



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 03:44 PM UTC

PDB ID : 7OOD / pdb_00007ood
EMDB ID : EMD-11999
Title : Mycoplasma pneumoniae 50S subunit of ribosomes in chloramphenicol-treated cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-05-27
Resolution : 3.40 Å (reported)
Based on initial models : 4YBB, 3J9W, 1ZAV, 1DIV

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:

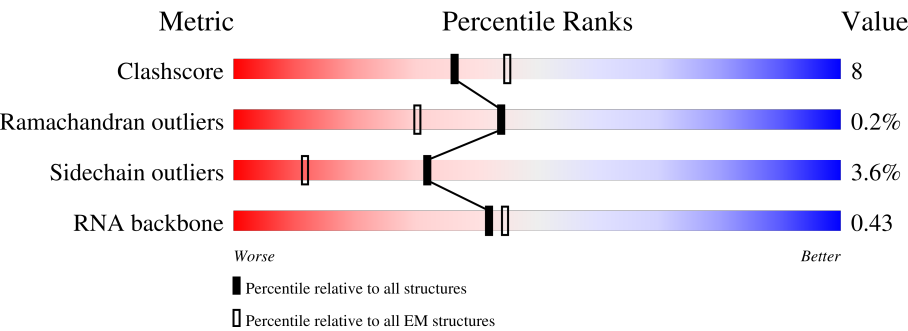
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

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	3	2907	99% 63% 29% 7% .
2	4	108	97% 58% 27% 10% ..
3	w	111	89% 61% 26% 11% .
4	a	287	99% 66% 32% ..
5	c	212	99% 67% 30% ..
6	e	184	96% 65% 29% ..
7	k	151	98% 67% 30% ..

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Mol	Chain	Length	Quality of chain
8	i	146	
9	m	124	
10	q	100	
11	u	104	
12	y	57	
13	0	48	
14	2	37	
15	1	59	
16	o	119	
17	s	237	
18	v	65	
19	x	97	
20	z	53	
21	d	180	
22	b	287	
23	l	139	
24	p	127	
25	j	122	
26	n	116	
27	t	111	
28	r	159	
29	f	149	
30	h	137	
31	g	161	

2 Entry composition

There are 35 unique types of molecules in this entry. The entry contains 89509 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 ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	3	2879	Total	C	N	O	P	0	0
			61690	27566	11236	20009	2879		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	4	105	Total	C	N	O	P	0	0
			2245	1003	409	728	105		

- Molecule 3 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	w	99	Total	C	N	O	0	0
			798	505	149	144		

- Molecule 4 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	a	285	Total	C	N	O	S	0	0
			2199	1370	433	390	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	c	210	Total	C	N	O	S	0	0
			1613	1026	294	290	3		

- Molecule 6 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	e	176	Total	C	N	O	0	0
			1349	867	240	242		

- Molecule 7 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	k	148	Total	C	N	O	0	0
			1138	722	223	193		

- Molecule 8 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	i	144	Total	C	N	O	S	0	0
			1158	733	212	208	5		

- Molecule 9 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	m	119	Total	C	N	O	S	0	0
			957	609	175	170	3		

- Molecule 10 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	q	99	Total	C	N	O	S	0	0
			809	525	148	133	3		

- Molecule 11 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	u	86	Total	C	N	O	S	0	0
			641	397	127	116	1		

- Molecule 12 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	y	56	Total	C	N	O	S	0	0
			436	262	96	73	5		

- Molecule 13 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	0	47	Total	C	N	O	S	0	0
			377	234	81	61	1		

- Molecule 14 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	2	37	Total	C	N	O	S	0	0
			303	189	65	45	4		

- Molecule 15 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	1	59	Total	C	N	O	S	0	0
			477	300	99	77	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	o	115	Total	C	N	O	S	0	0
			895	568	169	157	1		

- Molecule 17 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	s	92	Total	C	N	O	S	0	0
			714	470	121	122	1		

- Molecule 18 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	v	63	Total	C	N	O	S	0	0
			504	312	107	84	1		

- Molecule 19 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	x	44	Total	C	N	O	0	0
			218	130	44	44		

- Molecule 20 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	z	50	Total	C	N	O	S	0	0
			408	255	81	68	4		

- Molecule 21 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	d	175	Total	C	N	O	S	0	0
			1244	797	214	229	4		

- Molecule 22 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	b	229	Total	C	N	O	S	0	0
			1758	1116	317	318	7		

- Molecule 23 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	l	136	Total	C	N	O	S	0	0
			1057	680	193	177	7		

- Molecule 24 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	p	114	Total	C	N	O	S	0	0
			941	600	185	154	2		

- Molecule 25 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	j	122	Total	C	N	O	S	0	0
			944	595	178	167	4		

- Molecule 26 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	n	112	Total	C	N	O	S	0	0
			853	534	169	149	1		

- Molecule 27 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	t	96	Total	C	N	O	S	0	0
			706	449	132	122	3		

- Molecule 28 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	r	139	Total	C	N	O	S	0	0
			1068	663	207	191	7		

- Molecule 29 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	f	144	Total	C	N	O	0	0
			713	425	144	144		

- Molecule 30 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	h	128	Total	C	N	O	0	0
			630	374	128	128		

- Molecule 31 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	g	125	Total	C	N	O	0	0
			617	367	125	125		

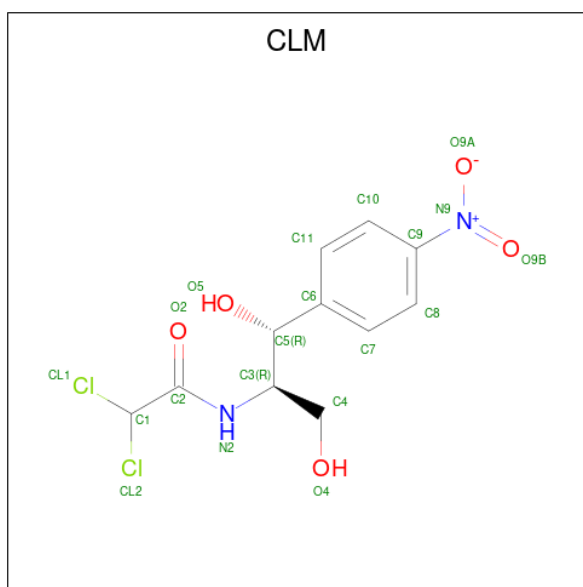
- Molecule 32 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
32	3	1	Total	K	0
			1	1	

- Molecule 33 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
33	3	24	Total	Mg	0
			24	24	
33	y	1	Total	Mg	0
			1	1	

- Molecule 34 is CHLORAMPHENICOL (CCD ID: CLM) (formula: C₁₁H₁₂Cl₂N₂O₅).



Mol	Chain	Residues	Atoms					AltConf
34	3	1	Total	C	Cl	N	O	0
			20	11	2	2	5	

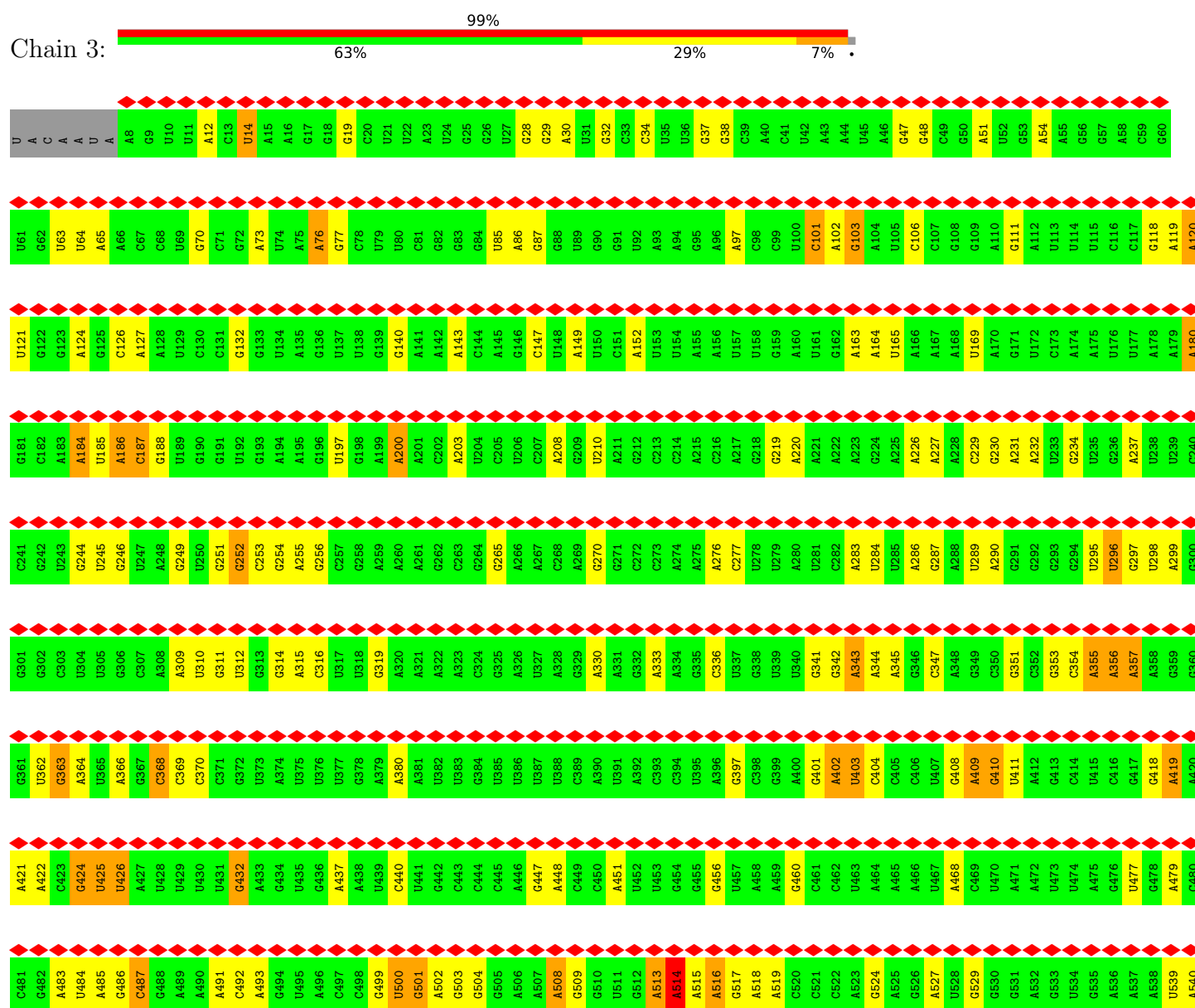
- Molecule 35 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
35	y	1	Total	Zn	0
			1	1	
35	2	1	Total	Zn	0
			1	1	
35	z	1	Total	Zn	0
			1	1	

3 Residue-property plots

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

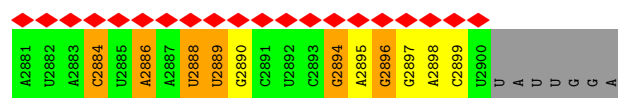
- Molecule 1: 23S ribosomal RNA



U1261	G541	U601	G661	U781	C901	U961	C1021	A1081	U1141	A1201	U1261	U1261
G1262	A542	U602	U662	U782	U902	U962	C1022	A1082	G1142	A1202	G1262	G1262
U1263	U543	G603	A663	G783	A903	U963	C1023	A1083	U1143	G1203	U1263	U1263
U1264	U544	A604	G664	A784	C904	G944	A1024	C1084	C1144	A1204	U1264	U1264
G1265	C545	A605	G665	A785	U905	U965	G1025	A1085	G1145	U1205	G1265	G1265
U1266	U546	G606	G666	A786	G906	U966	A1026	G1086	A1146	U1206	G1266	G1266
A1267	G547	U607	U667	C787	A907	U967	U1027	C1087	G1147	U1207	A1267	A1267
U1268	A548	A608	A668	G788	A908	U968	A1028	A1088	U1148	U1208	U1268	U1268
C1269	A549	A609	A669	A789	U909	A969	A1029	A1089	G1149	A1209	C1269	C1269
C1270	A550	G610	G670	U790	G910	U970	U1030	G1090	U1150	A1210	C1270	C1270
A1271	C551	A611	C671	A791	U911	U971	U1031	G1091	U1151	U1211	A1271	A1271
U1272	C552	G612	G672	G792	A912	C972	A1032	U1092	U1152	C1212	U1272	U1272
A1273	A553	C613	A673	C793	U913	U973	A1033	U1093	U1153	U1213	A1273	A1273
A1274	U554	C614	A674	G794	G914	C974	A1034	G1094	U1154	U1214	A1274	A1274
C1275	A555	G615	U675	G795	A915	G975	U1035	U1095	G1155	G1215	C1275	C1275
A1276	U556	G616	U676	A796	U916	C976	A1036	U1096	C1156	U1216	A1276	A1276
A1277	G557	C617	U677	U797	G917	A977	A1037	G1097	G1157	G1217	A1277	A1277
G1278	C558	G618	U678	U798	G918	G978	G1038	G1098	C1158	G1218	G1278	G1278
U1279	C559	A619	A679	A799	C919	U979	G1039	C1099	C1159	U1219	U1279	U1279
G1280	U560	G620	A680	C900	G920	C980	U1040	U1100	G1160	A1220	G1280	G1280
A1281	A561	U621	A681	U801	C921	A981	C1041	U1101	A1161	A1221	A1281	A1281
A1282	C562	U622	A682	U802	C922	G982	C1042	A1102	A1162	G1222	A1282	A1282
A1283	A563	G623	G683	G803	A923	A983	C1043	G1103	G1163	C1223	A1283	A1283
U1284	U564	U624	A684	U804	C924	C984	C1044	A1104	A1164	G1224	U1284	U1284
U1285	C565	G625	G685	G805	C925	A985	A1045	A1105	U1165	A1225	U1285	U1285
G1286	U566	A626	G686	A806	U926	G986	A1046	G1106	G1166	G1226	G1286	G1286
C1287	U567	U627	G687	U807	A927	U987	A1047	C1107	U1167	C1227	C1287	C1287
C1288	G568	A628	U688	U808	G928	G988	A1048	A1108	A1168	G1228	C1288	C1288
G1289	U569	G629	U689	A809	C929	G989	U1049	G1109	A1169	U1229	G1289	G1289
U1290	C570	C630	U690	G810	C930	G990	A1050	C1110	C1170	U1230	U1290	U1290
C1291	A571	A631	G691	G811	C931	G991	U1051	C1111	G1171	G1231	C1291	C1291
A1292	G572	G632	U692	G812	U932	G992	A1052	A1112	G1172	U1232	A1292	A1292
U1293	A573	G633	U693	G813	C933	A993	C1053	U1113	G1173	A1233	U1293	U1293
G1294	G574	G634	U694	U814	C934	U994	U1054	C1114	G1174	U1234	G1294	G1294
A1295	C575	G635	G695	G815	U935	A995	A1055	G1115	C1175	U1285	A1295	A1295
U1296	A576	A636	U696	A816	G936	A996	A1056	U1116	U1176	G1236	U1296	U1296
U1297	C577	U637	U697	A817	A937	G997	G1057	U1117	A1177	G1237	U1297	U1297
A1298	A578	A638	U698	A818	A938	C998	U1058	U1118	A1178	A1238	A1298	A1298
A1299	U579	G639	U699	U819	U939	U999	G1059	A1119	G1179	G1239	A1299	A1299
C1300	U580	U640	U700	U820	A940	U1000	G1060	A1120	U1180	U1240	C1300	C1300
G1301	A581	U641	A701	C921	C941	C1001	A1061	G1121	A1181	U1241	G1301	G1301
C1302	U582	A642	U702	C922	A942	A1002	A1062	G1122	U1182	G1242	C1302	C1302
U1303	U583	A643	A703	A823	A943	U1003	A1063	A1123	A1183	A1243	U1303	U1303
U1304	G584	C644	G704	A824	U944	U1004	A1064	G1124	U1184	A1244	U1304	U1304
G1305	U585	C645	A705	U825	U945	G1005	G1065	U1125	U1185	G1245	G1305	G1305
C1306	G586	A646	C706	C926	A946	U1006	G1066	G1126	A1186	U1246	C1306	C1306
G1307	U587	G647	C707	G827	A947	A987	A1067	C1127	C1187	C1247	G1307	G1307
A1308	G588	A648	C708	A828	A948	A988	U1068	G1128	C1188	A1248	A1308	A1308
G1309	A589	A649	G709	A829	C949	G989	G1069	U1129	G1189	A1249	G1309	G1309
U1310	U590	U650	A710	A830	U950	U990	U1070	A1130	A1190	U1250	U1310	U1310
G1311	G591	A651	C711	U831	C951	A1011	G1071	A1131	A1191	G1251	G1311	G1311
A1312	C592	U652	A712	C932	U952	G1012	A1072	C1132	U1192	G1252	A1312	A1312
G1313	G593	G653	C713	C933	G953	G1013	A1073	A1133	U1193	U1253	G1313	G1313
A1314	U594	G654	G714	A834	A954	G1014	A1074	G1134	U1194	A1254	A1314	A1314
A1315	U595	G655	G715	U835	A955	G1015	G1075	C1135	A1195	G1255	A1315	A1315
U1316	C596	G656	G716	G836	U956	U1016	U1076	U1136	U1196	A1256	U1316	U1316
C1317	G597	A657	C717	A837	G957	A1017	G1077	C1137	G1197	G1257	C1317	C1317
U1318	U598	U658	G718	U838	C958	G1018	C1078	A1138	U1198	C1258	U1318	U1318
C1319	U599	C659	G719	A839	C959	A999	U1079	C1139	A1199	A1259	C1319	C1319
U1320	U600	U660	A720	G840	A960	G900	A1080	U1140	U1200	U1260	U1320	U1320

C2041	U1881	A1861	U1801	G1741	U1621	A	U1501	A1441	A1381	C1321
A2042	G1982	A1862	C1802	C1742	C1622	A	A1502	G1442	A1382	A1322
C2043	U1983	G1863	U1803	U1743	U1623	U	A1503	A1443	G1383	A1323
C2044	A1984	A1864	A1804	U1744	A1624	G	G1504	C1444	C1384	A1324
C2045	A1985	A1865	U1805	A1745	G1625	A	G1505	U1445	U1385	C1325
G2046	C1986	G1866	G1806	U1746	G1626	U	U1506	U1446	G1386	C1326
U2047	C1987	G1867	C1807	G1747	U1627	C	G1507	A1447	A1387	G1327
U2048	A1988	A1868	C1808	U1748	G1628	A	G1508	U1448	G1388	A1328
A2049	U1989	G1869	A1809	A1749	U1629		U1509	U1449	G1389	U1329
G2050	G1990	G1870	A1810	A1750	A1630		A1510	G1450	G1390	U1330
G2051	U1991	U1871	A1811	A1751	A1631		C1511	A1451	U1391	G1331
C2052	C1992	U1872	C1812	A1752	C1632		A1512	G1452	G1392	A1332
G2053	U1993	A1873	C1813	U1753	C1633		A1513	U1453	A1393	C1333
C2054	U1994	G1874	G1814	U1754	A1634		U1514	G1454	A1394	U1334
A2055	G1995	C1875	U1815	A1755	G1635		A1515	A1455	A1395	A1335
A2056	A1996	G1876	A1816	A1756	U1636		G1516	C1456	A1396	A1336
C2057	U1997	A1877	A1817	G1757	C1637		G1517	A1457	G1397	G1337
G2058	C1998	C1878	G1818	C1758	C1638		U1518	A1458	C1398	G1338
G2059	G1999	A1879	U1819	C1759	C1639		A1519	A1459	G1399	U1339
G2060	U2000	G1880	U1820	G1760	G1640		A1520	G1460	U1400	U1340
A2061	C2001	C1881	G1821	C1761	A1641		A1521	A1461	A1401	U1341
C2062	U2002	G1882	A1822	A1762	G1642		U1522	A1462	G1402	C1342
G2063	C2003	A1883	U1823	G1763	A1643		C1523	G1463	G1403	C1343
G2064	G2004	A1884	G1824	U1764	A1644		G1524	G1464	C1404	U1344
A2065	G2005	G1885	U1825	G1765	C1645		G1525	U1465	G1405	G1345
A2066	C2006	C1886	A1826	A1766	G1646		U1526	U1466	A1406	G1346
U2067	U2007	U1887	U1827	A1767	A1647		U1527	U1467	U1407	A1347
G2068	A2008	U1888	A1828	G1768	A1648		U1528	U1468	G1408	C1348
A2069	U2009	U1889	U1829	A1769	C1649		U1529	G1469	G1409	C1349
C2070	A2010	U1890	G1830	A1770	A1650		G1530	C1470	A1410	A1350
C2071	G2011	A1891	G1831	C1771	C1651		C1531	A1471	C1411	G1351
A2072	A2012	A1892	G1832	G1772	A1652		U1532	C1472	A1412	G1352
C2073	C2013	C1893	G1833	A1773	C1653		U1533	C1473	A1413	G1353
G2074	G2014	U1894	U1834	U1774	G1654		A1534	C1474	C1414	U1354
U2075	C2015	G1895	G1835	G1775	U1655		A1535	C1475	A1415	C1355
G2076	G2016	A1896	A1836	G1776	A1656		G1536	C1476	G1416	G1356
A2077	U2017	G1897	C1837	G1777	G1657		U1537	A1477	G1417	U1357
C2078	U2018	C1898	A1838	G1778	U1658		U1538	U1478	U1418	C1358
G2079	G2019	C1899	C1839	G1779	C1659		U1539	A1479	U1419	C1359
C2080	A2020	C1900	G1840	C1780	A1660		G1540	U1480	A1420	U1360
U2081	A2021	C1901	U1841	C1781	A1661		A1541	U1481	A1421	G1361
A2082	A2022	C1902	G1842	U1782	G1662		G1542	U1482	U1422	C1362
U2083	U2023	A1903	C1843	G1783	G1663		U1543	G1483	A1423	C1363
C2084	C2024	G1904	U1844	U1784	A1664		G1544	G1484	U1424	A1364
G2085	C2025	U1905	C1845	U1785	G1665		U1545	A1485	U1425	G1365
U2086	A2026	G1906	A1846	U1786	A1666		U1546	U1486	C1426	G1366
G2087	G2027	A1907	G1847	A1787	G1667		G1547	U1487	C1427	G1367
U2088	G2028	A1908	U1848	A1788	G1668		A1548	U1488	U1428	U1368
A2089	U2029	C1909	G1849	C1789	U1669		U1549	G1489	G1429	U1369
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G2095	U2035	C1915	A1855	C1795	A1675		G1555	A1495	A1435	G1375
C2096	G2036	C1916	G1856	A1796	G1676		U1556	A1496	C1436	G1376
A2097	A2037	G1917	G1857	C1797	G1677		G1557	A1497	A1437	A1377
U2098	A2038	U1918	U1858	A1798	U1678		U1558	U1498	G1438	C1378
G2099	G2039	A1919	U1859	A1799	U1679		A1559	C1499	U1439	C1379
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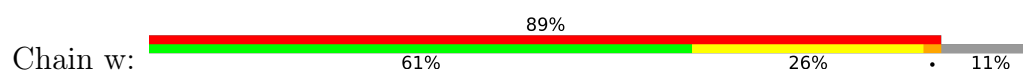
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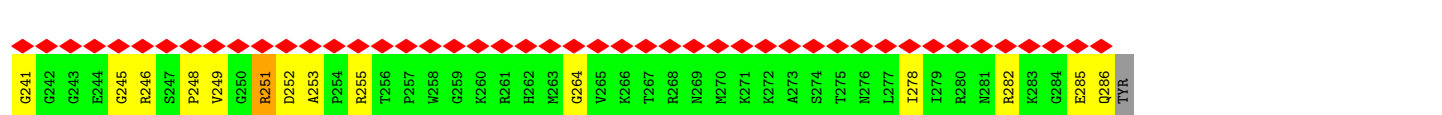
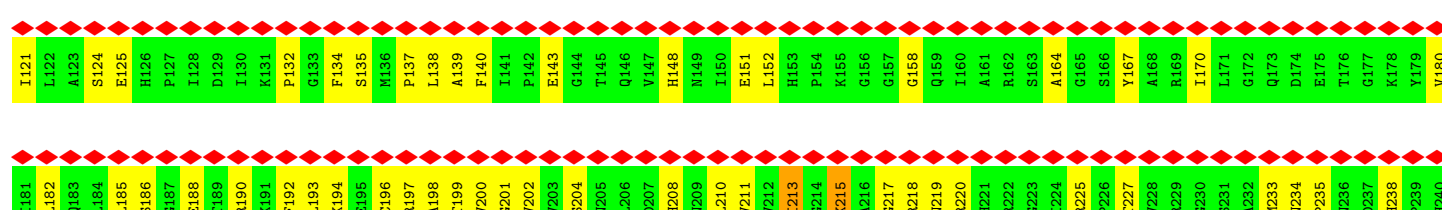
• Molecule 2: 5S ribosomal RNA



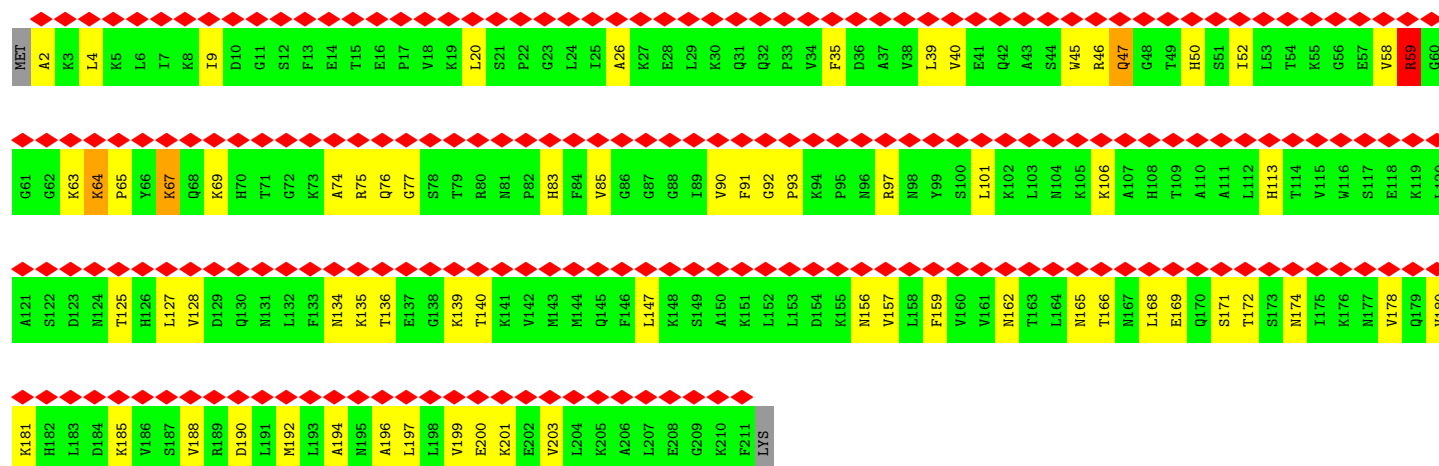
• Molecule 3: 50S ribosomal protein L29



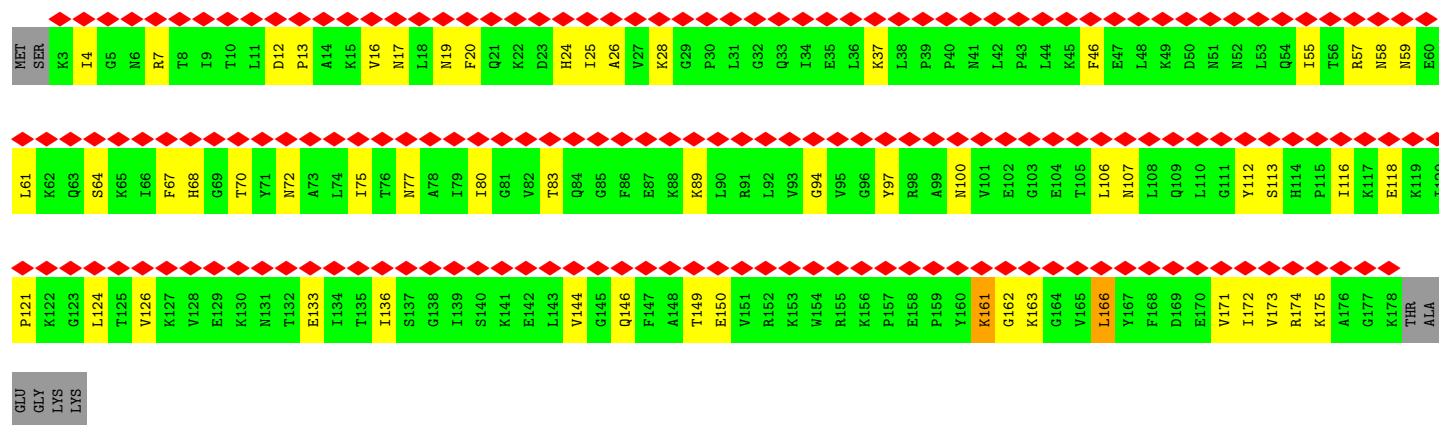
• Molecule 4: 50S ribosomal protein L2



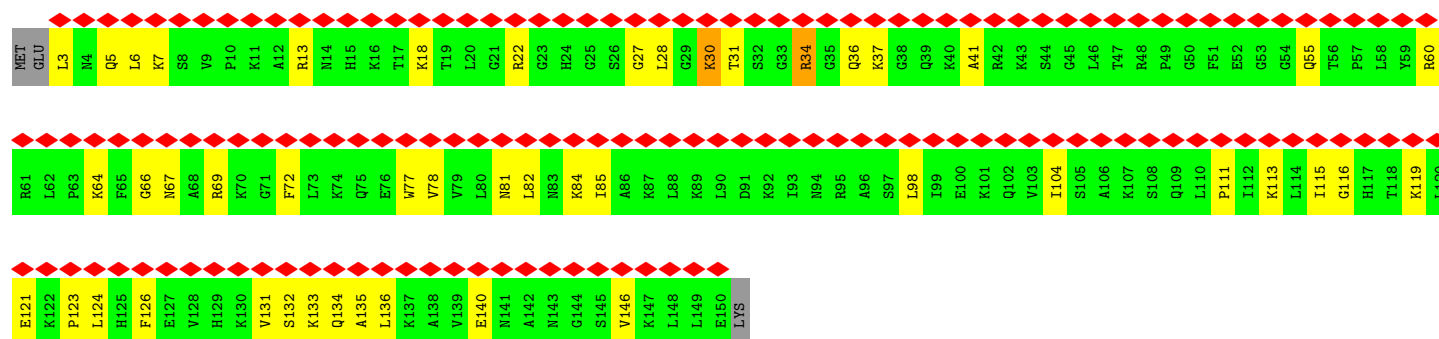
• Molecule 5: 50S ribosomal protein L4



• Molecule 6: 50S ribosomal protein L6



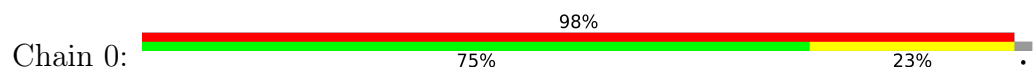
• Molecule 7: 50S ribosomal protein L15



• Molecule 8: 50S ribosomal protein L13



• Molecule 13: 50S ribosomal protein L34



• Molecule 14: 50S ribosomal protein L36



• Molecule 15: 50S ribosomal protein L35



• Molecule 16: 50S ribosomal protein L19

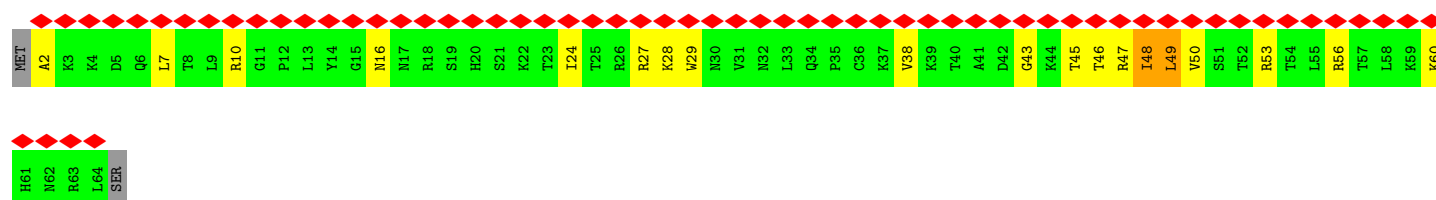


• Molecule 17: 50S ribosomal protein L23

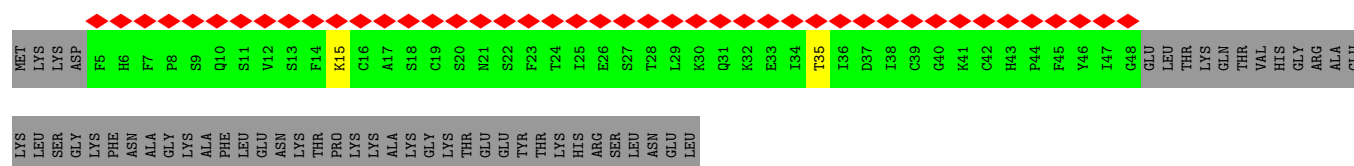


[illegible]

Chain v: 97% 68% 26%



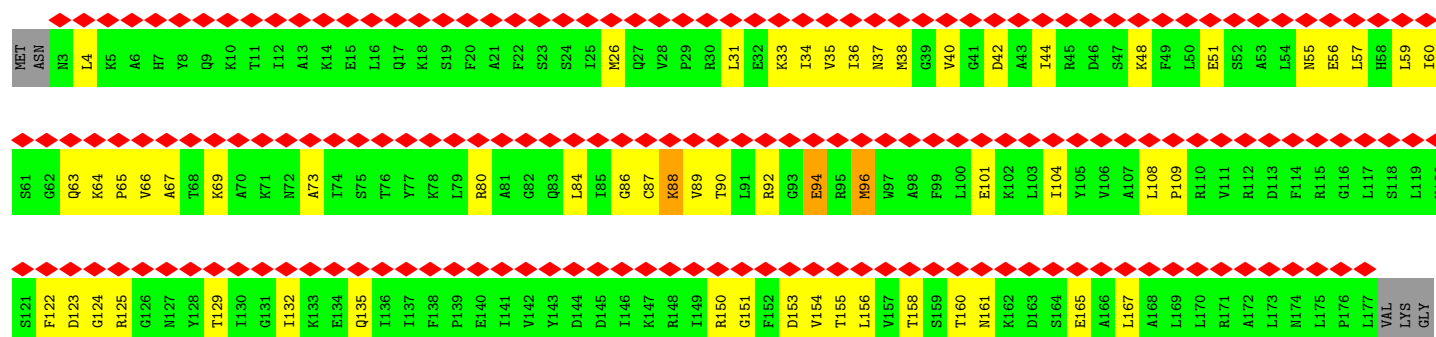
Chain x: 45% 43% 55%



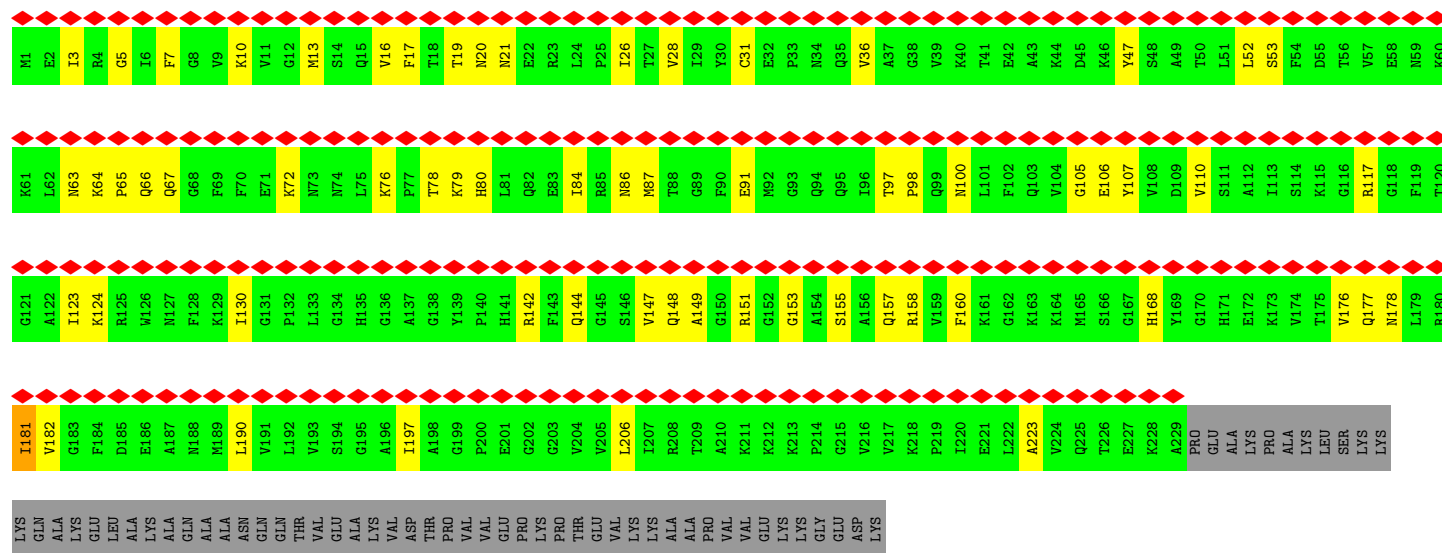
Chain z: 94% 72% 23% 6%



Chain d: 97% 65% 31%



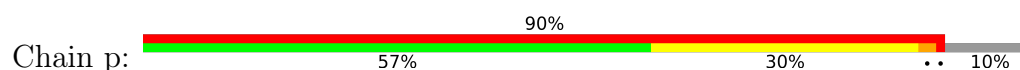
Chain b:



• Molecule 23: 50S ribosomal protein L16



• Molecule 24: 50S ribosomal protein L20

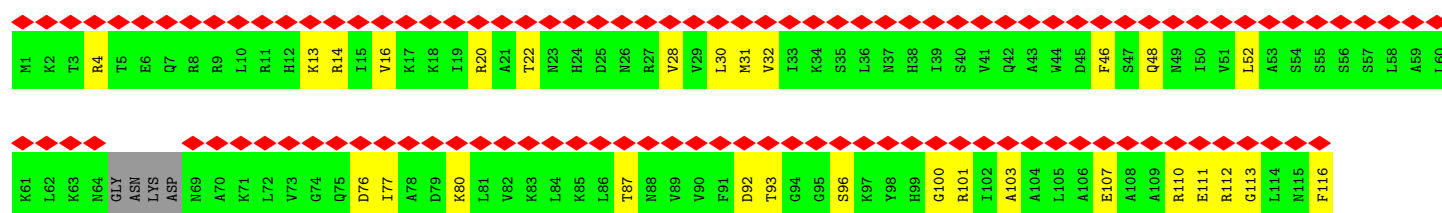
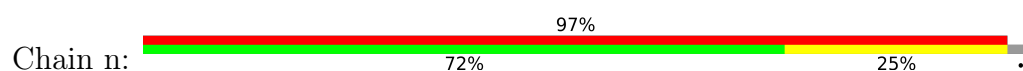


• Molecule 25: 50S ribosomal protein L14

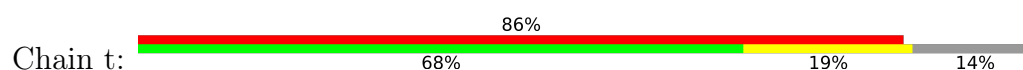




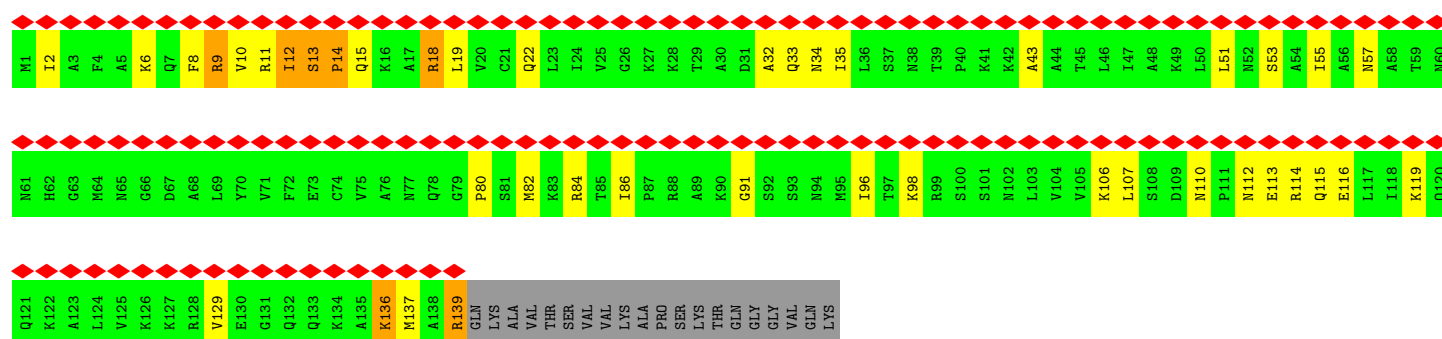
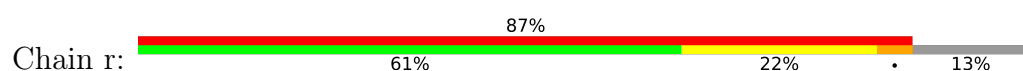
• Molecule 26: 50S ribosomal protein L18



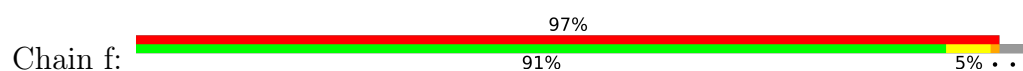
• Molecule 27: 50S ribosomal protein L24

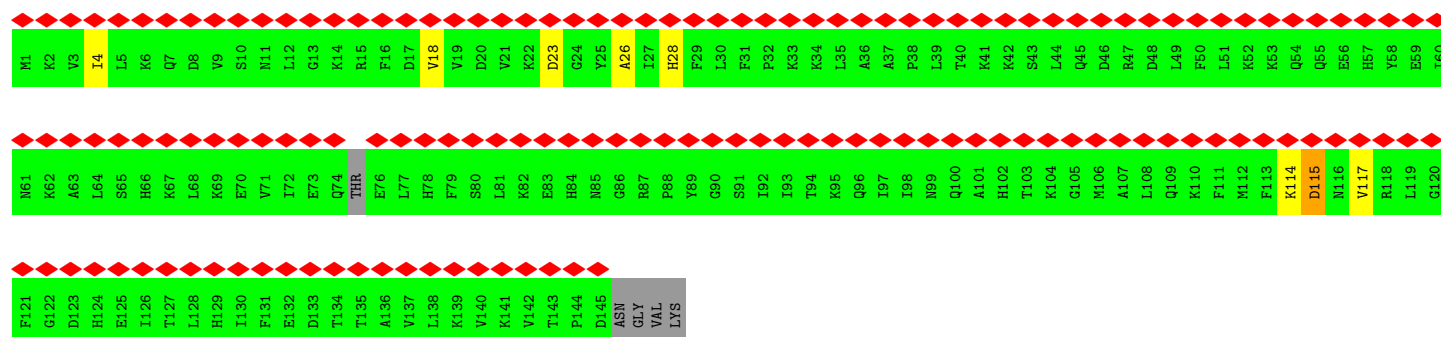


• Molecule 28: 50S ribosomal protein L22

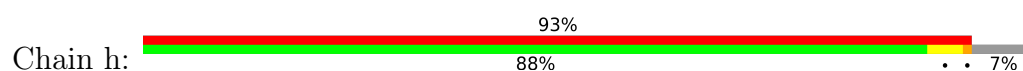


• Molecule 29: 50S ribosomal protein L9

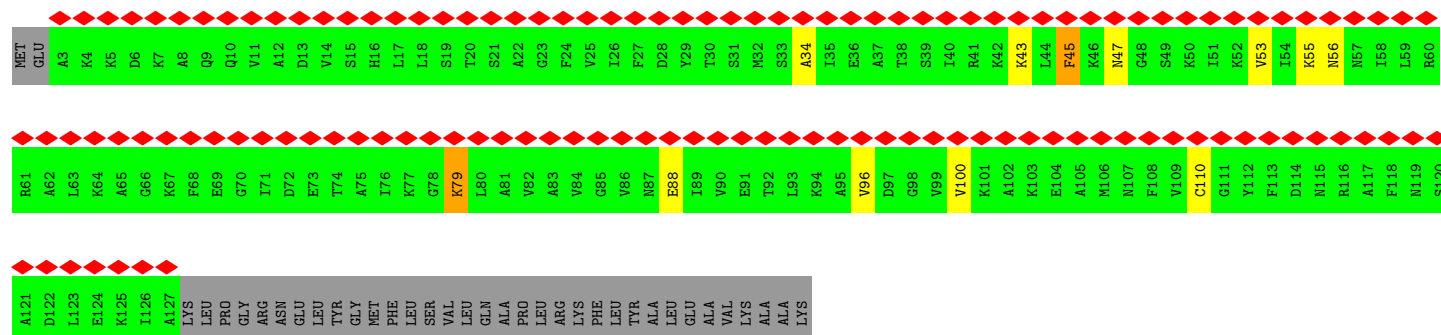
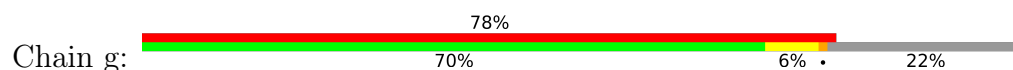




• Molecule 30: 50S ribosomal protein L11



• Molecule 31: 50S ribosomal protein L10



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	17890	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 ($e^-/\text{\AA}^2$)	3.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3750	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.022	Depositor
Minimum map value	-0.010	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0023	Depositor
Map size (Å)	323.076, 323.076, 323.076	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8502, 0.8502, 0.8502	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	3	0.67	21/69100 (0.0%)	0.85	71/107749 (0.1%)
2	4	0.52	0/2511	0.76	5/3910 (0.1%)
3	w	0.51	0/806	0.85	3/1080 (0.3%)
4	a	0.54	1/2241 (0.0%)	0.80	3/3013 (0.1%)
5	c	0.44	0/1639	0.77	4/2209 (0.2%)
6	e	0.34	0/1373	0.58	1/1854 (0.1%)
7	k	0.43	0/1155	0.72	0/1541
8	i	0.43	0/1180	0.61	0/1585
9	m	0.39	0/972	0.61	2/1308 (0.2%)
10	q	0.39	0/826	0.68	0/1109
11	u	0.37	0/649	0.59	0/867
12	y	0.59	0/440	1.15	4/582 (0.7%)
13	0	0.35	0/380	0.49	0/501
14	2	0.86	1/305 (0.3%)	1.18	3/401 (0.7%)
15	1	0.50	0/484	0.73	0/637
16	o	0.43	0/905	0.72	2/1211 (0.2%)
17	s	0.31	0/726	0.46	0/981
18	v	0.39	0/510	0.74	1/684 (0.1%)
19	x	0.14	0/217	0.40	0/301
20	z	0.31	0/412	0.52	0/547
21	d	0.29	0/1264	0.58	1/1719 (0.1%)
22	b	0.40	0/1791	0.57	0/2408
23	l	0.42	0/1082	0.57	0/1456
24	p	0.49	0/955	0.70	3/1271 (0.2%)
25	j	0.48	0/953	0.71	2/1275 (0.2%)
26	n	0.29	0/861	0.49	0/1156
27	t	0.28	0/712	0.41	0/954
28	r	0.57	2/1077 (0.2%)	0.73	2/1441 (0.1%)
29	f	0.67	0/711	1.09	1/988 (0.1%)
30	h	1.01	0/629	1.69	2/873 (0.2%)
31	g	1.21	0/616	1.76	7/856 (0.8%)
All	All	0.63	25/97482 (0.0%)	0.83	117/146467 (0.1%)

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	a	89	ASP	C-N	12.74	1.50	1.33
14	2	12	LYS	C-N	10.99	1.47	1.33
28	r	13	SER	CA-CB	-7.11	1.42	1.53
28	r	14	PRO	C-O	-6.69	1.16	1.24
1	3	611	A	P-OP2	6.57	1.62	1.49
1	3	2735	G	O3'-P	-6.19	1.51	1.61
1	3	2057	C	O3'-P	-6.11	1.51	1.61
1	3	2606	A	P-OP2	6.05	1.61	1.49
1	3	1222	A	O3'-P	-5.94	1.52	1.61
1	3	979	U	O3'-P	-5.78	1.52	1.61
1	3	1704	C	O3'-P	-5.60	1.52	1.61
1	3	614	C	O3'-P	-5.58	1.52	1.61
1	3	2358	U	O3'-P	-5.58	1.52	1.61
1	3	784	A	O3'-P	-5.57	1.52	1.61
1	3	2851	U	O3'-P	-5.47	1.52	1.61
1	3	926	U	C1'-N1	5.42	1.56	1.48
1	3	925	C	C1'-N1	5.36	1.55	1.47
1	3	197	U	O3'-P	-5.36	1.53	1.61
1	3	875	G	O3'-P	-5.21	1.53	1.61
1	3	2509	C	O3'-P	5.20	1.69	1.61
1	3	30	A	O3'-P	-5.18	1.53	1.61
1	3	546	U	P-OP2	5.09	1.59	1.49
1	3	2475	C	O3'-P	-5.05	1.53	1.61
1	3	2558	G	O3'-P	-5.02	1.53	1.61
1	3	587	U	O3'-P	-5.00	1.53	1.61

All (117) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	a	89	ASP	CA-C-N	16.05	136.94	119.28
4	a	89	ASP	C-N-CA	16.05	136.94	119.28
14	2	12	LYS	CA-C-N	-12.24	103.50	122.60
14	2	12	LYS	C-N-CA	-12.24	103.50	122.60
16	o	83	ASN	CB-CA-C	-9.62	99.08	110.15
1	3	881	A	C2'-C3'-O3'	8.43	122.15	109.50
1	3	1297	U	C2'-C3'-O3'	8.07	125.81	113.70
5	c	47	GLN	CB-CA-C	-8.04	97.19	110.85
14	2	12	LYS	O-C-N	7.82	132.80	122.33
1	3	2668	A	C2'-C3'-O3'	7.57	120.85	109.50
24	p	93	VAL	N-CA-C	-7.55	105.07	111.56
2	4	10	C	C2'-C3'-O3'	7.19	120.28	109.50
1	3	1295	A	C4'-C3'-O3'	-7.06	98.81	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	o	84	PRO	N-CA-C	-7.06	100.81	111.41
1	3	296	U	C4'-C3'-O3'	7.01	119.91	109.40
5	c	59	ARG	N-CA-C	-6.93	99.63	109.96
29	f	117	VAL	N-CA-C	6.92	117.98	108.84
12	y	48	TYR	CB-CA-C	-6.89	99.56	110.79
1	3	688	U	C4'-C3'-O3'	6.87	123.31	113.00
2	4	54	U	C2'-C3'-O3'	6.82	119.73	109.50
1	3	1371	G	N9-C1'-C2'	6.79	122.19	112.00
31	g	100	VAL	CB-CA-C	-6.78	102.98	112.14
1	3	1703	A	P-O5'-C5'	-6.76	110.76	120.90
2	4	39	U	C4'-C3'-O3'	6.75	119.52	109.40
12	y	46	GLY	N-CA-C	-6.72	106.04	115.32
3	w	61	ARG	N-CA-C	-6.69	101.69	110.53
1	3	14	U	N1-C1'-C2'	6.69	122.03	112.00
31	g	56	ASN	CB-CA-C	-6.52	99.97	110.79
2	4	39	U	C2'-C3'-O3'	6.39	119.08	109.50
1	3	2636	U	P-O5'-C5'	-6.35	111.38	120.90
1	3	410	G	C2'-C3'-O3'	6.30	118.96	109.50
1	3	605	A	C4'-C3'-O3'	-6.30	103.55	113.00
2	4	59	A	C2'-C3'-O3'	6.30	123.15	113.70
1	3	2506	C	C4'-C3'-O3'	6.29	122.43	113.00
1	3	1486	U	N1-C1'-C2'	6.22	121.33	112.00
1	3	2435	C	C4'-C3'-O3'	-6.14	103.79	113.00
28	r	136	LYS	N-CA-C	-6.13	105.80	113.28
1	3	1970	C	N1-C1'-C2'	6.03	121.05	112.00
1	3	1368	U	P-O5'-C5'	-6.02	111.87	120.90
1	3	2693	U	P-O5'-C5'	-6.02	111.87	120.90
1	3	1222	A	C2'-C3'-O3'	-6.02	104.67	113.70
1	3	2736	U	C4'-C3'-O3'	6.01	118.41	109.40
1	3	980	C	P-O5'-C5'	-5.99	111.91	120.90
1	3	2430	C	C2'-C3'-O3'	-5.99	104.72	113.70
1	3	38	G	C3'-C2'-O2'	-5.96	101.75	110.70
1	3	1698	A	N9-C1'-C2'	5.96	120.94	112.00
30	h	23	PRO	N-CA-C	5.95	124.72	112.47
12	y	31	GLN	N-CA-C	-5.95	102.86	110.53
1	3	2465	U	P-O5'-C5'	-5.94	111.99	120.90
1	3	1809	A	C3'-C2'-O2'	-5.94	101.79	110.70
1	3	1699	A	P-O5'-C5'	-5.92	112.03	120.90
1	3	598	G	P-O5'-C5'	-5.91	112.04	120.90
1	3	410	G	C4'-C3'-O3'	5.90	118.25	109.40
1	3	1761	C	C4'-C3'-O3'	-5.90	104.15	113.00
1	3	127	A	C4'-C3'-O3'	-5.90	104.16	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	p	104	LYS	N-CA-C	-5.87	106.46	113.97
1	3	1303	U	C2'-C3'-O3'	5.87	122.50	113.70
1	3	426	U	N1-C1'-C2'	5.85	120.78	112.00
1	3	514	A	C4'-C3'-O3'	-5.85	104.23	113.00
1	3	619	A	C5'-C4'-O4'	-5.77	101.14	109.80
5	c	45	TRP	N-CA-C	-5.77	105.44	112.88
1	3	2583	U	C2'-C3'-O3'	-5.75	105.07	113.70
1	3	1297	U	P-O3'-C3'	5.74	128.81	120.20
1	3	1235	U	P-O5'-C5'	-5.74	112.29	120.90
1	3	230	G	C4'-C3'-O3'	-5.73	104.41	113.00
24	p	88	GLU	CB-CG-CD	-5.71	102.89	112.60
1	3	1209	U	C2'-C3'-O3'	5.66	118.00	109.50
1	3	1836	A	C2'-C3'-O3'	5.62	122.13	113.70
1	3	1285	U	C4'-C3'-O3'	-5.59	104.61	113.00
1	3	1303	U	C4'-C3'-O3'	-5.59	104.62	113.00
1	3	1583	G	C2'-C3'-O3'	5.57	122.05	113.70
1	3	513	A	C2'-C3'-O3'	5.57	122.05	113.70
9	m	3	TYR	CA-C-O	-5.55	116.60	119.77
1	3	616	G	P-O5'-C5'	-5.53	112.61	120.90
5	c	47	GLN	CB-CG-CD	-5.53	103.21	112.60
1	3	1048	A	C4'-C3'-O3'	5.51	121.27	113.00
3	w	61	ARG	CA-C-N	-5.51	114.31	122.41
3	w	61	ARG	C-N-CA	-5.51	114.31	122.41
25	j	89	GLU	CA-C-N	-5.50	114.97	121.90
25	j	89	GLU	C-N-CA	-5.50	114.97	121.90
31	g	79	LYS	CA-C-N	-5.50	113.80	122.76
31	g	79	LYS	C-N-CA	-5.50	113.80	122.76
1	3	180	A	C2'-C3'-O3'	-5.48	105.47	113.70
1	3	2886	A	P-O5'-C5'	-5.47	112.70	120.90
1	3	1219	U	P-O5'-C5'	-5.42	112.76	120.90
1	3	1341	U	N1-C1'-C2'	5.41	120.12	112.00
31	g	56	ASN	N-CA-C	5.41	117.17	111.28
6	e	161	LYS	N-CA-C	-5.39	100.98	109.50
1	3	816	A	C4'-C3'-O3'	-5.38	104.93	113.00
1	3	425	U	C2'-C3'-O3'	5.36	117.54	109.50
1	3	2060	G	O5'-P-OP1	5.34	124.02	108.00
31	g	96	VAL	CA-C-N	5.32	127.41	120.28
31	g	96	VAL	C-N-CA	5.32	127.41	120.28
28	r	14	PRO	N-CA-C	-5.29	106.31	113.40
1	3	2305	C	P-O5'-C5'	-5.28	112.98	120.90
1	3	2438	A	C2'-C3'-O3'	-5.27	105.80	113.70
30	h	23	PRO	O-C-N	-5.25	115.55	122.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	3	1302	C	C2'-C3'-O3'	5.18	121.47	113.70
1	3	1482	U	C2'-C3'-O3'	5.17	117.26	109.50
4	a	213	ILE	N-CA-C	-5.17	102.18	109.63
1	3	487	C	C2'-C3'-O3'	-5.16	105.96	113.70
12	y	31	GLN	CA-C-O	-5.15	116.02	121.94
1	3	2570	U	C2'-C3'-O3'	-5.13	106.00	113.70
1	3	785	A	C2'-C3'-O3'	-5.12	106.02	113.70
1	3	2066	A	C4'-C3'-O3'	-5.12	105.33	113.00
1	3	2026	A	C3'-C2'-O2'	5.11	118.37	110.70
1	3	1281	A	P-O5'-C5'	-5.11	113.24	120.90
1	3	1618	U	C4'-C3'-O3'	5.11	117.06	109.40
1	3	354	C	P-O5'-C5'	-5.09	113.26	120.90
1	3	1507	G	C2'-C3'-O3'	5.07	117.11	109.50
9	m	3	TYR	N-CA-C	5.07	116.21	108.30
21	d	94	GLU	N-CA-C	-5.05	105.77	111.28
1	3	764	G	P-O5'-C5'	-5.04	113.34	120.90
1	3	2605	G	C4'-C3'-O3'	-5.04	105.44	113.00
18	v	43	GLY	N-CA-C	-5.04	103.73	111.24
1	3	619	A	C1'-C2'-O2'	-5.01	100.89	108.40
1	3	773	G	N9-C1'-C2'	5.00	119.50	112.00

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	3	61690	0	30961	509	0
2	4	2245	0	1135	27	0
3	w	798	0	838	34	0
4	a	2199	0	2248	84	0
5	c	1613	0	1676	56	0
6	e	1349	0	1373	36	0
7	k	1138	0	1223	48	0
8	i	1158	0	1176	52	0
9	m	957	0	1008	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	q	809	0	852	26	0
11	u	641	0	650	27	0
12	y	436	0	441	22	0
13	0	377	0	422	14	0
14	2	303	0	348	22	0
15	1	477	0	530	30	0
16	o	895	0	932	39	0
17	s	714	0	785	26	0
18	v	504	0	542	15	0
19	x	218	0	90	1	0
20	z	408	0	436	12	0
21	d	1244	0	1160	66	0
22	b	1758	0	1797	54	0
23	l	1057	0	1088	44	0
24	p	941	0	1017	61	0
25	j	944	0	1019	26	0
26	n	853	0	873	22	0
27	t	706	0	726	15	0
28	r	1068	0	1150	32	0
29	f	713	0	313	4	0
30	h	630	0	309	5	0
31	g	617	0	308	11	0
32	3	1	0	0	0	0
33	3	24	0	0	0	0
33	y	1	0	0	0	0
34	3	20	0	10	4	0
35	2	1	0	0	0	0
35	y	1	0	0	0	0
35	z	1	0	0	0	0
All	All	89509	0	57436	1098	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 8.

All (1098) 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)
14:2:11:CYS:SG	14:2:32:HIS:HE1	1.46	1.35
1:3:1142:G:OP1	31:g:55:LYS:CB	2.02	1.07
1:3:573:A:H5'	8:i:11:GLN:HG3	1.37	1.03
14:2:14:CYS:SG	14:2:27:CYS:HB2	1.99	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:w:16:VAL:HG21	3:w:68:GLU:CG	1.88	1.03
3:w:16:VAL:HG21	3:w:68:GLU:HG2	1.03	1.03
3:w:16:VAL:CG2	3:w:68:GLU:HG2	1.89	1.00
2:4:43:A:H1'	21:d:92:ARG:HH22	1.29	0.98
1:3:709:G:O2'	5:c:75:ARG:HD3	1.68	0.94
1:3:1806:G:C8	4:a:188:GLU:OE1	2.20	0.94
1:3:254:G:OP2	15:1:10:ARG:NH2	2.01	0.93
1:3:2853:U:OP1	16:o:97:ARG:NH1	2.01	0.93
3:w:16:VAL:HG11	3:w:68:GLU:HB3	1.49	0.92
1:3:1831:G:OP2	4:a:57:HIS:NE2	2.03	0.92
1:3:2888:U:O4	12:y:37:LYS:NZ	2.03	0.91
21:d:132:ILE:O	21:d:151:GLY:HA3	1.68	0.91
1:3:1142:G:OP1	31:g:55:LYS:CA	2.18	0.91
1:3:1686:U:OP1	9:m:36:LYS:HE2	1.70	0.91
1:3:1246:U:OP2	24:p:7:LYS:NZ	2.05	0.90
24:p:61:ILE:HD11	24:p:92:LYS:HD3	1.53	0.90
1:3:1173:G:H21	8:i:111:MET:HE2	1.36	0.90
24:p:27:ARG:HD3	24:p:37:THR:HG21	1.54	0.89
1:3:1392:G:N7	18:v:2:ALA:N	2.21	0.89
2:4:43:A:C1'	21:d:92:ARG:HH22	1.87	0.88
28:r:86:ILE:HD12	28:r:96:ILE:HD11	1.56	0.87
1:3:2692:U:P	16:o:56:ARG:HH21	1.98	0.87
1:3:1286:G:O2'	5:c:76:GLN:NE2	2.07	0.87
1:3:253:C:O2	15:1:9:LYS:NZ	2.09	0.86
1:3:1648:A:N6	28:r:91:GLY:HA2	1.90	0.85
1:3:1636:U:OP2	17:s:61:LYS:NZ	2.07	0.85
1:3:1173:G:N2	8:i:111:MET:HE2	1.91	0.85
8:i:42:LYS:HD2	24:p:62:LEU:HD11	1.59	0.85
21:d:33:LYS:HD3	21:d:92:ARG:HH11	1.40	0.85
27:t:31:ARG:HG3	27:t:33:GLN:HG2	1.60	0.83
1:3:996:A:H61	23:l:83:MET:HE2	1.43	0.82
10:q:6:VAL:HG22	10:q:11:GLN:HG2	1.61	0.82
1:3:992:G:O2'	23:l:83:MET:HE1	1.80	0.82
6:e:4:ILE:O	6:e:72:ASN:ND2	2.13	0.81
1:3:2270:U:P	11:u:33:LYS:NZ	2.53	0.81
2:4:43:A:O4'	21:d:92:ARG:NH2	2.14	0.81
1:3:486:G:OP1	5:c:52:ILE:HD11	1.80	0.81
1:3:2057:C:O2'	22:b:144:GLN:NE2	2.14	0.81
24:p:61:ILE:HD11	24:p:92:LYS:CD	2.10	0.80
29:f:114:LYS:O	29:f:115:ASP:CB	2.30	0.80
1:3:1635:G:OP1	17:s:59:ILE:HD11	1.81	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:1824:G:OP1	4:a:92:ARG:NH2	2.15	0.80
1:3:2492:G:OP1	23:l:45:ARG:HG2	1.81	0.79
1:3:2026:A:OP2	12:y:6:ARG:NH2	2.14	0.79
2:4:41:C:H5'	21:d:63:GLN:NE2	1.97	0.79
1:3:573:A:H4'	8:i:11:GLN:CB	2.13	0.79
1:3:147:C:H4'	3:w:66:GLN:HG2	1.63	0.79
1:3:1628:G:OP1	3:w:95:LYS:HE2	1.81	0.79
14:2:16:ILE:HG12	14:2:25:VAL:HG12	1.62	0.78
22:b:153:GLY:HA2	22:b:157:GLN:HG3	1.66	0.78
4:a:124:SER:O	4:a:197:ARG:NH2	2.17	0.78
24:p:96:GLU:OE2	24:p:100:LYS:NZ	2.18	0.77
1:3:573:A:H4'	8:i:11:GLN:HB3	1.64	0.77
2:4:43:A:C1'	21:d:92:ARG:NH2	2.47	0.77
1:3:1806:G:H8	4:a:188:GLU:OE1	1.65	0.76
1:3:1690:C:OP1	22:b:142:ARG:NH1	2.18	0.76
16:o:56:ARG:HH11	16:o:56:ARG:HG2	1.49	0.76
1:3:1142:G:OP1	31:g:55:LYS:HA	1.84	0.76
9:m:106:ARG:HE	9:m:113:MET:HE2	1.49	0.76
6:e:16:VAL:HA	6:e:28:LYS:O	1.86	0.76
1:3:2692:U:OP2	16:o:56:ARG:NH2	2.17	0.76
2:4:77:G:OP1	23:l:20:LYS:NZ	2.19	0.75
1:3:1482:U:O2	9:m:61:ARG:NH1	2.19	0.75
1:3:591:G:OP1	8:i:116:ARG:HB2	1.86	0.75
1:3:1043:C:OP1	8:i:42:LYS:NZ	2.18	0.75
2:4:40:U:O2	21:d:63:GLN:NE2	2.19	0.75
1:3:817:A:C2	4:a:233:MET:SD	2.80	0.75
1:3:1507:G:O2'	1:3:1508:G:OP1	2.05	0.74
10:q:11:GLN:OE1	24:p:91:ARG:CB	2.36	0.73
1:3:2321:C:O4'	21:d:37:ASN:ND2	2.21	0.73
1:3:32:G:OP2	24:p:4:LYS:NZ	2.17	0.73
1:3:1462:A:O2'	1:3:1463:G:O4'	2.07	0.73
1:3:1186:A:O2'	24:p:80:ASN:OD1	2.07	0.72
6:e:67:PHE:HA	6:e:70:THR:HG22	1.70	0.72
24:p:61:ILE:CD1	24:p:92:LYS:HD3	2.18	0.72
25:j:63:VAL:HG12	25:j:106:LEU:HD11	1.70	0.72
1:3:1628:G:P	3:w:95:LYS:NZ	2.62	0.72
3:w:22:LEU:HB3	3:w:51:LEU:HD11	1.72	0.72
4:a:151:GLU:OE1	4:a:197:ARG:N	2.22	0.72
23:l:41:TRP:HB3	23:l:94:VAL:HG21	1.71	0.72
1:3:780:G:O2'	1:3:783:G:O2'	2.08	0.71
1:3:2880:A:O2'	16:o:6:LYS:NZ	2.22	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:2123:A:N7	1:3:2169:G:O2'	2.24	0.71
1:3:1370:A:O2'	1:3:1372:U:OP2	2.09	0.71
1:3:2400:A:H5'	15:1:25:TYR:CE2	2.26	0.71
24:p:69:ARG:HE	24:p:74:THR:HG22	1.54	0.71
1:3:2826:G:O2'	1:3:2828:C:OP2	2.08	0.71
1:3:1128:G:H21	1:3:1133:A:H62	1.39	0.71
21:d:4:LEU:HD22	21:d:101:GLU:HB3	1.71	0.71
1:3:1647:A:H61	1:3:1651:C:H2'	1.55	0.70
28:r:18:ARG:O	28:r:22:GLN:HG2	1.90	0.70
1:3:1446:G:N2	1:3:1613:A:OP2	2.24	0.70
10:q:34:GLN:HG2	10:q:56:VAL:HG22	1.73	0.70
1:3:1906:G:H22	1:3:1909:C:H41	1.40	0.70
1:3:813:G:H5''	4:a:52:LYS:HE3	1.73	0.70
1:3:1628:G:P	3:w:95:LYS:HZ1	2.14	0.70
1:3:2270:U:P	11:u:33:LYS:HZ1	2.12	0.70
23:l:34:LEU:HB2	23:l:118:LEU:HD12	1.73	0.70
21:d:101:GLU:HA	21:d:104:ILE:HG12	1.73	0.69
12:y:36:LYS:HG3	28:r:34:ASN:HD22	1.57	0.69
1:3:1055:A:N1	1:3:1176:U:O2'	2.25	0.69
1:3:2460:C:C2	34:3:3026:CLM:H11	2.27	0.69
1:3:343:A:N3	1:3:363:G:O2'	2.24	0.69
1:3:2668:A:O2'	1:3:2669:G:O5'	2.10	0.69
1:3:1628:G:OP1	3:w:95:LYS:CE	2.41	0.69
1:3:1498:U:O4'	3:w:105:ARG:NH1	2.26	0.69
1:3:1627:U:O3'	3:w:95:LYS:NZ	2.25	0.69
24:p:93:VAL:O	24:p:96:GLU:N	2.24	0.69
1:3:799:A:N3	4:a:220:ARG:HD2	2.08	0.69
1:3:1971:G:O2'	1:3:1974:U:OP2	2.11	0.68
28:r:15:GLN:O	28:r:15:GLN:HG2	1.94	0.68
1:3:419:A:H5'	18:v:16:ASN:ND2	2.08	0.68
1:3:1647:A:N6	1:3:1651:C:H2'	2.09	0.68
1:3:1646:G:C4	1:3:1654:G:N2	2.62	0.68
2:4:47:C:OP1	26:n:101:ARG:N	2.24	0.68
1:3:1063:A:OP2	1:3:1161:A:N6	2.27	0.68
17:s:63:THR:H	17:s:75:SER:HG	1.40	0.68
1:3:1823:U:C5	4:a:66:TYR:CD2	2.83	0.67
1:3:2293:C:P	20:z:27:LYS:HZ3	2.15	0.67
21:d:92:ARG:HA	21:d:96:MET:HB2	1.75	0.67
1:3:1099:C:N4	1:3:1105:A:OP1	2.27	0.67
1:3:2593:U:O2'	1:3:2594:C:OP2	2.12	0.67
21:d:66:VAL:HG13	21:d:88:LYS:HG2	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:637:U:H5	7:k:84:LYS:O	1.77	0.67
21:d:31:LEU:HD21	21:d:34:ILE:HD11	1.76	0.67
17:s:3:VAL:HG13	17:s:5:ASN:H	1.58	0.67
1:3:842:U:OP1	7:k:37:LYS:NZ	2.28	0.67
1:3:2013:C:H6	1:3:2013:C:O5'	1.78	0.67
8:i:7:LEU:HD13	24:p:60:TRP:HE1	1.60	0.67
7:k:13:ARG:HD2	7:k:13:ARG:O	1.95	0.67
1:3:1115:G:O2'	30:h:122:LYS:O	2.14	0.67
1:3:500:U:HO2'	13:0:12:ARG:HH12	1.43	0.66
1:3:608:A:OP2	1:3:2507:C:O2'	2.11	0.66
1:3:1648:A:H62	28:r:91:GLY:HA2	1.61	0.66
1:3:948:A:C5	23:l:9:TYR:HD2	2.13	0.66
24:p:93:VAL:O	24:p:96:GLU:HB3	1.96	0.66
1:3:673:A:H5'	7:k:134:GLN:NE2	2.10	0.66
1:3:1142:G:H4'	31:g:79:LYS:HA	1.77	0.66
1:3:1686:U:H5'	9:m:36:LYS:HZ3	1.61	0.66
1:3:1691:U:OP1	22:b:142:ARG:HB2	1.95	0.66
2:4:10:C:H3'	11:u:87:GLY:O	1.96	0.66
7:k:131:VAL:HG11	7:k:146:VAL:HG11	1.77	0.66
1:3:1100:U:O2'	1:3:1101:U:O4'	2.08	0.66
4:a:83:VAL:HG21	4:a:115:ILE:HD12	1.77	0.66
6:e:58:ASN:OD1	6:e:59:ASN:ND2	2.29	0.66
10:q:47:ALA:HB3	10:q:48:PRO:HD3	1.78	0.66
16:o:57:GLY:HA3	16:o:62:GLU:HA	1.77	0.65
21:d:129:THR:HG22	21:d:155:THR:HG22	1.78	0.65
1:3:2453:G:OP1	5:c:75:ARG:NH2	2.29	0.65
1:3:558:C:O2	1:3:587:U:O2'	2.13	0.65
1:3:1047:A:P	24:p:76:SER:HG	2.19	0.65
1:3:1389:G:O2'	1:3:2223:C:O2'	2.15	0.65
1:3:2141:A:N6	1:3:2164:G:O2'	2.30	0.65
1:3:2400:A:H5'	15:1:25:TYR:HE2	1.59	0.65
26:n:30:LEU:HD11	26:n:77:ILE:HD11	1.78	0.65
1:3:2270:U:P	11:u:33:LYS:HZ3	2.17	0.65
2:4:3:U:OP1	2:4:59:A:O2'	2.15	0.65
1:3:2266:C:O2'	1:3:2435:C:OP2	2.15	0.64
16:o:100:TYR:OH	16:o:105:ARG:NH2	2.24	0.64
1:3:2122:G:O2'	1:3:2175:U:O2	2.15	0.64
21:d:122:PHE:CE2	21:d:167:LEU:HD22	2.32	0.64
1:3:2321:C:C4'	21:d:37:ASN:HD22	2.10	0.64
5:c:9:ILE:HG21	5:c:135:LYS:HD2	1.79	0.64
1:3:2861:G:N2	1:3:2864:A:OP2	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:i:8:THR:HG21	24:p:100:LYS:HG3	1.78	0.64
1:3:2794:U:OP1	22:b:72:LYS:NZ	2.31	0.64
28:r:10:VAL:HG23	28:r:12:ILE:HG22	1.79	0.64
1:3:1628:G:OP1	3:w:95:LYS:NZ	2.30	0.64
1:3:2400:A:C5'	15:l:25:TYR:CE2	2.81	0.64
22:b:110:VAL:HG11	22:b:197:ILE:HD12	1.79	0.64
1:3:1047:A:H5''	24:p:76:SER:OG	1.98	0.64
23:l:17:TYR:CZ	23:l:40:ASN:HA	2.33	0.64
1:3:548:A:H1'	24:p:10:ARG:NH2	2.13	0.64
1:3:2383:G:N2	1:3:2386:A:OP2	2.30	0.64
1:3:1323:A:O3'	9:m:16:MET:HE2	1.98	0.63
5:c:65:PRO:HD2	5:c:77:GLY:O	1.97	0.63
1:3:666:G:N2	1:3:669:A:OP2	2.31	0.63
1:3:2429:G:N7	15:l:28:HIS:CE1	2.67	0.63
1:3:2732:A:O2'	1:3:2733:A:H5'	1.98	0.63
1:3:608:A:O2'	1:3:2509:C:OP1	2.16	0.63
1:3:1242:G:O2'	1:3:1266:G:N2	2.29	0.63
8:i:7:LEU:HD11	24:p:63:ARG:HH21	1.64	0.63
1:3:85:U:O4	1:3:103:G:O2'	2.16	0.63
21:d:40:VAL:H	21:d:86:GLY:HA2	1.64	0.63
1:3:1392:G:N2	1:3:1395:A:OP2	2.32	0.63
1:3:907:A:OP1	23:l:6:ARG:NH1	2.32	0.63
1:3:1426:C:O3'	17:s:26:LYS:NZ	2.26	0.63
1:3:1558:A:OP2	1:3:1571:G:N2	2.32	0.62
1:3:2700:C:O2	1:3:2851:U:O2'	2.16	0.62
1:3:2880:A:H4'	16:o:6:LYS:HD3	1.81	0.62
23:l:116:LYS:HD2	23:l:120:ARG:HH11	1.64	0.62
2:4:45:C:OP2	26:n:4:ARG:NH1	2.29	0.62
8:i:115:ASN:OD1	8:i:116:ARG:N	2.32	0.62
22:b:28:VAL:HG12	22:b:190:LEU:HD11	1.80	0.62
4:a:125:GLU:HG2	4:a:197:ARG:HH22	1.63	0.62
1:3:2516:G:O2'	1:3:2562:U:O2'	2.17	0.62
1:3:2682:A:H4'	25:j:30:LYS:HD2	1.82	0.62
1:3:1000:U:O2'	1:3:2281:A:N3	2.28	0.62
1:3:366:A:O2'	1:3:368:C:OP2	2.14	0.62
1:3:1095:U:P	30:h:72:VAL:H	2.23	0.62
1:3:2446:U:O2'	1:3:2448:C:OP1	2.17	0.62
1:3:663:A:O4'	1:3:673:A:N6	2.32	0.62
1:3:1890:U:O2'	1:3:1891:A:O4'	2.18	0.61
6:e:17:ASN:OD1	6:e:28:LYS:HB3	1.99	0.61
21:d:36:ILE:HG13	21:d:154:VAL:HG12	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:1962:U:O4	1:3:2564:C:N4	2.33	0.61
24:p:106:ASN:HA	24:p:109:VAL:HG12	1.81	0.61
1:3:330:A:O3'	27:t:100:LYS:NZ	2.32	0.61
1:3:2460:C:N3	34:3:3026:CLM:H11	2.15	0.61
1:3:421:A:N6	1:3:424:G:OP2	2.32	0.61
1:3:874:U:O2'	1:3:1222:A:N3	2.34	0.61
1:3:1702:A:O2'	1:3:1708:G:N7	2.29	0.61
6:e:126:VAL:HG12	6:e:136:ILE:HG12	1.83	0.61
10:q:1:MET:N	10:q:42:ASP:OD1	2.34	0.61
1:3:824:A:H2	13:0:3:ARG:NH2	1.99	0.61
23:l:37:THR:OG1	23:l:128:THR:OG1	2.14	0.61
31:g:43:LYS:C	31:g:45:PHE:H	2.07	0.61
3:w:26:LEU:HD11	3:w:48:ARG:HG2	1.82	0.61
5:c:127:LEU:HD11	5:c:201:LYS:HA	1.82	0.61
1:3:1585:A:O2'	1:3:1586:U:OP1	2.16	0.60
5:c:52:ILE:HG21	5:c:92:GLY:HA3	1.83	0.60
6:e:7:ARG:HB3	6:e:72:ASN:HD21	1.64	0.60
23:l:31:GLU:OE2	23:l:31:GLU:N	2.34	0.60
1:3:2750:A:H5''	14:2:1:MET:CE	2.31	0.60
2:4:41:C:H5'	21:d:63:GLN:HE22	1.65	0.60
1:3:2400:A:C5'	15:1:25:TYR:CD2	2.85	0.60
1:3:2400:A:H5''	15:1:25:TYR:HD2	1.67	0.60
4:a:113:ASP:HB2	4:a:204:SER:HA	1.82	0.60
4:a:66:TYR:HA	4:a:91:ASN:HD21	1.66	0.60
21:d:38:MET:HE1	21:d:57:LEU:HD22	1.82	0.60
2:4:47:C:OP1	26:n:100:GLY:HA3	2.01	0.60
22:b:36:VAL:HG21	22:b:91:GLU:O	2.02	0.60
25:j:19:VAL:HG22	25:j:43:VAL:HG12	1.83	0.60
1:3:824:A:N6	1:3:1648:A:OP2	2.35	0.60
1:3:2344:A:H61	11:u:57:THR:HG21	1.67	0.60
4:a:148:HIS:ND1	4:a:201:GLY:O	2.34	0.60
7:k:34:ARG:HG2	7:k:41:ALA:HA	1.82	0.60
13:0:24:THR:HG23	13:0:27:GLY:H	1.66	0.60
1:3:1278:G:OP1	24:p:1:MET:N	2.27	0.60
1:3:637:U:C4	7:k:84:LYS:HB3	2.37	0.60
1:3:2844:U:H5''	9:m:50:THR:HG21	1.84	0.60
18:v:38:VAL:HG11	18:v:48:ILE:HD11	1.84	0.60
1:3:948:A:C5	23:l:9:TYR:CD2	2.89	0.59
28:r:53:SER:O	28:r:57:ASN:ND2	2.35	0.59
1:3:1296:G:N2	1:3:2020:A:OP2	2.31	0.59
1:3:2289:C:O2'	1:3:2290:G:H5'	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:e:94:GLY:HA2	6:e:163:LYS:HG2	1.84	0.59
1:3:409:A:O2'	18:v:60:LYS:NZ	2.31	0.59
1:3:1119:A:C2	31:g:53:VAL:CB	2.86	0.59
1:3:573:A:C5'	8:i:11:GLN:HG3	2.23	0.59
1:3:1786:U:OP2	1:3:1791:A:N6	2.32	0.59
4:a:143:GLU:HA	4:a:170:ILE:HB	1.84	0.59
16:o:56:ARG:HG2	16:o:56:ARG:NH1	2.16	0.59
1:3:2491:C:H42	23:l:124:LYS:NZ	2.00	0.59
1:3:2623:U:C2	12:y:4:GLN:HA	2.38	0.59
7:k:30:LYS:HG3	7:k:31:THR:N	2.17	0.59
10:q:71:ILE:HD12	10:q:82:LYS:HE2	1.85	0.59
1:3:1686:U:OP1	9:m:36:LYS:CE	2.47	0.58
1:3:2886:A:OP1	9:m:99:ARG:NH2	2.29	0.58
2:4:45:C:P	26:n:4:ARG:HH11	2.25	0.58
4:a:125:GLU:OE2	4:a:197:ARG:NH1	2.35	0.58
8:i:117:LEU:O	8:i:121:TRP:N	2.31	0.58
16:o:84:PRO:HG3	22:b:223:ALA:HB1	1.86	0.58
1:3:1028:C:OP1	10:q:72:LYS:NZ	2.36	0.58
2:4:12:U:O4'	2:4:96:G:N2	2.36	0.58
1:3:19:G:OP1	12:y:11:HIS:HD2	1.87	0.58
1:3:518:A:N6	1:3:541:G:O2'	2.37	0.58
11:u:29:ASP:OD2	11:u:30:SER:N	2.29	0.58
1:3:1190:A:OP1	24:p:54:ARG:HG3	2.04	0.58
4:a:116:LYS:N	4:a:119:ASP:OD2	2.24	0.58
1:3:721:G:N2	13:0:5:TYR:HE1	2.01	0.58
1:3:2313:U:H5	21:d:153:ASP:OD1	1.85	0.58
1:3:1142:G:P	31:g:55:LYS:CB	2.92	0.58
1:3:34:C:N4	1:3:483:A:OP2	2.36	0.58
1:3:637:U:C5	7:k:84:LYS:HB3	2.39	0.58
1:3:806:A:O2'	1:3:1383:G:O2'	2.22	0.58
12:y:54:LYS:HG2	12:y:55:LYS:H	1.67	0.58
28:r:9:ARG:HG3	28:r:80:PRO:HG2	1.85	0.58
1:3:2390:G:H21	15:1:39:ARG:HH12	1.52	0.58
23:l:43:ASP:HA	23:l:94:VAL:HA	1.85	0.58
27:t:76:LEU:HD12	27:t:89:ILE:HG13	1.85	0.58
26:n:87:THR:OG1	26:n:113:GLY:O	2.22	0.57
16:o:96:VAL:HG22	16:o:98:ARG:H	1.69	0.57
1:3:1104:A:OP1	1:3:1131:A:O2'	2.21	0.57
1:3:2274:A:N6	1:3:2281:A:OP2	2.37	0.57
1:3:649:A:H62	5:c:47:GLN:NE2	2.03	0.57
14:2:27:CYS:SG	14:2:29:THR:OG1	2.53	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:740:A:OP2	1:3:761:G:N2	2.32	0.57
9:m:71:ASN:OD1	9:m:72:LEU:N	2.38	0.57
10:q:41:LEU:HD23	10:q:42:ASP:HB2	1.87	0.57
17:s:76:LYS:HE3	17:s:76:LYS:HA	1.86	0.57
23:l:40:ASN:OD1	23:l:41:TRP:N	2.34	0.57
25:j:97:ARG:HE	25:j:99:PHE:HE1	1.51	0.57
1:3:637:U:O4	7:k:85:ILE:N	2.38	0.57
1:3:828:A:OP2	1:3:2078:A:O2'	2.22	0.57
1:3:2663:G:O2'	1:3:2672:G:O6	2.19	0.57
4:a:253:ALA:H	4:a:255:ARG:HH11	1.51	0.57
26:n:28:VAL:HG21	26:n:52:LEU:HD12	1.86	0.57
1:3:1166:G:C4	8:i:80:HIS:ND1	2.72	0.57
1:3:2644:U:O2'	22:b:47:TYR:OH	2.20	0.57
10:q:38:VAL:HG13	10:q:50:LEU:HB3	1.86	0.57
21:d:73:ALA:HA	21:d:80:ARG:HA	1.86	0.57
1:3:1987:C:O2'	1:3:1989:U:OP2	2.20	0.56
4:a:48:ASN:OD1	4:a:49:ASN:N	2.36	0.56
1:3:370:C:H5'	27:t:3:ARG:HH22	1.70	0.56
1:3:1406:A:O2'	1:3:1407:U:OP2	2.19	0.56
1:3:1603:A:O5'	4:a:63:LYS:NZ	2.38	0.56
1:3:2293:C:P	20:z:27:LYS:NZ	2.78	0.56
7:k:119:LYS:NZ	7:k:121:GLU:OE2	2.24	0.56
1:3:2798:A:H5'	1:3:2896:G:H21	1.70	0.56
4:a:188:GLU:HG3	4:a:282:ARG:HG2	1.85	0.56
4:a:215:LYS:HG2	4:a:218:ARG:H	1.71	0.56
23:l:73:SER:OG	23:l:74:LYS:N	2.34	0.56
1:3:524:G:N2	1:3:527:A:OP2	2.39	0.56
1:3:998:C:O2'	1:3:2504:C:O2'	2.20	0.56
1:3:1723:A:OP2	1:3:1732:A:N6	2.38	0.56
8:i:38:LEU:HD22	8:i:57:LEU:HD13	1.88	0.56
1:3:548:A:H1'	24:p:10:ARG:HH21	1.71	0.56
25:j:23:LYS:O	25:j:40:VAL:HG12	2.05	0.56
21:d:88:LYS:NZ	21:d:88:LYS:HB3	2.21	0.56
1:3:740:A:H4'	4:a:9:ARG:NE	2.21	0.56
1:3:1128:G:N2	1:3:1133:A:H62	2.04	0.56
1:3:2491:C:H42	23:l:124:LYS:HZ2	1.52	0.56
14:2:25:VAL:HG22	14:2:34:GLN:HB2	1.87	0.56
15:1:4:LYS:HE2	15:1:58:LEU:HD11	1.87	0.56
16:o:84:PRO:HD2	22:b:17:PHE:CD1	2.40	0.56
20:z:31:LYS:HE2	20:z:48:LYS:HB3	1.87	0.56
26:n:31:MET:HA	26:n:92:ASP:HB3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:1727:U:O2	4:a:14:ILE:CD1	2.54	0.56
5:c:74:ALA:HB3	5:c:76:GLN:HG2	1.88	0.56
1:3:580:U:OP1	1:3:1249:A:O2'	2.14	0.55
8:i:60:ILE:HG23	8:i:131:ASP:HA	1.88	0.55
1:3:362:U:H4'	27:t:70:PHE:HD2	1.71	0.55
1:3:1303:U:H5'	9:m:6:LYS:HB2	1.88	0.55
1:3:1350:A:O3'	28:r:84:ARG:NH2	2.33	0.55
1:3:1635:G:P	17:s:59:ILE:HD11	2.46	0.55
1:3:54:A:OP2	1:3:120:A:N6	2.34	0.55
1:3:514:A:N7	1:3:516:A:N6	2.54	0.55
1:3:2400:A:H4'	15:1:25:TYR:CE2	2.42	0.55
1:3:2888:U:H5	12:y:40:HIS:HD2	1.53	0.55
25:j:61:VAL:HG21	25:j:111:TYR:CE1	2.42	0.55
1:3:518:A:OP2	1:3:542:A:N6	2.40	0.55
1:3:1444:C:O2'	1:3:1445:U:O5'	2.20	0.55
1:3:1587:U:O2'	1:3:1588:A:OP1	2.22	0.55
1:3:2455:G:N2	1:3:2458:A:OP2	2.36	0.55
1:3:1803:U:O2'	4:a:264:GLY:N	2.39	0.55
1:3:2151:G:H1'	1:3:2154:A:H61	1.71	0.55
1:3:1295:A:C8	1:3:1297:U:C4	2.94	0.55
1:3:2123:A:OP1	1:3:2174:G:N2	2.40	0.55
7:k:82:LEU:HA	7:k:85:ILE:HG22	1.89	0.55
29:f:4:ILE:HA	29:f:18:VAL:HA	1.88	0.55
10:q:4:ILE:HG12	24:p:94:LEU:HD23	1.88	0.55
1:3:499:G:N2	1:3:502:A:OP2	2.36	0.54
5:c:134:ASN:C	5:c:136:THR:H	2.15	0.54
24:p:86:ASN:O	24:p:88:GLU:HG2	2.06	0.54
1:3:1447:A:O2'	1:3:1449:G:N7	2.39	0.54
1:3:2303:U:H5	26:n:14:ARG:HH22	1.54	0.54
1:3:2888:U:C5	12:y:40:HIS:HD2	2.25	0.54
4:a:167:TYR:HB3	4:a:202:VAL:HG12	1.89	0.54
21:d:69:LYS:HA	21:d:84:LEU:HA	1.88	0.54
1:3:1831:G:OP2	4:a:57:HIS:CE1	2.60	0.54
1:3:491:A:N6	1:3:508:A:N7	2.54	0.54
1:3:1727:U:O2	4:a:14:ILE:HD11	2.07	0.54
25:j:58:LEU:HD22	25:j:86:LEU:HD23	1.89	0.54
1:3:1325:C:H42	1:3:1677:G:H1	1.54	0.54
1:3:2511:A:O2'	1:3:2513:G:OP2	2.25	0.54
21:d:33:LYS:HB3	21:d:92:ARG:HE	1.71	0.54
1:3:503:G:O2'	1:3:831:U:O2'	2.26	0.54
1:3:2032:G:OP1	22:b:158:ARG:NH1	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:2372:C:H5''	11:u:70:ASP:HB2	1.88	0.54
11:u:51:ILE:HD11	11:u:75:ALA:HB2	1.90	0.54
24:p:86:ASN:O	24:p:88:GLU:CG	2.56	0.54
24:p:93:VAL:O	24:p:96:GLU:CB	2.55	0.54
27:t:7:GLY:H	27:t:24:VAL:HG13	1.72	0.54
1:3:1166:G:C8	8:i:80:HIS:CE1	2.95	0.54
16:o:35:ILE:HG12	16:o:86:ILE:HD11	1.89	0.54
23:l:109:ILE:HG13	23:l:110:PRO:HD2	1.89	0.54
25:j:111:TYR:HB3	25:j:114:ILE:HG13	1.90	0.54
6:e:94:GLY:HA3	6:e:97:TYR:CD2	2.43	0.54
21:d:35:VAL:HG22	21:d:155:THR:OG1	2.08	0.54
26:n:93:THR:O	26:n:96:SER:OG	2.22	0.54
1:3:824:A:C2	13:0:3:ARG:CZ	2.91	0.53
6:e:106:LEU:HD12	6:e:126:VAL:HG21	1.90	0.53
22:b:10:LYS:NZ	22:b:197:ILE:O	2.36	0.53
22:b:97:THR:OG1	22:b:100:ASN:OD1	2.25	0.53
28:r:12:ILE:HD11	28:r:43:ALA:HB2	1.90	0.53
1:3:666:G:OP2	15:1:20:LYS:NZ	2.40	0.53
1:3:918:G:O6	1:3:932:U:N3	2.42	0.53
10:q:45:ILE:HD11	24:p:108:ILE:HD13	1.89	0.53
11:u:79:GLY:HA3	11:u:98:VAL:O	2.07	0.53
18:v:16:ASN:HB3	18:v:24:ILE:HG13	1.91	0.53
1:3:140:G:N2	1:3:143:A:OP2	2.41	0.53
1:3:1117:U:H5'	30:h:115:ASN:H	1.73	0.53
1:3:451:A:O2'	1:3:1873:A:OP1	2.26	0.53
1:3:2572:A:OP1	1:3:2656:G:O2'	2.25	0.53
6:e:100:ASN:OD1	6:e:107:ASN:ND2	2.42	0.53
8:i:7:LEU:HD13	24:p:60:TRP:NE1	2.23	0.53
21:d:135:GLN:N	21:d:150:ARG:O	2.41	0.53
1:3:1329:U:H5	1:3:1675:A:H61	1.57	0.53
1:3:1823:U:C5	4:a:66:TYR:CE2	2.96	0.53
5:c:140:THR:HG22	5:c:171:SER:HA	1.89	0.53
25:j:1:MET:SD	25:j:67:LYS:HG2	2.48	0.53
22:b:7:PHE:CE2	22:b:206:LEU:HB2	2.43	0.53
28:r:116:GLU:OE1	28:r:116:GLU:N	2.40	0.53
1:3:200:A:O2'	1:3:840:G:O6	2.21	0.53
1:3:2270:U:OP1	11:u:33:LYS:NZ	2.42	0.53
1:3:648:G:H1	5:c:181:LYS:HE2	1.74	0.53
1:3:1650:A:H3'	1:3:1651:C:H5''	1.89	0.53
6:e:162:GLY:HA2	6:e:172:ILE:HD11	1.89	0.53
8:i:20:ILE:HD13	8:i:58:ILE:HB	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:d:66:VAL:O	21:d:88:LYS:N	2.40	0.53
22:b:26:ILE:HD11	22:b:182:VAL:HG21	1.90	0.53
14:2:27:CYS:SG	14:2:28:LYS:N	2.82	0.53
1:3:827:G:O2'	1:3:2448:C:N3	2.39	0.53
23:l:77:LYS:HD3	23:l:78:PRO:HD2	1.90	0.53
1:3:824:A:H2	13:0:3:ARG:CZ	2.22	0.52
1:3:945:U:OP2	23:l:22:LYS:NZ	2.42	0.52
5:c:127:LEU:HD12	5:c:199:VAL:O	2.09	0.52
24:p:61:ILE:HD11	24:p:92:LYS:HD2	1.91	0.52
1:3:1298:A:N3	1:3:2020:A:C6	2.77	0.52
1:3:1907:A:O2'	1:3:1908:A:OP1	2.24	0.52
1:3:2400:A:H5''	15:1:25:TYR:CD2	2.45	0.52
1:3:1369:U:OP2	1:3:1422:U:O2'	2.23	0.52
3:w:10:LYS:HG2	3:w:13:GLU:H	1.73	0.52
5:c:172:THR:HB	5:c:178:VAL:HG23	1.90	0.52
1:3:591:G:H5'	8:i:117:LEU:CD1	2.40	0.52
20:z:13:ASP:O	20:z:15:ARG:NH2	2.43	0.52
21:d:33:LYS:HB3	21:d:92:ARG:NE	2.24	0.52
23:l:35:VAL:HG22	23:l:102:VAL:HG22	1.92	0.52
1:3:2690:U:C5	22:b:13:MET:HE2	2.45	0.52
3:w:18:LEU:O	3:w:22:LEU:HD23	2.09	0.52
5:c:50:HIS:ND1	5:c:93:PRO:HB2	2.25	0.52
1:3:355:A:OP2	5:c:139:LYS:HA	2.10	0.52
1:3:1295:A:O4'	1:3:1297:U:C6	2.62	0.52
1:3:2344:A:H61	11:u:57:THR:CG2	2.23	0.52
4:a:137:PRO:HA	4:a:196:CYS:O	2.10	0.52
28:r:51:LEU:O	28:r:55:ILE:HG12	2.10	0.52
1:3:603:G:N1	1:3:2507:C:OP1	2.42	0.52
1:3:637:U:C4	7:k:84:LYS:CB	2.93	0.52
1:3:1046:A:H5''	24:p:65:ASN:HD22	1.74	0.52
8:i:52:ASP:HA	8:i:121:TRP:HE1	1.75	0.52
3:w:10:LYS:HD3	3:w:13:GLU:HB2	1.92	0.52
7:k:6:LEU:HD12	7:k:7:LYS:HG2	1.92	0.52
12:y:36:LYS:HG3	28:r:34:ASN:ND2	2.24	0.52
1:3:614:C:OP2	24:p:32:LYS:HE2	2.10	0.52
7:k:18:LYS:HE3	7:k:28:LEU:CD2	2.40	0.52
22:b:110:VAL:HG11	22:b:197:ILE:HG23	1.92	0.52
1:3:620:G:H22	7:k:34:ARG:CD	2.22	0.51
1:3:996:A:N6	23:l:83:MET:HE2	2.19	0.51
1:3:2259:G:N7	23:l:82:ARG:NH2	2.52	0.51
2:4:43:A:H1'	21:d:92:ARG:NH2	2.08	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:500:U:O2'	1:3:501:G:OP1	2.25	0.51
1:3:1046:A:O3'	24:p:76:SER:OG	2.28	0.51
1:3:2649:G:OP2	8:i:88:LYS:HE3	2.11	0.51
2:4:77:G:OP1	23:l:20:LYS:CE	2.58	0.51
1:3:479:A:C8	5:c:46:ARG:HD3	2.45	0.51
1:3:635:G:O2'	1:3:638:A:O2'	2.24	0.51
1:3:2586:G:H4'	1:3:2586:G:OP2	2.10	0.51
1:3:721:G:O6	13:0:16:HIS:NE2	2.43	0.51
1:3:2429:G:N7	15:1:28:HIS:HE1	2.08	0.51
21:d:88:LYS:NZ	21:d:88:LYS:CB	2.73	0.51
1:3:501:G:OP1	13:0:12:ARG:NH2	2.42	0.51
1:3:2750:A:H5''	14:2:1:MET:HE2	1.91	0.51
2:4:40:U:H4'	21:d:64:LYS:HB3	1.92	0.51
23:l:29:PHE:HB2	23:l:105:GLU:OE2	2.11	0.51
24:p:17:LEU:HD21	24:p:31:TYR:HA	1.93	0.51
25:j:106:LEU:HB2	25:j:115:LEU:HD21	1.91	0.51
1:3:1686:U:H5'	9:m:36:LYS:NZ	2.25	0.51
1:3:2059:G:H4'	22:b:148:GLN:NE2	2.25	0.51
1:3:2414:U:H5''	7:k:72:PHE:HZ	1.75	0.51
2:4:7:G:O3'	26:n:20:ARG:NH2	2.43	0.51
1:3:1029:A:OP1	24:p:49:ARG:NE	2.43	0.51
5:c:159:PHE:CD2	5:c:168:LEU:HD11	2.46	0.51
11:u:45:ILE:HD12	11:u:75:ALA:HB2	1.93	0.51
17:s:56:ASN:HB2	17:s:82:VAL:CG2	2.40	0.51
21:d:42:ASP:O	21:d:44:ILE:HD12	2.10	0.51
1:3:1030:U:O2	10:q:10:LYS:HE3	2.11	0.51
1:3:1298:A:C2	1:3:2020:A:C5	2.99	0.51
8:i:7:LEU:HD22	24:p:60:TRP:HE1	1.76	0.51
11:u:68:GLY:O	11:u:71:ASP:N	2.44	0.51
7:k:77:TRP:CZ3	7:k:111:PRO:HB2	2.46	0.51
14:2:8:LYS:HB2	14:2:8:LYS:NZ	2.25	0.51
1:3:402:A:O2'	1:3:403:U:O5'	2.27	0.51
3:w:26:LEU:HD21	3:w:30:ARG:HH21	1.76	0.51
16:o:83:ASN:HA	22:b:17:PHE:CE1	2.45	0.51
16:o:113:LYS:H	16:o:113:LYS:HD2	1.76	0.51
1:3:1368:U:OP2	17:s:60:ARG:NH1	2.43	0.50
4:a:182:LEU:HD12	4:a:192:PHE:CD1	2.46	0.50
24:p:57:ARG:O	24:p:61:ILE:HG12	2.11	0.50
1:3:356:A:OP2	5:c:174:ASN:HB2	2.11	0.50
1:3:1278:G:C8	24:p:1:MET:O	2.63	0.50
1:3:1298:A:C2	1:3:2020:A:C4	2.99	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:1447:A:OP2	1:3:1611:C:N4	2.44	0.50
25:j:1:MET:HB3	25:j:32:TYR:CD1	2.46	0.50
1:3:2548:G:O2'	1:3:2748:A:N3	2.44	0.50
5:c:181:LYS:NZ	5:c:190:ASP:OD1	2.35	0.50
31:g:43:LYS:C	31:g:45:PHE:N	2.69	0.50
1:3:2283:C:O2'	23:l:85:SER:N	2.39	0.50
5:c:192:MET:HE2	7:k:5:GLN:HG3	1.92	0.50
1:3:640:U:OP2	5:c:106:LYS:NZ	2.31	0.50
1:3:672:G:O6	7:k:113:LYS:NZ	2.33	0.50
1:3:824:A:C2	13:0:3:ARG:NH2	2.78	0.50
1:3:980:C:HO2'	1:3:981:A:P	2.35	0.50
4:a:124:SER:OG	4:a:125:GLU:N	2.44	0.50
1:3:673:A:OP1	7:k:134:GLN:NE2	2.45	0.50
1:3:1367:G:H21	1:3:1637:A:H1'	1.76	0.50
1:3:1806:G:N7	4:a:188:GLU:OE1	2.44	0.50
1:3:2259:G:OP1	23:l:82:ARG:NH1	2.45	0.50
1:3:2888:U:O2'	1:3:2889:U:O5'	2.25	0.50
1:3:504:G:OP2	13:0:37:LYS:NZ	2.38	0.50
1:3:553:A:H2'	1:3:554:U:H5'	1.92	0.50
1:3:619:A:H5''	5:c:90:VAL:HG11	1.93	0.50
1:3:1293:U:O2	12:y:4:GLN:NE2	2.45	0.50
1:3:1306:G:OP1	9:m:33:THR:OG1	2.28	0.50
1:3:2599:C:OP2	4:a:246:ARG:HB2	2.12	0.50
9:m:112:GLU:OE1	12:y:41:ARG:NH2	2.43	0.50
22:b:64:LYS:HA	22:b:67:GLN:HG2	1.94	0.50
24:p:46:TYR:O	24:p:50:ARG:HD2	2.12	0.50
1:3:184:A:O2'	1:3:186:A:N7	2.43	0.50
1:3:2580:A:OP2	22:b:151:ARG:N	2.44	0.50
24:p:46:TYR:OH	24:p:50:ARG:NH2	2.44	0.50
25:j:104:ARG:NH1	25:j:122:VAL:OXT	2.45	0.50
1:3:650:G:O6	5:c:185:LYS:HD2	2.11	0.50
1:3:869:U:H5'	15:1:54:ARG:HH11	1.77	0.50
1:3:2287:G:N7	11:u:28:ARG:NH2	2.59	0.50
1:3:2384:A:N3	26:n:110:ARG:NH2	2.59	0.50
5:c:157:VAL:HA	5:c:196:ALA:O	2.12	0.50
21:d:66:VAL:HG12	21:d:88:LYS:O	2.12	0.50
5:c:162:ASN:HB2	5:c:203:VAL:HG12	1.93	0.49
16:o:31:VAL:HG12	16:o:90:LEU:HA	1.94	0.49
21:d:34:ILE:CD1	21:d:96:MET:HG3	2.42	0.49
1:3:2355:C:O2'	20:z:19:TYR:OH	2.19	0.49
27:t:90:LYS:HD3	27:t:103:VAL:HG13	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:251:G:O6	15:1:9:LYS:NZ	2.32	0.49
1:3:620:G:H22	7:k:34:ARG:NE	2.10	0.49
1:3:1443:A:O2'	1:3:1445:U:OP2	2.23	0.49
1:3:2788:U:OP2	8:i:120:ARG:NH2	2.45	0.49
4:a:99:ILE:HG21	4:a:121:ILE:HD11	1.94	0.49
7:k:131:VAL:HG21	7:k:136:LEU:HD12	1.94	0.49
9:m:54:VAL:HB	9:m:59:ASN:ND2	2.27	0.49
14:2:2:LYS:O	14:2:34:GLN:HA	2.13	0.49
22:b:53:SER:HB2	22:b:78:THR:OG1	2.12	0.49
23:l:17:TYR:CE1	23:l:40:ASN:HA	2.47	0.49
24:p:50:ARG:HH11	24:p:50:ARG:HG3	1.77	0.49
1:3:673:A:OP2	7:k:116:GLY:N	2.35	0.49
1:3:923:A:H3'	1:3:924:C:C6	2.47	0.49
5:c:192:MET:HE3	7:k:3:LEU:N	2.27	0.49
18:v:56:ARG:HH11	18:v:56:ARG:HG2	1.76	0.49
23:l:42:ILE:HD11	23:l:97:VAL:HG21	1.94	0.49
2:4:10:C:O2'	2:4:11:A:O5'	2.26	0.49
4:a:217:GLY:O	4:a:220:ARG:N	2.45	0.49
15:1:35:THR:O	15:1:39:ARG:HG2	2.13	0.49
21:d:123:ASP:OD1	21:d:124:GLY:N	2.46	0.49
1:3:1047:A:OP1	24:p:76:SER:OG	2.29	0.49
18:v:7:LEU:HD23	18:v:50:VAL:HG22	1.94	0.49
1:3:2111:U:N3	1:3:2112:A:N7	2.59	0.49
1:3:2691:C:H5''	16:o:56:ARG:HH22	1.78	0.49
18:v:10:ARG:HH12	18:v:53:ARG:HD2	1.77	0.49
1:3:610:G:H5'	1:3:610:G:H8	1.76	0.49
26:n:103:ALA:O	26:n:107:GLU:HG2	2.12	0.49
1:3:54:A:OP2	1:3:118:G:N1	2.46	0.49
1:3:1097:G:O6	1:3:1112:A:N6	2.45	0.49
2:4:40:U:O2'	2:4:41:C:O5'	2.31	0.49
7:k:136:LEU:O	7:k:140:GLU:HG2	2.13	0.49
1:3:856:A:N6	1:3:1008:A:O2'	2.46	0.48
1:3:928:G:H2'	1:3:929:G:H8	1.78	0.48
7:k:81:ASN:OD1	7:k:82:LEU:N	2.45	0.48
11:u:54:GLN:NE2	11:u:73:LEU:HD23	2.27	0.48
17:s:9:LYS:O	17:s:30:VAL:HG12	2.13	0.48
21:d:35:VAL:HG12	21:d:90:THR:HG22	1.95	0.48
27:t:28:MET:HE2	27:t:33:GLN:HB2	1.94	0.48
1:3:563:A:H2	8:i:119:ARG:CZ	2.26	0.48
1:3:2474:C:H5'	14:2:5:ALA:HB3	1.95	0.48
1:3:2580:A:OP2	22:b:151:ARG:O	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:2751:C:OP2	1:3:2763:C:N4	2.46	0.48
22:b:148:GLN:OE1	22:b:149:ALA:N	2.45	0.48
1:3:1255:G:OP1	10:q:67:LYS:NZ	2.43	0.48
1:3:1314:A:O2'	1:3:1316:U:OP2	2.31	0.48
1:3:2367:C:O2'	15:l:51:ASP:OD1	2.29	0.48
4:a:220:ARG:HH22	4:a:225:ARG:HE	1.59	0.48
1:3:227:A:O2'	1:3:456:G:N3	2.44	0.48
1:3:1091:G:O2'	1:3:1138:A:N6	2.46	0.48
1:3:1445:U:O4	1:3:1614:G:O6	2.31	0.48
5:c:76:GLN:HA	5:c:76:GLN:OE1	2.12	0.48
21:d:165:GLU:N	21:d:165:GLU:OE1	2.46	0.48
5:c:97:ARG:HG2	5:c:97:ARG:HH21	1.78	0.48
9:m:21:GLN:OE1	9:m:41:THR:OG1	2.20	0.48
12:y:40:HIS:O	12:y:41:ARG:HD3	2.13	0.48
25:j:58:LEU:HD23	25:j:94:ARG:NH1	2.29	0.48
1:3:1672:C:O2	1:3:2706:U:O2'	2.30	0.48
1:3:2275:A:H5''	1:3:2276:A:H5''	1.95	0.48
8:i:7:LEU:HD11	24:p:63:ARG:NH2	2.26	0.48
16:o:76:GLU:OE2	16:o:105:ARG:NH1	2.47	0.48
1:3:1431:A:HO2'	1:3:1497:A:HO2'	1.62	0.48
4:a:251:ARG:HE	4:a:251:ARG:HB3	1.34	0.48
14:2:14:CYS:HA	14:2:26:ILE:O	2.14	0.48
28:r:32:ALA:HA	28:r:35:ILE:HG22	1.95	0.48
27:t:18:LYS:HA	27:t:18:LYS:HE2	1.94	0.48
1:3:880:C:H4'	1:3:881:A:C5	2.49	0.48
6:e:136:ILE:HG22	6:e:144:VAL:HG23	1.95	0.48
20:z:8:ARG:HE	20:z:17:ILE:HG21	1.78	0.48
22:b:19:THR:HG22	22:b:20:ASN:H	1.79	0.48
1:3:70:G:N2	1:3:76:A:O4'	2.47	0.47
1:3:485:A:OP1	5:c:85:VAL:O	2.31	0.47
1:3:2622:A:O4'	12:y:2:ALA:HB3	2.13	0.47
1:3:1278:G:H3'	1:3:1279:U:C5'	2.44	0.47
1:3:2297:G:C2'	1:3:2298:G:H5'	2.44	0.47
1:3:2598:C:OP2	4:a:245:GLY:HA2	2.14	0.47
10:q:2:HIS:CE1	10:q:40:MET:HE3	2.49	0.47
13:0:34:ARG:NE	13:0:42:LEU:O	2.34	0.47
23:l:42:ILE:HG22	23:l:126:PRO:HD2	1.96	0.47
1:3:1104:A:O2'	1:3:1108:A:N6	2.32	0.47
1:3:1311:G:N2	1:3:1314:A:OP2	2.46	0.47
1:3:2122:G:H2'	1:3:2124:A:H62	1.79	0.47
1:3:2573:A:H62	25:j:28:THR:HG21	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:e:112:TYR:HD1	6:e:116:ILE:HD11	1.79	0.47
22:b:63:ASN:OD1	22:b:65:PRO:HD2	2.14	0.47
1:3:948:A:H2'	23:l:9:TYR:HE2	1.78	0.47
1:3:1278:G:H3'	1:3:1279:U:H5'	1.96	0.47
1:3:2400:A:C5'	15:1:25:TYR:HE2	2.22	0.47
1:3:2458:A:OP1	1:3:2505:A:O2'	2.20	0.47
6:e:57:ARG:HD3	6:e:68:HIS:ND1	2.29	0.47
8:i:28:LEU:HD22	8:i:103:LEU:HD21	1.96	0.47
15:1:21:ARG:HD3	15:1:47:VAL:HG12	1.97	0.47
1:3:1281:A:OP1	24:p:9:THR:OG1	2.31	0.47
1:3:1297:U:H2'	1:3:1297:U:O2	2.15	0.47
1:3:2429:G:C8	15:1:28:HIS:HE1	2.32	0.47
1:3:2884:C:O2	9:m:96:GLY:HA3	2.14	0.47
10:q:5:VAL:HG21	10:q:55:VAL:HG11	1.96	0.47
10:q:36:ASP:HA	10:q:54:ARG:HG3	1.97	0.47
1:3:730:G:OP1	1:3:1408:G:O2'	2.32	0.47
4:a:217:GLY:O	4:a:218:ARG:C	2.55	0.47
1:3:922:C:H2'	1:3:923:A:C8	2.49	0.47
1:3:2547:C:C5'	14:2:3:VAL:HG11	2.44	0.47
1:3:2826:G:OP1	22:b:168:HIS:NE2	2.34	0.47
4:a:33:PRO:HB2	4:a:38:LEU:HD11	1.97	0.47
5:c:76:GLN:CD	5:c:83:HIS:HE2	2.21	0.47
7:k:133:LYS:HB2	7:k:133:LYS:HE2	1.73	0.47
11:u:77:SER:HB3	11:u:99:LYS:HE3	1.95	0.47
22:b:5:GLY:HA3	22:b:84:ILE:HD13	1.97	0.47
1:3:572:G:O2'	8:i:11:GLN:OE1	2.33	0.47
1:3:1628:G:P	3:w:95:LYS:HZ3	2.36	0.47
6:e:20:PHE:HD1	6:e:25:ILE:HG12	1.78	0.47
8:i:99:GLN:O	8:i:99:GLN:HG2	2.14	0.47
10:q:15:HIS:HB2	10:q:18:ASP:OD2	2.15	0.47
28:r:114:ARG:HD2	28:r:114:ARG:HA	1.48	0.47
1:3:2750:A:OP1	14:2:1:MET:HE3	2.15	0.47
1:3:2880:A:H4'	16:o:6:LYS:CD	2.43	0.47
4:a:20:ILE:HD12	4:a:20:ILE:H	1.80	0.47
5:c:127:LEU:HD21	5:c:201:LYS:HG3	1.97	0.47
14:2:19:ARG:HG2	14:2:20:HIS:ND1	2.30	0.47
15:1:18:GLN:OE1	15:1:18:GLN:HA	2.14	0.47
17:s:56:ASN:HB2	17:s:82:VAL:HG22	1.95	0.47
3:w:8:ARG:HA	3:w:8:ARG:CZ	2.44	0.47
6:e:121:PRO:HG2	6:e:124:LEU:HD22	1.95	0.47
16:o:78:ASN:O	25:j:75:THR:HA	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:2691:C:OP1	16:o:58:LYS:HE2	2.15	0.46
10:q:71:ILE:HG22	24:p:42:ALA:CB	2.45	0.46
26:n:30:LEU:HD11	26:n:77:ILE:CD1	2.46	0.46
4:a:89:ASP:HB3	4:a:96:VAL:CG2	2.44	0.46
4:a:132:PRO:HA	4:a:200:VAL:HG23	1.97	0.46
9:m:22:VAL:HA	9:m:25:VAL:HG12	1.96	0.46
12:y:31:GLN:CD	12:y:31:GLN:H	2.23	0.46
15:1:21:ARG:HG2	15:1:45:GLY:O	2.15	0.46
1:3:903:A:O2'	1:3:904:C:OP1	2.29	0.46
1:3:2022:A:C2	12:y:3:VAL:HG12	2.51	0.46
3:w:40:LYS:HB3	3:w:42:HIS:CE1	2.51	0.46
5:c:147:LEU:HD11	5:c:157:VAL:HG11	1.96	0.46
1:3:187:C:O2'	1:3:468:A:N3	2.46	0.46
1:3:529:G:N2	28:r:57:ASN:OD1	2.48	0.46
8:i:84:ILE:HD11	22:b:160:PHE:CE2	2.50	0.46
15:1:11:PHE:CE2	15:1:55:ILE:HD12	2.51	0.46
22:b:5:GLY:H	22:b:87:MET:HE2	1.80	0.46
1:3:1806:G:H8	4:a:188:GLU:CD	2.24	0.46
1:3:1807:C:H3'	4:a:152:LEU:HD12	1.98	0.46
1:3:2400:A:C4'	15:1:25:TYR:CE2	2.98	0.46
3:w:16:VAL:HG21	3:w:68:GLU:CB	2.43	0.46
16:o:17:GLN:NE2	22:b:223:ALA:H	2.13	0.46
16:o:38:LYS:NZ	22:b:21:ASN:HD21	2.14	0.46
1:3:1653:C:H6	1:3:1653:C:O5'	1.98	0.46
1:3:579:U:H5''	28:r:129:VAL:HG11	1.98	0.46
1:3:1023:C:O2'	1:3:1036:A:N3	2.46	0.46
1:3:2888:U:H5	12:y:40:HIS:CD2	2.34	0.46
4:a:190:ARG:HG3	4:a:278:ILE:HD13	1.97	0.46
4:a:213:ILE:HG21	4:a:219:ASN:HB2	1.98	0.46
8:i:19:TYR:CD1	8:i:143:LEU:HD22	2.51	0.46
10:q:24:LYS:HA	10:q:90:THR:HG23	1.97	0.46
1:3:249:G:OP1	7:k:67:ASN:ND2	2.49	0.46
1:3:251:G:N2	1:3:255:A:OP2	2.42	0.46
1:3:1827:U:O2'	4:a:164:ALA:O	2.22	0.46
1:3:2436:G:N2	7:k:55:GLN:HE21	2.14	0.46
3:w:62:LYS:HD2	3:w:62:LYS:HA	1.73	0.46
16:o:35:ILE:HG12	16:o:86:ILE:CD1	2.44	0.46
27:t:66:GLU:OE2	27:t:66:GLU:N	2.49	0.46
1:3:185:U:N1	13:0:36:LYS:NZ	2.63	0.46
1:3:341:G:N1	1:3:344:A:OP2	2.42	0.46
1:3:2270:U:OP1	11:u:33:LYS:CE	2.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:2424:C:OP1	7:k:66:GLY:HA3	2.16	0.46
1:3:564:A:OP1	8:i:116:ARG:NE	2.49	0.46
5:c:26:ALA:HB2	5:c:113:HIS:NE2	2.31	0.46
17:s:56:ASN:O	17:s:81:ALA:HA	2.16	0.46
25:j:71:ARG:NE	25:j:105:GLU:OE2	2.49	0.46
1:3:2013:C:O2'	1:3:2827:A:N3	2.48	0.45
5:c:59:ARG:HE	5:c:59:ARG:HB3	1.25	0.45
8:i:19:TYR:HD1	8:i:143:LEU:HD22	1.80	0.45
16:o:25:PHE:HB3	16:o:90:LEU:HD12	1.98	0.45
1:3:1547:G:C5'	3:w:104:LYS:HE2	2.46	0.45
1:3:2009:U:O4	1:3:2010:A:N6	2.48	0.45
1:3:2067:A:N6	5:c:75:ARG:HH22	2.14	0.45
1:3:2691:C:O2	25:j:70:GLN:NE2	2.48	0.45
1:3:2759:G:O3'	6:e:4:ILE:HD11	2.16	0.45
4:a:139:ALA:HB2	4:a:194:LYS:HB2	1.98	0.45
1:3:1278:G:H2'	24:p:1:MET:O	2.17	0.45
1:3:2390:G:N2	15:l:39:ARG:HH12	2.14	0.45
5:c:197:LEU:HD13	5:c:199:VAL:HG23	1.98	0.45
9:m:90:TYR:HB3	9:m:97:TYR:CE2	2.51	0.45
25:j:1:MET:HE1	25:j:67:LYS:NZ	2.30	0.45
28:r:13:SER:OG	28:r:14:PRO:HD2	2.16	0.45
1:3:97:A:O2'	3:w:42:HIS:ND1	2.29	0.45
4:a:41:LEU:HG	4:a:66:TYR:HB2	1.98	0.45
17:s:70:ARG:O	17:s:71:PHE:HD1	1.98	0.45
22:b:63:ASN:OD1	22:b:64:LYS:N	2.49	0.45
1:3:185:U:O4'	13:0:36:LYS:CE	2.64	0.45
1:3:1173:G:C2	8:i:111:MET:HE2	2.50	0.45
1:3:1426:C:O2'	17:s:26:LYS:NZ	2.49	0.45
1:3:1659:C:H2'	1:3:1660:A:C5'	2.47	0.45
1:3:591:G:O3'	8:i:115:ASN:ND2	2.50	0.45
1:3:1691:U:OP1	22:b:142:ARG:CB	2.65	0.45
1:3:2387:U:O2'	26:n:22:THR:HG21	2.17	0.45
1:3:2538:A:N7	6:e:175:LYS:NZ	2.64	0.45
11:u:52:TYR:HB3	11:u:73:LEU:HB2	1.99	0.45
16:o:56:ARG:HG2	16:o:57:GLY:N	2.32	0.45
1:3:678:U:O2'	1:3:680:A:N7	2.40	0.45
1:3:1391:U:O2'	1:3:1816:A:N3	2.45	0.45
1:3:2059:G:OP1	22:b:147:VAL:HG22	2.17	0.45
1:3:2579:U:O2'	22:b:155:SER:HB3	2.17	0.45
3:w:53:THR:O	3:w:56:THR:HB	2.17	0.45
23:l:8:LYS:HE3	23:l:9:TYR:CZ	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:p:47:ARG:NH2	24:p:48:ASP:OD1	2.50	0.45
25:j:85:VAL:HG21	25:j:114:ILE:HD13	1.98	0.45
27:t:20:GLY:O	27:t:39:LEU:HD11	2.16	0.45
1:3:1659:C:H2'	1:3:1660:A:H5'	1.98	0.45
1:3:2339:G:O2'	11:u:57:THR:HG22	2.16	0.45
1:3:2460:C:C2	34:3:3026:CLM:C11	2.96	0.45
17:s:41:LYS:HB3	17:s:55:VAL:HG21	1.99	0.45
17:s:85:LEU:HD23	17:s:85:LEU:HA	1.83	0.45
26:n:76:ASP:O	26:n:80:LYS:HG3	2.16	0.45
1:3:548:A:C1'	24:p:10:ARG:NH2	2.80	0.45
1:3:780:G:H21	1:3:785:A:H61	1.64	0.45
1:3:1383:G:OP2	4:a:42:LYS:NZ	2.32	0.45
3:w:26:LEU:HD21	3:w:30:ARG:NH2	2.32	0.45
4:a:215:LYS:HB3	4:a:215:LYS:HE3	1.56	0.45
7:k:123:PRO:O	7:k:124:LEU:HD23	2.17	0.45
11:u:35:LEU:HD22	11:u:55:ARG:HG2	1.98	0.45
12:y:37:LYS:HB3	12:y:43:CYS:HB3	1.99	0.45
1:3:1815:U:O2'	1:3:1816:A:O5'	2.31	0.45
1:3:2306:A:H62	1:3:2326:G:H21	1.65	0.45
5:c:40:VAL:HG23	5:c:101:LEU:HB2	1.99	0.45
6:e:7:ARG:HB3	6:e:72:ASN:ND2	2.32	0.45
8:i:9:LYS:NZ	8:i:49:PRO:HD2	2.32	0.45
22:b:123:ILE:HD13	22:b:130:ILE:HG12	1.98	0.45
1:3:2100:G:OP1	29:f:23:ASP:O	2.34	0.44
4:a:22:TYR:HA	4:a:26:LEU:HD13	1.99	0.44
21:d:88:LYS:O	21:d:88:LYS:HG3	2.17	0.44
1:3:29:G:N2	1:3:548:A:OP2	2.50	0.44
1:3:1165:U:C5	22:b:155:SER:O	2.71	0.44
1:3:1315:A:O5'	9:m:106:ARG:HD3	2.17	0.44
1:3:2400:A:H4'	15:1:25:TYR:CD2	2.53	0.44
4:a:233:MET:HG3	4:a:238:HIS:HB2	1.99	0.44
15:1:44:GLN:H	15:1:44:GLN:HG2	1.47	0.44
18:v:7:LEU:HD21	18:v:48:ILE:HD12	1.99	0.44
18:v:27:ARG:HD2	18:v:28:LYS:N	2.32	0.44
21:d:122:PHE:HE2	21:d:167:LEU:HD22	1.81	0.44
27:t:36:VAL:HG21	27:t:74:LEU:HD11	1.99	0.44
1:3:419:A:H5'	18:v:16:ASN:HD21	1.82	0.44
1:3:687:G:OP1	15:1:15:LYS:O	2.35	0.44
1:3:980:C:O2'	1:3:981:A:OP2	2.30	0.44
2:4:41:C:C5'	21:d:63:GLN:NE2	2.75	0.44
9:m:54:VAL:HB	9:m:59:ASN:HD21	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:u:46:ARG:HA	11:u:78:ASP:OD1	2.17	0.44
22:b:79:LYS:HG2	22:b:80:HIS:ND1	2.32	0.44
2:4:55:A:C6	21:d:26:MET:HE3	2.52	0.44
8:i:39:ILE:O	8:i:54:GLY:HA3	2.17	0.44
11:u:57:THR:O	11:u:57:THR:HG23	2.18	0.44
16:o:33:VAL:HG13	16:o:33:VAL:O	2.17	0.44
17:s:44:PHE:HA	17:s:47:VAL:HG12	2.00	0.44
22:b:63:ASN:HB3	22:b:66:GLN:OE1	2.18	0.44
28:r:115:GLN:N	28:r:115:GLN:OE1	2.50	0.44
1:3:2547:C:H5'	14:2:3:VAL:HG11	2.00	0.44
4:a:251:ARG:H	4:a:251:ARG:HG2	1.50	0.44
5:c:188:VAL:O	5:c:192:MET:HG2	2.16	0.44
9:m:53:LYS:HD3	9:m:91:GLU:HA	1.98	0.44
21:d:31:LEU:HD11	21:d:156:LEU:HD22	1.99	0.44
21:d:108:LEU:N	21:d:109:PRO:HD2	2.32	0.44
26:n:111:GLU:OE1	26:n:112:ARG:HD2	2.18	0.44
1:3:819:U:H3	1:3:828:A:H62	1.65	0.44
1:3:1525:G:N2	4:a:103:ASN:O	2.45	0.44
1:3:2323:U:O2	21:d:125:ARG:NH2	2.50	0.44
1:3:2439:U:N3	1:3:2442:A:OP2	2.48	0.44
5:c:200:GLU:HG2	5:c:203:VAL:HG13	2.00	0.44
10:q:50:LEU:HD12	10:q:50:LEU:HA	1.77	0.44
12:y:54:LYS:CG	12:y:55:LYS:H	2.31	0.44
18:v:49:LEU:HD13	18:v:49:LEU:HA	1.76	0.44
22:b:16:VAL:HG12	22:b:26:ILE:HG13	1.99	0.44
26:n:112:ARG:NE	26:n:112:ARG:HA	2.33	0.44
28:r:2:ILE:HD11	28:r:113:GLU:OE2	2.18	0.44
4:a:138:LEU:HB3	4:a:180:VAL:HG11	1.99	0.44
22:b:76:LYS:HA	22:b:76:LYS:HD3	1.79	0.44
24:p:46:TYR:CZ	24:p:50:ARG:NH2	2.85	0.44
1:3:1047:A:P	24:p:76:SER:OG	2.75	0.44
1:3:1633:C:OP2	17:s:37:LYS:HD3	2.18	0.44
1:3:2273:U:H3'	1:3:2274:A:H5''	2.00	0.44
9:m:90:TYR:HB3	9:m:97:TYR:HE2	1.82	0.44
21:d:38:MET:HE3	21:d:56:GLU:OE2	2.18	0.44
22:b:3:ILE:HD12	22:b:86:ASN:HB2	1.99	0.44
1:3:477:U:O2'	5:c:47:GLN:NE2	2.51	0.44
1:3:553:A:C2'	1:3:554:U:H5'	2.48	0.44
3:w:9:GLN:O	3:w:11:SER:N	2.51	0.44
4:a:134:PHE:O	4:a:199:THR:HG23	2.17	0.44
5:c:90:VAL:HG13	5:c:91:PHE:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:p:61:ILE:CD1	24:p:92:LYS:CD	2.86	0.44
1:3:637:U:C5	7:k:84:LYS:O	2.65	0.43
1:3:880:C:H1'	1:3:968:U:H3	1.82	0.43
1:3:2675:C:N3	6:e:113:SER:OG	2.39	0.43
2:4:41:C:C5'	21:d:63:GLN:HE22	2.30	0.43
5:c:35:PHE:CZ	5:c:39:LEU:HD11	2.53	0.43
5:c:67:LYS:HB3	5:c:67:LYS:HE3	1.82	0.43
6:e:61:LEU:O	6:e:64:SER:OG	2.25	0.43
17:s:70:ARG:O	17:s:71:PHE:CD1	2.71	0.43
23:l:73:SER:HB2	23:l:93:TRP:CZ3	2.53	0.43
1:3:591:G:OP1	8:i:116:ARG:CB	2.63	0.43
1:3:960:A:H4'	11:u:43:GLN:CG	2.48	0.43
1:3:1235:U:OP1	5:c:156:ASN:ND2	2.51	0.43
1:3:2502:G:O2'	23:l:80:GLU:HA	2.18	0.43
21:d:57:LEU:HD21	21:d:89:VAL:HG23	1.99	0.43
25:j:87:ILE:O	25:j:94:ARG:NH1	2.51	0.43
1:3:591:G:P	8:i:116:ARG:HB2	2.58	0.43
1:3:2794:U:H5''	22:b:72:LYS:NZ	2.33	0.43
4:a:71:PHE:HB3	4:a:158:GLY:H	1.83	0.43
7:k:98:LEU:C	7:k:104:ILE:HG22	2.43	0.43
18:v:56:ARG:HG2	18:v:56:ARG:NH1	2.33	0.43
28:r:13:SER:OG	28:r:14:PRO:CD	2.66	0.43
28:r:19:LEU:HD23	28:r:19:LEU:HA	1.75	0.43
1:3:1119:A:N3	31:g:53:VAL:CB	2.81	0.43
1:3:1684:A:H1'	9:m:111:THR:HG22	2.00	0.43
5:c:165:ASN:OD1	5:c:166:THR:N	2.50	0.43
17:s:26:LYS:HG2	17:s:84:THR:HG22	2.00	0.43
1:3:548:A:C2'	24:p:10:ARG:NH2	2.82	0.43
1:3:1278:G:C3'	1:3:1279:U:C5'	2.97	0.43
1:3:2299:U:O2'	1:3:2382:A:N3	2.52	0.43
3:w:45:ASN:ND2	3:w:49:ARG:HH21	2.17	0.43
1:3:401:G:O2'	1:3:402:A:OP1	2.31	0.43
1:3:1120:A:N6	31:g:34:ALA:HA	2.34	0.43
1:3:1876:G:N2	1:3:1879:A:OP2	2.38	0.43
4:a:185:LEU:HA	4:a:185:LEU:HD12	1.77	0.43
4:a:190:ARG:HB3	4:a:192:PHE:CE1	2.54	0.43
5:c:194:ALA:C	5:c:196:ALA:H	2.26	0.43
21:d:57:LEU:HD23	21:d:65:PRO:HB3	2.00	0.43
23:l:8:LYS:HG2	23:l:9:TYR:CD1	2.54	0.43
1:3:548:A:N3	24:p:10:ARG:NH2	2.67	0.43
3:w:45:ASN:HD21	3:w:49:ARG:HH21	1.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:e:118:GLU:OE2	6:e:150:GLU:HB3	2.18	0.43
7:k:126:PHE:HB2	7:k:146:VAL:HG22	2.00	0.43
7:k:132:SER:HB2	7:k:135:ALA:HB3	2.01	0.43
16:o:84:PRO:HG3	22:b:223:ALA:CB	2.48	0.43
25:j:113:LYS:HB2	25:j:113:LYS:HE2	1.47	0.43
28:r:139:ARG:H	28:r:139:ARG:HG2	1.48	0.43
1:3:1475:C:O2'	1:3:1577:A:N3	2.49	0.43
1:3:2721:C:H3'	1:3:2722:G:H5''	2.00	0.43
1:3:2884:C:O2	9:m:96:GLY:CA	2.67	0.43
6:e:166:LEU:HD21	6:e:172:ILE:HG21	2.01	0.43
1:3:2321:C:N4	1:3:2322:G:O6	2.52	0.43
1:3:2513:G:O5'	34:3:3026:CLM:O4	2.37	0.43
4:a:135:SER:HA	4:a:198:ALA:O	2.19	0.43
7:k:27:GLY:O	7:k:28:LEU:C	2.60	0.43
19:x:15:LYS:O	19:x:35:THR:HA	2.19	0.43
1:3:432:G:OP2	18:v:10:ARG:HD2	2.19	0.43
1:3:916:U:O4	1:3:936:G:N2	2.52	0.43
1:3:1652:A:C6	9:m:4:ILE:HG12	2.54	0.43
2:4:78:C:H41	2:4:86:G:H1	1.67	0.43
8:i:9:LYS:HZ1	8:i:49:PRO:HD2	1.84	0.43
8:i:18:TRP:CE2	8:i:56:TYR:HD1	2.37	0.43
11:u:45:ILE:O	11:u:78:ASP:HA	2.19	0.43
17:s:48:TYR:OH	17:s:93:VAL:HA	2.19	0.43
21:d:158:THR:HG23	21:d:160:THR:H	1.83	0.43
1:3:1351:G:H5''	28:r:84:ARG:HE	1.84	0.42
17:s:32:ASN:OD1	17:s:33:PRO:HD2	2.19	0.42
21:d:67:ALA:HA	21:d:87:CYS:HA	2.01	0.42
26:n:13:LYS:HA	26:n:16:VAL:HG12	2.01	0.42
1:3:1095:U:OP1	30:h:72:VAL:N	2.47	0.42
1:3:1601:A:O2'	4:a:31:ASN:ND2	2.52	0.42
1:3:2820:G:O4'	12:y:40:HIS:ND1	2.52	0.42
8:i:15:ARG:O	8:i:15:ARG:HG2	2.18	0.42
16:o:14:GLU:O	16:o:18:LEU:HG	2.19	0.42
30:h:98:MET:N	30:h:136:ILE:O	2.52	0.42
1:3:86:A:N6	1:3:101:C:O4'	2.52	0.42
1:3:637:U:C5	7:k:84:LYS:C	2.97	0.42
4:a:208:HIS:O	4:a:211:VAL:HG12	2.19	0.42
6:e:77:ASN:HA	6:e:80:ILE:HG22	2.00	0.42
6:e:80:ILE:HA	6:e:83:THR:HG22	2.01	0.42
7:k:18:LYS:HE3	7:k:28:LEU:HD21	2.00	0.42
1:3:637:U:O4	7:k:84:LYS:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:1804:A:H5'	4:a:264:GLY:HA2	2.00	0.42
5:c:128:VAL:O	5:c:200:GLU:HA	2.19	0.42
9:m:109:ASP:HB2	9:m:111:THR:HG23	2.01	0.42
11:u:75:ALA:O	11:u:76:LEU:HD12	2.19	0.42
16:o:36:LYS:O	16:o:37:LEU:HD23	2.19	0.42
21:d:66:VAL:CG1	21:d:88:LYS:HG2	2.47	0.42
22:b:105:GLY:HA2	22:b:181:ILE:O	2.19	0.42
23:l:27:VAL:HG23	23:l:105:GLU:OE1	2.20	0.42
27:t:31:ARG:HG3	27:t:33:GLN:CG	2.40	0.42
1:3:1601:A:C8	4:a:88:TYR:HE2	2.37	0.42
4:a:12:SER:O	4:a:12:SER:OG	2.35	0.42
16:o:53:LEU:HD12	16:o:65:ILE:HG21	2.00	0.42
21:d:44:ILE:HD12	21:d:44:ILE:H	1.83	0.42
22:b:79:LYS:HG2	22:b:80:HIS:CE1	2.54	0.42
25:j:57:VAL:C	25:j:58:LEU:HD12	2.45	0.42
25:j:90:ASP:OD1	25:j:91:LYS:N	2.48	0.42
1:3:893:A:H61	1:3:957:G:H1	1.68	0.42
1:3:1120:A:H61	31:g:34:ALA:HA	1.84	0.42
1:3:2321:C:C4'	21:d:37:ASN:ND2	2.80	0.42
4:a:140:PHE:CD1	4:a:140:PHE:N	2.86	0.42
4:a:253:ALA:H	4:a:255:ARG:NH1	2.17	0.42
16:o:33:VAL:HG22	16:o:86:ILE:HD12	2.01	0.42
17:s:27:TYR:OH	17:s:91:ILE:N	2.45	0.42
1:3:356:A:H3'	5:c:174:ASN:OD1	2.20	0.42
1:3:637:U:O4	7:k:84:LYS:HB2	2.20	0.42
1:3:1360:U:C5	1:3:1643:A:C4	3.07	0.42
1:3:1910:G:OP2	4:a:248:PRO:HB2	2.20	0.42
1:3:2006:C:O2'	1:3:2007:U:H5'	2.19	0.42
4:a:151:GLU:OE2	4:a:151:GLU:N	2.53	0.42
6:e:146:GLN:HA	6:e:146:GLN:NE2	2.35	0.42
10:q:14:VAL:CG1	10:q:94:VAL:HG11	2.49	0.42
1:3:252:G:O2'	1:3:2440:A:OP1	2.20	0.42
1:3:333:A:N3	1:3:353:G:O2'	2.42	0.42
1:3:2253:U:O2'	1:3:2444:G:OP2	2.35	0.42
1:3:2353:G:OP2	20:z:36:LYS:HG2	2.20	0.42
5:c:20:LEU:HA	5:c:20:LEU:HD23	1.82	0.42
6:e:46:PHE:HA	6:e:55:ILE:HG22	2.01	0.42
7:k:36:GLN:HA	7:k:36:GLN:OE1	2.20	0.42
13:0:27:GLY:HA2	13:0:30:VAL:HG12	2.02	0.42
6:e:24:HIS:HD2	6:e:37:LYS:HA	1.85	0.42
10:q:21:PHE:HD1	10:q:91:LYS:HB2	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:q:28:PRO:HG2	10:q:31:LYS:HD2	2.02	0.42
14:2:12:LYS:HB2	14:2:12:LYS:HE3	1.85	0.42
15:1:11:PHE:HE2	15:1:55:ILE:HD12	1.84	0.42
17:s:65:ILE:C	17:s:67:GLY:H	2.28	0.42
24:p:61:ILE:HD12	24:p:75:TYR:CZ	2.55	0.42
25:j:34:PHE:N	25:j:37:ASP:OD2	2.52	0.42
27:t:3:ARG:HE	27:t:4:ILE:HG12	1.83	0.42
28:r:33:GLN:HE21	28:r:55:ILE:HG13	1.84	0.42
1:3:590:U:O2'	8:i:117:LEU:HD11	2.20	0.42
1:3:770:A:H1'	1:3:1668:G:H21	1.85	0.42
1:3:2814:A:H62	1:3:2894:G:H21	1.68	0.42
2:4:40:U:C5	21:d:66:VAL:HG11	2.55	0.42
4:a:67:ARG:HH21	4:a:89:ASP:HB2	1.85	0.42
4:a:234:ASN:C	4:a:241:GLY:HA3	2.44	0.42
6:e:166:LEU:HD23	6:e:166:LEU:HA	1.79	0.42
12:y:32:LYS:HD2	12:y:32:LYS:HA	1.82	0.42
21:d:88:LYS:CB	21:d:88:LYS:HZ2	2.33	0.42
26:n:46:PHE:C	26:n:48:GLN:H	2.28	0.42
1:3:1275:C:H4'	5:c:39:LEU:HD22	2.00	0.41
1:3:1827:U:OP1	4:a:185:LEU:HD23	2.19	0.41
1:3:2118:U:OP2	1:3:2152:C:N4	2.53	0.41
8:i:56:TYR:CE2	8:i:124:LYS:HD2	2.55	0.41
24:p:86:ASN:O	24:p:88:GLU:HG3	2.20	0.41
28:r:106:LYS:C	28:r:107:LEU:HD12	2.45	0.41
28:r:112:ASN:C	28:r:114:ARG:H	2.27	0.41
1:3:1826:A:O2'	4:a:186:SER:HB3	2.19	0.41
1:3:2239:U:H5''	18:v:29:TRP:HD1	1.85	0.41
21:d:125:ARG:HA	21:d:161:ASN:O	2.19	0.41
25:j:23:LYS:HB3	25:j:40:VAL:CG1	2.50	0.41
4:a:285:GLU:HB3	4:a:286:GLN:OE1	2.21	0.41
14:2:2:LYS:HB2	14:2:34:GLN:HG3	2.02	0.41
21:d:48:LYS:O	21:d:51:GLU:HG2	2.19	0.41
21:d:92:ARG:HA	21:d:96:MET:CB	2.49	0.41
22:b:31:CYS:SG	22:b:98:PRO:HD3	2.59	0.41
22:b:52:LEU:HD12	22:b:84:ILE:HD12	2.02	0.41
23:l:51:ARG:HG3	23:l:66:ILE:HD11	2.02	0.41
7:k:18:LYS:HE3	7:k:28:LEU:HD22	2.02	0.41
20:z:8:ARG:HH11	20:z:8:ARG:HG3	1.86	0.41
23:l:66:ILE:HG12	23:l:104:PHE:CE2	2.56	0.41
27:t:90:LYS:HG3	27:t:105:LYS:HG2	2.03	0.41
1:3:254:G:H4'	7:k:60:ARG:HE	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:357:A:H2'	1:3:357:A:N3	2.36	0.41
1:3:960:A:H4'	11:u:43:GLN:HG2	2.02	0.41
1:3:1727:U:C2	4:a:14:ILE:HD11	2.55	0.41
1:3:2504:C:OP2	23:l:82:ARG:HD3	2.19	0.41
1:3:2540:G:N2	1:3:2671:G:O2'	2.54	0.41
4:a:182:LEU:HD23	4:a:182:LEU:HA	1.85	0.41
7:k:78:VAL:HG12	7:k:111:PRO:O	2.20	0.41
8:i:10:GLU:HG2	8:i:48:THR:OG1	2.20	0.41
9:m:18:VAL:O	9:m:22:VAL:HG22	2.21	0.41
16:o:17:GLN:HE21	22:b:223:ALA:H	1.68	0.41
17:s:28:VAL:HG23	17:s:82:VAL:HG12	2.01	0.41
20:z:18:ASN:HB3	20:z:19:TYR:CD1	2.54	0.41
21:d:88:LYS:HB3	21:d:88:LYS:HZ3	1.84	0.41
21:d:125:ARG:O	21:d:161:ASN:HA	2.20	0.41
28:r:82:MET:HB2	28:r:98:LYS:HB2	2.02	0.41
4:a:234:ASN:HB3	4:a:235:PRO:HD2	2.01	0.41
5:c:64:LYS:HZ2	5:c:64:LYS:HG2	1.79	0.41
6:e:173:VAL:C	6:e:174:ARG:HD2	2.46	0.41
8:i:18:TRP:NE1	8:i:138:GLN:HE21	2.18	0.41
9:m:44:ARG:NH2	9:m:47:LYS:HD2	2.35	0.41
14:2:7:VAL:HG23	14:2:7:VAL:O	2.20	0.41
17:s:23:GLU:N	17:s:23:GLU:OE1	2.53	0.41
25:j:90:ASP:CG	25:j:91:LYS:H	2.27	0.41
28:r:110:ASN:OD1	28:r:113:GLU:HB2	2.20	0.41
28:r:119:LYS:HA	28:r:119:LYS:HD3	1.92	0.41
1:3:605:A:H61	1:3:2036:G:H21	1.67	0.41
1:3:672:G:O2'	1:3:673:A:O5'	2.39	0.41
1:3:1303:U:H5'	9:m:6:LYS:CB	2.50	0.41
1:3:1444:C:HO2'	1:3:1445:U:P	2.44	0.41
4:a:67:ARG:HD2	4:a:67:ARG:N	2.35	0.41
8:i:145:TRP:N	8:i:145:TRP:CD1	2.89	0.41
12:y:28:SER:HB2	12:y:39:PHE:HD1	1.85	0.41
14:2:17:ILE:CD1	14:2:26:ILE:HD11	2.51	0.41
14:2:20:HIS:O	14:2:22:ILE:HG12	2.21	0.41
16:o:6:LYS:HD3	16:o:6:LYS:HA	1.78	0.41
20:z:27:LYS:HE3	20:z:27:LYS:HB2	1.65	0.41
21:d:123:ASP:CG	21:d:125:ARG:H	2.25	0.41
6:e:75:ILE:HD13	6:e:75:ILE:HA	1.96	0.41
9:m:100:VAL:HG22	9:m:116:LEU:HD13	2.01	0.41
20:z:28:ASN:OD1	20:z:28:ASN:N	2.53	0.41
23:l:58:LEU:HD11	23:l:62:GLY:HA3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:p:35:LYS:O	24:p:39:ILE:HG12	2.20	0.41
26:n:110:ARG:HG2	26:n:116:PHE:CZ	2.56	0.41
1:3:573:A:H4'	8:i:11:GLN:CG	2.50	0.41
1:3:948:A:C6	23:l:9:TYR:CD2	3.09	0.41
1:3:1379:C:O2'	1:3:1605:A:N3	2.52	0.41
1:3:1698:A:H61	1:3:2003:C:N4	2.19	0.41
1:3:2813:A:H3'	1:3:2814:A:H5'	2.03	0.41
2:4:39:U:O2	2:4:39:U:H2'	2.20	0.41
3:w:33:LEU:HB2	3:w:38:LEU:HD22	2.03	0.41
4:a:193:LEU:H	4:a:193:LEU:HD12	1.86	0.41
5:c:4:LEU:HD11	5:c:125:THR:O	2.21	0.41
9:m:3:TYR:N	9:m:3:TYR:CD1	2.89	0.41
9:m:34:THR:HG22	9:m:36:LYS:H	1.85	0.41
16:o:22:VAL:HG13	16:o:22:VAL:O	2.20	0.41
16:o:52:VAL:HA	16:o:65:ILE:O	2.21	0.41
16:o:113:LYS:HD2	16:o:113:LYS:N	2.36	0.41
21:d:57:LEU:HA	21:d:60:ILE:HG22	2.01	0.41
29:f:26:ALA:C	29:f:28:HIS:N	2.78	0.41
1:3:571:A:H2'	1:3:572:G:H5'	2.03	0.41
1:3:780:G:O4'	9:m:3:TYR:HE1	2.04	0.41
1:3:1498:U:C4'	3:w:105:ARG:HH11	2.33	0.41
1:3:2352:U:OP1	20:z:35:ASN:OD1	2.39	0.41
4:a:170:ILE:HD13	4:a:182:LEU:HD21	2.03	0.41
5:c:169:GLU:HB3	5:c:180:VAL:HG11	2.03	0.41
6:e:89:LYS:HE2	6:e:133:GLU:HG3	2.03	0.41
14:2:25:VAL:CG2	14:2:34:GLN:HB2	2.49	0.41
26:n:32:VAL:HG12	26:n:92:ASP:O	2.21	0.41
1:3:85:U:O2'	1:3:86:A:H5'	2.21	0.40
1:3:721:G:H3'	1:3:722:C:H5'	2.02	0.40
1:3:923:A:C2	1:3:924:C:H1'	2.56	0.40
1:3:2886:A:P	9:m:99:ARG:HH21	2.40	0.40
7:k:69:ARG:HG2	7:k:72:PHE:HB2	2.04	0.40
8:i:84:ILE:HD11	22:b:160:PHE:CD2	2.56	0.40
8:i:96:LEU:HD23	8:i:96:LEU:HA	1.93	0.40
23:l:2:LEU:HD23	23:l:69:PHE:CE1	2.56	0.40
1:3:289:U:O4	1:3:290:A:N6	2.53	0.40
1:3:710:A:N3	1:3:2451:C:O2'	2.47	0.40
11:u:28:ARG:HE	11:u:28:ARG:HB2	1.63	0.40
23:l:116:LYS:O	23:l:116:LYS:HD3	2.20	0.40
24:p:50:ARG:HH11	24:p:50:ARG:CG	2.34	0.40
24:p:100:LYS:N	24:p:100:LYS:HD3	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:1186:A:O3'	24:p:80:ASN:ND2	2.54	0.40
1:3:1481:U:O2'	1:3:1482:U:OP2	2.36	0.40
1:3:1686:U:C5'	9:m:36:LYS:NZ	2.84	0.40
1:3:2692:U:P	16:o:56:ARG:NH2	2.79	0.40
5:c:2:ALA:N	5:c:20:LEU:HB2	2.36	0.40
6:e:146:GLN:O	6:e:149:THR:HG22	2.22	0.40
7:k:22:ARG:HA	7:k:22:ARG:HD3	1.88	0.40
10:q:73:HIS:HD2	10:q:80:LEU:HD13	1.87	0.40
21:d:55:ASN:O	21:d:59:LEU:HG	2.20	0.40
22:b:13:MET:HG3	22:b:26:ILE:O	2.21	0.40
1:3:715:G:OP2	1:3:811:G:N2	2.54	0.40
1:3:849:C:OP1	10:q:81:LYS:HA	2.21	0.40
1:3:1047:A:OP1	24:p:76:SER:CB	2.70	0.40
6:e:19:ASN:ND2	6:e:26:ALA:HB3	2.36	0.40
8:i:7:LEU:CD1	24:p:60:TRP:HE1	2.32	0.40
9:m:19:ARG:NH2	9:m:68:LEU:HD21	2.36	0.40
10:q:42:ASP:C	10:q:44:LYS:N	2.80	0.40
21:d:35:VAL:HA	21:d:89:VAL:O	2.21	0.40
22:b:106:GLU:OE1	22:b:107:TYR:N	2.54	0.40
28:r:112:ASN:O	28:r:114:ARG:N	2.54	0.40
1:3:1160:G:O6	1:3:1161:A:N6	2.55	0.40
1:3:1547:G:H5'	3:w:104:LYS:HE2	2.03	0.40
1:3:2024:C:O2	12:y:7:ARG:HB3	2.22	0.40
1:3:2844:U:C5'	9:m:50:THR:HG21	2.49	0.40
3:w:22:LEU:HD13	3:w:25:GLU:OE2	2.22	0.40
6:e:12:ASP:HA	6:e:13:PRO:HD3	1.87	0.40
7:k:115:ILE:HD13	7:k:115:ILE:HG21	1.83	0.40
16:o:33:VAL:HG11	16:o:79:PHE:CE1	2.56	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	
3	w	95/111 (86%)	89 (94%)	6 (6%)	0	100	100
4	a	283/287 (99%)	253 (89%)	30 (11%)	0	100	100
5	c	208/212 (98%)	186 (89%)	22 (11%)	0	100	100
6	e	174/184 (95%)	165 (95%)	9 (5%)	0	100	100
7	k	146/151 (97%)	126 (86%)	20 (14%)	0	100	100
8	i	142/146 (97%)	134 (94%)	8 (6%)	0	100	100
9	m	117/124 (94%)	111 (95%)	6 (5%)	0	100	100
10	q	97/100 (97%)	85 (88%)	12 (12%)	0	100	100
11	u	84/104 (81%)	76 (90%)	8 (10%)	0	100	100
12	y	54/57 (95%)	48 (89%)	6 (11%)	0	100	100
13	0	45/48 (94%)	43 (96%)	2 (4%)	0	100	100
14	2	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
15	1	57/59 (97%)	53 (93%)	4 (7%)	0	100	100
16	o	113/119 (95%)	95 (84%)	18 (16%)	0	100	100
17	s	90/237 (38%)	82 (91%)	8 (9%)	0	100	100
18	v	61/65 (94%)	53 (87%)	8 (13%)	0	100	100
19	x	42/97 (43%)	31 (74%)	11 (26%)	0	100	100
20	z	48/53 (91%)	45 (94%)	3 (6%)	0	100	100
21	d	173/180 (96%)	154 (89%)	19 (11%)	0	100	100
22	b	227/287 (79%)	199 (88%)	28 (12%)	0	100	100
23	l	134/139 (96%)	118 (88%)	16 (12%)	0	100	100
24	p	112/127 (88%)	104 (93%)	8 (7%)	0	100	100
25	j	120/122 (98%)	105 (88%)	15 (12%)	0	100	100
26	n	108/116 (93%)	91 (84%)	17 (16%)	0	100	100
27	t	92/111 (83%)	84 (91%)	8 (9%)	0	100	100
28	r	137/159 (86%)	123 (90%)	14 (10%)	0	100	100
29	f	140/149 (94%)	121 (86%)	18 (13%)	1 (1%)	18	47
30	h	126/137 (92%)	116 (92%)	8 (6%)	2 (2%)	7	29
31	g	123/161 (76%)	115 (94%)	4 (3%)	4 (3%)	3	17
All	All	3383/3879 (87%)	3039 (90%)	337 (10%)	7 (0%)	44	71

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
29	f	115	ASP
30	h	20	LYS
31	g	45	PHE
31	g	110	CYS
30	h	23	PRO
31	g	88	GLU
31	g	47	ASN

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	w	83/98 (85%)	78 (94%)	5 (6%)	17	43
4	a	233/243 (96%)	226 (97%)	7 (3%)	36	59
5	c	174/184 (95%)	168 (97%)	6 (3%)	32	57
6	e	138/159 (87%)	135 (98%)	3 (2%)	45	63
7	k	118/126 (94%)	115 (98%)	3 (2%)	42	62
8	i	124/128 (97%)	120 (97%)	4 (3%)	34	58
9	m	104/109 (95%)	103 (99%)	1 (1%)	68	75
10	q	88/91 (97%)	84 (96%)	4 (4%)	24	51
11	u	64/85 (75%)	63 (98%)	1 (2%)	55	68
12	y	45/49 (92%)	39 (87%)	6 (13%)	4	15
13	0	39/41 (95%)	39 (100%)	0	100	100
14	2	35/35 (100%)	31 (89%)	4 (11%)	5	21
15	1	51/51 (100%)	47 (92%)	4 (8%)	11	37
16	o	91/105 (87%)	86 (94%)	5 (6%)	19	46
17	s	80/208 (38%)	80 (100%)	0	100	100
18	v	55/60 (92%)	50 (91%)	5 (9%)	9	30
20	z	47/50 (94%)	47 (100%)	0	100	100
21	d	111/154 (72%)	108 (97%)	3 (3%)	39	60
22	b	185/233 (79%)	179 (97%)	6 (3%)	34	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	l	107/115 (93%)	106 (99%)	1 (1%)	70	76
24	p	99/108 (92%)	96 (97%)	3 (3%)	36	59
25	j	103/103 (100%)	96 (93%)	7 (7%)	14	40
26	n	85/99 (86%)	85 (100%)	0	100	100
27	t	69/96 (72%)	68 (99%)	1 (1%)	59	70
28	r	116/132 (88%)	107 (92%)	9 (8%)	11	37
All	All	2444/2862 (85%)	2356 (96%)	88 (4%)	32	56

All (88) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	w	37	GLU
3	w	39	ASP
3	w	65	TRP
3	w	66	GLN
3	w	68	GLU
4	a	89	ASP
4	a	210	LEU
4	a	215	LYS
4	a	227	THR
4	a	249	VAL
4	a	251	ARG
4	a	252	ASP
5	c	58	VAL
5	c	59	ARG
5	c	63	LYS
5	c	64	LYS
5	c	67	LYS
5	c	69	LYS
6	e	161	LYS
6	e	166	LEU
6	e	171	VAL
7	k	30	LYS
7	k	34	ARG
7	k	64	LYS
8	i	127	VAL
8	i	129	LYS
8	i	131	ASP
8	i	132	LYS
9	m	3	TYR

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Mol	Chain	Res	Type
10	q	94	VAL
10	q	95	VAL
10	q	96	ARG
10	q	99	HIS
11	u	43	GLN
12	y	10	LYS
12	y	32	LYS
12	y	33	CYS
12	y	50	ASP
12	y	52	ARG
12	y	53	VAL
14	2	8	LYS
14	2	34	GLN
14	2	35	ARG
14	2	36	GLN
15	1	4	LYS
15	1	42	ARG
15	1	44	GLN
15	1	46	THR
16	o	80	GLN
16	o	81	ILE
16	o	86	ILE
16	o	87	SER
16	o	88	ILE
18	v	45	THR
18	v	46	THR
18	v	47	ARG
18	v	48	ILE
18	v	49	LEU
21	d	88	LYS
21	d	94	GLU
21	d	96	MET
22	b	117	ARG
22	b	124	LYS
22	b	176	VAL
22	b	177	GLN
22	b	178	ASN
22	b	181	ILE
23	l	16	SER
24	p	50	ARG
24	p	86	ASN
24	p	93	VAL

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Mol	Chain	Res	Type
25	j	22	ILE
25	j	24	VAL
25	j	25	LEU
25	j	113	LYS
25	j	114	ILE
25	j	115	LEU
25	j	119	VAL
27	t	45	HIS
28	r	6	LYS
28	r	8	PHE
28	r	9	ARG
28	r	11	ARG
28	r	12	ILE
28	r	18	ARG
28	r	136	LYS
28	r	137	MET
28	r	139	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
4	a	11	ASN
4	a	91	ASN
5	c	47	GLN
5	c	76	GLN
5	c	156	ASN
6	e	21	GLN
6	e	107	ASN
8	i	126	HIS
8	i	138	GLN
9	m	20	GLN
9	m	81	HIS
9	m	117	GLN
11	u	43	GLN
14	2	30	GLN
14	2	36	GLN
15	1	28	HIS
17	s	20	GLN
17	s	56	ASN
18	v	16	ASN
18	v	34	GLN
21	d	63	GLN

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Mol	Chain	Res	Type
22	b	20	ASN
22	b	188	ASN
23	l	123	HIS
24	p	65	ASN
25	j	70	GLN
26	n	38	HIS
27	t	17	ASN
28	r	38	ASN
28	r	121	GLN
28	r	132	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3	2876/2907 (98%)	669 (23%)	58 (2%)
2	4	103/108 (95%)	32 (31%)	6 (5%)
All	All	2979/3015 (98%)	701 (23%)	64 (2%)

All (701) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3	12	A
1	3	14	U
1	3	28	G
1	3	37	G
1	3	47	G
1	3	48	G
1	3	51	A
1	3	63	U
1	3	64	U
1	3	65	A
1	3	73	A
1	3	76	A
1	3	77	G
1	3	87	G
1	3	101	C
1	3	102	A
1	3	103	G
1	3	106	C
1	3	111	G
1	3	119	A

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Mol	Chain	Res	Type
1	3	120	A
1	3	121	U
1	3	124	A
1	3	126	C
1	3	132	G
1	3	149	A
1	3	152	A
1	3	163	A
1	3	164	A
1	3	165	U
1	3	169	U
1	3	180	A
1	3	184	A
1	3	186	A
1	3	187	C
1	3	188	G
1	3	200	A
1	3	203	A
1	3	208	A
1	3	210	U
1	3	219	G
1	3	220	A
1	3	226	A
1	3	229	C
1	3	231	A
1	3	232	A
1	3	234	G
1	3	237	A
1	3	244	G
1	3	245	U
1	3	246	G
1	3	252	G
1	3	256	G
1	3	265	G
1	3	270	G
1	3	276	A
1	3	277	C
1	3	283	A
1	3	284	U
1	3	286	A
1	3	287	G
1	3	295	U

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Mol	Chain	Res	Type
1	3	296	U
1	3	297	G
1	3	298	U
1	3	299	A
1	3	309	A
1	3	310	U
1	3	311	G
1	3	312	U
1	3	314	G
1	3	315	A
1	3	316	C
1	3	319	G
1	3	336	C
1	3	342	G
1	3	343	A
1	3	345	A
1	3	347	C
1	3	351	G
1	3	355	A
1	3	356	A
1	3	357	A
1	3	363	G
1	3	364	A
1	3	369	C
1	3	380	A
1	3	397	G
1	3	402	A
1	3	403	U
1	3	404	C
1	3	408	G
1	3	409	A
1	3	410	G
1	3	411	U
1	3	418	G
1	3	419	A
1	3	422	A
1	3	424	G
1	3	425	U
1	3	426	U
1	3	432	G
1	3	437	A
1	3	440	C

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Mol	Chain	Res	Type
1	3	447	G
1	3	448	A
1	3	460	G
1	3	484	U
1	3	487	C
1	3	492	C
1	3	493	A
1	3	500	U
1	3	501	G
1	3	509	G
1	3	514	A
1	3	515	A
1	3	516	A
1	3	517	G
1	3	519	A
1	3	539	U
1	3	540	A
1	3	543	U
1	3	554	U
1	3	562	C
1	3	566	G
1	3	567	U
1	3	568	G
1	3	573	A
1	3	581	A
1	3	583	U
1	3	589	A
1	3	596	G
1	3	604	A
1	3	605	A
1	3	606	G
1	3	608	A
1	3	609	U
1	3	610	G
1	3	620	G
1	3	636	U
1	3	637	U
1	3	638	A
1	3	647	G
1	3	648	G
1	3	649	A
1	3	650	G

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Mol	Chain	Res	Type
1	3	652	U
1	3	657	A
1	3	663	A
1	3	670	G
1	3	673	A
1	3	681	A
1	3	682	A
1	3	689	U
1	3	691	G
1	3	705	A
1	3	706	C
1	3	721	G
1	3	722	C
1	3	752	C
1	3	765	A
1	3	771	C
1	3	781	U
1	3	782	U
1	3	786	A
1	3	800	C
1	3	810	G
1	3	811	G
1	3	812	G
1	3	817	A
1	3	818	A
1	3	819	U
1	3	820	U
1	3	824	A
1	3	825	U
1	3	827	G
1	3	828	A
1	3	829	A
1	3	835	U
1	3	837	A
1	3	840	G
1	3	841	C
1	3	847	C
1	3	854	A
1	3	862	U
1	3	880	C
1	3	881	A
1	3	882	C

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Mol	Chain	Res	Type
1	3	883	A
1	3	895	G
1	3	902	U
1	3	904	C
1	3	906	G
1	3	914	G
1	3	917	G
1	3	920	G
1	3	923	A
1	3	924	C
1	3	925	C
1	3	927	A
1	3	928	G
1	3	930	C
1	3	932	U
1	3	935	U
1	3	936	G
1	3	944	U
1	3	947	A
1	3	949	C
1	3	951	C
1	3	952	U
1	3	953	G
1	3	970	U
1	3	981	A
1	3	982	G
1	3	994	U
1	3	995	A
1	3	997	G
1	3	1005	G
1	3	1008	A
1	3	1009	A
1	3	1010	G
1	3	1016	A
1	3	1026	A
1	3	1027	U
1	3	1032	A
1	3	1041	C
1	3	1049	U
1	3	1052	A
1	3	1057	G
1	3	1061	A

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Mol	Chain	Res	Type
1	3	1068	U
1	3	1075	G
1	3	1078	C
1	3	1080	A
1	3	1081	A
1	3	1082	A
1	3	1095	U
1	3	1102	A
1	3	1103	G
1	3	1104	A
1	3	1105	A
1	3	1107	C
1	3	1112	A
1	3	1118	U
1	3	1121	A
1	3	1123	A
1	3	1124	G
1	3	1125	U
1	3	1126	G
1	3	1132	C
1	3	1137	C
1	3	1146	A
1	3	1147	G
1	3	1151	U
1	3	1154	U
1	3	1160	G
1	3	1164	A
1	3	1165	U
1	3	1167	U
1	3	1168	A
1	3	1169	A
1	3	1170	C
1	3	1171	G
1	3	1176	U
1	3	1177	A
1	3	1178	A
1	3	1186	A
1	3	1190	A
1	3	1204	A
1	3	1207	U
1	3	1208	A
1	3	1209	U

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Mol	Chain	Res	Type
1	3	1210	A
1	3	1212	C
1	3	1215	G
1	3	1217	G
1	3	1219	U
1	3	1234	U
1	3	1235	U
1	3	1250	A
1	3	1251	G
1	3	1253	G
1	3	1256	A
1	3	1268	U
1	3	1278	G
1	3	1279	U
1	3	1281	A
1	3	1283	A
1	3	1285	U
1	3	1286	G
1	3	1292	A
1	3	1295	A
1	3	1298	A
1	3	1301	G
1	3	1302	C
1	3	1303	U
1	3	1304	U
1	3	1316	U
1	3	1328	A
1	3	1329	U
1	3	1330	U
1	3	1337	G
1	3	1338	G
1	3	1349	C
1	3	1360	U
1	3	1366	G
1	3	1369	U
1	3	1370	A
1	3	1380	U
1	3	1393	A
1	3	1402	G
1	3	1406	A
1	3	1407	U
1	3	1412	A

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Mol	Chain	Res	Type
1	3	1423	A
1	3	1424	U
1	3	1431	A
1	3	1434	U
1	3	1437	A
1	3	1444	C
1	3	1445	U
1	3	1448	U
1	3	1455	A
1	3	1456	C
1	3	1457	A
1	3	1462	A
1	3	1463	G
1	3	1467	U
1	3	1480	A
1	3	1481	U
1	3	1482	U
1	3	1483	G
1	3	1486	U
1	3	1487	U
1	3	1494	U
1	3	1502	A
1	3	1504	G
1	3	1507	G
1	3	1508	G
1	3	1510	A
1	3	1513	A
1	3	1514	U
1	3	1515	A
1	3	1518	C
1	3	1519	A
1	3	1520	A
1	3	1522	U
1	3	1532	A
1	3	1533	U
1	3	1534	A
1	3	1541	A
1	3	1548	A
1	3	1557	G
1	3	1559	A
1	3	1571	G
1	3	1580	G

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Mol	Chain	Res	Type
1	3	1582	G
1	3	1584	U
1	3	1585	A
1	3	1586	U
1	3	1587	U
1	3	1588	A
1	3	1589	A
1	3	1592	A
1	3	1601	A
1	3	1603	A
1	3	1612	U
1	3	1615	G
1	3	1617	U
1	3	1618	U
1	3	1619	A
1	3	1641	A
1	3	1643	A
1	3	1644	A
1	3	1650	A
1	3	1651	C
1	3	1652	A
1	3	1653	C
1	3	1655	U
1	3	1656	A
1	3	1668	G
1	3	1679	U
1	3	1680	A
1	3	1681	G
1	3	1682	C
1	3	1688	A
1	3	1694	A
1	3	1699	A
1	3	1706	C
1	3	1707	U
1	3	1708	G
1	3	1727	U
1	3	1732	A
1	3	1733	G
1	3	1735	A
1	3	1737	G
1	3	1748	U
1	3	1751	A

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Mol	Chain	Res	Type
1	3	1761	C
1	3	1762	A
1	3	1763	G
1	3	1764	U
1	3	1765	G
1	3	1769	A
1	3	1770	A
1	3	1771	C
1	3	1780	A
1	3	1788	A
1	3	1789	C
1	3	1790	U
1	3	1791	A
1	3	1807	C
1	3	1809	A
1	3	1815	U
1	3	1816	A
1	3	1821	G
1	3	1822	A
1	3	1823	U
1	3	1834	U
1	3	1837	C
1	3	1841	U
1	3	1842	G
1	3	1854	A
1	3	1865	A
1	3	1866	G
1	3	1867	G
1	3	1869	G
1	3	1870	G
1	3	1876	G
1	3	1880	G
1	3	1891	A
1	3	1898	G
1	3	1903	A
1	3	1906	G
1	3	1907	A
1	3	1908	A
1	3	1910	G
1	3	1913	G
1	3	1920	A
1	3	1921	C

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Mol	Chain	Res	Type
1	3	1926	A
1	3	1934	A
1	3	1936	G
1	3	1937	G
1	3	1938	U
1	3	1945	A
1	3	1952	G
1	3	1962	U
1	3	1972	C
1	3	1977	A
1	3	1978	U
1	3	1979	G
1	3	1998	U
1	3	2000	U
1	3	2009	U
1	3	2011	G
1	3	2025	C
1	3	2027	G
1	3	2028	G
1	3	2038	A
1	3	2040	A
1	3	2041	C
1	3	2043	C
1	3	2050	G
1	3	2056	A
1	3	2062	C
1	3	2063	G
1	3	2067	A
1	3	2068	G
1	3	2069	A
1	3	2076	G
1	3	2084	A
1	3	2099	U
1	3	2100	G
1	3	2106	G
1	3	2107	A
1	3	2110	U
1	3	2111	U
1	3	2112	A
1	3	2114	C
1	3	2115	A
1	3	2117	G

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Mol	Chain	Res	Type
1	3	2123	A
1	3	2124	A
1	3	2125	U
1	3	2128	G
1	3	2130	A
1	3	2131	G
1	3	2132	G
1	3	2133	A
1	3	2139	C
1	3	2140	G
1	3	2153	U
1	3	2166	U
1	3	2171	A
1	3	2180	U
1	3	2181	A
1	3	2182	C
1	3	2193	U
1	3	2195	U
1	3	2196	G
1	3	2198	G
1	3	2199	C
1	3	2200	U
1	3	2201	G
1	3	2202	U
1	3	2203	U
1	3	2207	A
1	3	2211	G
1	3	2212	U
1	3	2219	U
1	3	2220	A
1	3	2221	U
1	3	2222	C
1	3	2223	C
1	3	2231	A
1	3	2233	A
1	3	2246	G
1	3	2247	G
1	3	2259	G
1	3	2274	A
1	3	2275	A
1	3	2276	A
1	3	2286	A

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Mol	Chain	Res	Type
1	3	2291	U
1	3	2292	A
1	3	2294	A
1	3	2295	A
1	3	2296	A
1	3	2298	G
1	3	2305	C
1	3	2312	G
1	3	2313	U
1	3	2316	G
1	3	2317	A
1	3	2324	A
1	3	2327	U
1	3	2329	G
1	3	2330	A
1	3	2332	U
1	3	2333	G
1	3	2335	A
1	3	2341	G
1	3	2342	U
1	3	2343	A
1	3	2344	A
1	3	2346	G
1	3	2353	G
1	3	2355	C
1	3	2358	U
1	3	2366	A
1	3	2380	U
1	3	2391	G
1	3	2393	C
1	3	2410	C
1	3	2411	C
1	3	2414	U
1	3	2415	A
1	3	2418	G
1	3	2422	G
1	3	2431	U
1	3	2433	A
1	3	2435	C
1	3	2436	G
1	3	2438	A
1	3	2449	U

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Mol	Chain	Res	Type
1	3	2453	G
1	3	2456	A
1	3	2457	U
1	3	2477	A
1	3	2484	A
1	3	2486	A
1	3	2488	C
1	3	2492	G
1	3	2499	U
1	3	2505	A
1	3	2506	C
1	3	2507	C
1	3	2509	C
1	3	2510	G
1	3	2512	U
1	3	2513	G
1	3	2521	A
1	3	2526	A
1	3	2527	U
1	3	2528	C
1	3	2543	G
1	3	2555	U
1	3	2557	G
1	3	2562	U
1	3	2570	U
1	3	2574	A
1	3	2575	G
1	3	2580	A
1	3	2581	C
1	3	2584	G
1	3	2590	G
1	3	2594	C
1	3	2605	G
1	3	2610	A
1	3	2617	U
1	3	2618	C
1	3	2621	U
1	3	2622	A
1	3	2623	U
1	3	2631	G
1	3	2637	A
1	3	2638	G

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Mol	Chain	Res	Type
1	3	2639	G
1	3	2642	G
1	3	2646	G
1	3	2654	U
1	3	2656	G
1	3	2664	U
1	3	2668	A
1	3	2669	G
1	3	2672	G
1	3	2687	A
1	3	2697	C
1	3	2698	U
1	3	2722	G
1	3	2734	C
1	3	2737	G
1	3	2740	U
1	3	2741	A
1	3	2747	U
1	3	2752	G
1	3	2753	C
1	3	2756	A
1	3	2760	C
1	3	2765	A
1	3	2772	A
1	3	2784	A
1	3	2786	A
1	3	2788	U
1	3	2797	C
1	3	2798	A
1	3	2799	U
1	3	2800	U
1	3	2801	U
1	3	2808	A
1	3	2809	A
1	3	2811	G
1	3	2812	U
1	3	2813	A
1	3	2814	A
1	3	2815	G
1	3	2822	C
1	3	2824	A
1	3	2825	A

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Mol	Chain	Res	Type
1	3	2826	G
1	3	2829	G
1	3	2835	G
1	3	2839	A
1	3	2853	U
1	3	2863	G
1	3	2870	U
1	3	2871	G
1	3	2876	G
1	3	2884	C
1	3	2888	U
1	3	2889	U
1	3	2890	G
1	3	2894	G
1	3	2895	A
1	3	2896	G
1	3	2897	G
1	3	2898	A
1	3	2899	C
2	4	10	C
2	4	11	A
2	4	12	U
2	4	13	G
2	4	16	G
2	4	23	A
2	4	31	G
2	4	33	U
2	4	35	C
2	4	40	U
2	4	41	C
2	4	42	G
2	4	43	A
2	4	49	G
2	4	50	C
2	4	51	A
2	4	54	U
2	4	55	A
2	4	60	C
2	4	63	U
2	4	64	G
2	4	65	G
2	4	71	A

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Mol	Chain	Res	Type
2	4	78	C
2	4	80	G
2	4	85	A
2	4	86	G
2	4	88	G
2	4	89	A
2	4	96	G
2	4	99	A
2	4	108	C

All (64) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	3	296	U
1	3	311	G
1	3	315	A
1	3	357	A
1	3	368	C
1	3	410	G
1	3	425	U
1	3	447	G
1	3	500	U
1	3	508	A
1	3	513	A
1	3	514	A
1	3	604	A
1	3	647	G
1	3	648	G
1	3	688	U
1	3	781	U
1	3	811	G
1	3	881	A
1	3	901	C
1	3	903	A
1	3	952	U
1	3	980	C
1	3	1048	A
1	3	1209	U
1	3	1211	U
1	3	1297	U
1	3	1302	C
1	3	1328	A

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Mol	Chain	Res	Type
1	3	1329	U
1	3	1462	A
1	3	1507	G
1	3	1519	A
1	3	1583	G
1	3	1585	A
1	3	1587	U
1	3	1588	A
1	3	1618	U
1	3	1644	A
1	3	1680	A
1	3	1820	U
1	3	2029	U
1	3	2180	U
1	3	2290	G
1	3	2304	U
1	3	2332	U
1	3	2342	U
1	3	2504	C
1	3	2506	C
1	3	2604	U
1	3	2621	U
1	3	2622	A
1	3	2668	A
1	3	2787	U
1	3	2823	A
1	3	2862	U
1	3	2889	U
1	3	2897	G
2	4	10	C
2	4	34	U
2	4	38	U
2	4	54	U
2	4	59	A
2	4	70	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 30 ligands modelled in this entry, 29 are monoatomic - leaving 1 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
34	CLM	3	3026	-	20,20,20	2.41	7 (35%)	23,27,27	1.36	2 (8%)

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
34	CLM	3	3026	-	-	3/20/22/22	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	3	3026	CLM	O9B-N9	-5.88	1.12	1.22
34	3	3026	CLM	C2-N2	4.23	1.43	1.34
34	3	3026	CLM	C1-C2	3.76	1.58	1.53
34	3	3026	CLM	O2-C2	-3.54	1.16	1.23
34	3	3026	CLM	O5-C5	-3.21	1.36	1.42
34	3	3026	CLM	C3-N2	-3.06	1.41	1.46
34	3	3026	CLM	C11-C6	-2.60	1.35	1.39

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	3	3026	CLM	C4-C3-N2	-3.09	104.40	109.28
34	3	3026	CLM	C3-N2-C2	-2.94	118.14	123.25

There are no chirality outliers.

All (3) torsion outliers are listed below:

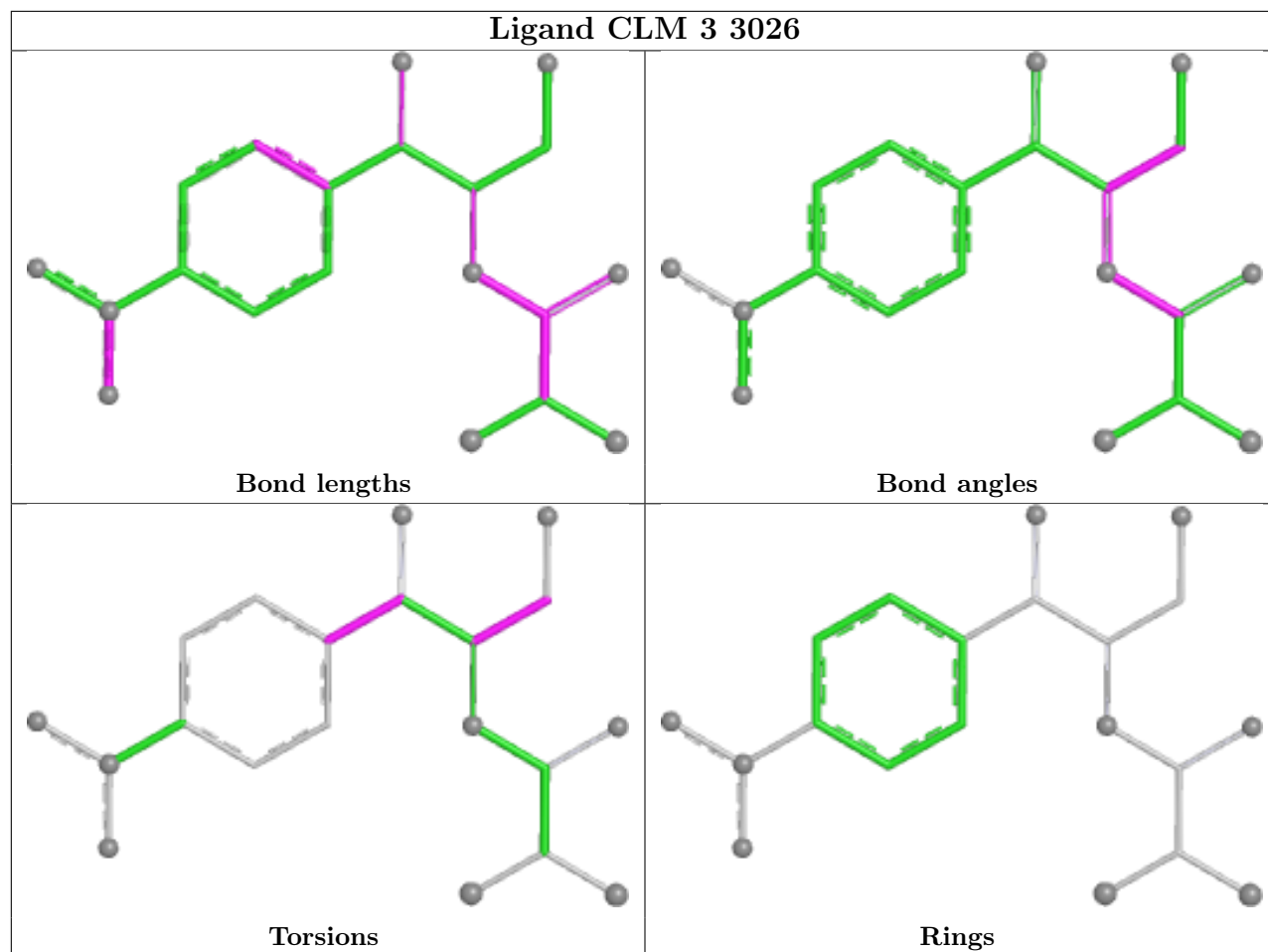
Mol	Chain	Res	Type	Atoms
34	3	3026	CLM	C3-C5-C6-C7
34	3	3026	CLM	C3-C5-C6-C11
34	3	3026	CLM	N2-C3-C4-O4

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
34	3	3026	CLM	4	0

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.

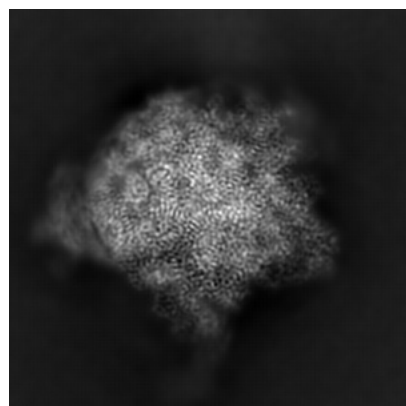
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11999. These allow visual inspection of the internal detail of the map and identification of artifacts.

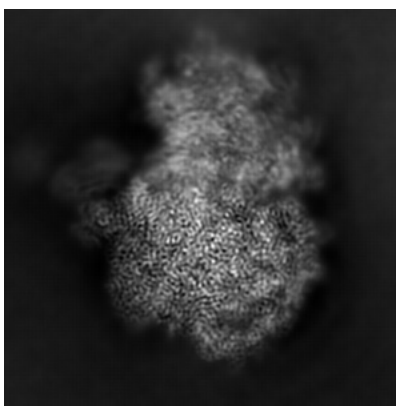
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

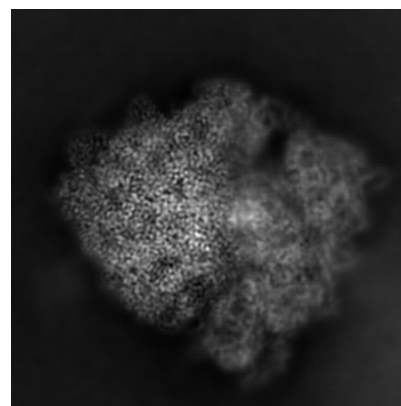
6.1.1 Primary map



X

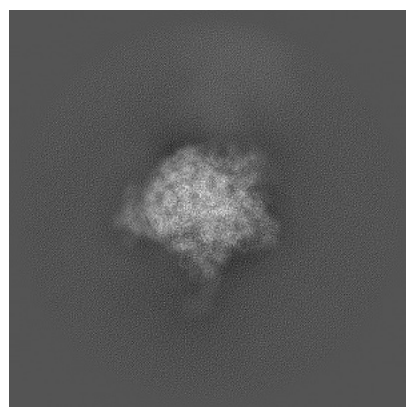


Y

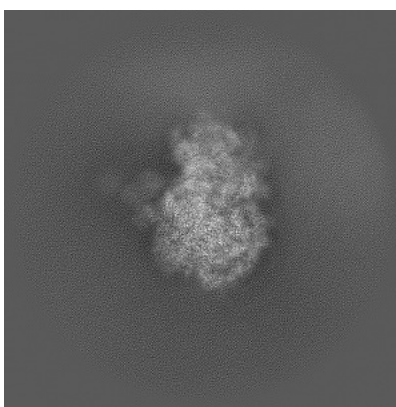


Z

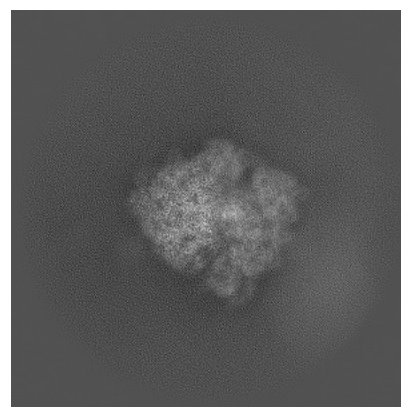
6.1.2 Raw map



X



Y

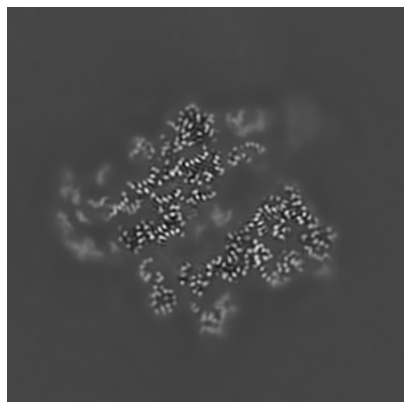


Z

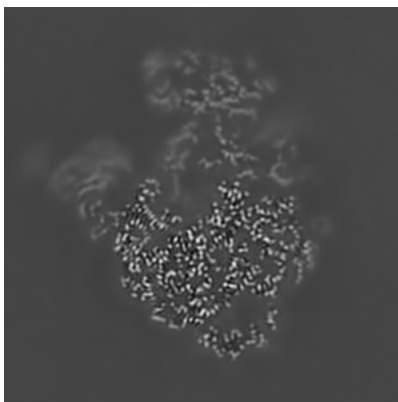
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

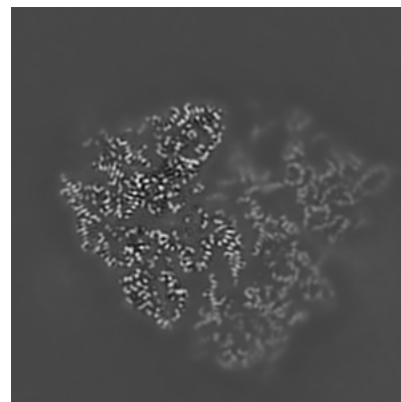
6.2.1 Primary map



X Index: 190

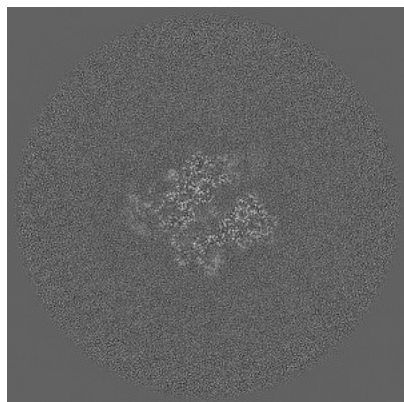


Y Index: 190

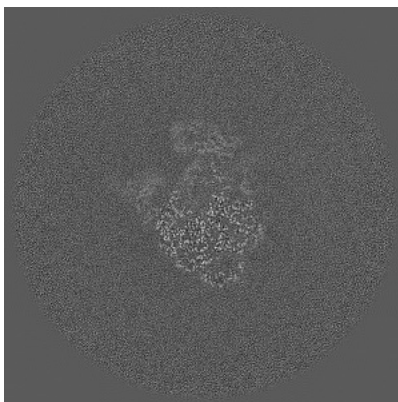


Z Index: 190

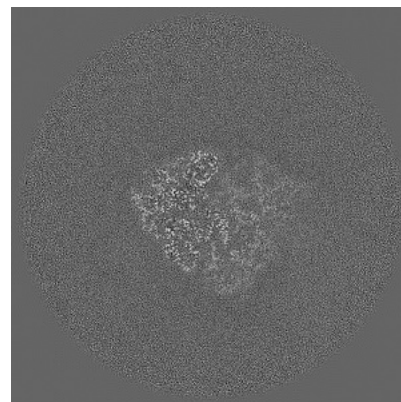
6.2.2 Raw map



X Index: 176



Y Index: 176

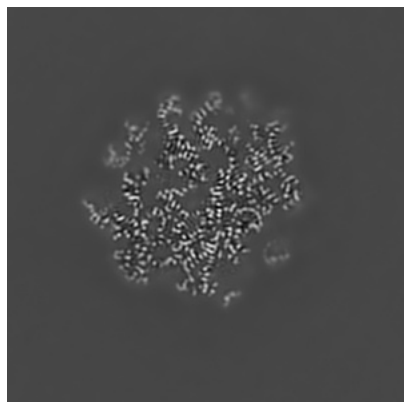


Z Index: 176

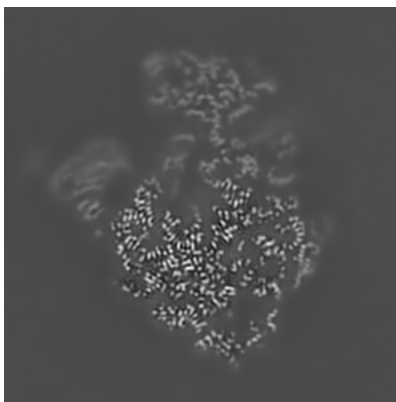
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

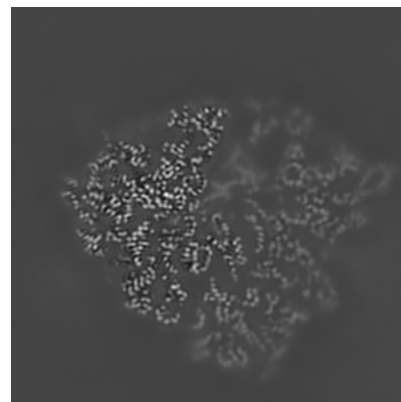
6.3.1 Primary map



X Index: 146

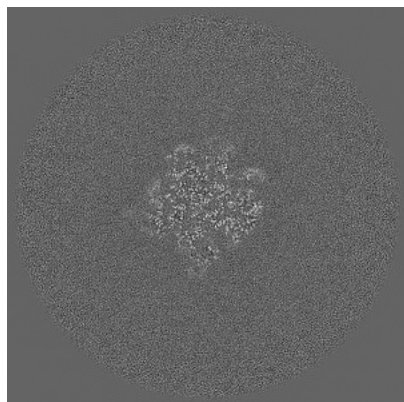


Y Index: 194

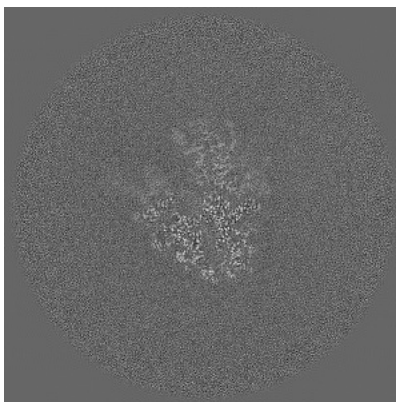


Z Index: 186

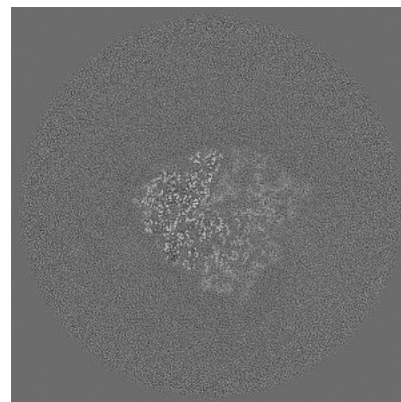
6.3.2 Raw map



X Index: 165



Y Index: 169

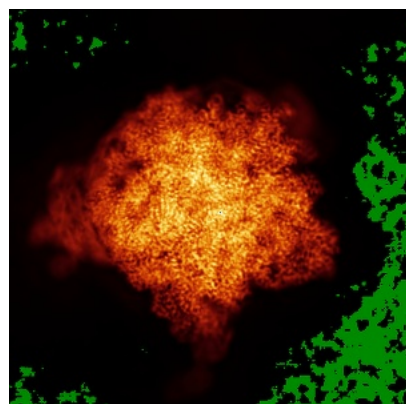


Z Index: 173

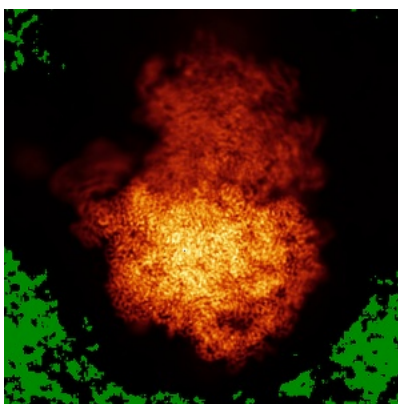
The images above show the largest variance slices of the map in three orthogonal directions.

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

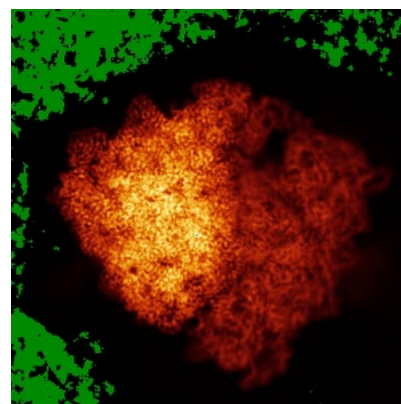
6.4.1 Primary map



X

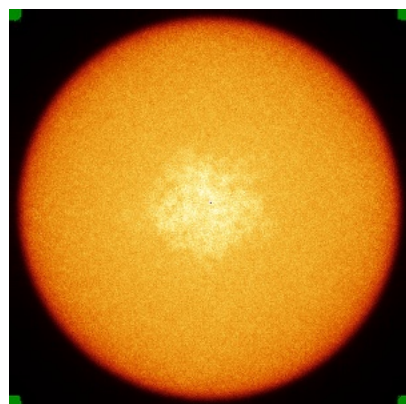


Y

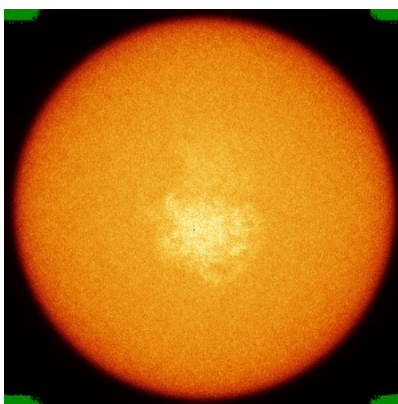


Z

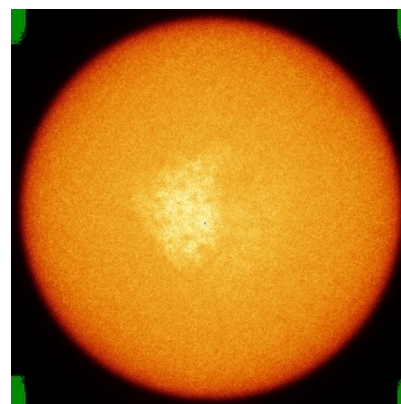
6.4.2 Raw map



X



Y



Z

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

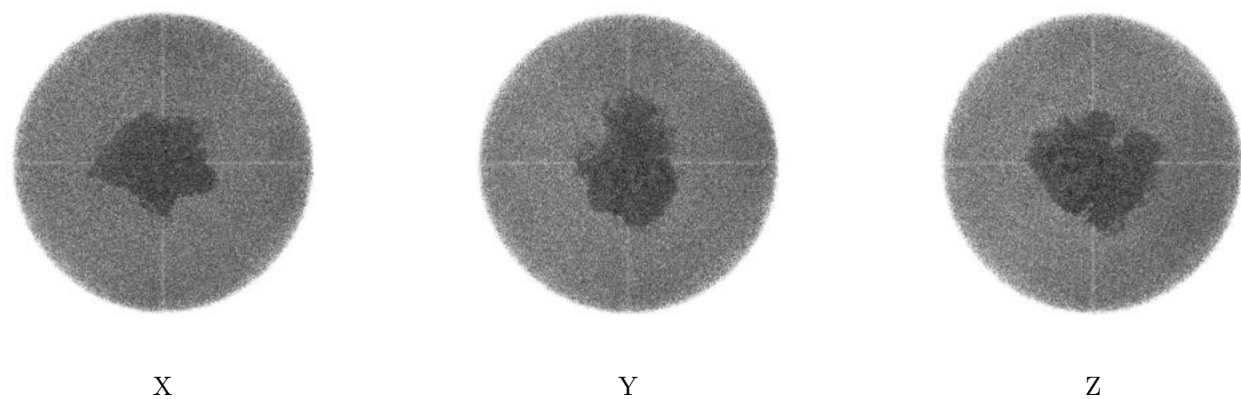
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0023. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

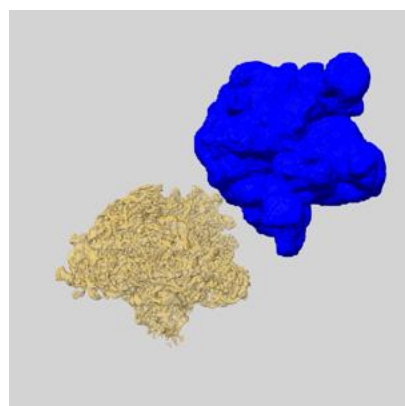
6.6 Mask visualisation [i](#)

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

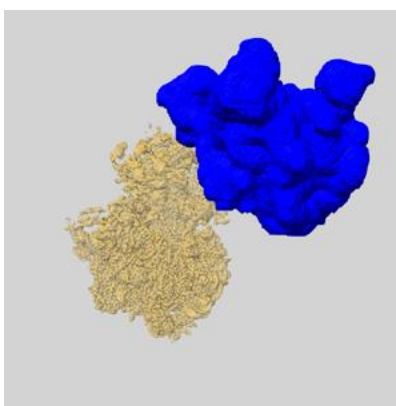
A mask typically either:

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

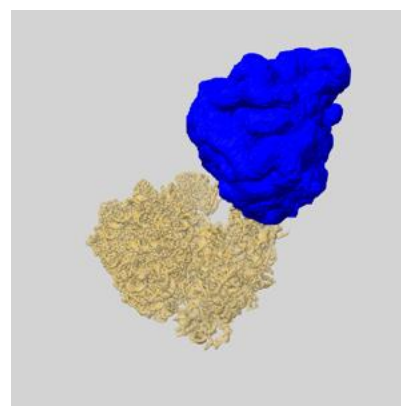
6.6.1 emd_11999_msk_1.map [i](#)



X



Y

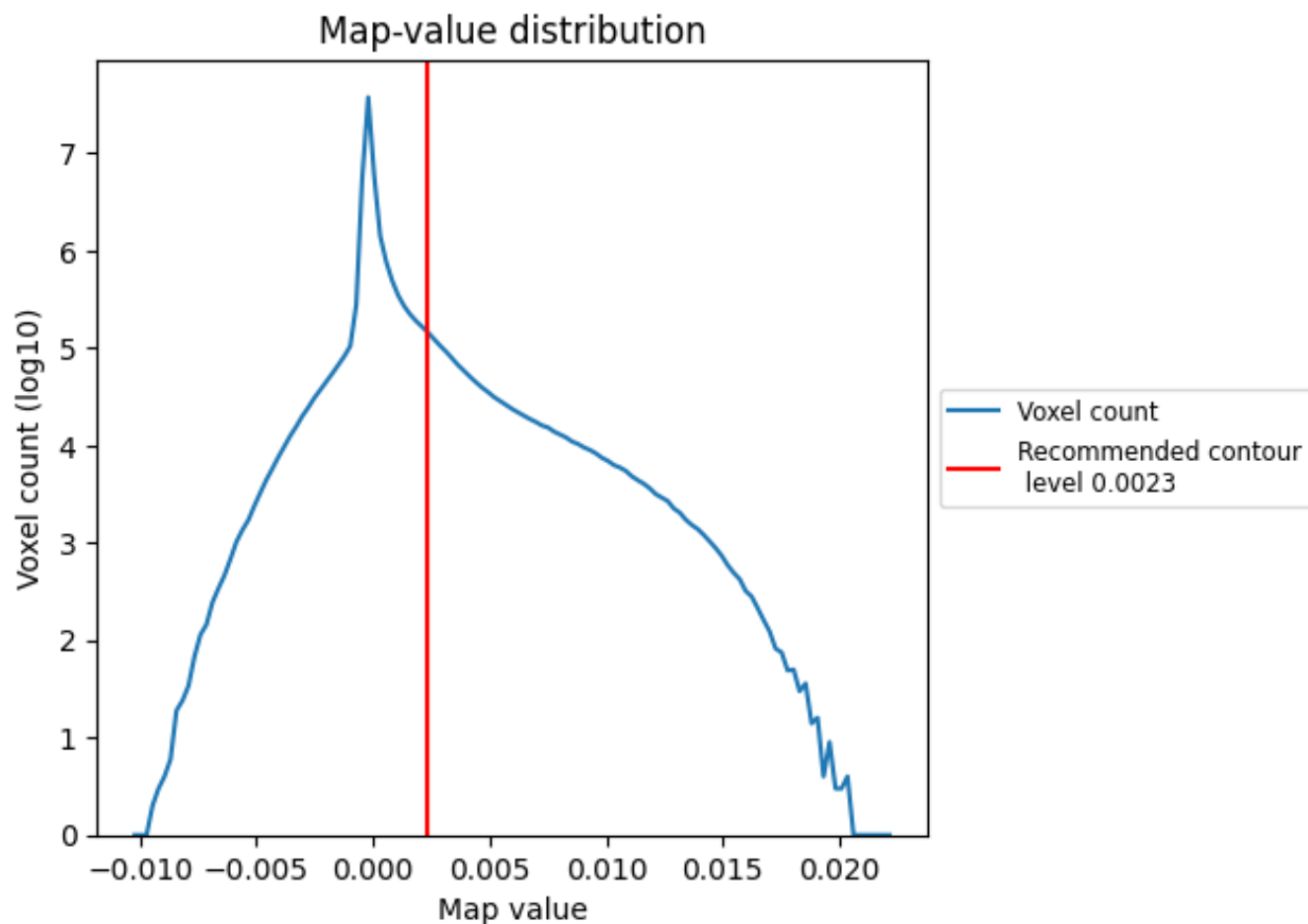


Z

7 Map analysis [i](#)

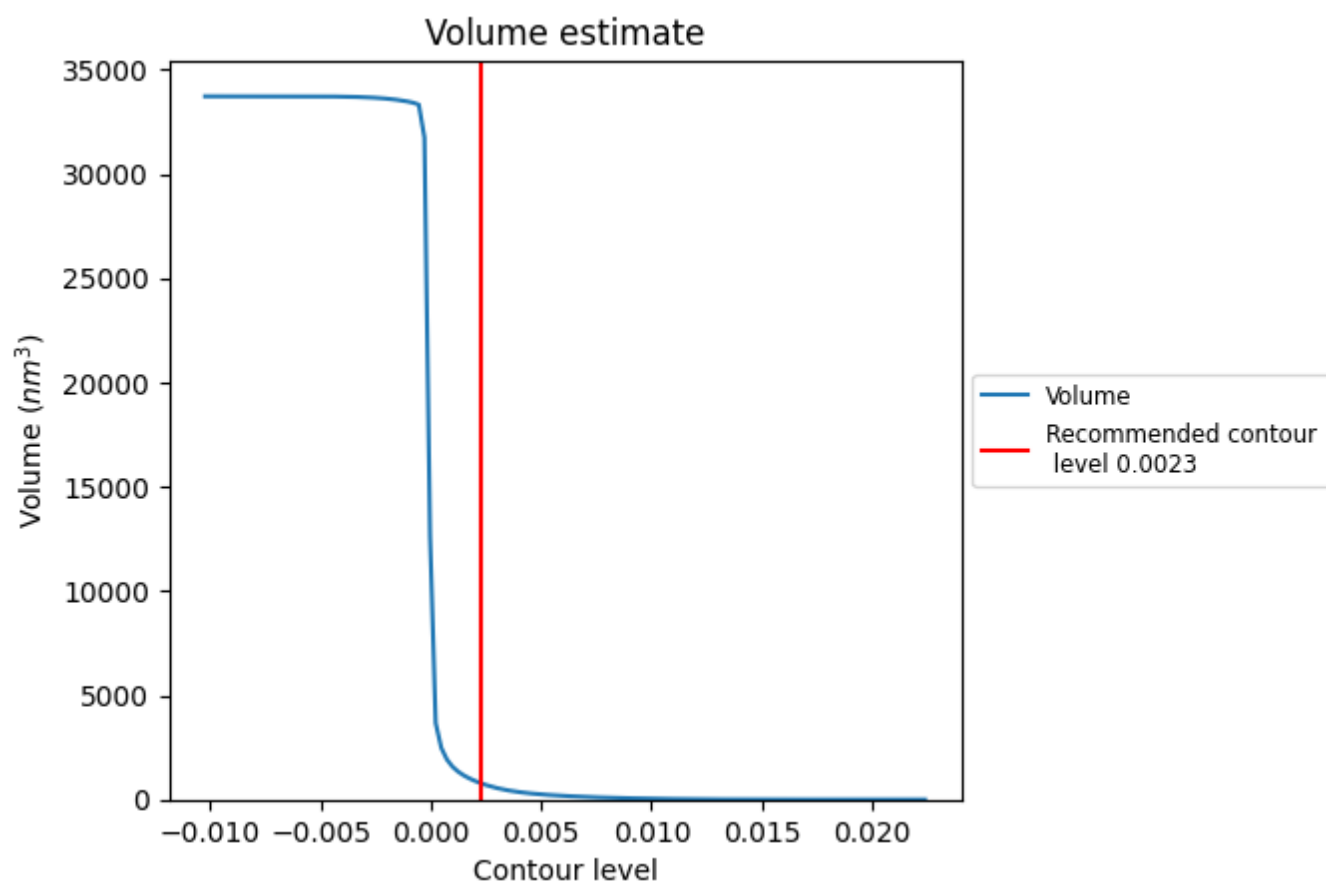
This section contains the results of statistical analysis of the map.

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.

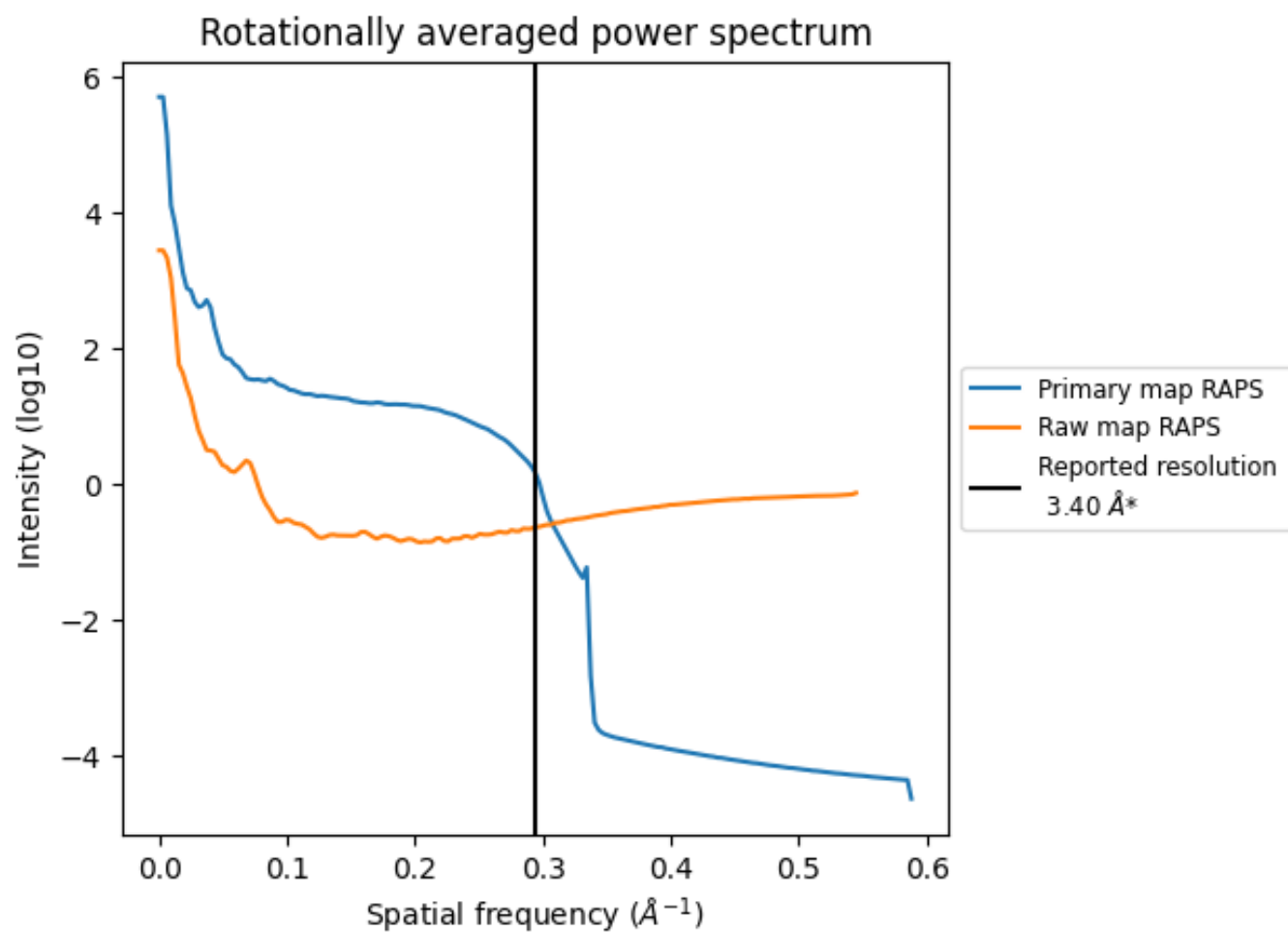
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 773 nm³; this corresponds to an approximate mass of 698 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 ⓘ

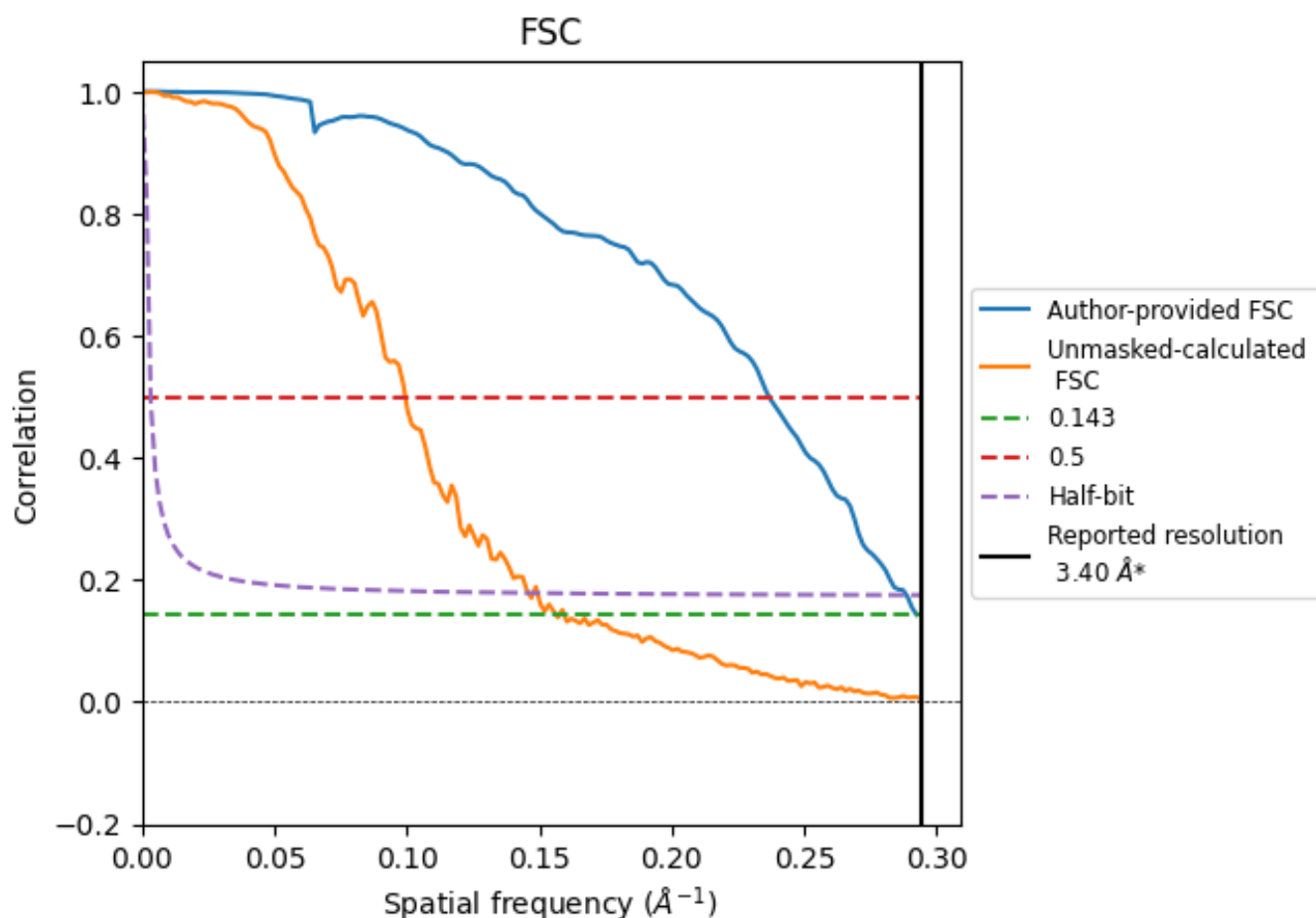


*Reported resolution corresponds to spatial frequency of 0.294 $\text{\AA}^{-1}$

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 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

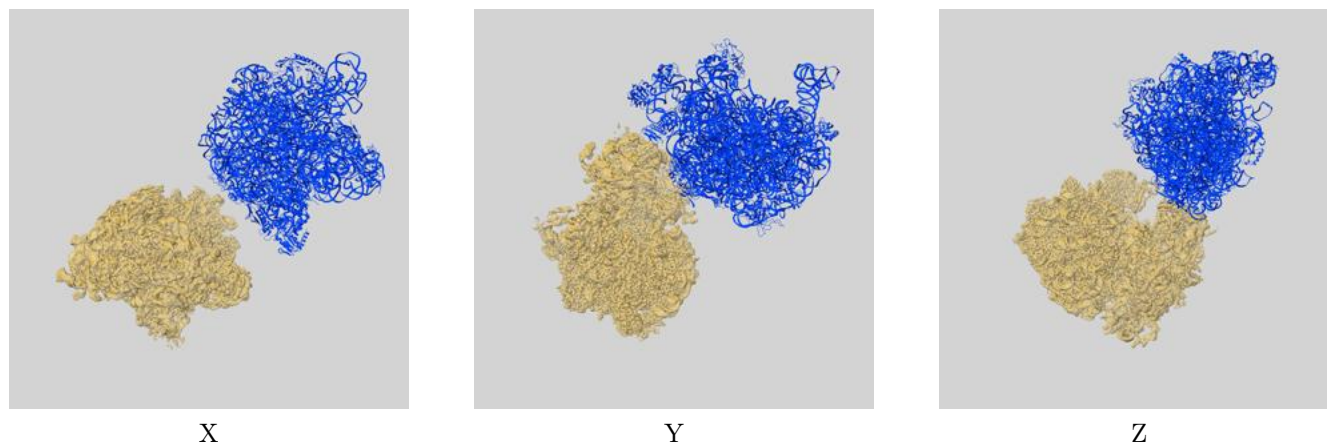
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.42	4.22	3.47
Unmasked-calculated*	6.40	10.06	6.85

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.40 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

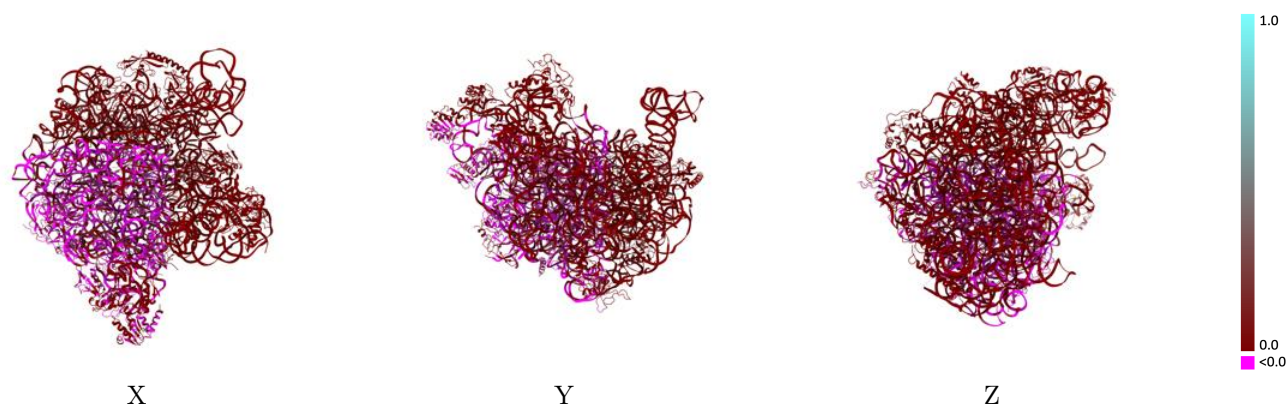
This section contains information regarding the fit between EMDB map EMD-11999 and PDB model 7OOD. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

9.1 Map-model overlay [i](#)



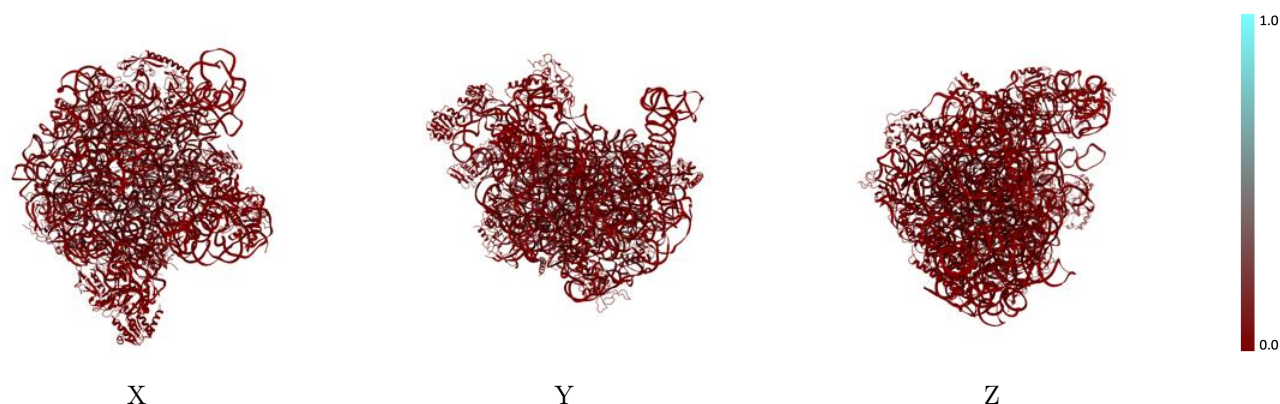
The images above show the 3D surface view of the map at the recommended contour level 0.0023 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



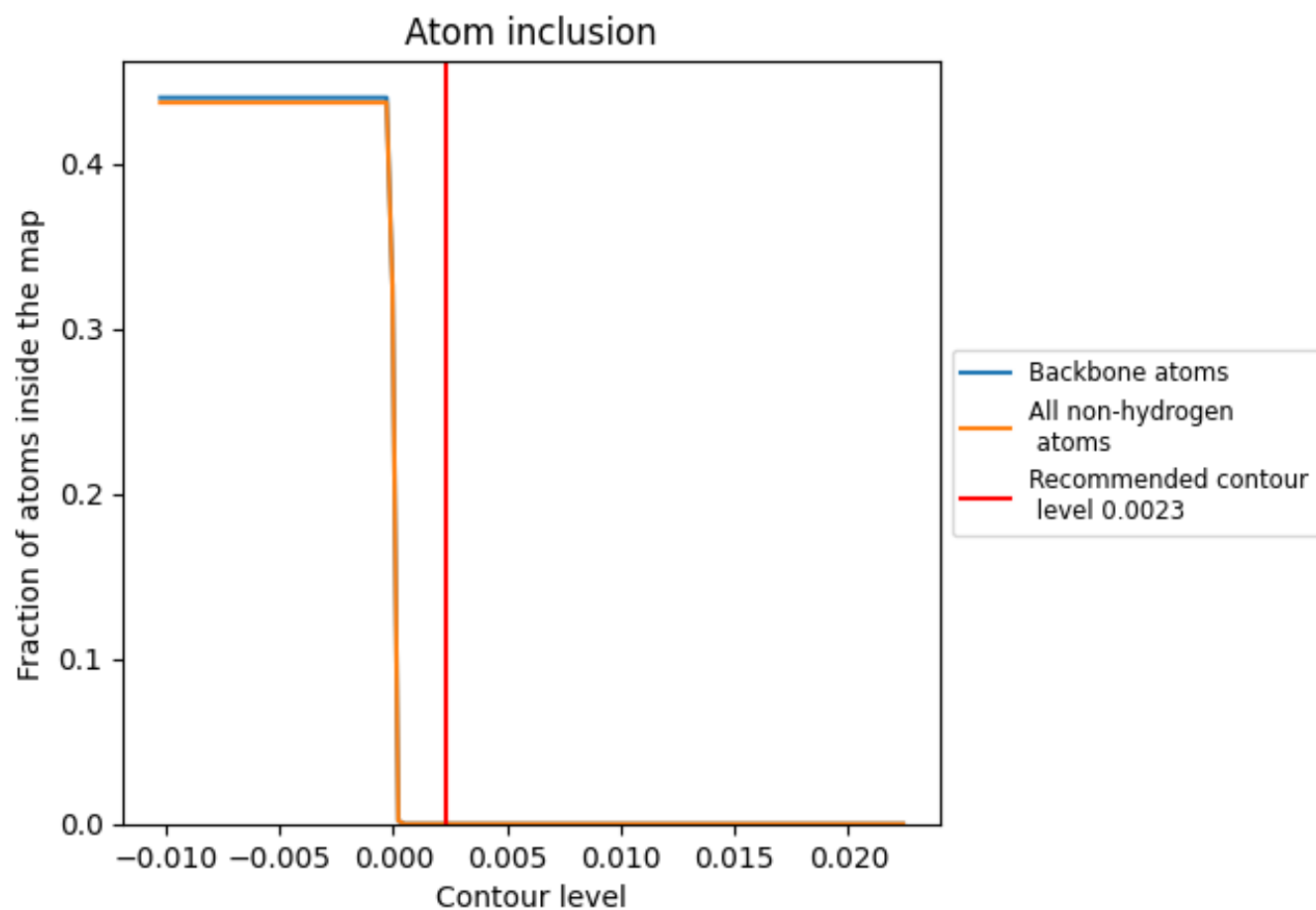
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0023).

9.4 Atom inclusion [i](#)



At the recommended contour level, 0% of all backbone atoms, 0% 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 (0.0023) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.0000	-0.0010
0	0.0000	0.0030
1	0.0000	0.0000
2	0.0000	-0.0030
3	0.0000	-0.0010
4	0.0000	0.0000
a	0.0000	-0.0050
b	0.0000	0.0030
c	0.0000	0.0080
d	0.0000	0.0000
e	0.0000	-0.0050
f	0.0000	0.0000
g	0.0000	0.0030
h	0.0000	0.0000
i	0.0000	0.0030
j	0.0000	-0.0190
k	0.0000	0.0030
l	0.0000	-0.0160
m	0.0000	0.0050
n	0.0000	0.0000
o	0.0000	-0.0060
p	0.0000	-0.0090
q	0.0000	0.0060
r	0.0000	0.0070
s	0.0000	-0.0010
t	0.0000	0.0020
u	0.0000	-0.0040
v	0.0000	0.0000
w	0.0000	0.0000
x	0.0000	0.0000
y	0.0000	-0.0320
z	0.0000	0.0000

