



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 09:00 PM UTC

PDB ID : 1YJN / pdb_00001yjn
Title : Crystal Structure Of Clindamycin Bound To The G2099A Mutant 50S Ribosomal Subunit Of Haloarcula Marismortui
Authors : Tu, D.; Blaha, G.; Moore, P.B.; Steitz, T.A.
Deposited on : 2005-01-14
Resolution : 3.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

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:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

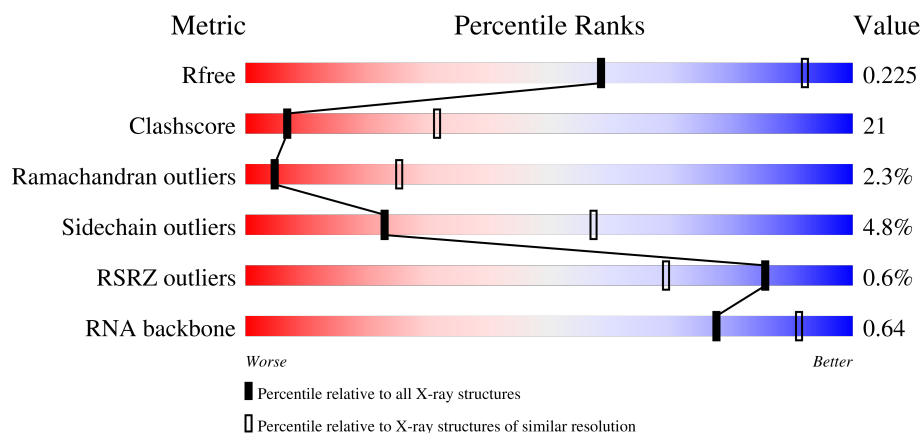
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

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



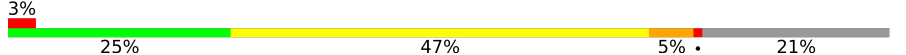
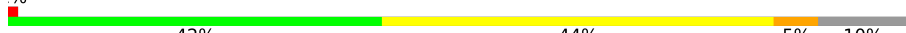
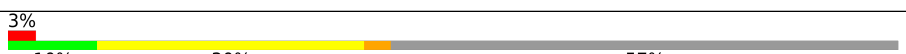
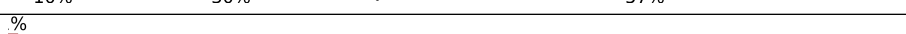
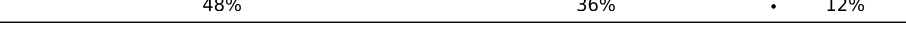
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)
RNA backbone	3983	1109 (3.20-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	2922	
2	9	122	
3	A	240	
4	B	338	

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Mol	Chain	Length	Quality of chain
5	C	246	
6	D	177	
7	E	178	
8	F	120	
9	G	348	
10	H	177	
11	I	162	
12	J	145	
13	K	132	
14	L	165	
15	M	195	
16	N	187	
17	O	116	
18	P	149	
19	Q	96	
20	R	155	
21	S	85	
22	T	120	
23	U	66	
24	V	71	
25	W	154	
26	X	92	
27	Y	241	
28	Z	83	
29	1	57	

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Mol	Chain	Length	Quality of chain
30	2	50	
31	3	92	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
36	CL	J	8802	-	-	X	-

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 99060 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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					ZeroOcc	AltConf	Trace
1	0	2754	Total	C	N	O	P	0	0	0
			59020	26349	10873	19053	2745			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	628	1MA	A	modified residue	GB 55229667
0	2099	A	G	engineered mutation	GB 55229667
0	2587	OMU	U	modified residue	GB 55229667
0	2588	OMG	G	modified residue	GB 55229667
0	2619	UR3	U	modified residue	GB 55229667
0	2621	PSU	U	modified residue	GB 55229667

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	9	122	Total	C	N	O	P	0	0	0
			2599	1160	471	847	121			

- Molecule 3 is a protein called 50S ribosomal protein L2P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	237	Total	C	N	O	S	0	0	0
			1753	1072	352	324	5			

- Molecule 4 is a protein called 50S ribosomal protein L3P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	B	337	Total	C	N	O	S	0	0	0
			2625	1616	493	511	5			

- Molecule 5 is a protein called 50S ribosomal protein L4E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	C	246	Total	C	N	O	S	0	0	0
			1859	1131	344	383	1			

- Molecule 6 is a protein called 50S ribosomal protein L5P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	D	140	Total	C	N	O	S	0	0	0
			1094	685	195	210	4			

- Molecule 7 is a protein called 50S ribosomal protein L6P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	E	172	Total	C	N	O	S	0	0	0
			1357	840	224	289	4			

- Molecule 8 is a protein called 50S ribosomal protein L7AE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	F	119	Total	C	N	O	S	0	0	0
			890	551	141	197	1			

- Molecule 9 is a protein called ACIDIC RIBOSOMAL PROTEIN P0 HOMOLOG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	G	29	Total	C	N	O	S	0	0	0
			240	149	39	51	1			

- Molecule 10 is a protein called 50S RIBOSOMAL PROTEIN L10E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	H	160	Total	C	N	O	S	0	0	0
			1282	798	240	238	6			

- Molecule 11 is a protein called 50S RIBOSOMAL PROTEIN L11P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	I	70	Total	C	N	O	S	0	0	0
			519	323	81	114	1			

- Molecule 12 is a protein called 50S ribosomal protein L13P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	J	142	Total	C	N	O	S	0	0	0
			1120	696	199	222	3			

- Molecule 13 is a protein called 50S ribosomal protein L14P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	K	132	Total	C	N	O	S	0	0	0
			992	609	187	192	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	44	LEU	HIS	conflict	UNP P22450

- Molecule 14 is a protein called 50S ribosomal protein L15P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	L	145	Total	C	N	O	S	0	0	0
			1118	670	222	226				

- Molecule 15 is a protein called 50S Ribosomal Protein L15E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	M	194	Total	C	N	O	S	0	0	0
			1558	942	332	283	1			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	13	GLU	LYS	conflict	GB 55231501

- Molecule 16 is a protein called 50S ribosomal protein L18P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	N	186	Total	C	N	O	S	0	0	0
			1445	895	262	286	2			

- Molecule 17 is a protein called 50S ribosomal protein L18e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	O	115	Total	C	N	O	S	0	0	0
			865	529	161	175				

- Molecule 18 is a protein called 50S ribosomal protein L19E.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	P	143	Total	C	N	O	0	0	0
			1136	683	229	224			

- Molecule 19 is a protein called 50S ribosomal protein L21e.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
19	Q	95	Total	C	N	O	0	0	0
			735	450	141	144			

- Molecule 20 is a protein called 50S ribosomal protein L22P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	R	150	Total	C	N	O	S	0	0	0
			1149	713	209	223	4			

- Molecule 21 is a protein called 50S ribosomal protein L23P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	S	81	Total	C	N	O	S	0	0	0
			641	389	111	138	3			

- Molecule 22 is a protein called 50S ribosomal protein L24P.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
22	T	119	Total	C	N	O	0	0	0
			950	568	180	202			

- Molecule 23 is a protein called 50S ribosomal protein L24E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	U	53	Total	C	N	O	S	0	0	0
			410	244	75	86	5			

- Molecule 24 is a protein called 50S ribosomal protein L29P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	V	65	Total	C	N	O	S	0	0	0
			499	304	94	100	1			

- Molecule 25 is a protein called 50S ribosomal protein L30P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	W	154	Total	C	N	O	S	0	0	0
			1196	737	209	244	6			

- Molecule 26 is a protein called 50S ribosomal protein L31e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	X	82	Total	C	N	O	S	0	0	0
			654	402	129	122	1			

- Molecule 27 is a protein called 50S ribosomal protein L32E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	Y	142	Total	C	N	O	S	0	0	0
			1130	686	228	216				

- Molecule 28 is a protein called 50S ribosomal protein L37Ae.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	Z	73	Total	C	N	O	S	0	0	0
			578	346	116	111	5			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Z	10	ARG	SER	conflict	GB 55231162

- Molecule 29 is a protein called 50S ribosomal protein L37e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	1	56	Total	C	N	O	S	0	0	0
			431	258	86	83	4			

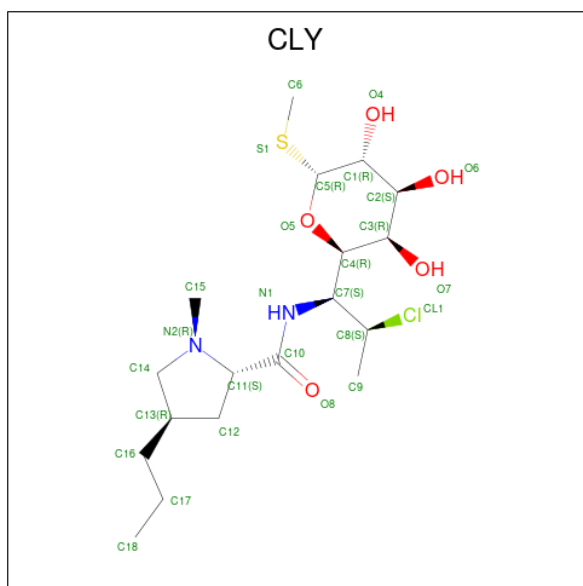
- Molecule 30 is a protein called 50S ribosomal protein L39e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	2	46	Total	C	N	O	S	0	0	0
			396	239	89	67	1			

- Molecule 31 is a protein called 50S ribosomal protein L44E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	3	92	Total	C	N	O	S	0	0	0
			755	458	153	137	7			

- Molecule 32 is CLINDAMYCIN (CCD ID: CLY) (formula: $C_{18}H_{33}ClN_2O_5S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
32	0	1	Total	C	Cl	N	O	S	
			27	18	1	2	5	1	

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
33	0	110	Total	Mg	0	0
			110	110		
33	9	1	Total	Mg	0	0
			1	1		
33	B	1	Total	Mg	0	0
			1	1		
33	K	1	Total	Mg	0	0
			1	1		
33	T	1	Total	Mg	0	0
			1	1		
33	Y	1	Total	Mg	0	0
			1	1		
33	3	1	Total	Mg	0	0
			1	1		

- Molecule 34 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
34	0	2	Total K 2 2	0	0

- Molecule 35 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
35	0	72	Total Na 72 72	0	0
35	9	2	Total Na 2 2	0	0
35	A	1	Total Na 1 1	0	0
35	B	1	Total Na 1 1	0	0
35	C	1	Total Na 1 1	0	0
35	H	1	Total Na 1 1	0	0
35	J	1	Total Na 1 1	0	0
35	L	1	Total Na 1 1	0	0
35	M	1	Total Na 1 1	0	0
35	Q	1	Total Na 1 1	0	0
35	R	2	Total Na 2 2	0	0
35	S	1	Total Na 1 1	0	0
35	T	1	Total Na 1 1	0	0

- Molecule 36 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
36	0	10	Total Cl 10 10	0	0
36	A	1	Total Cl 1 1	0	0
36	B	1	Total Cl 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
36	J	3	Total 3	Cl 3	0	0
36	L	1	Total 1	Cl 1	0	0
36	M	1	Total 1	Cl 1	0	0
36	N	1	Total 1	Cl 1	0	0
36	O	1	Total 1	Cl 1	0	0
36	R	1	Total 1	Cl 1	0	0
36	Y	1	Total 1	Cl 1	0	0
36	3	1	Total 1	Cl 1	0	0

- Molecule 37 is CADMIUM ION (CCD ID: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
37	O	1	Total 1	Cd 1	0	0
37	U	1	Total 1	Cd 1	0	0
37	Z	1	Total 1	Cd 1	0	0
37	1	1	Total 1	Cd 1	0	0
37	3	1	Total 1	Cd 1	0	0

- Molecule 38 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	0	5892	Total 5892	O 5892	0	0
38	9	139	Total 139	O 139	0	0
38	A	120	Total 120	O 120	0	0
38	B	146	Total 146	O 146	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	C	169	Total 169	O 169	0	0
38	D	49	Total 49	O 49	0	0
38	E	41	Total 41	O 41	0	0
38	F	25	Total 25	O 25	0	0
38	G	19	Total 19	O 19	0	0
38	H	68	Total 68	O 68	0	0
38	I	10	Total 10	O 10	0	0
38	J	56	Total 56	O 56	0	0
38	K	60	Total 60	O 60	0	0
38	L	82	Total 82	O 82	0	0
38	M	128	Total 128	O 128	0	0
38	N	64	Total 64	O 64	0	0
38	O	44	Total 44	O 44	0	0
38	P	64	Total 64	O 64	0	0
38	Q	49	Total 49	O 49	0	0
38	R	79	Total 79	O 79	0	0
38	S	31	Total 31	O 31	0	0
38	T	36	Total 36	O 36	0	0
38	U	27	Total 27	O 27	0	0
38	V	14	Total 14	O 14	0	0
38	W	68	Total 68	O 68	0	0

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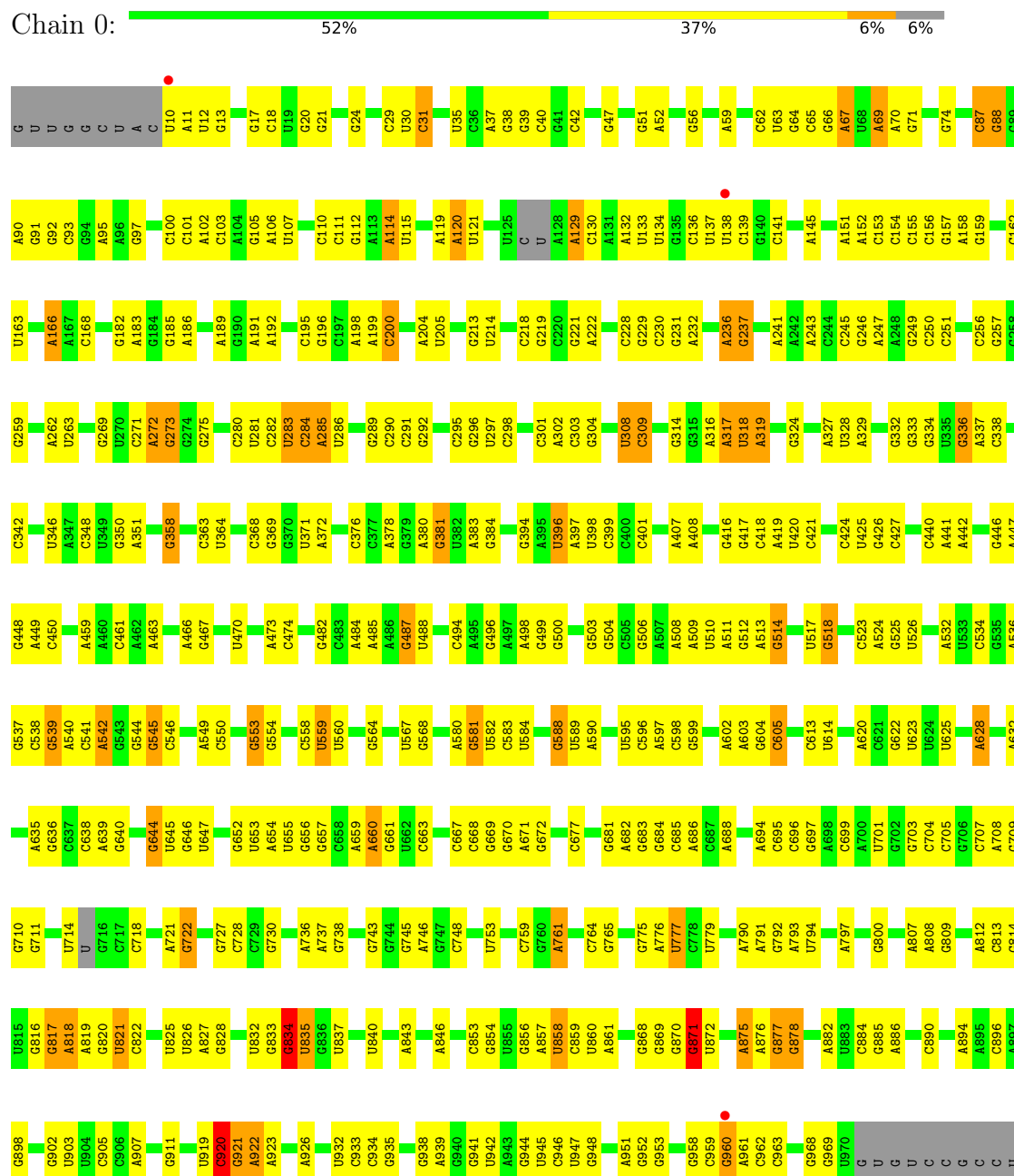
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	X	24	Total 24	O 24	0	0
38	Y	101	Total 101	O 101	0	0
38	Z	31	Total 31	O 31	0	0
38	1	57	Total 57	O 57	0	0
38	2	39	Total 39	O 39	0	0
38	3	74	Total 74	O 74	0	0

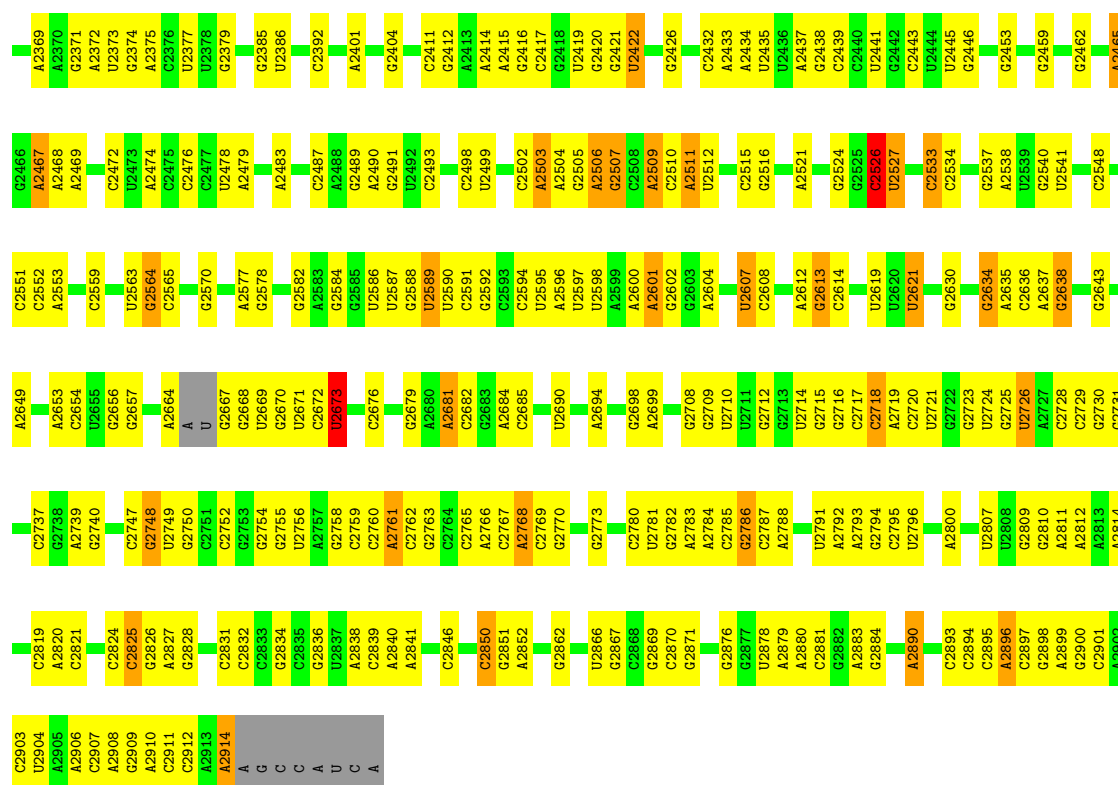
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

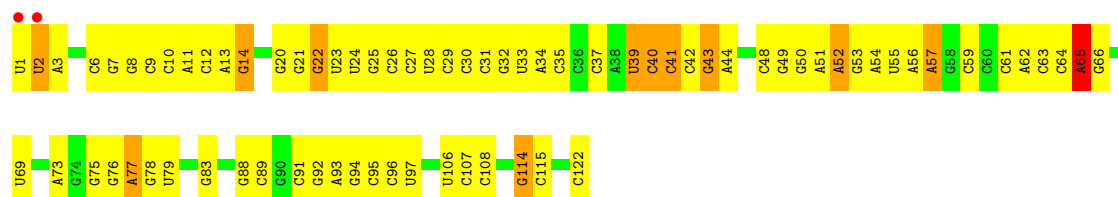
• Molecule 1: 23S Ribosomal RNA



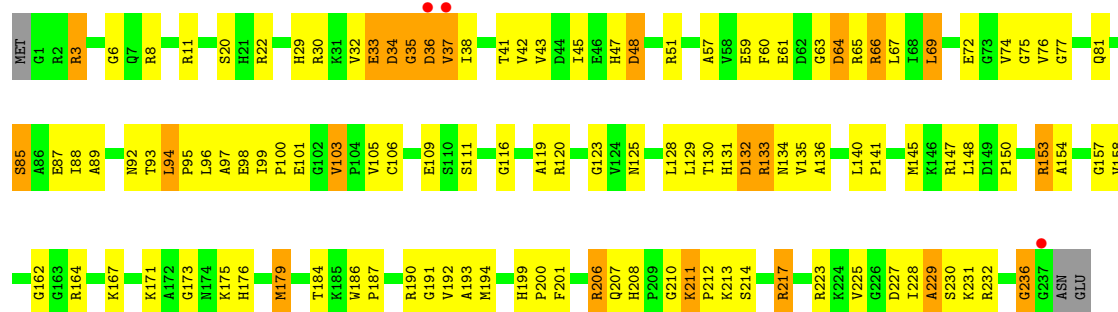
U2276	C	G	A2039	G1951	G1851	A1767	A1667	G1568	C1477	U1383	U1266	G1175	G1071	C
U2277	A	U	A1852	U	A1852	C1768	U1668	U1569	U1478	U1384	C1267	C1176	G1072	C
U2278	G	C	C1853	A	C1853	G1769	G1669	U1572	A1480	C1388	G1268	U1180	A1078	G
C2281	C	C	C1856	C	C1856	U1771	A1670	A1580	C1483	U1389	G1269	A1181	A1079	A
U2282	C	C	C1861	U	C1861	G1772	C1679	U1587	G1484	A1393	C1273	C1182	C1080	A
C2281	A	A	C1862	U	C1862	G1773	G1680	U1588	A1485	C1394	C1278	C1183	A1081	G
C2281	C	C	C1863	U	C1863	G1774	G1681	U1589	U1488	A1406	U1279	U1185	A1086	G
C2281	G	G	C1868	A	C1868	A1778	G1682	U1590	G1489	C1398	C1289	C1186	A1087	A
A2300	C	C	G1868	C	G1868	A1779	C1685	U1591	U1488	A1399	C1289	U1187	A1088	U
A2301	C	C	C1872	C	C1872	A1783	C1686	U1592	A1494	C1400	C1289	A1188	A1097	C
A2302	C	C	G1873	U	G1873	U1784	C1687	C1593	C1495	A1406	U1293	A1189	A1098	G
A2303	A	A	G1874	U	G1874	U1784	C1687	C1594	C1496	A1407	U1293	A1191	A1099	C
C2309	U	C	U1874	U	U1874	C1787	C1692	U1595	G1497	A1407	A1296	A1192	A1098	C
C2313	C	U	G1877	U	G1877	U1788	C1692	U1596	G1497	A1407	A1296	A1192	A1098	C
C2316	C	U	G1878	U	G1878	U1788	C1692	U1596	G1497	A1407	A1296	A1192	A1098	C
C2317	C	U	G1879	U	G1879	C1790	U1702	U1598	U1499	G1409	U1298	A1193	A1099	C
C2320	C	U	U1791	U	U1791	U1791	U1702	U1599	U1500	G1409	U1298	A1193	A1099	C
C2321	C	U	C1882	U	C1882	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2324	C	A	U1883	U	U1883	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2325	C	U	G1884	U	G1884	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2326	C	U	A1885	U	A1885	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2329	C	U	A1886	U	A1886	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2330	C	U	U1890	U	U1890	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2336	C	U	G1891	U	G1891	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2337	C	U	A1895	U	A1895	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2338	C	U	G1896	U	G1896	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2344	C	U	U1899	U	U1899	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2345	C	U	G1899	U	G1899	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2346	C	U	A1899	U	A1899	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2350	C	U	G1909	U	G1909	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2351	C	U	A1909	U	A1909	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2352	C	U	G1919	U	G1919	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2353	C	U	A1921	U	A1921	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2354	C	U	G1923	U	G1923	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2355	C	U	A1926	U	A1926	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2356	C	U	G1927	U	G1927	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2357	C	U	A1928	U	A1928	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2358	C	U	G1929	U	G1929	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2360	C	U	A1930	U	A1930	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2361	C	U	G1931	U	G1931	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2362	C	U	A1932	U	A1932	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2363	C	U	G1933	U	G1933	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2364	C	U	A1934	U	A1934	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2365	C	U	G1935	U	G1935	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2366	C	U	A1936	U	A1936	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2367	C	U	G1937	U	G1937	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2368	C	U	A1938	U	A1938	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2369	C	U	G1939	U	G1939	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2370	C	U	A1940	U	A1940	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2371	C	U	G1941	U	G1941	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2372	C	U	A1942	U	A1942	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2373	C	U	G1943	U	G1943	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2374	C	U	A1944	U	A1944	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2375	C	U	G1945	U	G1945	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2376	C	U	A1946	U	A1946	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2377	C	U	G1947	U	G1947	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2378	C	U	A1948	U	A1948	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2379	C	U	G1949	U	G1949	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2380	C	U	A1950	U	A1950	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2381	C	U	G1951	U	G1951	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2382	C	U	A1952	U	A1952	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2383	C	U	G1953	U	G1953	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2384	C	U	A1954	U	A1954	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2385	C	U	G1955	U	G1955	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2386	C	U	A1956	U	A1956	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2387	C	U	G1957	U	G1957	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2388	C	U	A1958	U	A1958	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2389	C	U	G1959	U	G1959	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2390	C	U	A1960	U	A1960	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2391	C	U	G1961	U	G1961	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2392	C	U	A1962	U	A1962	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2393	C	U	G1963	U	G1963	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2394	C	U	A1964	U	A1964	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2395	C	U	G1965	U	G1965	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2396	C	U	A1966	U	A1966	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2397	C	U	G1967	U	G1967	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2398	C	U	A1968	U	A1968	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2399	C	U	G1969	U	G1969	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2400	C	U	A1970	U	A1970	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2401	C	U	G1971	U	G1971	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2402	C	U	A1972	U	A1972	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2403	C	U	G1973	U	G1973	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2404	C	U	A1974	U	A1974	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2405	C	U	G1975	U	G1975	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2406	C	U	A1976	U	A1976	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2407	C	U	G1977	U	G1977	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2408	C	U	A1978	U	A1978	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2409	C	U	G1979	U	G1979	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2410	C	U	A1980	U	A1980	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2411	C	U	G1981	U	G1981	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2412	C	U	A1982	U	A1982	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2413	C	U	G1983	U	G1983	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2414	C	U	A1984	U	A1984	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2415	C	U	G1985	U	G1985	C1798	A1710	U1600	U1503	A1414	U1304	G1197	U1116	A
C2416	C	U	A1986	U	A1986	C1798	A1							



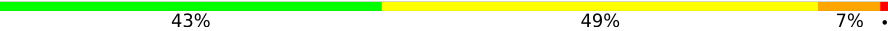
• Molecule 2: 5S Ribosomal RNA

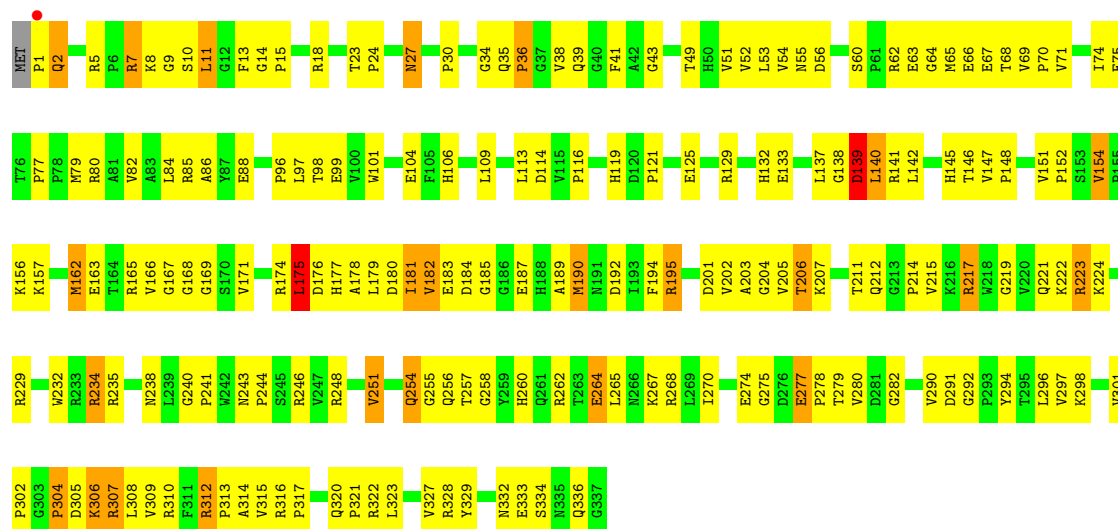


• Molecule 3: 50S ribosomal protein L2P



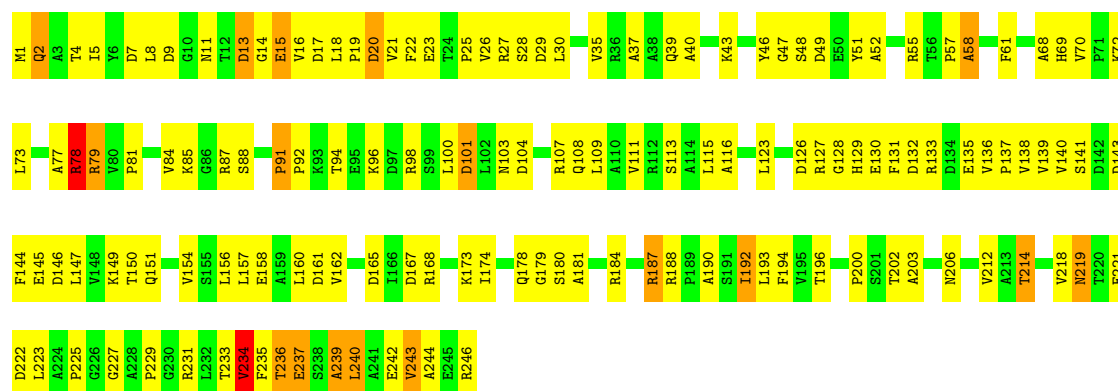
• Molecule 4: 50S ribosomal protein L3P

Chain B:  43% 49% 7%

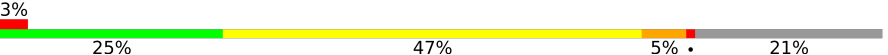


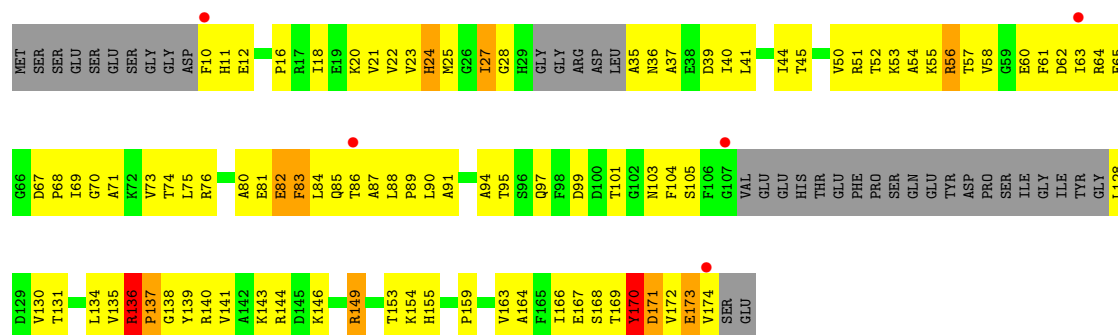
• Molecule 5: 50S ribosomal protein L4E

Chain C:  42% 50% 7%



• Molecule 6: 50S ribosomal protein L5P

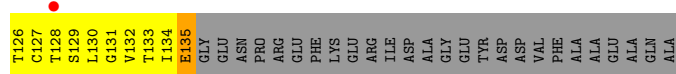
Chain D:  3% 25% 47% 5% 21%



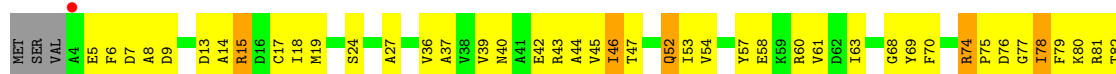
• Molecule 7: 50S ribosomal protein L6P



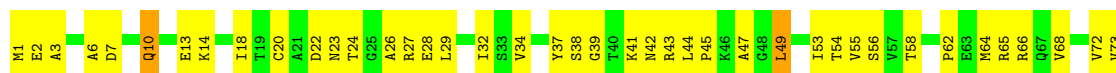
• Molecule 11: 50S RIBOSOMAL PROTEIN L11P



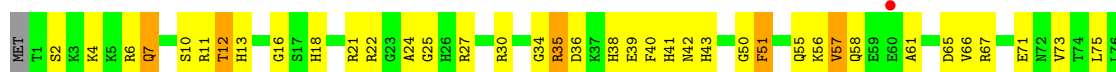
• Molecule 12: 50S ribosomal protein L13P



• Molecule 13: 50S ribosomal protein L14P

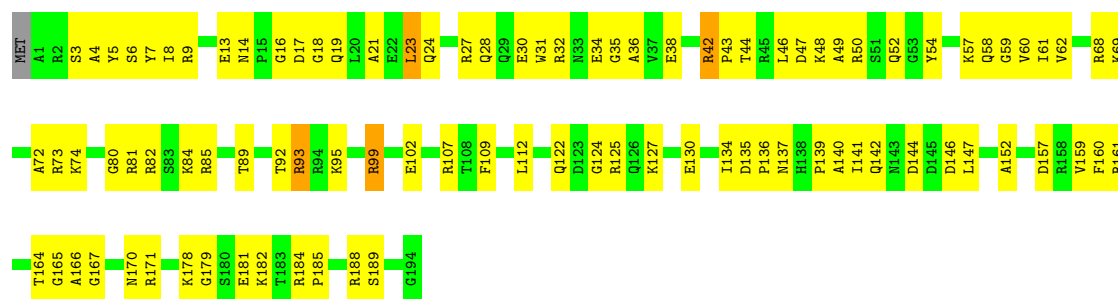


• Molecule 14: 50S ribosomal protein L15P

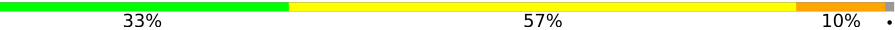


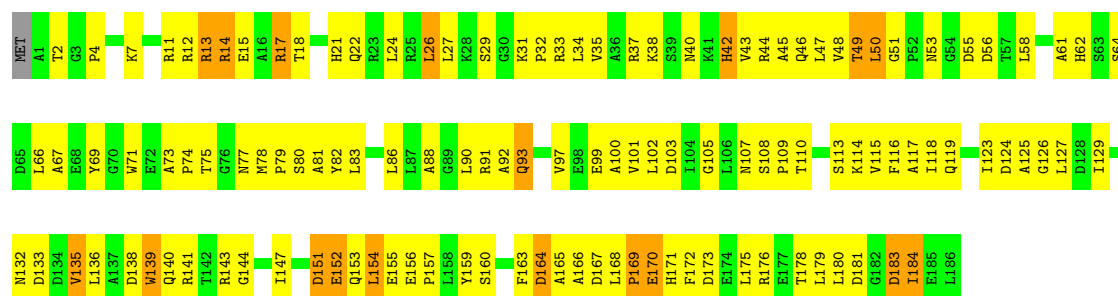
• Molecule 15: 50S Ribosomal Protein L15E

Chain M: 



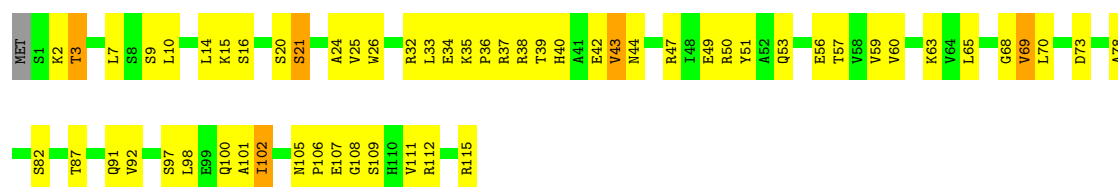
• Molecule 16: 50S ribosomal protein L18P

Chain N: 



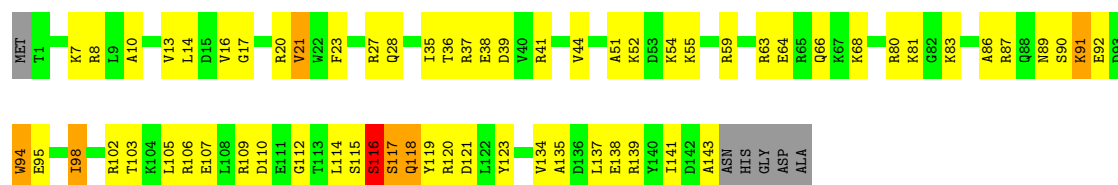
• Molecule 17: 50S ribosomal protein L18e

Chain O: 



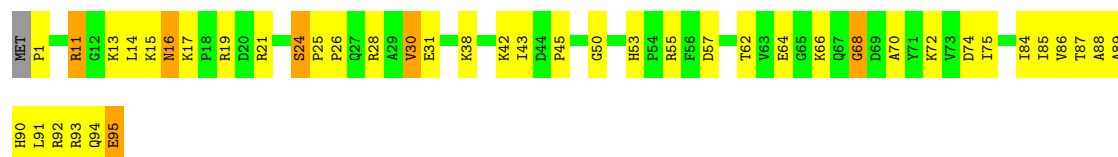
• Molecule 18: 50S ribosomal protein L19E

Chain P: 



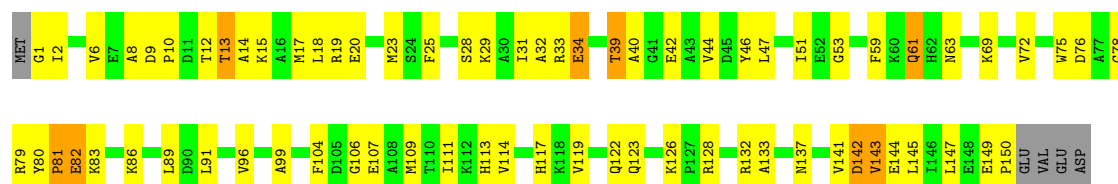
• Molecule 19: 50S ribosomal protein L21e

Chain Q: 



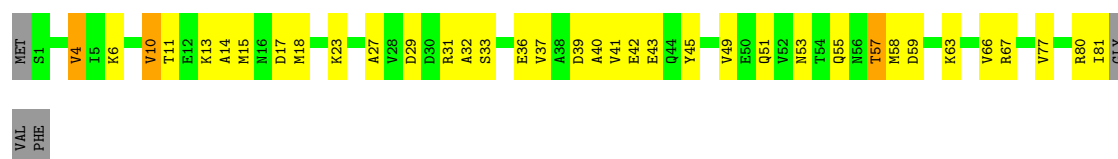
- Molecule 20: 50S ribosomal protein L22P

Chain R: 50% 41% 5% .



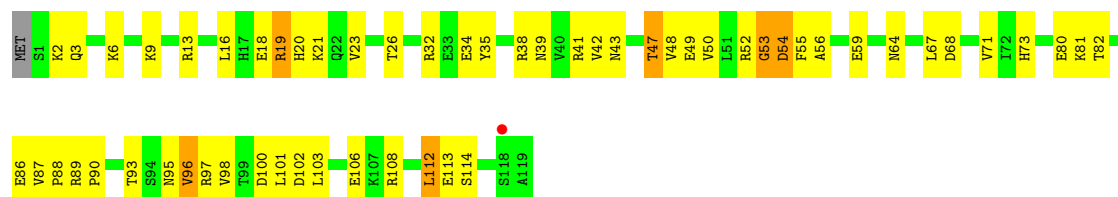
- Molecule 21: 50S ribosomal protein L23P

Chain S: 53% 39% . 5%



- Molecule 22: 50S ribosomal protein L24P

Chain T: % 52% 42% 5% .



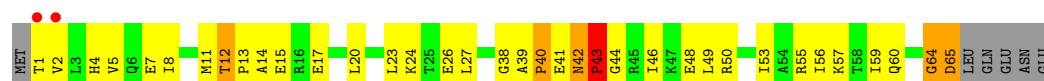
- Molecule 23: 50S ribosomal protein L24E

Chain U: 38% 41% . 20%

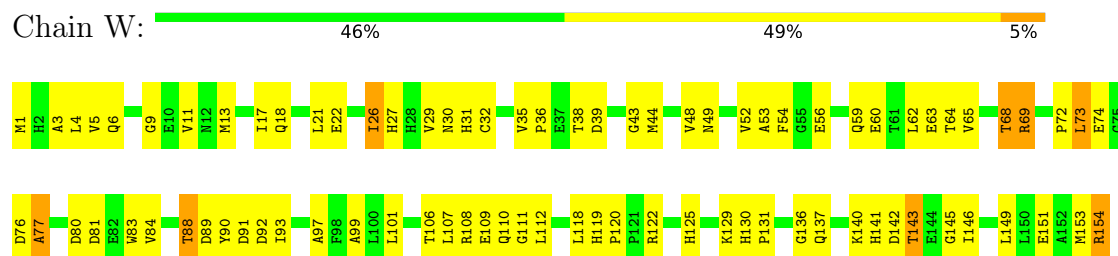


- Molecule 24: 50S ribosomal protein L29P

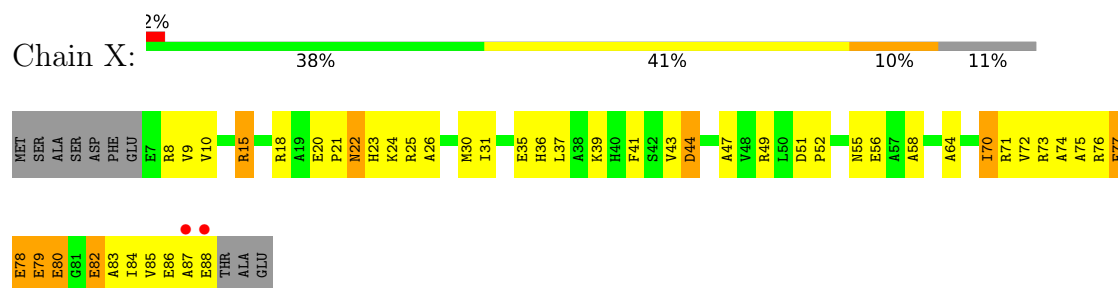
Chain V: 3% 41% 42% 7% . 8%



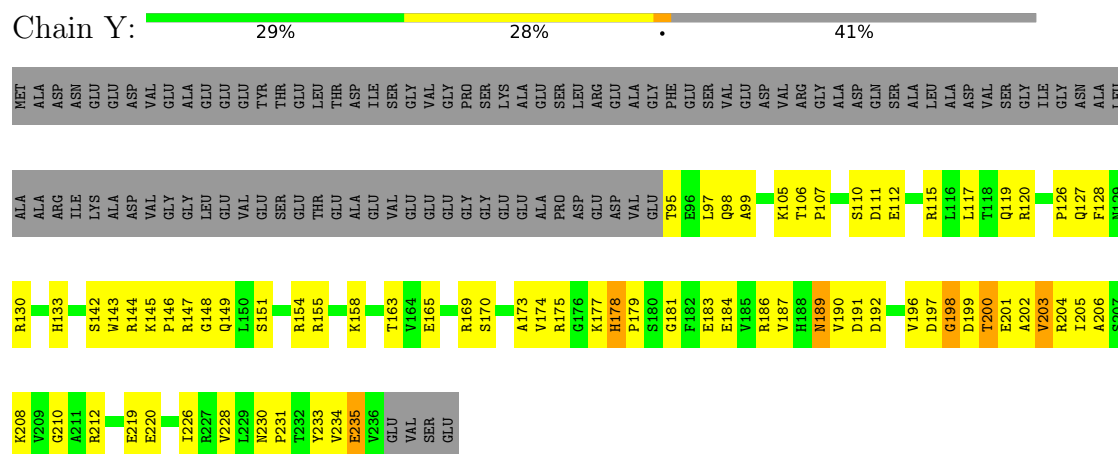
- Molecule 25: 50S ribosomal protein L30P



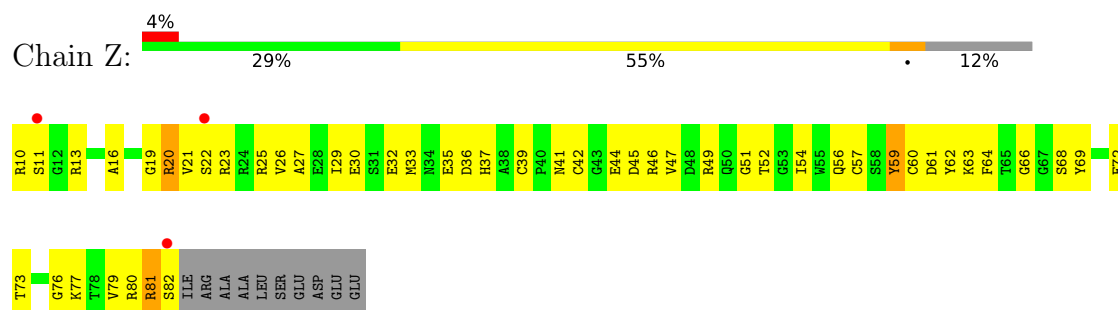
- Molecule 26: 50S ribosomal protein L31e



- Molecule 27: 50S ribosomal protein L32E

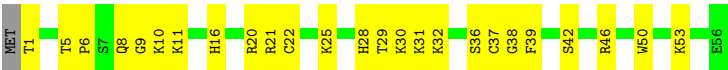


- Molecule 28: 50S ribosomal protein L37Ae



- Molecule 29: 50S ribosomal protein L37e

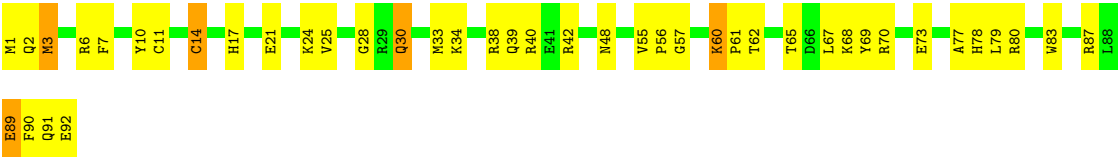




• Molecule 30: 50S ribosomal protein L39e



• Molecule 31: 50S ribosomal protein L44E



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	212.51Å 300.12Å 573.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.97 – 3.00 29.97 – 3.00	Depositor EDS
% Data completeness (in resolution range)	92.0 (29.97-3.00) 92.0 (29.97-3.00)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.00 (at 3.01Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.170 , 0.228 0.169 , 0.225	Depositor DCC
R_{free} test set	3275 reflections (0.98%)	wwPDB-VP
Wilson B-factor (Å ²)	53.3	Xtriage
Anisotropy	0.318	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 78.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	99060	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.79% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CD, 1MA, OMG, MG, K, UR3, NA, CL, PSU, OMU, CLY

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	0	0.38	0/65957	0.61	20/102867 (0.0%)
2	9	0.38	0/2904	0.61	3/4526 (0.1%)
3	A	0.43	0/1786	1.00	7/2408 (0.3%)
4	B	0.45	0/2690	1.01	13/3652 (0.4%)
5	C	0.50	0/1884	1.01	7/2551 (0.3%)
6	D	0.37	0/1111	0.95	4/1498 (0.3%)
7	E	0.41	0/1382	0.96	5/1880 (0.3%)
8	F	0.38	0/901	0.91	2/1224 (0.2%)
9	G	0.41	0/241	0.77	0/324
10	H	0.43	0/1302	0.99	6/1743 (0.3%)
11	I	0.38	0/526	0.91	3/716 (0.4%)
12	J	0.48	0/1136	0.95	6/1530 (0.4%)
13	K	0.45	0/1001	0.99	3/1347 (0.2%)
14	L	0.39	0/1130	0.98	4/1509 (0.3%)
15	M	0.45	0/1582	0.96	6/2117 (0.3%)
16	N	0.40	0/1474	1.07	12/1999 (0.6%)
17	O	0.46	0/874	0.91	3/1181 (0.3%)
18	P	0.44	0/1147	0.90	1/1528 (0.1%)
19	Q	0.46	0/749	1.08	6/1005 (0.6%)
20	R	0.50	0/1172	0.96	6/1578 (0.4%)
21	S	0.41	0/648	0.89	4/875 (0.5%)
22	T	0.41	0/958	0.99	3/1289 (0.2%)
23	U	0.41	0/417	0.96	1/562 (0.2%)
24	V	0.40	0/502	1.05	4/675 (0.6%)
25	W	0.51	0/1219	1.03	3/1655 (0.2%)
26	X	0.47	0/664	1.00	2/895 (0.2%)
27	Y	0.47	0/1146	0.96	4/1536 (0.3%)
28	Z	0.38	0/589	0.89	0/787
29	1	0.47	0/438	0.89	0/578
30	2	0.41	0/401	0.77	0/529
31	3	0.37	0/771	0.86	2/1024 (0.2%)
All	All	0.40	0/98702	0.73	140/147588 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	0	0	30
2	9	0	1
All	All	0	31

There are no bond length outliers.

The worst 5 of 140 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	1563	G	C2'-C3'-O3'	13.40	129.59	109.50
16	N	135	VAL	N-CA-C	-10.68	102.64	112.90
19	Q	17	LYS	N-CA-C	-9.57	98.06	109.93
18	P	118	GLN	N-CA-C	-9.35	100.19	111.69
6	D	136	ARG	CA-C-N	8.81	130.85	119.84

There are no chirality outliers.

5 of 31 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	324	G	Sidechain
1	0	396	U	Sidechain
1	0	518	G	Sidechain
1	0	722	G	Sidechain
1	0	761	A	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	59020	0	29807	1150	0
2	9	2599	0	1325	94	0
3	A	1753	0	1766	158	0
4	B	2625	0	2533	208	0
5	C	1859	0	1816	159	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	D	1094	0	1085	132	0
7	E	1357	0	1266	81	0
8	F	890	0	843	76	0
9	G	240	0	231	22	0
10	H	1282	0	1292	100	0
11	I	519	0	500	70	0
12	J	1120	0	1098	83	0
13	K	992	0	1031	90	0
14	L	1118	0	1076	62	0
15	M	1558	0	1566	87	0
16	N	1445	0	1401	142	0
17	O	865	0	873	53	0
18	P	1136	0	1123	79	0
19	Q	735	0	729	37	0
20	R	1149	0	1122	75	0
21	S	641	0	605	37	0
22	T	950	0	923	63	0
23	U	410	0	364	33	0
24	V	499	0	511	40	0
25	W	1196	0	1137	108	0
26	X	654	0	653	57	0
27	Y	1130	0	1133	69	0
28	Z	578	0	540	52	0
29	1	431	0	426	34	0
30	2	396	0	413	26	0
31	3	755	0	729	38	0
32	0	27	0	32	5	0
33	0	110	0	0	0	0
33	3	1	0	0	0	0
33	9	1	0	0	0	0
33	B	1	0	0	0	0
33	K	1	0	0	0	0
33	T	1	0	0	0	0
33	Y	1	0	0	0	0
34	0	2	0	0	0	0
35	0	72	0	0	0	0
35	9	2	0	0	0	0
35	A	1	0	0	0	0
35	B	1	0	0	0	0
35	C	1	0	0	0	0
35	H	1	0	0	0	0
35	J	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	L	1	0	0	0	0
35	M	1	0	0	0	0
35	Q	1	0	0	0	0
35	R	2	0	0	0	0
35	S	1	0	0	0	0
35	T	1	0	0	0	0
36	0	10	0	0	0	0
36	3	1	0	0	0	0
36	A	1	0	0	0	0
36	B	1	0	0	0	0
36	J	3	0	0	3	0
36	L	1	0	0	0	0
36	M	1	0	0	0	0
36	N	1	0	0	0	0
36	O	1	0	0	1	0
36	R	1	0	0	0	0
36	Y	1	0	0	0	0
37	1	1	0	0	0	0
37	3	1	0	0	0	0
37	O	1	0	0	0	0
37	U	1	0	0	0	0
37	Z	1	0	0	0	0
38	0	5892	0	0	234	0
38	1	57	0	0	2	0
38	2	39	0	0	4	0
38	3	74	0	0	9	0
38	9	139	0	0	12	0
38	A	120	0	0	16	0
38	B	146	0	0	27	0
38	C	169	0	0	35	0
38	D	49	0	0	26	0
38	E	41	0	0	11	0
38	F	25	0	0	8	0
38	G	19	0	0	2	0
38	H	68	0	0	15	0
38	I	10	0	0	6	0
38	J	56	0	0	4	0
38	K	60	0	0	9	0
38	L	82	0	0	14	0
38	M	128	0	0	7	0
38	N	64	0	0	11	0
38	O	44	0	0	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	P	64	0	0	9	0
38	Q	49	0	0	6	0
38	R	79	0	0	8	0
38	S	31	0	0	4	0
38	T	36	0	0	9	0
38	U	27	0	0	3	0
38	V	14	0	0	4	0
38	W	68	0	0	15	0
38	X	24	0	0	8	0
38	Y	101	0	0	7	0
38	Z	31	0	0	7	0
All	All	99060	0	59949	3216	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 21.

The worst 5 of 3216 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:871:G:H5'	1:0:871:G:H8	1.15	1.12
2:9:6:C:H5''	16:N:37:ARG:HH12	1.16	1.10
13:K:10:GLN:H	13:K:10:GLN:NE2	1.49	1.09
13:K:10:GLN:HE21	13:K:10:GLN:N	1.52	1.07
4:B:62:ARG:HA	4:B:65:MET:HE3	1.36	1.06

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 X-ray entries followed by that with respect to entries of similar resolution.

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	A	235/240 (98%)	192 (82%)	34 (14%)	9 (4%)	2 15

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	B	335/338 (99%)	289 (86%)	38 (11%)	8 (2%)	4	24
5	C	244/246 (99%)	213 (87%)	24 (10%)	7 (3%)	3	20
6	D	134/177 (76%)	89 (66%)	35 (26%)	10 (8%)	1	4
7	E	170/178 (96%)	157 (92%)	13 (8%)	0	100	100
8	F	117/120 (98%)	95 (81%)	15 (13%)	7 (6%)	1	7
9	G	25/348 (7%)	22 (88%)	2 (8%)	1 (4%)	2	14
10	H	156/177 (88%)	140 (90%)	14 (9%)	2 (1%)	9	38
11	I	68/162 (42%)	45 (66%)	22 (32%)	1 (2%)	8	35
12	J	140/145 (97%)	124 (89%)	11 (8%)	5 (4%)	2	16
13	K	130/132 (98%)	114 (88%)	15 (12%)	1 (1%)	16	50
14	L	141/165 (86%)	118 (84%)	21 (15%)	2 (1%)	9	36
15	M	192/195 (98%)	172 (90%)	18 (9%)	2 (1%)	12	45
16	N	184/187 (98%)	151 (82%)	26 (14%)	7 (4%)	2	15
17	O	113/116 (97%)	100 (88%)	11 (10%)	2 (2%)	6	31
18	P	141/149 (95%)	128 (91%)	11 (8%)	2 (1%)	9	36
19	Q	93/96 (97%)	81 (87%)	11 (12%)	1 (1%)	11	43
20	R	148/155 (96%)	133 (90%)	13 (9%)	2 (1%)	9	36
21	S	79/85 (93%)	71 (90%)	8 (10%)	0	100	100
22	T	117/120 (98%)	102 (87%)	14 (12%)	1 (1%)	14	48
23	U	51/66 (77%)	44 (86%)	5 (10%)	2 (4%)	2	14
24	V	63/71 (89%)	56 (89%)	5 (8%)	2 (3%)	3	18
25	W	152/154 (99%)	141 (93%)	9 (6%)	2 (1%)	9	38
26	X	80/92 (87%)	67 (84%)	9 (11%)	4 (5%)	1	10
27	Y	140/241 (58%)	125 (89%)	13 (9%)	2 (1%)	9	36
28	Z	71/83 (86%)	57 (80%)	11 (16%)	3 (4%)	2	13
29	1	54/57 (95%)	50 (93%)	4 (7%)	0	100	100
30	2	42/50 (84%)	39 (93%)	3 (7%)	0	100	100
31	3	90/92 (98%)	81 (90%)	9 (10%)	0	100	100
All	All	3705/4437 (84%)	3196 (86%)	424 (11%)	85 (2%)	5	25

5 of 85 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	34	ASP
3	A	36	ASP
3	A	132	ASP
4	B	139	ASP
5	C	234	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	A	179/182 (98%)	167 (93%)	12 (7%)	15	46
4	B	282/283 (100%)	262 (93%)	20 (7%)	13	43
5	C	193/193 (100%)	180 (93%)	13 (7%)	15	46
6	D	117/148 (79%)	112 (96%)	5 (4%)	26	60
7	E	152/156 (97%)	142 (93%)	10 (7%)	15	46
8	F	93/94 (99%)	90 (97%)	3 (3%)	34	67
9	G	27/283 (10%)	25 (93%)	2 (7%)	13	42
10	H	134/145 (92%)	130 (97%)	4 (3%)	36	69
11	I	58/130 (45%)	57 (98%)	1 (2%)	53	78
12	J	118/121 (98%)	112 (95%)	6 (5%)	21	55
13	K	106/106 (100%)	103 (97%)	3 (3%)	38	70
14	L	113/127 (89%)	108 (96%)	5 (4%)	25	60
15	M	158/159 (99%)	154 (98%)	4 (2%)	42	72
16	N	149/150 (99%)	142 (95%)	7 (5%)	23	58
17	O	93/94 (99%)	88 (95%)	5 (5%)	20	53
18	P	113/117 (97%)	107 (95%)	6 (5%)	20	54
19	Q	79/80 (99%)	74 (94%)	5 (6%)	16	48
20	R	117/122 (96%)	112 (96%)	5 (4%)	26	60
21	S	71/74 (96%)	70 (99%)	1 (1%)	59	80
22	T	105/106 (99%)	99 (94%)	6 (6%)	18	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	U	44/52 (85%)	44 (100%)	0	100	100
24	V	51/57 (90%)	49 (96%)	2 (4%)	28	62
25	W	130/130 (100%)	124 (95%)	6 (5%)	24	58
26	X	66/74 (89%)	60 (91%)	6 (9%)	9	33
27	Y	120/196 (61%)	114 (95%)	6 (5%)	22	56
28	Z	60/68 (88%)	59 (98%)	1 (2%)	53	78
29	1	46/47 (98%)	46 (100%)	0	100	100
30	2	42/46 (91%)	42 (100%)	0	100	100
31	3	79/79 (100%)	75 (95%)	4 (5%)	21	55
All	All	3095/3619 (86%)	2947 (95%)	148 (5%)	23	57

5 of 148 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
20	R	143	VAL
28	Z	41	ASN
22	T	39	ASN
25	W	154	ARG
6	D	149	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 105 such sidechains are listed below:

Mol	Chain	Res	Type
18	P	118	GLN
22	T	39	ASN
30	2	45	ASN
19	Q	27	GLN
20	R	98	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	2745/2922 (93%)	248 (9%)	28 (1%)
2	9	121/122 (99%)	16 (13%)	1 (0%)
All	All	2866/3044 (94%)	264 (9%)	29 (1%)

5 of 264 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	0	31	C
1	0	67	A
1	0	69	A
1	0	70	A
1	0	71	G

5 of 29 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	0	1352	A
1	0	2791	U
1	0	1563	G
1	0	2526	C
1	0	1450	C

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	OMU	0	2587	1	19,22,23	0.25	0	25,31,34	0.40	0
1	OMG	0	2588	1	23,26,27	0.31	0	32,38,41	0.32	0
1	UR3	0	2619	1	19,22,23	0.45	0	26,32,35	0.67	1 (3%)
1	PSU	0	2621	1	18,21,22	1.58	2 (11%)	21,30,33	1.33	3 (14%)
1	1MA	0	628	1	21,25,26	0.72	1 (4%)	30,37,40	0.76	1 (3%)

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
1	OMU	0	2587	1	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMG	0	2588	1	-	0/9/27/28	0/3/3/3
1	UR3	0	2619	1	-	0/7/25/26	0/2/2/2
1	PSU	0	2621	1	-	0/7/25/26	0/2/2/2
1	1MA	0	628	1	-	2/7/25/26	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	0	2621	PSU	C2-N1	5.00	1.43	1.36
1	0	2621	PSU	C6-C5	3.48	1.39	1.35
1	0	628	1MA	C6-N6	2.42	1.33	1.28

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	2621	PSU	C6-N1-C2	-3.11	119.81	122.69
1	0	2621	PSU	O2-C2-N1	3.05	125.93	122.79
1	0	2621	PSU	C6-C5-C4	2.94	120.16	118.17
1	0	628	1MA	N1-C2-N3	2.90	129.44	126.00
1	0	2619	UR3	C4-N3-C2	2.62	126.69	124.58

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	0	628	1MA	C2'-C1'-N9-C8
1	0	628	1MA	C2'-C1'-N9-C4

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	0	2587	OMU	2	0
1	0	2588	OMG	1	0
1	0	2621	PSU	1	0
1	0	628	1MA	1	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 232 ligands modelled in this entry, 231 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
32	CLY	0	9000	-	26,28,28	1.90	9 (34%)	31,40,40	1.27	3 (9%)

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
32	CLY	0	9000	-	-	4/21/53/53	0/2/2/2

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	0	9000	CLY	C14-N2	4.32	1.53	1.47
32	0	9000	CLY	O5-C4	3.52	1.49	1.44
32	0	9000	CLY	C15-N2	3.36	1.53	1.46
32	0	9000	CLY	C10-N1	2.89	1.40	1.34
32	0	9000	CLY	C11-N2	2.37	1.52	1.46

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	0	9000	CLY	C11-C10-N1	-3.91	107.96	116.52
32	0	9000	CLY	O8-C10-N1	2.83	128.03	122.96
32	0	9000	CLY	C12-C13-C16	-2.46	111.86	114.68

There are no chirality outliers.

All (4) torsion outliers are listed below:

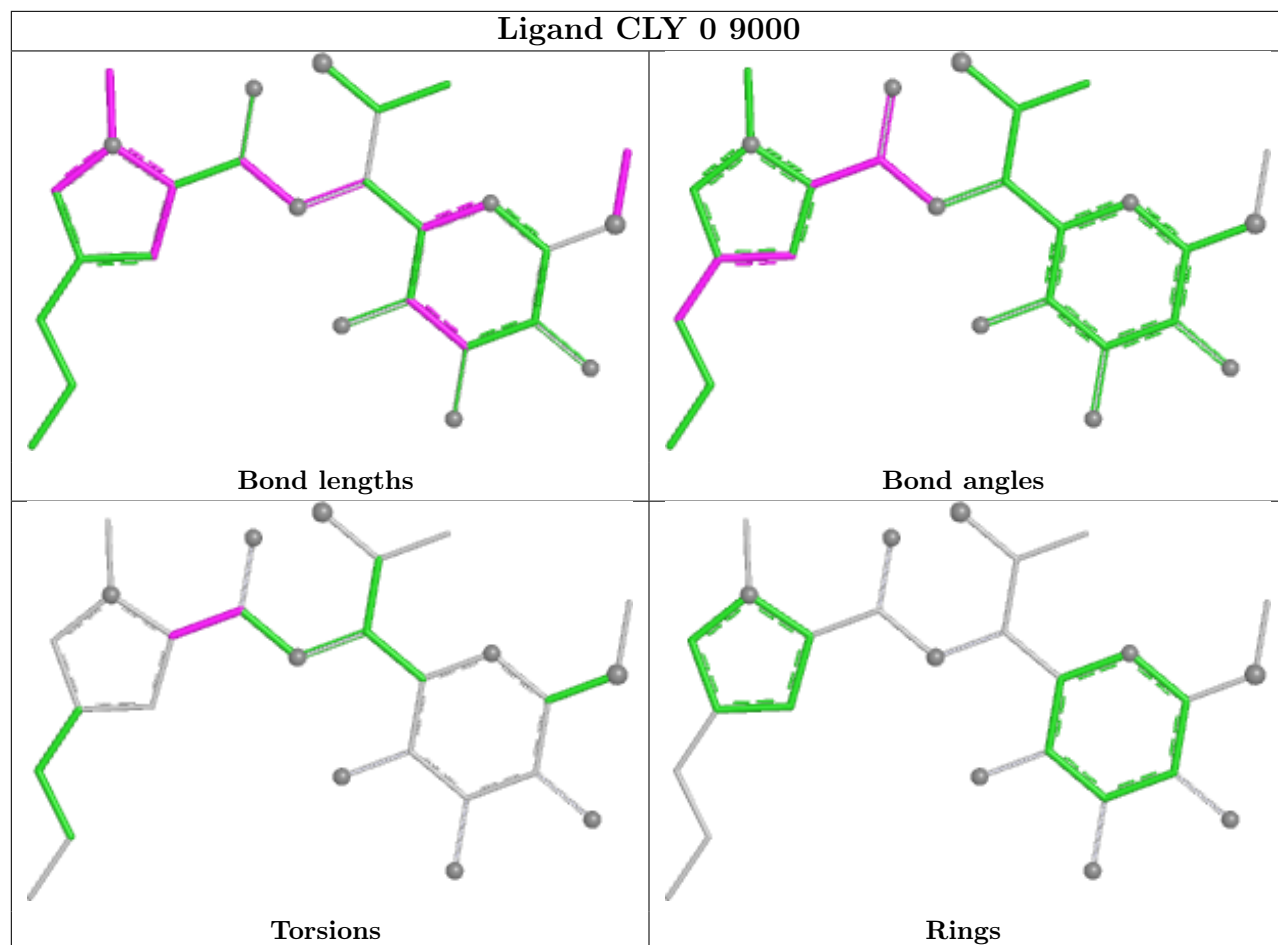
Mol	Chain	Res	Type	Atoms
32	0	9000	CLY	O8-C10-C11-C12
32	0	9000	CLY	N1-C10-C11-C12
32	0	9000	CLY	O8-C10-C11-N2
32	0	9000	CLY	N1-C10-C11-N2

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	0	9000	CLY	5	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 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	0	2749/2922 (94%)	-0.73	9 (0%) 90 79	23, 50, 94, 155	0
2	9	122/122 (100%)	-0.38	2 (1%) 70 47	37, 69, 94, 157	0
3	A	237/240 (98%)	-0.32	3 (1%) 75 53	31, 58, 94, 112	0
4	B	337/338 (99%)	-0.35	1 (0%) 90 79	30, 59, 85, 94	0
5	C	246/246 (100%)	-0.47	0 100 100	26, 48, 72, 82	0
6	D	140/177 (79%)	0.45	5 (3%) 46 26	63, 104, 125, 135	0
7	E	172/178 (96%)	-0.06	0 100 100	50, 72, 95, 99	0
8	F	119/120 (99%)	-0.11	0 100 100	51, 75, 98, 116	0
9	G	29/348 (8%)	0.34	0 100 100	77, 93, 105, 107	0
10	H	160/177 (90%)	-0.26	2 (1%) 75 53	43, 63, 96, 110	0
11	I	70/162 (43%)	0.88	5 (7%) 22 11	109, 125, 143, 145	0
12	J	142/145 (97%)	-0.39	1 (0%) 84 66	38, 54, 76, 92	0
13	K	132/132 (100%)	-0.36	0 100 100	37, 56, 77, 87	0
14	L	145/165 (87%)	-0.10	3 (2%) 63 40	28, 70, 108, 122	0
15	M	194/195 (99%)	-0.51	0 100 100	33, 47, 63, 70	0
16	N	186/187 (99%)	-0.09	0 100 100	45, 69, 114, 121	0
17	O	115/116 (99%)	-0.34	0 100 100	43, 58, 74, 78	0
18	P	143/149 (95%)	-0.29	0 100 100	41, 60, 75, 81	0
19	Q	95/96 (98%)	-0.56	0 100 100	36, 49, 65, 81	0
20	R	150/155 (96%)	-0.64	0 100 100	32, 47, 67, 79	0
21	S	81/85 (95%)	-0.38	0 100 100	45, 64, 82, 88	0
22	T	119/120 (99%)	-0.32	1 (0%) 82 64	40, 59, 86, 102	0
23	U	53/66 (80%)	-0.23	0 100 100	49, 62, 78, 88	0
24	V	65/71 (91%)	0.13	2 (3%) 51 30	59, 78, 115, 120	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	W	154/154 (100%)	-0.57	0 100 100	32, 49, 68, 82	0
26	X	82/92 (89%)	-0.20	2 (2%) 59 36	48, 62, 86, 100	0
27	Y	142/241 (58%)	-0.54	0 100 100	31, 48, 69, 90	0
28	Z	73/83 (87%)	0.34	3 (4%) 41 23	72, 83, 98, 107	0
29	1	56/57 (98%)	-0.82	0 100 100	27, 35, 41, 49	0
30	2	46/50 (92%)	-0.04	0 100 100	35, 66, 94, 108	0
31	3	92/92 (100%)	-0.12	0 100 100	53, 72, 82, 90	0
All	All	6646/7481 (88%)	-0.46	39 (0%) 85 69	23, 56, 102, 157	0

The worst 5 of 39 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	9	1	U	4.7
24	V	1	THR	4.4
11	I	128	THR	4.2
26	X	88	GLU	3.6
11	I	71	ALA	3.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	1MA	0	628	23/24	0.98	0.06	29,32,34,35	0
1	OMU	0	2587	21/22	0.98	0.06	37,39,41,44	0
1	OMG	0	2588	24/25	0.98	0.06	37,40,41,44	0
1	UR3	0	2619	21/22	0.98	0.06	39,43,46,50	0
1	PSU	0	2621	20/21	0.98	0.05	28,31,37,37	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
35	NA	0	8529	1/1	0.58	0.24	79,79,79,79	0
33	MG	0	8050	1/1	0.79	0.14	107,107,107,107	0
35	NA	0	8584	1/1	0.81	0.13	63,63,63,63	0
32	CLY	0	9000	27/27	0.82	0.19	50,56,61,61	0
33	MG	0	8092	1/1	0.82	0.22	89,89,89,89	0
35	NA	0	8582	1/1	0.83	0.20	66,66,66,66	0
35	NA	0	8508	1/1	0.84	0.18	59,59,59,59	0
33	MG	0	8090	1/1	0.84	0.12	74,74,74,74	0
35	NA	R	8586	1/1	0.84	0.21	63,63,63,63	0
35	NA	9	8551	1/1	0.86	0.18	46,46,46,46	0
33	MG	0	8082	1/1	0.86	0.17	70,70,70,70	0
35	NA	0	8506	1/1	0.87	0.22	40,40,40,40	0
35	NA	9	8583	1/1	0.87	0.16	70,70,70,70	0
35	NA	0	8577	1/1	0.87	0.16	65,65,65,65	0
35	NA	0	8571	1/1	0.88	0.25	52,52,52,52	0
35	NA	S	8512	1/1	0.88	0.06	32,32,32,32	0
35	NA	B	8561	1/1	0.89	0.20	70,70,70,70	0
35	NA	0	8572	1/1	0.89	0.28	66,66,66,66	0
33	MG	0	8011	1/1	0.89	0.13	8,8,8,8	0
35	NA	0	8585	1/1	0.90	0.21	52,52,52,52	0
33	MG	0	8045	1/1	0.90	0.09	54,54,54,54	0
35	NA	0	8518	1/1	0.90	0.07	28,28,28,28	0
35	NA	0	8569	1/1	0.91	0.30	86,86,86,86	0
33	MG	0	8087	1/1	0.91	0.13	51,51,51,51	0
33	MG	0	8067	1/1	0.91	0.08	60,60,60,60	0
35	NA	0	8573	1/1	0.91	0.08	61,61,61,61	0
35	NA	0	8513	1/1	0.91	0.05	52,52,52,52	0
33	MG	0	8049	1/1	0.91	0.19	79,79,79,79	0
35	NA	0	8522	1/1	0.91	0.28	61,61,61,61	0
35	NA	0	8524	1/1	0.91	0.14	44,44,44,44	0
35	NA	0	8525	1/1	0.91	0.10	54,54,54,54	0
33	MG	T	8073	1/1	0.91	0.07	59,59,59,59	0
35	NA	0	8534	1/1	0.91	0.12	49,49,49,49	0
35	NA	0	8555	1/1	0.91	0.15	81,81,81,81	0
35	NA	0	8566	1/1	0.91	0.05	48,48,48,48	0
33	MG	0	8104	1/1	0.92	0.07	56,56,56,56	0
35	NA	0	8528	1/1	0.92	0.08	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
35	NA	0	8560	1/1	0.92	0.17	63,63,63,63	0
35	NA	0	8563	1/1	0.92	0.13	46,46,46,46	0
35	NA	C	8504	1/1	0.92	0.06	29,29,29,29	0
35	NA	0	8511	1/1	0.92	0.22	58,58,58,58	0
35	NA	0	8533	1/1	0.92	0.10	44,44,44,44	0
36	CL	0	8816	1/1	0.92	0.12	74,74,74,74	0
36	CL	B	8819	1/1	0.92	0.16	62,62,62,62	0
35	NA	0	8526	1/1	0.93	0.20	57,57,57,57	0
35	NA	0	8562	1/1	0.93	0.22	66,66,66,66	0
33	MG	0	8113	1/1	0.93	0.06	69,69,69,69	0
35	NA	0	8540	1/1	0.93	0.12	49,49,49,49	0
35	NA	0	8568	1/1	0.93	0.11	84,84,84,84	0
35	NA	0	8552	1/1	0.93	0.13	49,49,49,49	0
33	MG	0	8070	1/1	0.93	0.08	52,52,52,52	0
36	CL	J	8802	1/1	0.93	0.07	83,83,83,83	0
33	MG	0	8046	1/1	0.94	0.06	43,43,43,43	0
35	NA	0	8523	1/1	0.94	0.09	42,42,42,42	0
35	NA	0	8556	1/1	0.94	0.18	49,49,49,49	0
35	NA	0	8557	1/1	0.94	0.08	45,45,45,45	0
35	NA	0	8558	1/1	0.94	0.25	70,70,70,70	0
35	NA	0	8531	1/1	0.94	0.23	77,77,77,77	0
35	NA	0	8502	1/1	0.94	0.09	45,45,45,45	0
36	CL	0	8822	1/1	0.94	0.11	92,92,92,92	0
33	MG	0	8075	1/1	0.94	0.09	73,73,73,73	0
35	NA	0	8507	1/1	0.94	0.10	65,65,65,65	0
36	CL	J	8821	1/1	0.94	0.06	61,61,61,61	0
36	CL	L	8810	1/1	0.94	0.11	74,74,74,74	0
36	CL	3	8804	1/1	0.94	0.07	76,76,76,76	0
34	K	0	8401	1/1	0.95	0.30	99,99,99,99	0
35	NA	0	8501	1/1	0.95	0.12	31,31,31,31	0
35	NA	0	8539	1/1	0.95	0.06	21,21,21,21	0
35	NA	0	8567	1/1	0.95	0.08	54,54,54,54	0
33	MG	0	8103	1/1	0.95	0.08	68,68,68,68	0
35	NA	L	8580	1/1	0.95	0.21	63,63,63,63	0
35	NA	Q	8548	1/1	0.95	0.07	49,49,49,49	0
35	NA	0	8503	1/1	0.95	0.37	68,68,68,68	0
35	NA	0	8554	1/1	0.95	0.10	44,44,44,44	0
33	MG	0	8053	1/1	0.95	0.06	37,37,37,37	0
33	MG	0	8111	1/1	0.95	0.07	38,38,38,38	0
36	CL	A	8809	1/1	0.95	0.11	84,84,84,84	0
35	NA	0	8574	1/1	0.95	0.17	62,62,62,62	0
36	CL	J	8801	1/1	0.95	0.07	80,80,80,80	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
35	NA	0	8575	1/1	0.95	0.15	67,67,67,67	0
33	MG	0	8076	1/1	0.95	0.07	79,79,79,79	0
33	MG	B	8055	1/1	0.95	0.06	45,45,45,45	0
36	CL	O	8808	1/1	0.95	0.11	90,90,90,90	0
33	MG	0	8096	1/1	0.95	0.07	47,47,47,47	0
35	NA	0	8505	1/1	0.96	0.12	35,35,35,35	0
35	NA	0	8527	1/1	0.96	0.06	41,41,41,41	0
35	NA	0	8559	1/1	0.96	0.14	61,61,61,61	0
33	MG	0	8094	1/1	0.96	0.14	66,66,66,66	0
33	MG	0	8115	1/1	0.96	0.04	58,58,58,58	0
35	NA	J	8546	1/1	0.96	0.05	52,52,52,52	0
33	MG	9	8095	1/1	0.96	0.06	54,54,54,54	0
35	NA	0	8532	1/1	0.96	0.03	53,53,53,53	0
33	MG	0	8041	1/1	0.96	0.07	56,56,56,56	0
33	MG	K	8069	1/1	0.96	0.05	59,59,59,59	0
35	NA	T	8543	1/1	0.96	0.11	31,31,31,31	0
36	CL	0	8815	1/1	0.96	0.09	92,92,92,92	0
35	NA	0	8535	1/1	0.96	0.10	42,42,42,42	0
36	CL	0	8817	1/1	0.96	0.06	68,68,68,68	0
35	NA	0	8516	1/1	0.96	0.16	39,39,39,39	0
33	MG	0	8101	1/1	0.96	0.09	56,56,56,56	0
35	NA	0	8541	1/1	0.96	0.06	50,50,50,50	0
35	NA	0	8549	1/1	0.96	0.11	50,50,50,50	0
33	MG	0	8081	1/1	0.96	0.05	56,56,56,56	0
33	MG	0	8042	1/1	0.96	0.04	36,36,36,36	0
35	NA	0	8581	1/1	0.96	0.07	70,70,70,70	0
33	MG	0	8105	1/1	0.96	0.06	64,64,64,64	0
36	CL	Y	8820	1/1	0.96	0.06	42,42,42,42	0
33	MG	0	8093	1/1	0.96	0.04	45,45,45,45	0
35	NA	A	8545	1/1	0.97	0.07	41,41,41,41	0
35	NA	0	8565	1/1	0.97	0.10	50,50,50,50	0
35	NA	0	8536	1/1	0.97	0.04	61,61,61,61	0
33	MG	0	8062	1/1	0.97	0.07	62,62,62,62	0
33	MG	0	8102	1/1	0.97	0.04	77,77,77,77	0
33	MG	0	8064	1/1	0.97	0.13	33,33,33,33	0
35	NA	0	8570	1/1	0.97	0.22	55,55,55,55	0
33	MG	0	8066	1/1	0.97	0.06	87,87,87,87	0
33	MG	0	8024	1/1	0.97	0.04	33,33,33,33	0
36	CL	0	8811	1/1	0.97	0.07	63,63,63,63	0
36	CL	0	8813	1/1	0.97	0.07	54,54,54,54	0
35	NA	0	8553	1/1	0.97	0.06	37,37,37,37	0
35	NA	0	8510	1/1	0.97	0.08	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
33	MG	0	8057	1/1	0.97	0.08	50,50,50,50	0
35	NA	0	8576	1/1	0.97	0.08	48,48,48,48	0
34	K	0	8402	1/1	0.97	0.12	73,73,73,73	0
35	NA	0	8578	1/1	0.97	0.13	52,52,52,52	0
35	NA	0	8579	1/1	0.97	0.07	39,39,39,39	0
35	NA	0	8530	1/1	0.97	0.06	41,41,41,41	0
35	NA	0	8515	1/1	0.97	0.08	46,46,46,46	0
33	MG	0	8098	1/1	0.97	0.11	45,45,45,45	0
36	CL	M	8818	1/1	0.97	0.05	50,50,50,50	0
36	CL	N	8807	1/1	0.97	0.07	58,58,58,58	0
35	NA	0	8517	1/1	0.97	0.07	48,48,48,48	0
33	MG	0	8114	1/1	0.97	0.03	52,52,52,52	0
35	NA	0	8520	1/1	0.97	0.06	29,29,29,29	0
35	NA	0	8564	1/1	0.98	0.05	48,48,48,48	0
35	NA	H	8509	1/1	0.98	0.05	40,40,40,40	0
33	MG	0	8112	1/1	0.98	0.04	50,50,50,50	0
33	MG	0	8091	1/1	0.98	0.09	53,53,53,53	0
35	NA	M	8547	1/1	0.98	0.05	33,33,33,33	0
33	MG	0	8018	1/1	0.98	0.04	55,55,55,55	0
35	NA	R	8537	1/1	0.98	0.04	50,50,50,50	0
35	NA	0	8514	1/1	0.98	0.06	28,28,28,28	0
33	MG	0	8012	1/1	0.98	0.04	43,43,43,43	0
35	NA	0	8538	1/1	0.98	0.05	54,54,54,54	0
36	CL	0	8803	1/1	0.98	0.08	75,75,75,75	0
33	MG	0	8052	1/1	0.98	0.04	51,51,51,51	0
36	CL	0	8812	1/1	0.98	0.09	51,51,51,51	0
33	MG	0	8043	1/1	0.98	0.06	43,43,43,43	0
33	MG	0	8097	1/1	0.98	0.04	39,39,39,39	0
35	NA	0	8544	1/1	0.98	0.04	24,24,24,24	0
33	MG	0	8044	1/1	0.98	0.05	35,35,35,35	0
35	NA	0	8550	1/1	0.98	0.09	52,52,52,52	0
35	NA	0	8521	1/1	0.98	0.09	53,53,53,53	0
33	MG	Y	8108	1/1	0.98	0.04	40,40,40,40	0
33	MG	0	8100	1/1	0.98	0.04	80,80,80,80	0
33	MG	0	8059	1/1	0.98	0.04	44,44,44,44	0
33	MG	0	8060	1/1	0.98	0.05	50,50,50,50	0
33	MG	0	8085	1/1	0.98	0.04	67,67,67,67	0
33	MG	0	8035	1/1	0.98	0.04	48,48,48,48	0
33	MG	0	8088	1/1	0.98	0.04	36,36,36,36	0
33	MG	0	8107	1/1	0.98	0.08	80,80,80,80	0
36	CL	R	8806	1/1	0.98	0.05	46,46,46,46	0
33	MG	0	8110	1/1	0.98	0.04	47,47,47,47	0

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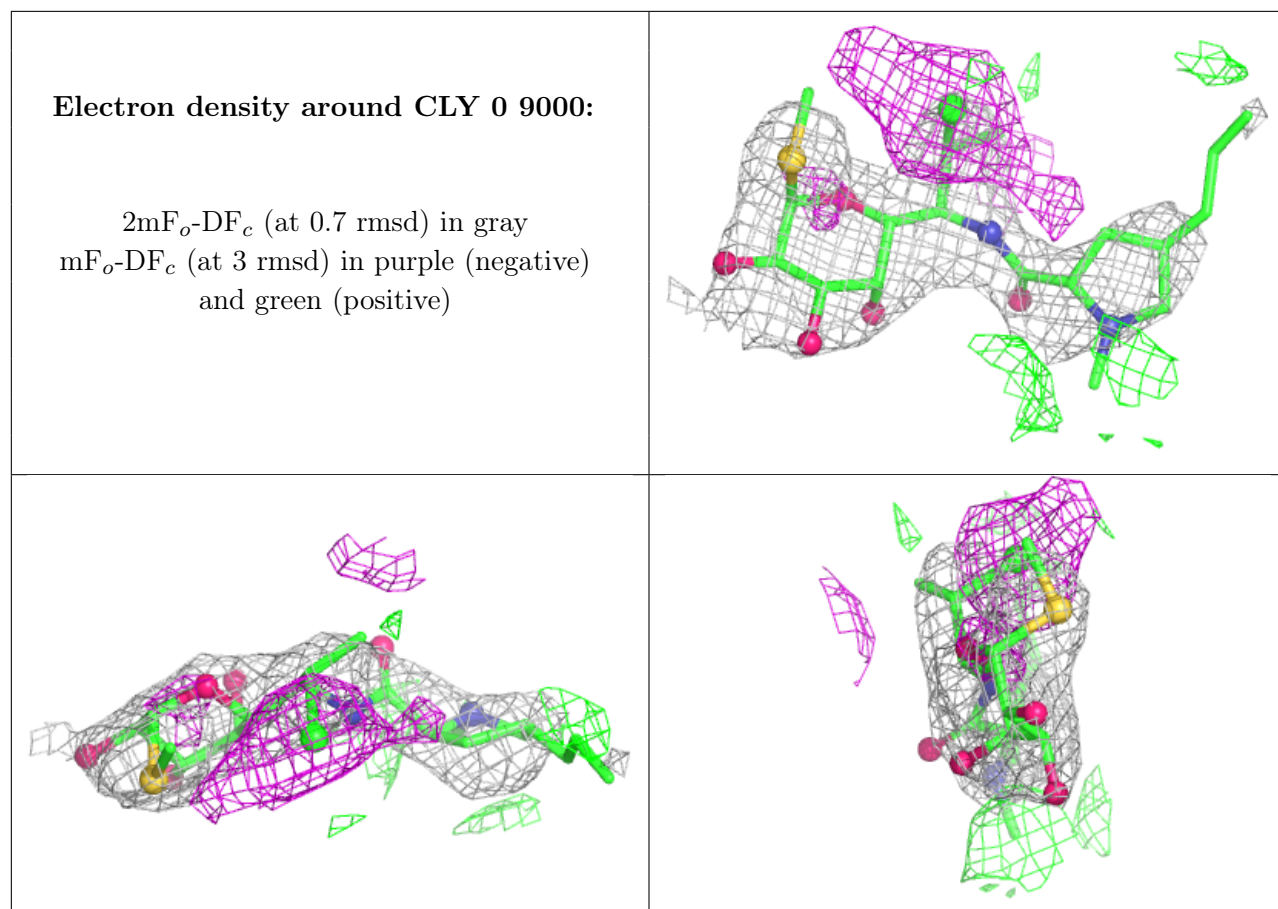
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
33	MG	0	8039	1/1	0.98	0.07	49,49,49,49	0
37	CD	O	8705	1/1	0.98	0.05	87,87,87,87	0
35	NA	0	8542	1/1	0.99	0.02	39,39,39,39	0
33	MG	0	8051	1/1	0.99	0.03	67,67,67,67	0
33	MG	0	8032	1/1	0.99	0.07	41,41,41,41	0
33	MG	0	8033	1/1	0.99	0.03	34,34,34,34	0
33	MG	0	8056	1/1	0.99	0.02	55,55,55,55	0
33	MG	0	8007	1/1	0.99	0.03	34,34,34,34	0
33	MG	0	8036	1/1	0.99	0.04	42,42,42,42	0
33	MG	0	8037	1/1	0.99	0.03	46,46,46,46	0
33	MG	0	8061	1/1	0.99	0.02	40,40,40,40	0
33	MG	0	8099	1/1	0.99	0.04	64,64,64,64	0
33	MG	0	8014	1/1	0.99	0.04	36,36,36,36	0
33	MG	0	8063	1/1	0.99	0.04	70,70,70,70	0
33	MG	0	8040	1/1	0.99	0.04	72,72,72,72	0
33	MG	0	8065	1/1	0.99	0.05	41,41,41,41	0
33	MG	0	8015	1/1	0.99	0.02	43,43,43,43	0
36	CL	0	8805	1/1	0.99	0.04	61,61,61,61	0
33	MG	0	8016	1/1	0.99	0.02	33,33,33,33	0
33	MG	0	8068	1/1	0.99	0.02	68,68,68,68	0
33	MG	0	8109	1/1	0.99	0.06	30,30,30,30	0
36	CL	0	8814	1/1	0.99	0.05	64,64,64,64	0
33	MG	0	8008	1/1	0.99	0.03	41,41,41,41	0
33	MG	0	8071	1/1	0.99	0.04	80,80,80,80	0
33	MG	0	8072	1/1	0.99	0.04	46,46,46,46	0
33	MG	0	8074	1/1	0.99	0.03	29,29,29,29	0
33	MG	0	8021	1/1	0.99	0.03	28,28,28,28	0
33	MG	0	8022	1/1	0.99	0.03	48,48,48,48	0
33	MG	0	8116	1/1	0.99	0.05	23,23,23,23	0
33	MG	0	8006	1/1	0.99	0.03	37,37,37,37	0
33	MG	0	8047	1/1	0.99	0.08	74,74,74,74	0
33	MG	0	8083	1/1	0.99	0.02	45,45,45,45	0
33	MG	0	8084	1/1	0.99	0.07	55,55,55,55	0
33	MG	0	8048	1/1	0.99	0.07	60,60,60,60	0
33	MG	3	8078	1/1	0.99	0.10	55,55,55,55	0
33	MG	0	8086	1/1	0.99	0.05	46,46,46,46	0
33	MG	0	8027	1/1	0.99	0.03	48,48,48,48	0
33	MG	0	8031	1/1	0.99	0.03	28,28,28,28	0
33	MG	0	8089	1/1	0.99	0.03	58,58,58,58	0
37	CD	3	8704	1/1	0.99	0.03	88,88,88,88	0
33	MG	0	8080	1/1	1.00	0.03	50,50,50,50	0
33	MG	0	8106	1/1	1.00	0.01	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
33	MG	0	8034	1/1	1.00	0.02	36,36,36,36	0
33	MG	0	8054	1/1	1.00	0.02	43,43,43,43	0
33	MG	0	8017	1/1	1.00	0.07	26,26,26,26	0
33	MG	0	8009	1/1	1.00	0.05	38,38,38,38	0
33	MG	0	8058	1/1	1.00	0.03	40,40,40,40	0
33	MG	0	8019	1/1	1.00	0.06	27,27,27,27	0
33	MG	0	8038	1/1	1.00	0.01	31,31,31,31	0
35	NA	0	8519	1/1	1.00	0.04	33,33,33,33	0
33	MG	0	8020	1/1	1.00	0.02	31,31,31,31	0
33	MG	0	8010	1/1	1.00	0.03	41,41,41,41	0
33	MG	0	8004	1/1	1.00	0.03	43,43,43,43	0
33	MG	0	8023	1/1	1.00	0.03	40,40,40,40	0
33	MG	0	8005	1/1	1.00	0.01	35,35,35,35	0
33	MG	0	8025	1/1	1.00	0.02	45,45,45,45	0
33	MG	0	8026	1/1	1.00	0.02	27,27,27,27	0
33	MG	0	8013	1/1	1.00	0.03	45,45,45,45	0
33	MG	0	8028	1/1	1.00	0.02	44,44,44,44	0
33	MG	0	8029	1/1	1.00	0.03	38,38,38,38	0
33	MG	0	8030	1/1	1.00	0.03	31,31,31,31	0
33	MG	0	8001	1/1	1.00	0.03	35,35,35,35	0
33	MG	0	8002	1/1	1.00	0.04	41,41,41,41	0
33	MG	0	8003	1/1	1.00	0.02	33,33,33,33	0
33	MG	0	8077	1/1	1.00	0.03	39,39,39,39	0
37	CD	U	8701	1/1	1.00	0.03	65,65,65,65	0
37	CD	Z	8703	1/1	1.00	0.04	97,97,97,97	0
37	CD	1	8702	1/1	1.00	0.03	64,64,64,64	0
33	MG	0	8079	1/1	1.00	0.03	33,33,33,33	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers ⓘ

There are no such residues in this entry.