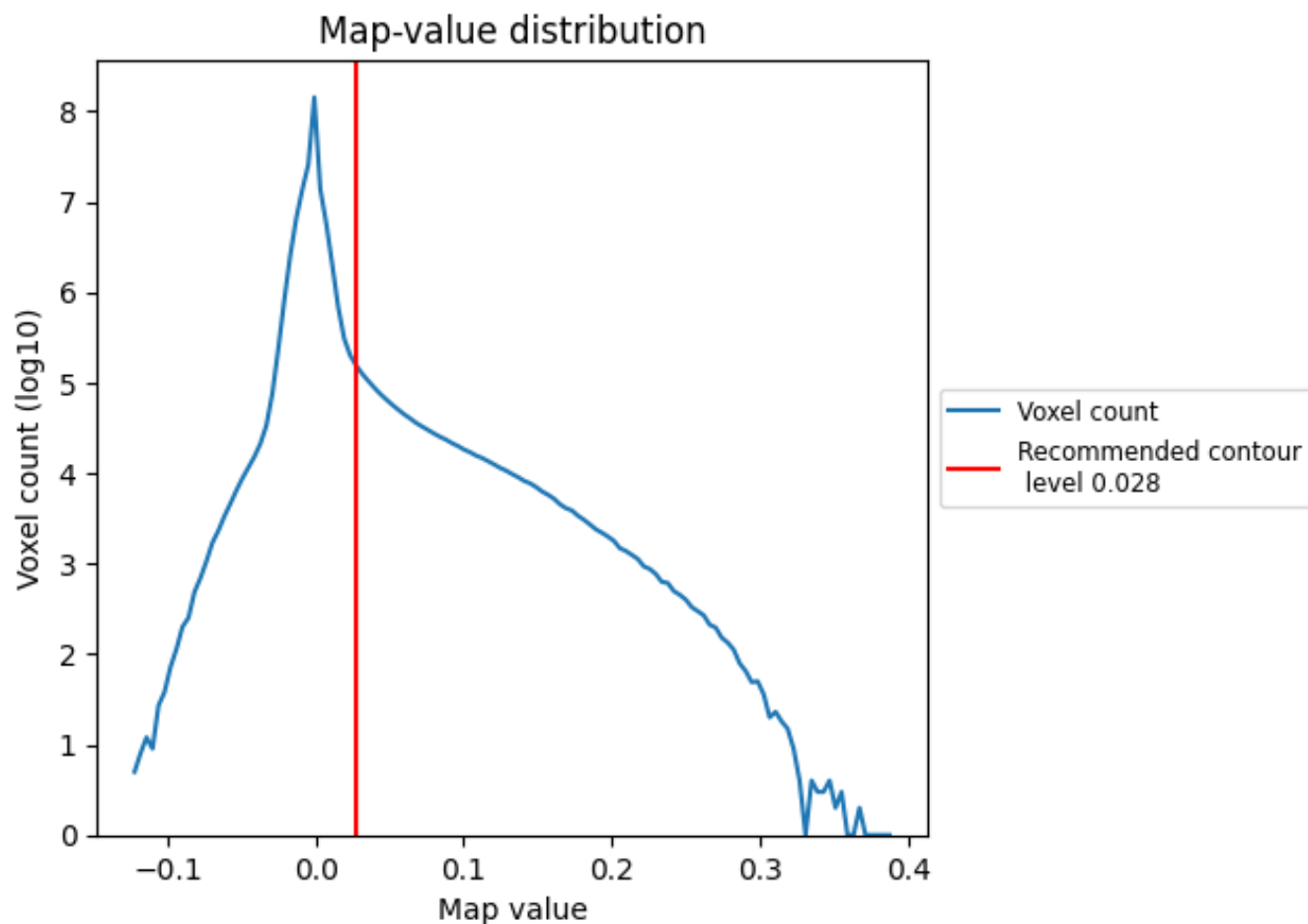
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

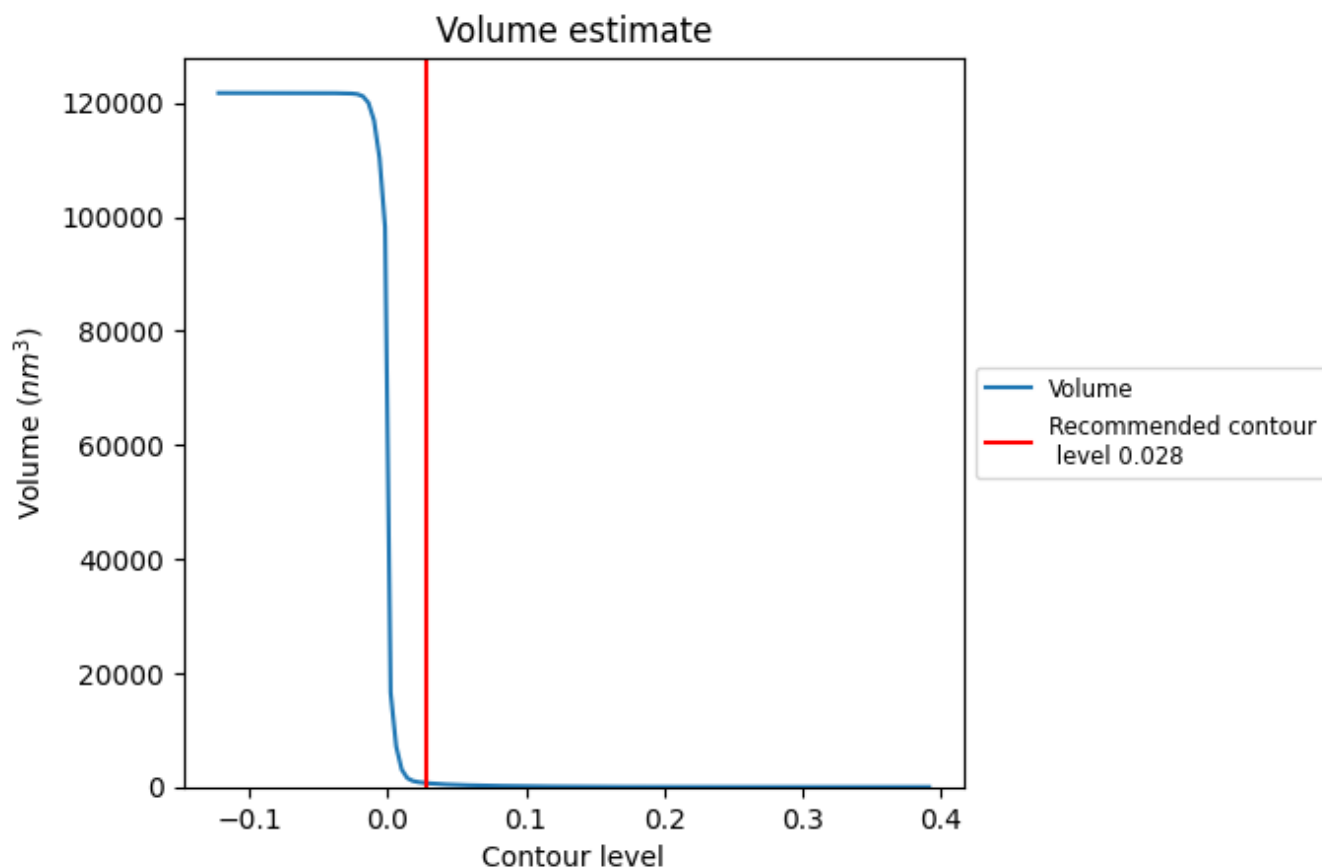
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

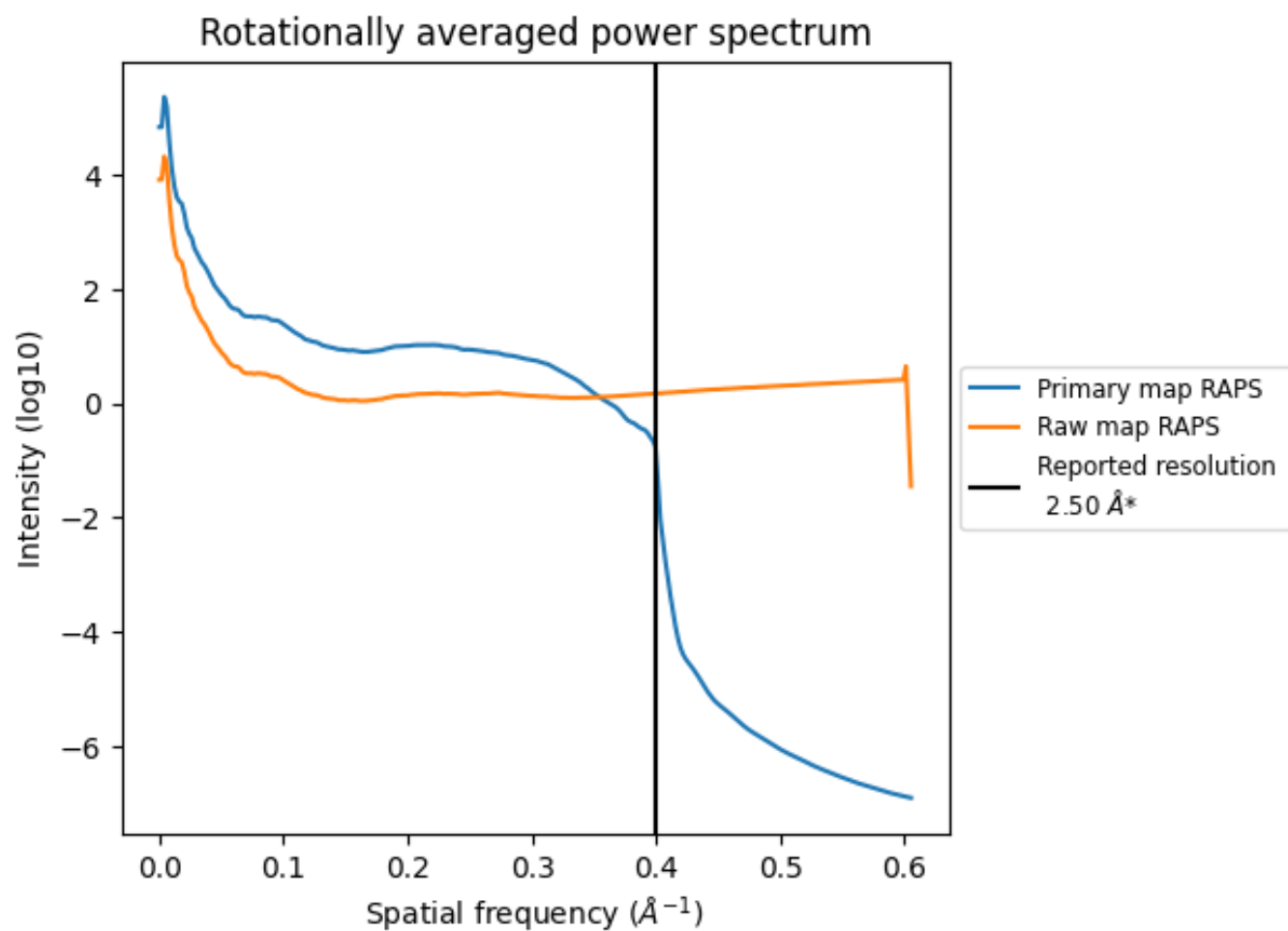
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 687 nm^3 ; this corresponds to an approximate mass of 621 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 ⓘ

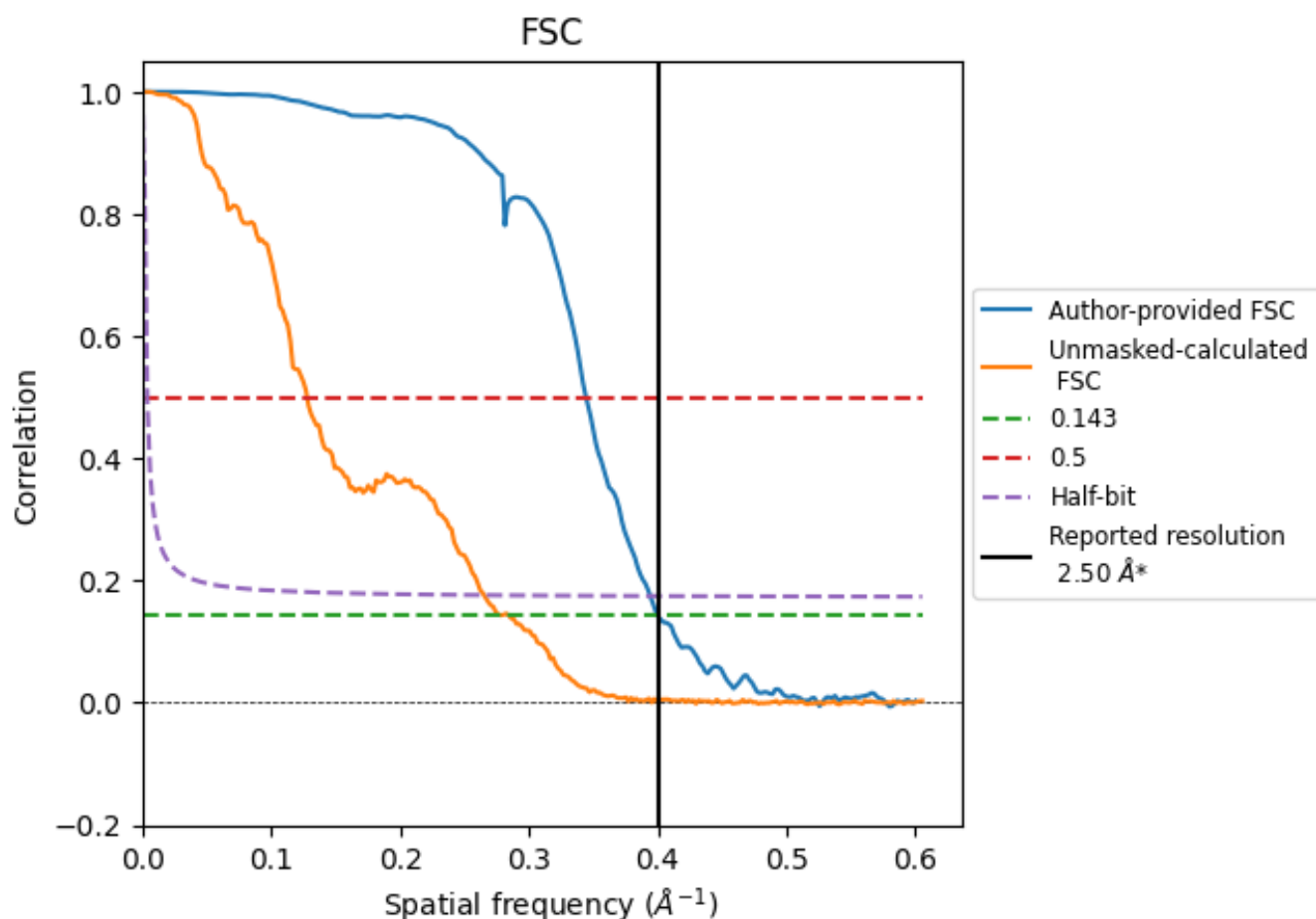


*Reported resolution corresponds to spatial frequency of 0.400 Å⁻¹

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 0.400 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

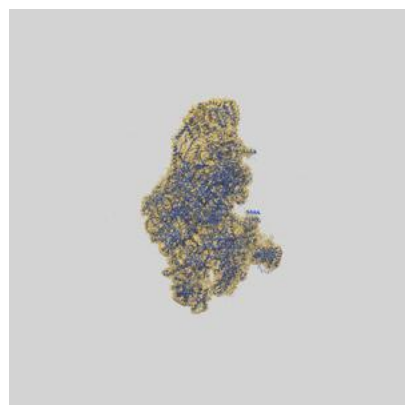
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.50	-	-
Author-provided FSC curve	2.50	2.90	2.54
Unmasked-calculated*	3.59	7.81	3.77

*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 3.59 differs from the reported value 2.5 by more than 10 %

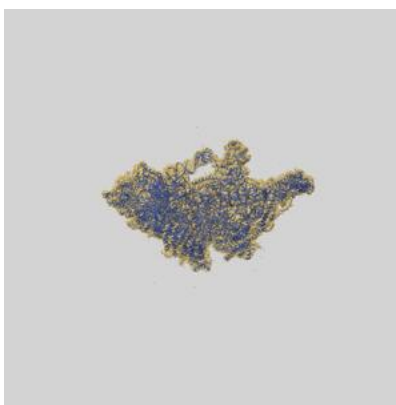
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-70544 and PDB model 9OJM. Per-residue inclusion information can be found in section [3](#) on page [15](#).

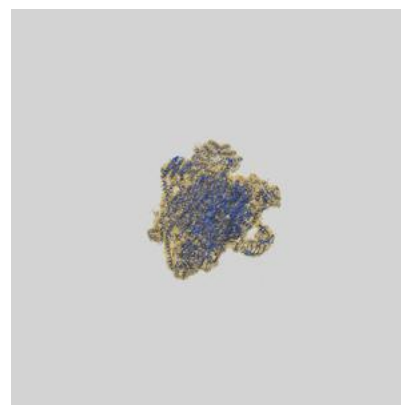
9.1 Map-model overlay [i](#)



X



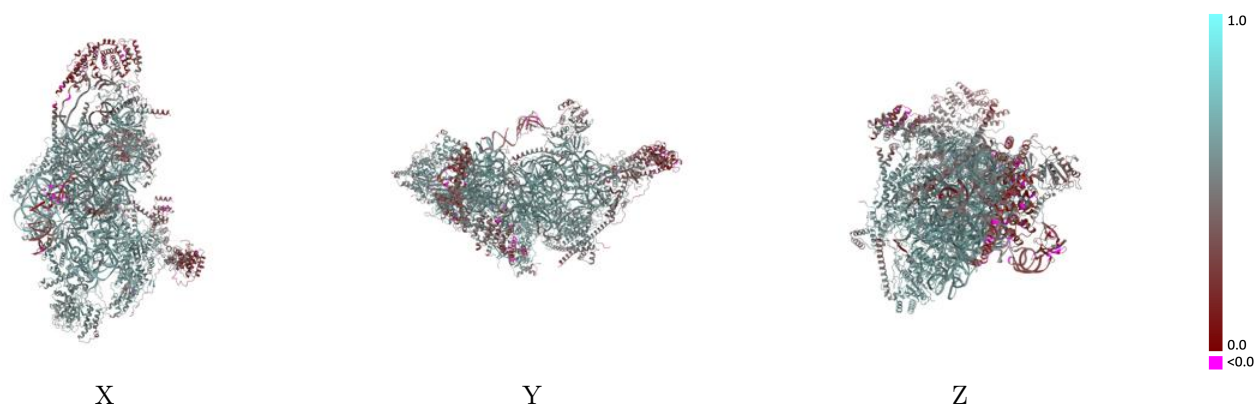
Y



Z

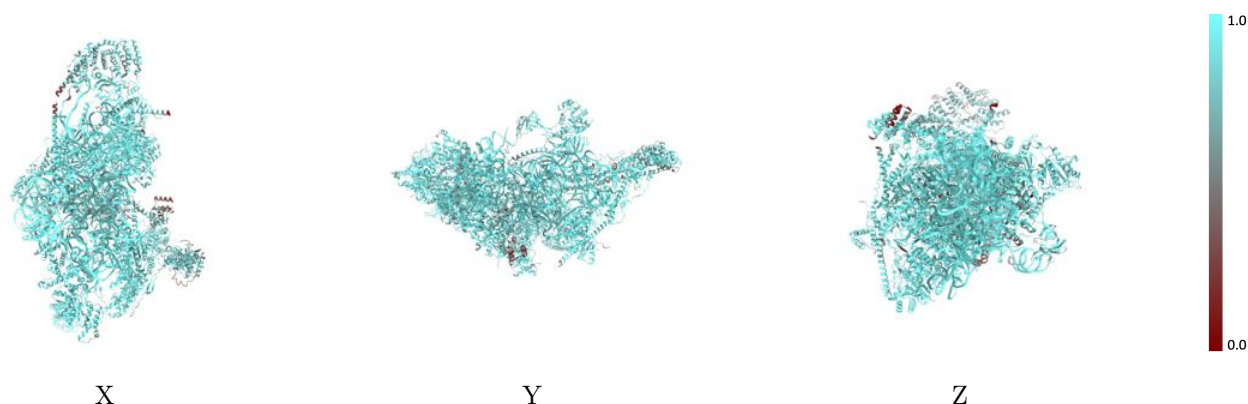
The images above show the 3D surface view of the map at the recommended contour level 0.028 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



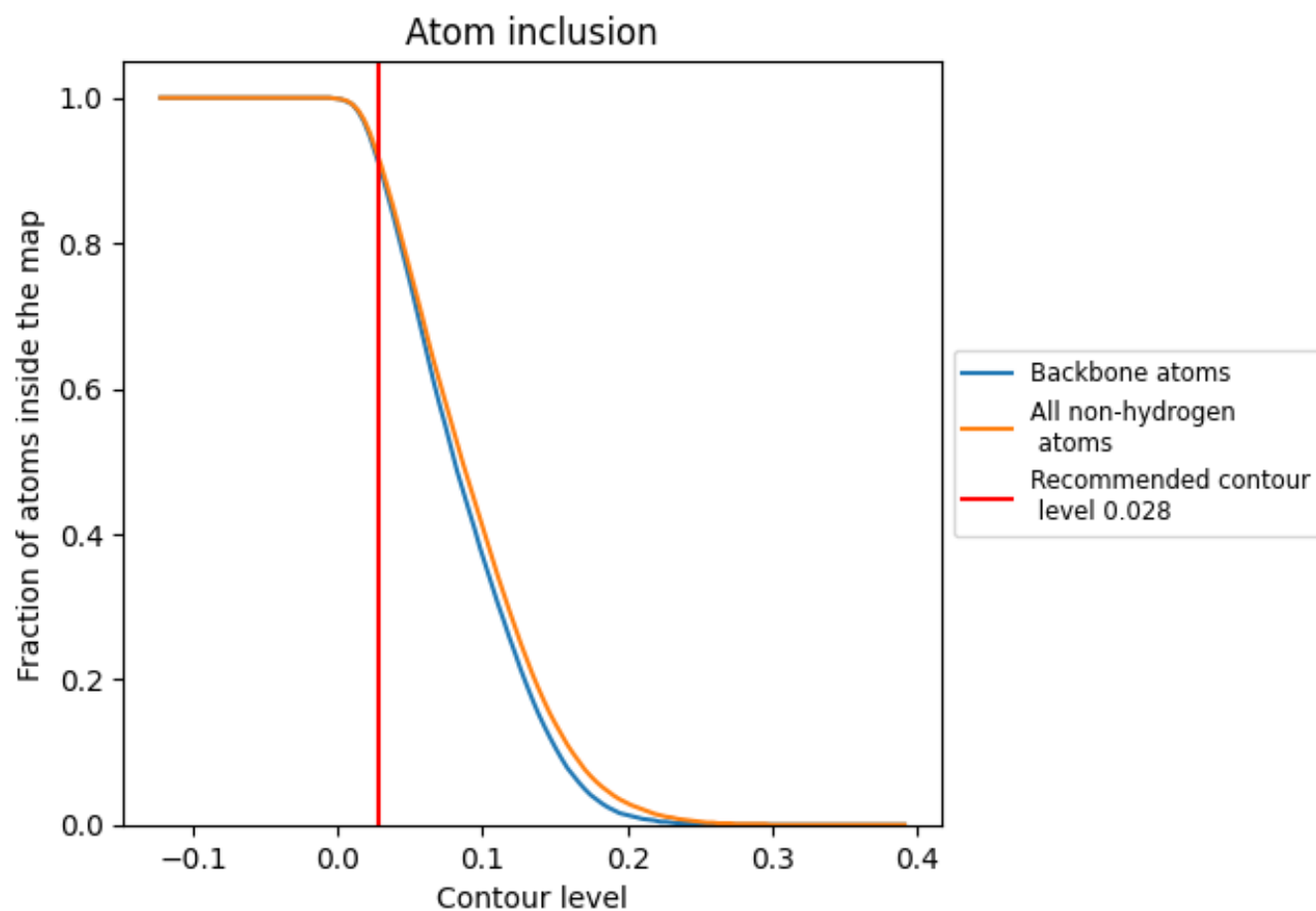
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.028).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 92% 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 (0.028) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9200	 0.5380
0	 0.8790	 0.4410
1	 0.9260	 0.5530
2	 0.9120	 0.5690
3	 0.9630	 0.6070
4	 0.7340	 0.3450
5	 0.9410	 0.3780
6	 0.9880	 0.5970
7	 0.8500	 0.4420
A	 0.9850	 0.6080
B	 0.9640	 0.6110
C	 0.9820	 0.6310
D	 0.9270	 0.5820
E	 0.9580	 0.6020
F	 0.9550	 0.5830
G	 0.9080	 0.5630
H	 0.9390	 0.5900
I	 0.9650	 0.6050
J	 0.9560	 0.6040
K	 0.9770	 0.6320
L	 0.9310	 0.5680
M	 0.9280	 0.5520
N	 0.9640	 0.6200
O	 0.9520	 0.5590
P	 0.9530	 0.6120
Q	 0.9760	 0.6310
R	 0.9240	 0.5240
S	 0.9390	 0.5600
T	 0.9420	 0.5870
U	 0.8970	 0.4960
V	 0.7370	 0.2380
W	 0.9530	 0.5990
X	 0.9420	 0.5500
Y	 0.7790	 0.4670
Z	 0.9320	 0.5740

