



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 10, 2025 – 03:33 PM EST

PDB ID : 4DV5
Title : Crystal structure of the Thermus thermophilus 30S ribosomal subunit with a 16S rRNA mutation, A914G, bound with streptomycin
Authors : Demirci, H.; Murphy IV, F.; Murphy, E.; Gregory, S.T.; Dahlberg, A.E.; Jogl, G.
Deposited on : 2012-02-22
Resolution : 3.68 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.21
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

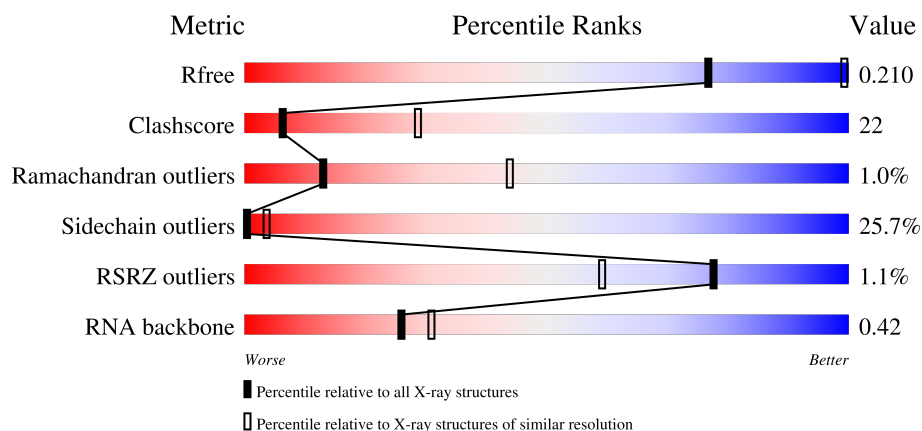
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.68 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}	164625	1132 (3.80-3.56)
Clashscore	180529	1194 (3.80-3.56)
Ramachandran outliers	177936	1173 (3.80-3.56)
Sidechain outliers	177891	1170 (3.80-3.56)
RSRZ outliers	164620	1132 (3.80-3.56)
RNA backbone	3690	1117 (4.30-3.00)

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	A	1522	<div> <div style="width: 15%; background-color: red;"></div> <div style="width: 41%; background-color: orange;"></div> <div style="width: 30%; background-color: yellow;"></div> <div style="width: 13%; background-color: green;"></div> <div style="width: 1%; background-color: grey;"></div> </div> <div>15% 41% 30% 13% •</div>
2	B	256	<div> <div style="width: 30%; background-color: green;"></div> <div style="width: 47%; background-color: yellow;"></div> <div style="width: 12%; background-color: orange;"></div> <div style="width: 9%; background-color: red;"></div> <div style="width: 2%; background-color: grey;"></div> </div> <div>30% 47% 12% 9%</div>
3	C	239	<div> <div style="width: 35%; background-color: green;"></div> <div style="width: 37%; background-color: yellow;"></div> <div style="width: 14%; background-color: orange;"></div> <div style="width: 14%; background-color: red;"></div> </div> <div>35% 37% 14% 14%</div>

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Mol	Chain	Length	Quality of chain
4	D	209	
5	E	162	
6	F	101	
7	G	156	
8	H	138	
9	I	128	
10	J	105	
11	K	129	
12	L	135	
13	M	126	
14	N	61	
15	O	89	
16	P	88	
17	Q	105	
18	R	88	
19	S	93	
20	T	106	
21	U	27	

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
1	5MC	A	1404	-	-	X	-
23	MG	A	1796	-	-	-	X

2 Entry composition

There are 25 unique types of molecules in this entry. The entry contains 52300 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 16S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1512	Total	C	N	O	P	0	0	0
			32508	14477	6011	10508	1512			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	914	G	A	engineered mutation	GB M26923.1
A	1534	C	A	conflict	GB M26923.1
A	1535	A	C	conflict	GB M26923.1

- Molecule 2 is a protein called ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	234	Total	C	N	O	S	0	0	0
			1900	1213	341	341	5			

- Molecule 3 is a protein called ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	206	Total	C	N	O	S	0	0	0
			1612	1016	314	281	1			

- Molecule 4 is a protein called ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	208	Total	C	N	O	S	0	0	0
			1703	1066	339	291	7			

- Molecule 5 is a protein called ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	150	Total	C	N	O	S	0	0	0
			1146	724	217	201	4			

- Molecule 6 is a protein called ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	101	Total	C	N	O	S	0	0	0
			843	531	155	154	3			

- Molecule 7 is a protein called ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	155	Total	C	N	O	S	0	0	0
			1257	781	252	218	6			

- Molecule 8 is a protein called ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	138	Total	C	N	O	S	0	0	0
			1116	705	215	193	3			

- Molecule 9 is a protein called ribosomal protein S9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	I	127	Total	C	N	O	0	0	0
			1010	639	197	174			

- Molecule 10 is a protein called ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	98	Total	C	N	O	S	0	0	0
			792	498	156	137	1			

- Molecule 11 is a protein called ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	116	Total	C	N	O	S	0	0	0
			864	537	164	160	3			

- Molecule 12 is a protein called ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	124	Total	C	N	O	S	0	0	0
			972	612	195	163	2			

- Molecule 13 is a protein called ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	118	Total	C	N	O	S	0	0	0
			937	579	193	163	2			

- Molecule 14 is a protein called ribosomal protein S14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			

- Molecule 15 is a protein called ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	O	87	Total	C	N	O	S	0	0	0
			729	457	146	124	2			

- Molecule 16 is a protein called ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	P	83	Total	C	N	O	S	0	0	0
			700	443	139	117	1			

- Molecule 17 is a protein called ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	Q	99	Total	C	N	O	S	0	0	0
			823	528	152	141	2			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	96	GLN	GLU	conflict	UNP Q5SHP7

- Molecule 18 is a protein called ribosomal protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	R	70	Total	C	N	O	0	0	0
			574	367	112	95			

- Molecule 19 is a protein called ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	S	80	Total	C	N	O	S	0	0	0
			647	414	119	112	2			

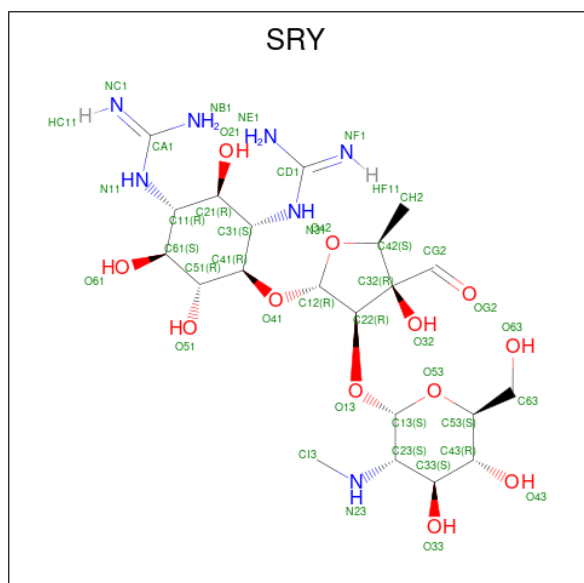
- Molecule 20 is a protein called ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	T	99	Total	C	N	O	S	0	0	0
			763	470	162	129	2			

- Molecule 21 is a protein called ribosomal protein THX.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	U	24	Total	C	N	O	0	0	0
			208	128	50	30			

- Molecule 22 is STREPTOMYCIN (three-letter code: SRY) (formula: $C_{21}H_{39}N_7O_{12}$).



- Molecule 23 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
23	A	253	Total 253	Mg 253	0	0
23	B	2	Total 2	Mg 2	0	0
23	D	1	Total 1	Mg 1	0	0
23	E	1	Total 1	Mg 1	0	0
23	H	4	Total 4	Mg 4	0	0
23	J	2	Total 2	Mg 2	0	0
23	M	2	Total 2	Mg 2	0	0
23	N	1	Total 1	Mg 1	0	0
23	P	3	Total 3	Mg 3	0	0
23	Q	1	Total 1	Mg 1	0	0
23	S	1	Total 1	Mg 1	0	0
23	T	2	Total 2	Mg 2	0	0

- Molecule 24 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
24	D	1	Total 1	Zn 1	0	0
24	N	1	Total 1	Zn 1	0	0

- Molecule 25 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
25	A	374	Total 374	O 374	0	0
25	B	1	Total 1	O 1	0	0
25	D	1	Total 1	O 1	0	0

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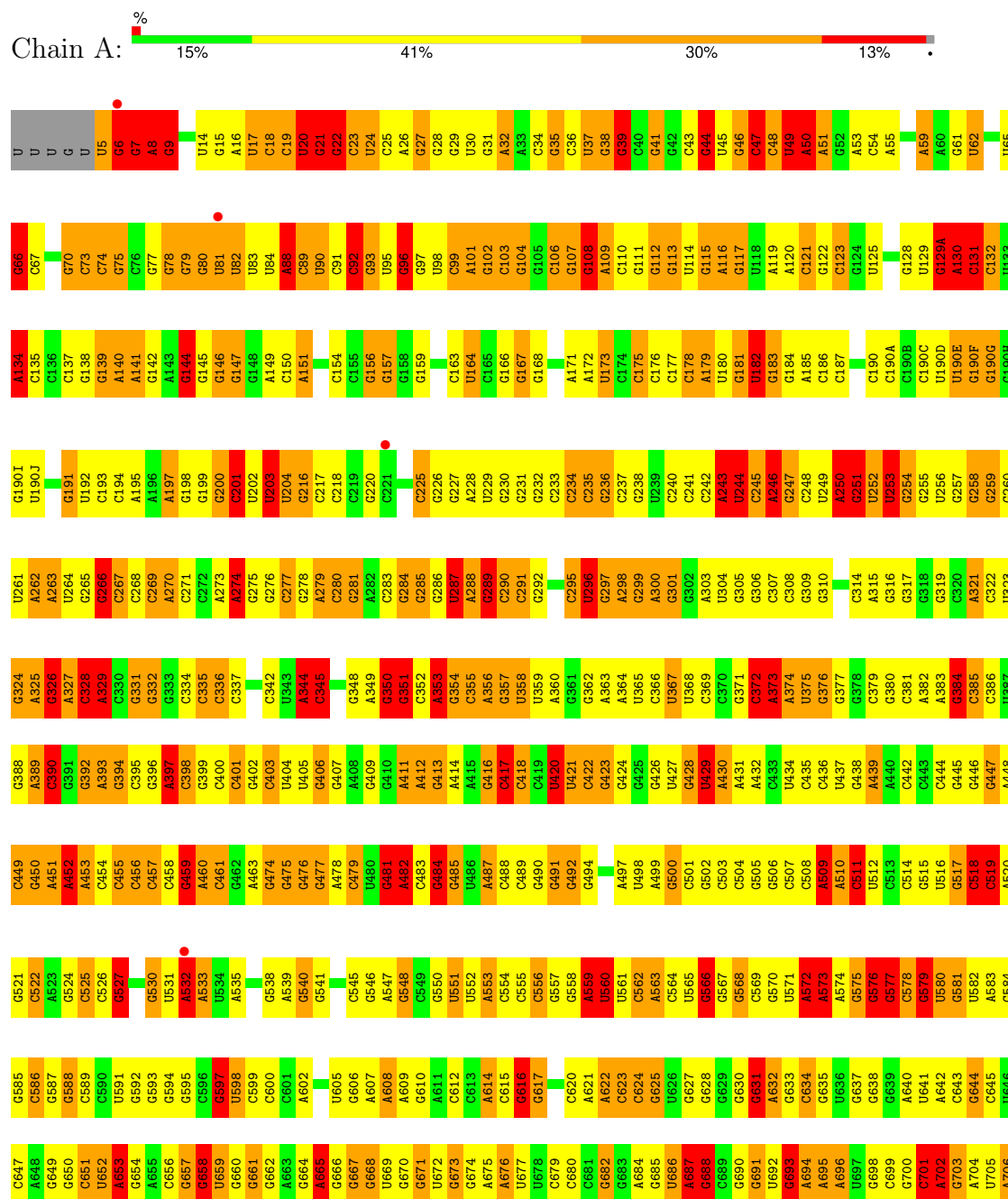
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
25	E	7	Total	O	0	0
			7	7		
25	L	1	Total	O	0	0
			1	1		
25	N	1	Total	O	0	0
			1	1		
25	P	2	Total	O	0	0
			2	2		
25	T	2	Total	O	0	0
			2	2		

3 Residue-property plots [i](#)

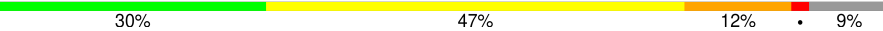
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

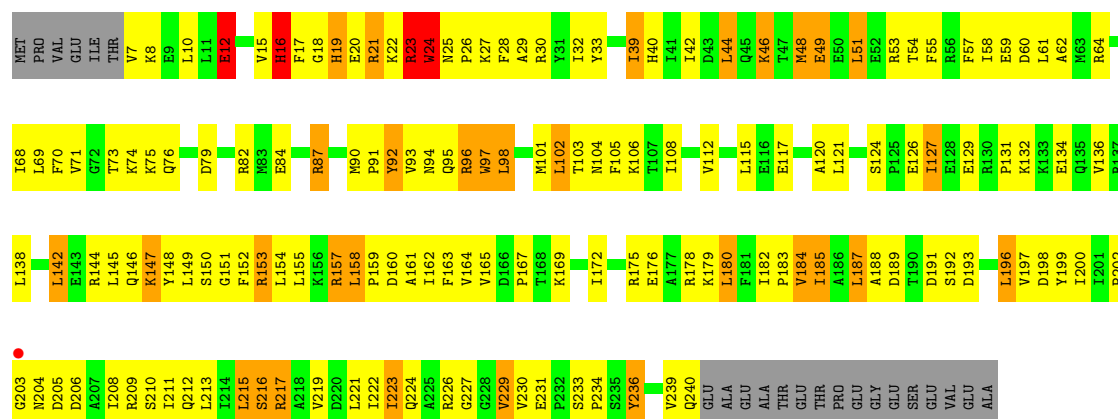
• Molecule 1: 16S rRNA



A1451	C1452	A1453	G1454	C1455	G1456	A1457	C1458	G1459	A1460	C1461	G1462	C1463	A1464	C1465	G1466	A1467	C1468	G1469	A1470	C1471	A1472	C1473	G1474	A1475	C1476	G1477	A1478	C1479	G1480	A1481	C1482	A1483	C1484	G1485	A1486	C1487	G1488	A1489	C1490	G1491	A1492	C1493	G1494	A1495	C1496	G1497	A1498	C1499	A1500	C1501	A1502	C1503	G1504	C1505	A1506	C1507	G1508	C1509	A1510	C1511	G1512	C1513	A1514	C1515	G1516	C1517	A1518	C1519	G1520	C1521	A1522	G1523	C1524	A1525	G1526	C1527	A1528	C1529	G1530	A1531	C1532	G1533	C	A	C	U	C	A1539	G1540	C1541	A1542	C1543	G1544																																																																																																																																																																																																																																																																																																																																									
U1381	C1322	C1260	U1199	G1138	G1077	C1019	G954	C894	A828	C768	C707	U1382	C1323	A1261	C1200	U1201	G1202	C1203	G1141	G1142	G1143	G1144	G1145	G1146	G1147	G1148	C1149	U1150	A1151	C1152	G1153	G1154	G1155	G1156	U1157	C1158	G1159	C1160	G1161	C1162	A1163	G1164	C1165	G1166	A1167	G1168	C1169	U1170	A1171	C1172	G1173	C1174	G1175	C1176	G1177	C1178	G1179	A1180	C1181	G1182	C1183	A1184	G1185	C1186	G1187	A1188	C1189	G1190	C1191	A1192	G1193	C1194	A1195	G1196	C1197	A1198	C1199	G1200	C1201	A1202	G1203	C1204	A1205	G1206	C1207	A1208	G1209	C1210	A1211	C1212	G1213	A1214	C1215	G1216	A1217	C1218	G1219	C1220	A1221	G1222	C1223	G1224	A1225	C1226	G1227	A1228	C1229	G1230	A1231	C1232	G1233	A1234	C1235	G1236	A1237	C1238	G1239	A1240	C1241	G1242	A1243	C1244	G1245	A1246	C1247	G1248	A1249	C1250	G1251	A1252	C1253	G1254	A1255	C1256	G1257	A1258	C1259	G1260	A1261	C1262	G1263	A1264	C1265	G1266	A1267	C1268	G1269	A1270	C1271	G1272	A1273	C1274	G1275	A1276	C1277	G1278	A1279	C1280	G1281	A1282	C1283	G1284	A1285	C1286	G1287	A1288	C1289	G1290	A1291	C1292	G1293	A1294	C1295	G1296	A1297	C1298	G1299	A1300	C1301	G1302	A1303	C1304	G1305	A1306	C1307	G1308	A1309	C1310	G1311	A1312	C1313	G1314	A1315	C1316	G1317	A1318	C1319	G1320	A1321	C1322	G1323	A1324	C1325	G1326	A1327	C1328	G1329	A1330	C1331	G1332	A1333	C1334	G1335	A1336	C1337	G1338	A1339	C1340	G1341	A1342	C1343	G1344	A1345	C1346	G1347	A1348	C1349	G1350	A1351	C1352	G1353	A1354	C1355	G1356	A1357	C1358	G1359	A1360	C1361	G1362	A1363	C1364	G1365	A1366	C1367	G1368	A1369	C1370	G1371	A1372	C1373	G1374	A1375	C1376	G1377	A1378	C1379	G1380	A1381	C1382	G1383	A1384	C1385	G1386	A1387	C1388	G1389	A1390	C1391	G1392	A1393	C1394	G1395	A1396	C1397	G1398	A1399	C1400	G1401	A1402	C1403	G1404	A1405	C1406	G1407	A1408	C1409	G1410	A1411	C1412	G1413	A1414	C1415	G1416	A1417	C1418	G1419	A1420	C1421	G1422	A1423	C1424	G1425	A1426	C1427	G1428	A1429	C1430	G1431	A1432	C1433	G1434	A1435	C1436	G1437	A1438	C1439	G1440	A1441	C1442	G1443	A1444	C1445	G1446	A1447	C1448	G1449	A1450	C1451	G1452	A1453	C1454	G1455	A1456	C1457	G1458	A1459	C1460	G1461	A1462	C1463	G1464	A1465	C1466	G1467	A1468	C1469	G1470	A1471	C1472	G1473	A1474	C1475	G1476	A1477	C1478	G1479	A1480	C1481	G1482	A1483	C1484	G1485	A1486	C1487	G1488	A1489	C1490	G1491	A1492	C1493	G1494	A1495	C1496	G1497	A1498	C1499	G1500	A1501	C1502	G1503	A1504	C1505	G1506	A1507	C1508	G1509	A1510	C1511	G1512	A1513	C1514	G1515	A1516	C1517	G1518	A1519	C1520	G1521	A1522	C1523	G1524	A1525	C1526	G1527	A1528	C1529	G1530	A1531	C1532	G1533	C	A	C	U	C	A1539	G1540	C1541	A1542	C1543	G1544
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U1381	C1322	C1260	U1199	G1138	G1077	C1019	G954	C894	A828	C768	C707	U1382	C1323	A1261	C1200	U1201	G1202	C1203																																																																																																																																																																																																																																																																																																																																																																																																																				

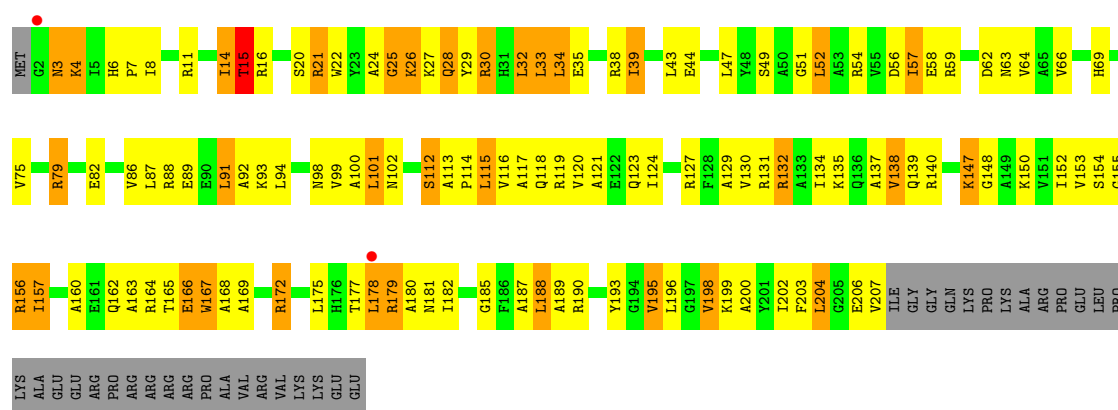
- Molecule 2: ribosomal protein S2

Chain B: 




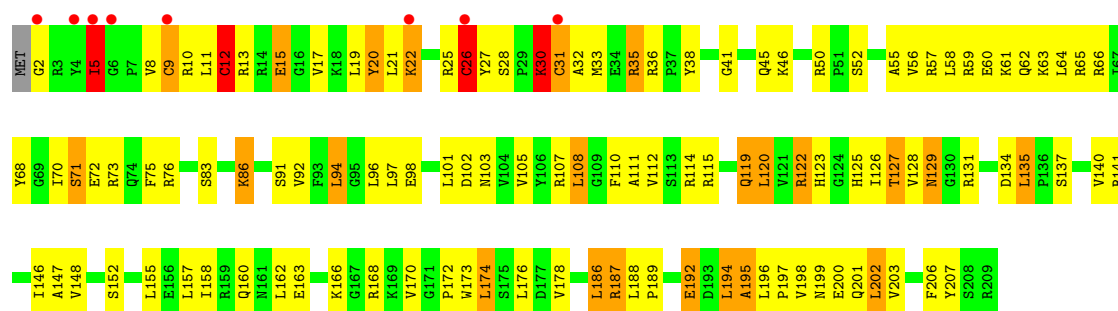
• Molecule 3: ribosomal protein S3

Chain C: 




• Molecule 4: ribosomal protein S4

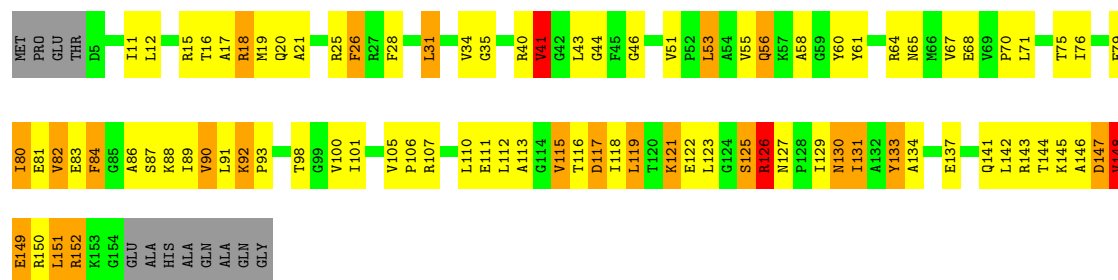
Chain D: 



• Molecule 5: ribosomal protein S5

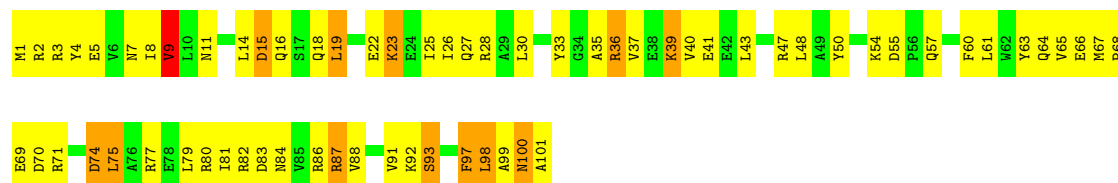
Chain E: 





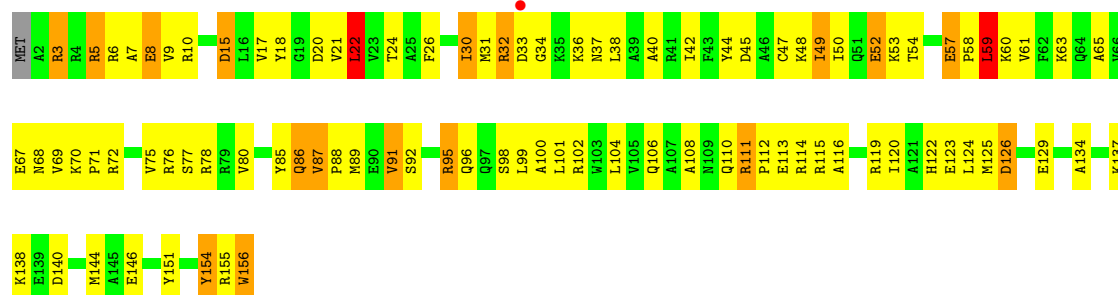
• Molecule 6: ribosomal protein S6

Chain F: 35% 52% 12%



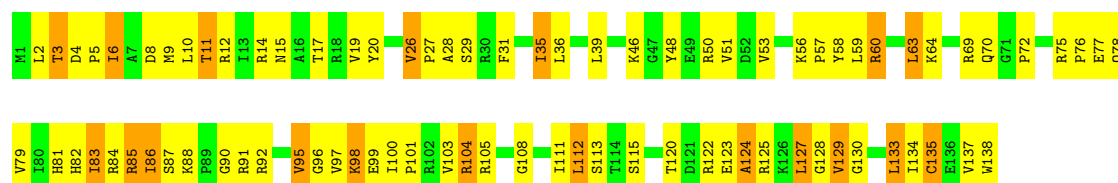
• Molecule 7: ribosomal protein S7

Chain G: 39% 48% 11%



• Molecule 8: ribosomal protein S8

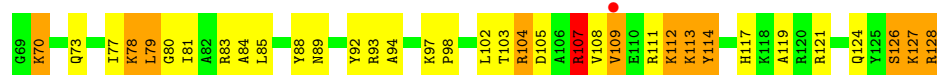
Chain H: 40% 46% 14%



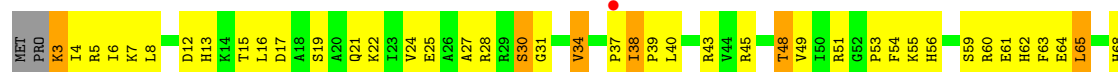
• Molecule 9: ribosomal protein S9

Chain I: 41% 45% 12%

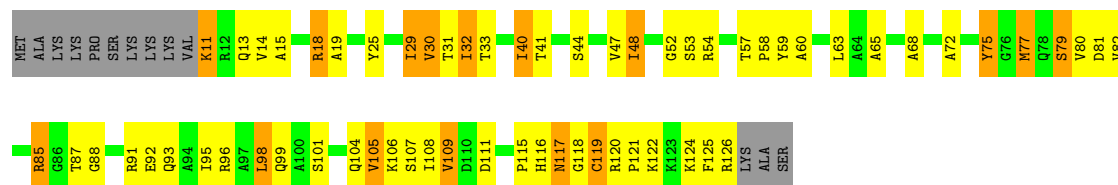




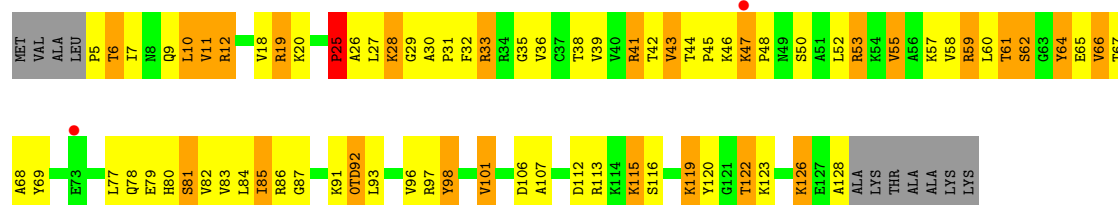
• Molecule 10: ribosomal protein S10



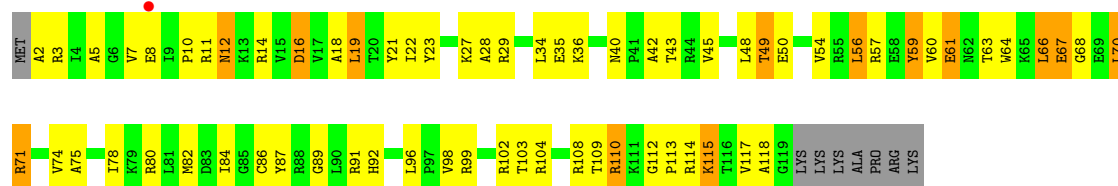
• Molecule 11: ribosomal protein S11



• Molecule 12: ribosomal protein S12



• Molecule 13: ribosomal protein S13

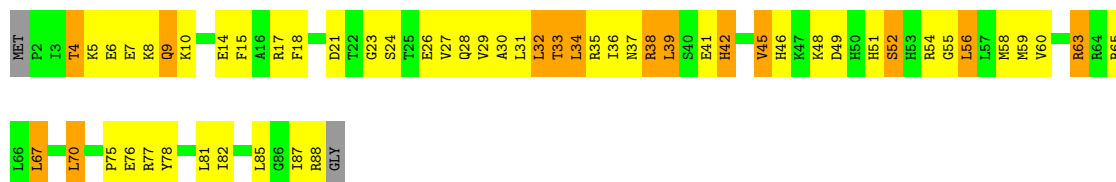


• Molecule 14: ribosomal protein S14

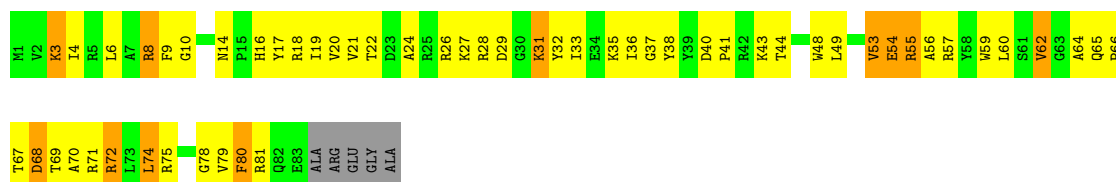




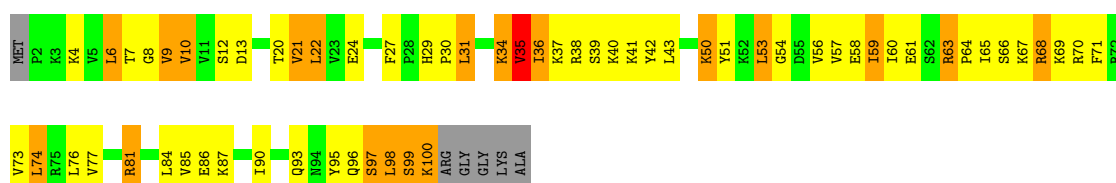
• Molecule 15: ribosomal protein S15



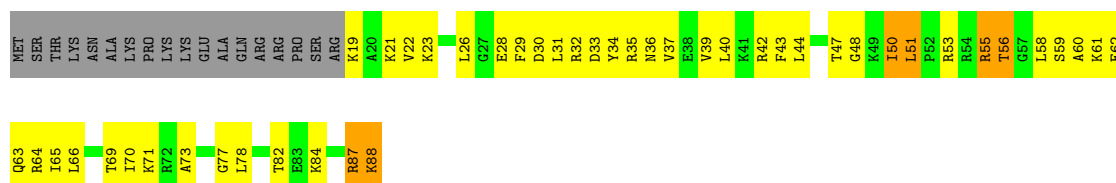
• Molecule 16: ribosomal protein S16



• Molecule 17: ribosomal protein S17

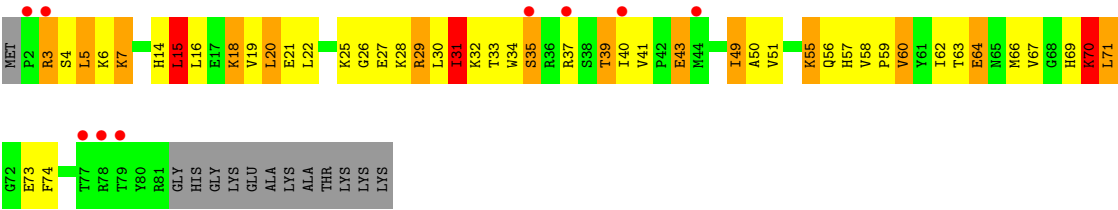


• Molecule 18: ribosomal protein S18



• Molecule 19: ribosomal protein S19

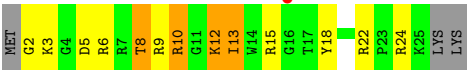




● Molecule 20: ribosomal protein S20



● Molecule 21: ribosomal protein THX



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	402.13Å 402.13Å 172.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.55 – 3.68 34.55 – 3.68	Depositor EDS
% Data completeness (in resolution range)	98.1 (34.55-3.68) 97.7 (34.55-3.68)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.92 (at 3.66Å)	Xtriage
Refinement program	PHENIX dev_978	Depositor
R, R_{free}	0.156 , 0.211 0.155 , 0.210	Depositor DCC
R_{free} test set	7392 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	122.3	Xtriage
Anisotropy	0.371	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 122.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	52300	wwPDB-VP
Average B, all atoms (Å ²)	148.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.44% 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: ZN, PSU, SRY, 7MG, MA6, 0TD, UR3, M2G, 2MG, MG, 5MC, 4OC

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	1.41	334/36041 (0.9%)	2.16	2692/56245 (4.8%)
2	B	0.91	1/1935 (0.1%)	1.06	7/2609 (0.3%)
3	C	0.70	0/1636	0.94	4/2205 (0.2%)
4	D	0.92	3/1733 (0.2%)	1.12	7/2318 (0.3%)
5	E	1.15	5/1162 (0.4%)	1.21	4/1564 (0.3%)
6	F	0.79	0/856	0.97	1/1154 (0.1%)
7	G	0.75	1/1276 (0.1%)	0.92	2/1709 (0.1%)
8	H	1.19	2/1136 (0.2%)	1.21	4/1527 (0.3%)
9	I	0.74	0/1029	0.98	1/1379 (0.1%)
10	J	0.70	0/805	0.95	0/1082
11	K	0.84	1/879 (0.1%)	1.05	1/1187 (0.1%)
12	L	0.97	1/977 (0.1%)	1.18	3/1306 (0.2%)
13	M	0.77	1/947 (0.1%)	0.95	0/1270
14	N	0.68	0/501	0.92	0/664
15	O	0.86	0/740	1.06	2/987 (0.2%)
16	P	0.95	1/716 (0.1%)	1.10	2/963 (0.2%)
17	Q	1.16	1/836 (0.1%)	1.32	9/1117 (0.8%)
18	R	0.81	0/579	0.97	0/768
19	S	0.67	0/661	0.90	1/890 (0.1%)
20	T	0.86	0/765	1.10	1/1007 (0.1%)
21	U	0.59	0/212	0.84	0/277
All	All	1.25	351/55422 (0.6%)	1.88	2741/82228 (3.3%)

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
3	C	0	2
4	D	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
7	G	0	1
8	H	0	1
9	I	0	1
10	J	0	2
12	L	0	1
17	Q	0	1
20	T	0	1
All	All	0	11

The worst 5 of 351 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	279	A	N9-C4	-14.20	1.29	1.37
1	A	1502	A	N9-C4	-12.65	1.30	1.37
1	A	917	G	N9-C4	-10.97	1.29	1.38
8	H	135	CYS	CB-SG	-10.53	1.64	1.82
1	A	1513	A	N9-C4	-10.06	1.31	1.37

The worst 5 of 2741 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	117	G	N1-C6-O6	20.89	132.43	119.90
1	A	279	A	C5-N7-C8	-17.64	95.08	103.90
1	A	1505	G	C8-N9-C4	-17.36	99.45	106.40
1	A	117	G	C5-C6-N1	-16.75	103.12	111.50
1	A	117	G	C2-N3-C4	-16.57	103.61	111.90

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	166	GLU	Peptide
3	C	24	ALA	Peptide
4	D	195	ALA	Peptide
7	G	154	TYR	Peptide
8	H	90	GLY	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32508	0	16426	863	0
2	B	1900	0	1951	117	0
3	C	1612	0	1677	93	0
4	D	1703	0	1763	100	0
5	E	1146	0	1207	73	0
6	F	843	0	857	55	0
7	G	1257	0	1296	76	0
8	H	1116	0	1177	70	0
9	I	1010	0	1037	76	0
10	J	792	0	835	50	0
11	K	864	0	881	51	0
12	L	972	0	1058	67	0
13	M	937	0	995	55	0
14	N	492	0	529	49	0
15	O	729	0	768	47	0
16	P	700	0	720	48	0
17	Q	823	0	893	52	0
18	R	574	0	644	47	0
19	S	647	0	673	37	0
20	T	763	0	861	49	0
21	U	208	0	221	20	0
22	A	40	0	37	7	0
23	A	253	0	0	0	0
23	B	2	0	0	0	0
23	D	1	0	0	0	0
23	E	1	0	0	0	0
23	H	4	0	0	0	0
23	J	2	0	0	0	0
23	M	2	0	0	0	0
23	N	1	0	0	0	0
23	P	3	0	0	0	0
23	Q	1	0	0	0	0
23	S	1	0	0	0	0
23	T	2	0	0	0	0
24	D	1	0	0	0	0
24	N	1	0	0	0	0
25	A	374	0	0	14	0
25	B	1	0	0	0	0
25	D	1	0	0	0	0
25	E	7	0	0	0	0
25	L	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	N	1	0	0	0	0
25	P	2	0	0	0	0
25	T	2	0	0	1	0
All	All	52300	0	36506	1903	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 22.

The worst 5 of 1903 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)
18:R:26:LEU:HD11	18:R:42:ARG:HD3	1.46	0.98
1:A:792:A:H1'	1:A:793:U:H2'	1.47	0.96
11:K:48:ILE:HD12	11:K:63:LEU:HB2	1.45	0.96
1:A:1326:C:OP2	21:U:6:ARG:NH2	2.00	0.93
12:L:87:GLY:HA2	12:L:98:TYR:HA	1.51	0.92

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	
2	B	232/256 (91%)	199 (86%)	30 (13%)	3 (1%)	10	39
3	C	204/239 (85%)	172 (84%)	30 (15%)	2 (1%)	13	44
4	D	206/209 (99%)	186 (90%)	17 (8%)	3 (2%)	8	37
5	E	148/162 (91%)	137 (93%)	9 (6%)	2 (1%)	9	38
6	F	99/101 (98%)	96 (97%)	3 (3%)	0	100	100
7	G	153/156 (98%)	137 (90%)	15 (10%)	1 (1%)	19	51
8	H	136/138 (99%)	129 (95%)	7 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	I	125/128 (98%)	112 (90%)	12 (10%)	1 (1%)	16	48
10	J	96/105 (91%)	74 (77%)	20 (21%)	2 (2%)	5	32
11	K	114/129 (88%)	98 (86%)	16 (14%)	0	100	100
12	L	121/135 (90%)	105 (87%)	14 (12%)	2 (2%)	7	35
13	M	116/126 (92%)	103 (89%)	10 (9%)	3 (3%)	4	28
14	N	58/61 (95%)	48 (83%)	10 (17%)	0	100	100
15	O	85/89 (96%)	75 (88%)	10 (12%)	0	100	100
16	P	81/88 (92%)	74 (91%)	6 (7%)	1 (1%)	11	41
17	Q	97/105 (92%)	90 (93%)	7 (7%)	0	100	100
18	R	68/88 (77%)	60 (88%)	8 (12%)	0	100	100
19	S	78/93 (84%)	70 (90%)	5 (6%)	3 (4%)	2	22
20	T	97/106 (92%)	81 (84%)	16 (16%)	0	100	100
21	U	22/27 (82%)	20 (91%)	2 (9%)	0	100	100
All	All	2336/2541 (92%)	2066 (88%)	247 (11%)	23 (1%)	13	44

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
19	S	31	ILE
19	S	70	LYS
2	B	21	ARG
2	B	24	TRP
3	C	15	THR

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	
2	B	202/220 (92%)	146 (72%)	56 (28%)	0	2
3	C	160/188 (85%)	107 (67%)	53 (33%)	0	1
4	D	180/181 (99%)	141 (78%)	39 (22%)	1	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	115/123 (94%)	78 (68%)	37 (32%)	0	1
6	F	90/90 (100%)	66 (73%)	24 (27%)	0	3
7	G	126/127 (99%)	92 (73%)	34 (27%)	0	3
8	H	119/119 (100%)	89 (75%)	30 (25%)	0	4
9	I	98/99 (99%)	77 (79%)	21 (21%)	1	6
10	J	87/92 (95%)	71 (82%)	16 (18%)	1	8
11	K	88/99 (89%)	66 (75%)	22 (25%)	0	4
12	L	103/110 (94%)	73 (71%)	30 (29%)	0	2
13	M	94/101 (93%)	71 (76%)	23 (24%)	0	4
14	N	49/50 (98%)	41 (84%)	8 (16%)	2	12
15	O	79/80 (99%)	61 (77%)	18 (23%)	0	5
16	P	72/74 (97%)	60 (83%)	12 (17%)	2	11
17	Q	94/97 (97%)	71 (76%)	23 (24%)	0	4
18	R	61/77 (79%)	45 (74%)	16 (26%)	0	3
19	S	71/80 (89%)	50 (70%)	21 (30%)	0	2
20	T	76/82 (93%)	54 (71%)	22 (29%)	0	2
21	U	19/22 (86%)	15 (79%)	4 (21%)	1	6
All	All	1983/2111 (94%)	1474 (74%)	509 (26%)	0	4

5 of 509 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	G	91	VAL
17	Q	96	GLN
9	I	107	ARG
17	Q	74	LEU
19	S	41	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
10	J	62	HIS
17	Q	16	GLN
19	S	14	HIS
18	R	63	GLN

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Mol	Chain	Res	Type
8	H	82	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1508/1522 (99%)	422 (27%)	62 (4%)

5 of 422 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	G
1	A	7	G
1	A	8	A
1	A	9	G
1	A	21	G

5 of 62 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	687	A
1	A	1346	A
1	A	975	A
1	A	1335	C
1	A	1504	G

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

15 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	7MG	A	527	1	23,26,27	4.20	4 (17%)	27,39,42	2.38	9 (33%)
1	PSU	A	516	1,23	18,21,22	1.70	2 (11%)	21,30,33	1.31	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	5MC	A	1404	1	19,22,23	1.47	4 (21%)	26,32,35	1.18	4 (15%)
1	5MC	A	967	1	19,22,23	1.38	2 (10%)	26,32,35	0.68	0
1	2MG	A	1207	1	18,26,27	2.04	4 (22%)	16,38,41	1.49	3 (18%)
1	4OC	A	1402	1	20,23,24	1.42	5 (25%)	25,32,35	0.85	2 (8%)
1	5MC	A	1407	1	19,22,23	1.33	2 (10%)	26,32,35	1.40	4 (15%)
1	PSU	A	1540	1	18,21,22	1.27	1 (5%)	21,30,33	1.99	4 (19%)
1	5MC	A	1400	1	19,22,23	1.55	3 (15%)	26,32,35	1.17	1 (3%)
1	M2G	A	966	1	20,27,28	0.69	0	19,40,43	1.70	2 (10%)
1	UR3	A	1498	1,23	19,22,23	1.29	4 (21%)	26,32,35	1.14	2 (7%)
12	0TD	L	92	12	8,9,10	1.67	3 (37%)	6,11,13	3.95	4 (66%)
1	PSU	A	1541	1	18,21,22	1.53	2 (11%)	21,30,33	2.20	6 (28%)
1	MA6	A	1519	1	19,26,27	1.90	5 (26%)	18,38,41	0.81	1 (5%)
1	MA6	A	1518	1	19,26,27	1.16	1 (5%)	18,38,41	1.05	2 (11%)

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	7MG	A	527	1	-	2/7/37/38	0/3/3/3
1	PSU	A	516	1,23	-	0/7/25/26	0/2/2/2
1	5MC	A	1404	1	-	0/7/25/26	0/2/2/2
1	5MC	A	967	1	-	0/7/25/26	0/2/2/2
1	2MG	A	1207	1	-	0/5/27/28	0/3/3/3
1	4OC	A	1402	1	-	2/9/29/30	0/2/2/2
1	5MC	A	1407	1	-	0/7/25/26	0/2/2/2
1	PSU	A	1540	1	-	3/7/25/26	0/2/2/2
1	5MC	A	1400	1	-	2/7/25/26	0/2/2/2
1	M2G	A	966	1	-	0/7/29/30	0/3/3/3
1	UR3	A	1498	1,23	-	0/7/25/26	0/2/2/2
12	0TD	L	92	12	-	2/7/12/14	-
1	PSU	A	1541	1	-	3/7/25/26	0/2/2/2
1	MA6	A	1519	1	-	4/7/29/30	0/3/3/3
1	MA6	A	1518	1	-	3/7/29/30	0/3/3/3

The worst 5 of 42 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	527	7MG	C8-N9	-18.09	1.34	1.45
1	A	516	PSU	C6-C5	5.58	1.41	1.35
1	A	1207	2MG	C2-N1	5.45	1.45	1.36
1	A	527	7MG	C5-N7	5.44	1.42	1.35
1	A	1541	PSU	C6-C5	4.99	1.40	1.35

The worst 5 of 48 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	L	92	0TD	CSB-SB-CB	-6.96	89.85	102.36
1	A	1541	PSU	C6-C5-C4	-6.84	113.56	118.17
12	L	92	0TD	CB-CA-N	-6.03	96.88	109.10
1	A	527	7MG	C5-C6-N1	5.37	120.39	110.94
1	A	1540	PSU	O2-C2-N1	-4.98	117.65	122.79

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1402	4OC	O4'-C4'-C5'-O5'
1	A	1518	MA6	C5-C6-N6-C10
1	A	1519	MA6	C5-C6-N6-C10
1	A	1519	MA6	N1-C6-N6-C9
1	A	1541	PSU	O4'-C4'-C5'-O5'

There are no ring outliers.

13 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	527	7MG	2	0
1	A	1404	5MC	7	0
1	A	967	5MC	1	0
1	A	1402	4OC	1	0
1	A	1407	5MC	1	0
1	A	1540	PSU	2	0
1	A	1400	5MC	1	0
1	A	966	M2G	1	0
1	A	1498	UR3	2	0
12	L	92	0TD	2	0
1	A	1541	PSU	2	0
1	A	1519	MA6	3	0
1	A	1518	MA6	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 276 ligands modelled in this entry, 275 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	$\# Z > 2$
22	SRY	A	1601	-	40,42,42	2.44	10 (25%)	49,63,63	2.78	22 (44%)

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 Torsions and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	SRY	A	1601	-	-	2/20/87/87	0/3/3/3

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	A	1601	SRY	CD1-N31	9.88	1.50	1.33
22	A	1601	SRY	CA1-N11	6.03	1.43	1.33
22	A	1601	SRY	O53-C53	-4.20	1.34	1.44
22	A	1601	SRY	CA1-NB1	3.36	1.46	1.34
22	A	1601	SRY	C11-N11	-3.34	1.40	1.45

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	A	1601	SRY	O13-C13-C23	7.13	119.64	108.07
22	A	1601	SRY	C13-O13-C22	-6.53	105.15	116.26
22	A	1601	SRY	C11-N11-CA1	-6.09	111.33	123.39
22	A	1601	SRY	C12-O42-C42	-5.59	99.45	108.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	A	1601	SRY	CI3-N23-C23	-5.12	107.62	114.23

There are no chirality outliers.

All (2) torsion outliers are listed below:

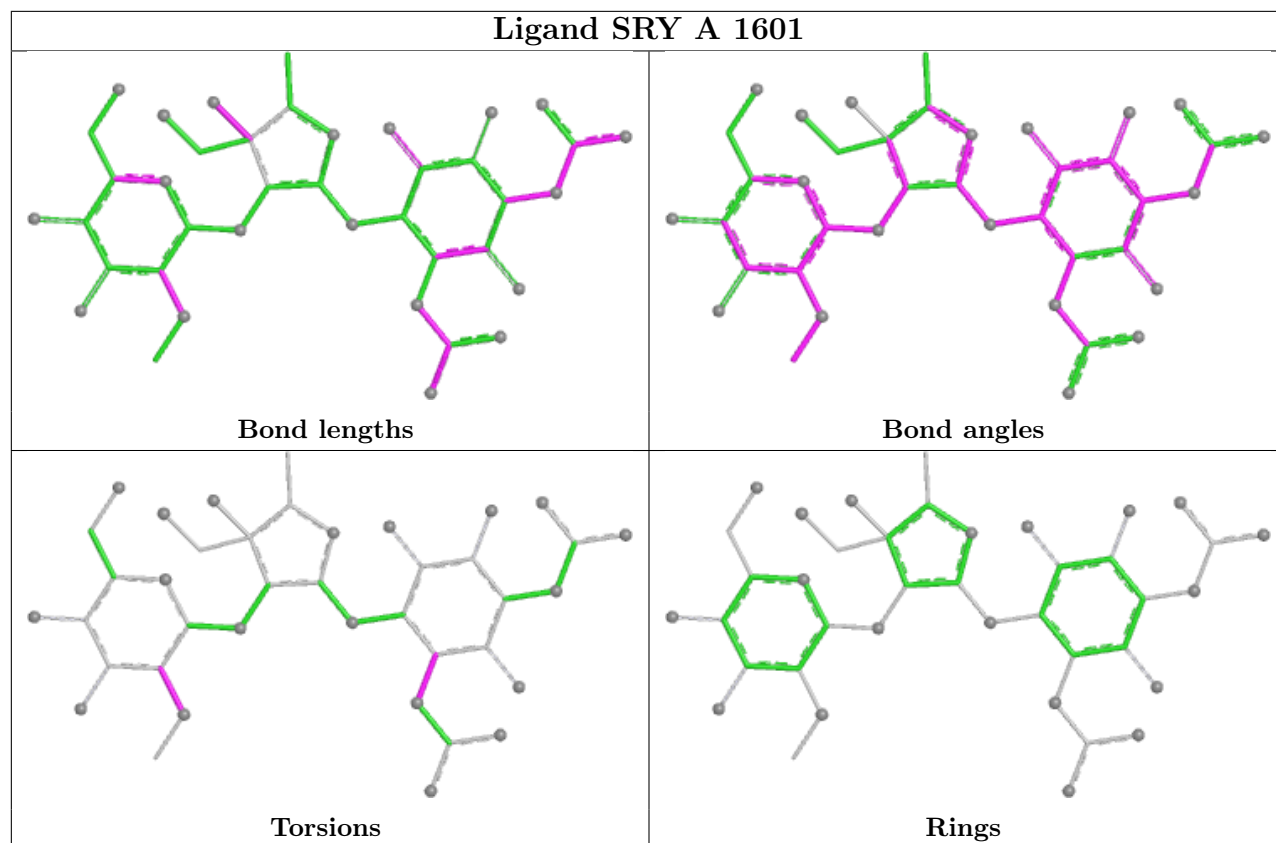
Mol	Chain	Res	Type	Atoms
22	A	1601	SRY	C13-C23-N23-CI3
22	A	1601	SRY	C21-C31-N31-CD1

There are no ring outliers.

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
22	A	1601	SRY	7	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	A	1498/1522 (98%)	-0.59	11 (0%) 84 68	74, 131, 262, 364	0
2	B	234/256 (91%)	-0.65	1 (0%) 89 76	82, 143, 231, 264	0
3	C	206/239 (86%)	-0.41	2 (0%) 79 61	123, 191, 239, 272	0
4	D	208/209 (99%)	-0.33	8 (3%) 44 32	85, 134, 177, 200	0
5	E	150/162 (92%)	-0.88	0 100 100	73, 106, 144, 182	0
6	F	101/101 (100%)	-0.79	0 100 100	106, 153, 181, 203	0
7	G	155/156 (99%)	-0.48	1 (0%) 85 70	128, 180, 226, 251	0
8	H	138/138 (100%)	-0.88	0 100 100	68, 96, 145, 159	0
9	I	127/128 (99%)	-0.31	3 (2%) 59 42	126, 199, 236, 258	0
10	J	98/105 (93%)	-0.13	1 (1%) 79 61	165, 229, 278, 305	0
11	K	116/129 (89%)	-0.52	0 100 100	94, 131, 177, 219	0
12	L	123/135 (91%)	-0.49	2 (1%) 70 51	71, 124, 172, 206	0
13	M	118/126 (93%)	-0.39	1 (0%) 82 66	122, 164, 204, 231	0
14	N	60/61 (98%)	-0.20	0 100 100	133, 189, 234, 267	0
15	O	87/89 (97%)	-0.79	0 100 100	74, 122, 165, 180	0
16	P	83/88 (94%)	-0.59	0 100 100	92, 125, 166, 203	0
17	Q	99/105 (94%)	-0.73	0 100 100	84, 107, 140, 168	0
18	R	70/88 (79%)	-0.84	0 100 100	92, 129, 180, 220	0
19	S	80/93 (86%)	0.14	9 (11%) 11 12	174, 217, 268, 283	0
20	T	99/106 (93%)	-0.55	1 (1%) 79 61	95, 130, 179, 210	0
21	U	24/27 (88%)	0.48	1 (4%) 41 30	151, 187, 219, 221	0
All	All	3874/4063 (95%)	-0.54	41 (1%) 77 59	68, 141, 239, 364	0

The worst 5 of 41 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
10	J	37	PRO	6.0
1	A	1129	C	5.7
20	T	106	ALA	4.9
12	L	73	GLU	4.8
19	S	2	PRO	4.3

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	PSU	A	1541	20/21	0.78	0.18	159,231,317,318	0
1	PSU	A	1540	20/21	0.80	0.21	207,241,323,324	0
1	MA6	A	1519	24/25	0.95	0.09	105,122,132,134	0
1	UR3	A	1498	21/22	0.96	0.10	112,123,141,146	0
1	PSU	A	516	20/21	0.96	0.08	110,141,152,153	0
1	2MG	A	1207	24/25	0.96	0.15	175,210,229,233	0
1	5MC	A	1404	21/22	0.96	0.13	114,124,129,132	0
1	MA6	A	1518	24/25	0.97	0.08	121,127,148,148	0
1	M2G	A	966	25/26	0.97	0.08	123,141,169,173	0
1	5MC	A	1407	21/22	0.97	0.07	136,148,157,159	0
1	7MG	A	527	24/25	0.97	0.07	103,112,124,131	0
1	5MC	A	1400	21/22	0.98	0.06	95,124,131,135	0
1	4OC	A	1402	22/23	0.98	0.07	108,117,120,127	0
1	5MC	A	967	21/22	0.98	0.07	129,133,145,149	0
12	0TD	L	92	10/11	0.99	0.07	87,120,138,251	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [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(\AA^2)	Q<0.9
23	MG	A	1853	1/1	-0.12	0.13	338,338,338,338	0
23	MG	A	1837	1/1	0.65	0.27	103,103,103,103	0
23	MG	A	1731	1/1	0.66	0.18	95,95,95,95	0
23	MG	A	1783	1/1	0.69	0.27	133,133,133,133	0
23	MG	A	1800	1/1	0.71	0.13	108,108,108,108	0
23	MG	A	1661	1/1	0.74	0.29	89,89,89,89	0
23	MG	H	204	1/1	0.74	0.31	105,105,105,105	0
23	MG	A	1761	1/1	0.75	0.24	97,97,97,97	0
23	MG	A	1765	1/1	0.76	0.26	124,124,124,124	0
23	MG	A	1737	1/1	0.76	0.18	128,128,128,128	0
23	MG	A	1748	1/1	0.77	0.08	143,143,143,143	0
23	MG	A	1755	1/1	0.77	0.10	159,159,159,159	0
23	MG	A	1715	1/1	0.77	0.33	120,120,120,120	0
23	MG	A	1788	1/1	0.79	0.29	99,99,99,99	0
23	MG	A	1767	1/1	0.80	0.13	93,93,93,93	0
23	MG	A	1713	1/1	0.80	0.46	96,96,96,96	0
23	MG	A	1702	1/1	0.80	0.21	106,106,106,106	0
23	MG	A	1796	1/1	0.80	0.55	107,107,107,107	0
23	MG	A	1718	1/1	0.81	0.13	95,95,95,95	0
23	MG	A	1821	1/1	0.82	0.15	338,338,338,338	0
23	MG	Q	201	1/1	0.82	0.11	115,115,115,115	0
23	MG	A	1624	1/1	0.83	0.20	97,97,97,97	0
23	MG	A	1794	1/1	0.83	0.20	127,127,127,127	0
23	MG	A	1698	1/1	0.83	0.19	170,170,170,170	0
23	MG	A	1782	1/1	0.84	0.11	108,108,108,108	0
23	MG	A	1671	1/1	0.84	0.47	125,125,125,125	0
23	MG	A	1801	1/1	0.84	0.21	111,111,111,111	0
23	MG	A	1795	1/1	0.84	0.13	107,107,107,107	0
23	MG	A	1730	1/1	0.85	0.23	91,91,91,91	0
23	MG	A	1699	1/1	0.85	0.12	221,221,221,221	0
23	MG	A	1798	1/1	0.85	0.16	122,122,122,122	0
23	MG	A	1792	1/1	0.85	0.12	111,111,111,111	0
23	MG	A	1720	1/1	0.85	0.16	112,112,112,112	0
23	MG	A	1741	1/1	0.86	0.41	113,113,113,113	0
23	MG	A	1727	1/1	0.86	0.18	95,95,95,95	0
23	MG	A	1832	1/1	0.86	0.37	109,109,109,109	0
23	MG	A	1682	1/1	0.86	0.07	171,171,171,171	0
23	MG	A	1847	1/1	0.86	0.19	296,296,296,296	0
23	MG	A	1797	1/1	0.86	0.23	127,127,127,127	0
23	MG	A	1709	1/1	0.86	0.73	117,117,117,117	0
23	MG	P	102	1/1	0.86	0.12	100,100,100,100	0
23	MG	P	103	1/1	0.86	0.10	102,102,102,102	0
23	MG	A	1685	1/1	0.86	0.08	269,269,269,269	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
23	MG	A	1760	1/1	0.87	0.41	105,105,105,105	0
23	MG	A	1739	1/1	0.87	0.68	92,92,92,92	0
23	MG	A	1667	1/1	0.87	0.16	100,100,100,100	0
23	MG	A	1623	1/1	0.88	0.16	146,146,146,146	0
23	MG	A	1726	1/1	0.88	0.23	91,91,91,91	0
23	MG	B	301	1/1	0.88	0.13	110,110,110,110	0
23	MG	D	302	1/1	0.88	0.16	123,123,123,123	0
23	MG	A	1665	1/1	0.88	0.11	176,176,176,176	0
23	MG	N	102	1/1	0.88	0.08	112,112,112,112	0
23	MG	A	1696	1/1	0.88	0.18	141,141,141,141	0
23	MG	A	1753	1/1	0.88	0.09	168,168,168,168	0
23	MG	A	1706	1/1	0.88	0.22	97,97,97,97	0
23	MG	A	1768	1/1	0.89	0.17	112,112,112,112	0
23	MG	A	1781	1/1	0.89	0.23	101,101,101,101	0
23	MG	A	1659	1/1	0.89	0.25	108,108,108,108	0
23	MG	A	1745	1/1	0.89	0.29	85,85,85,85	0
23	MG	A	1836	1/1	0.89	0.10	175,175,175,175	0
23	MG	A	1784	1/1	0.89	0.32	93,93,93,93	0
23	MG	A	1841	1/1	0.89	0.17	392,392,392,392	0
23	MG	A	1732	1/1	0.89	0.20	114,114,114,114	0
23	MG	A	1774	1/1	0.90	0.12	272,272,272,272	0
23	MG	A	1778	1/1	0.90	0.17	129,129,129,129	0
23	MG	A	1779	1/1	0.90	0.32	91,91,91,91	0
23	MG	A	1849	1/1	0.90	0.08	296,296,296,296	0
23	MG	A	1627	1/1	0.90	0.33	97,97,97,97	0
23	MG	A	1747	1/1	0.90	0.35	111,111,111,111	0
23	MG	A	1604	1/1	0.90	0.16	92,92,92,92	0
23	MG	A	1719	1/1	0.90	0.30	113,113,113,113	0
23	MG	J	201	1/1	0.90	0.18	107,107,107,107	0
23	MG	A	1804	1/1	0.90	0.23	77,77,77,77	0
23	MG	A	1626	1/1	0.90	0.39	146,146,146,146	0
23	MG	A	1772	1/1	0.90	0.22	117,117,117,117	0
23	MG	A	1793	1/1	0.90	0.23	105,105,105,105	0
23	MG	S	101	1/1	0.90	0.22	93,93,93,93	0
23	MG	A	1712	1/1	0.91	0.13	91,91,91,91	0
23	MG	A	1668	1/1	0.91	0.24	149,149,149,149	0
23	MG	A	1664	1/1	0.91	0.17	133,133,133,133	0
23	MG	A	1852	1/1	0.91	0.08	404,404,404,404	0
23	MG	A	1835	1/1	0.91	0.29	128,128,128,128	0
23	MG	A	1695	1/1	0.91	0.31	121,121,121,121	0
23	MG	A	1738	1/1	0.91	0.29	89,89,89,89	0
23	MG	A	1684	1/1	0.92	0.07	133,133,133,133	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
23	MG	A	1656	1/1	0.92	0.08	152,152,152,152	0
23	MG	A	1750	1/1	0.92	0.37	115,115,115,115	0
23	MG	A	1693	1/1	0.92	0.10	104,104,104,104	0
23	MG	A	1799	1/1	0.92	0.35	109,109,109,109	0
23	MG	A	1663	1/1	0.92	0.10	109,109,109,109	0
23	MG	A	1758	1/1	0.92	0.16	98,98,98,98	0
23	MG	A	1723	1/1	0.92	0.23	92,92,92,92	0
23	MG	A	1725	1/1	0.92	0.14	91,91,91,91	0
23	MG	M	201	1/1	0.92	0.16	101,101,101,101	0
23	MG	A	1645	1/1	0.92	0.13	138,138,138,138	0
23	MG	A	1834	1/1	0.92	0.36	130,130,130,130	0
23	MG	A	1660	1/1	0.92	0.09	173,173,173,173	0
23	MG	A	1746	1/1	0.92	0.18	123,123,123,123	0
23	MG	A	1769	1/1	0.92	0.12	112,112,112,112	0
23	MG	A	1603	1/1	0.93	0.13	126,126,126,126	0
23	MG	A	1634	1/1	0.93	0.10	82,82,82,82	0
23	MG	A	1848	1/1	0.93	0.12	336,336,336,336	0
23	MG	A	1762	1/1	0.93	0.18	122,122,122,122	0
23	MG	A	1644	1/1	0.93	0.09	117,117,117,117	0
23	MG	A	1608	1/1	0.93	0.12	80,80,80,80	0
23	MG	A	1802	1/1	0.93	0.26	86,86,86,86	0
23	MG	A	1787	1/1	0.93	0.20	81,81,81,81	0
23	MG	H	202	1/1	0.93	0.10	83,83,83,83	0
23	MG	A	1650	1/1	0.93	0.22	127,127,127,127	0
23	MG	A	1823	1/1	0.93	0.20	317,317,317,317	0
23	MG	A	1721	1/1	0.93	0.22	115,115,115,115	0
23	MG	A	1833	1/1	0.93	0.34	98,98,98,98	0
23	MG	A	1654	1/1	0.93	0.50	143,143,143,143	0
23	MG	A	1616	1/1	0.93	0.44	90,90,90,90	0
23	MG	A	1775	1/1	0.93	0.06	235,235,235,235	0
23	MG	A	1740	1/1	0.93	0.09	123,123,123,123	0
23	MG	T	201	1/1	0.93	0.11	92,92,92,92	0
23	MG	A	1810	1/1	0.94	0.21	85,85,85,85	0
23	MG	A	1815	1/1	0.94	0.15	355,355,355,355	0
23	MG	A	1744	1/1	0.94	0.20	99,99,99,99	0
23	MG	A	1651	1/1	0.94	0.30	108,108,108,108	0
23	MG	E	201	1/1	0.94	0.05	228,228,228,228	0
23	MG	A	1735	1/1	0.94	0.19	95,95,95,95	0
23	MG	A	1632	1/1	0.94	0.35	105,105,105,105	0
23	MG	A	1637	1/1	0.94	0.15	127,127,127,127	0
23	MG	A	1638	1/1	0.94	0.22	96,96,96,96	0
23	MG	A	1673	1/1	0.94	0.19	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
23	MG	A	1785	1/1	0.94	0.08	74,74,74,74	0
23	MG	A	1678	1/1	0.94	0.19	149,149,149,149	0
23	MG	A	1743	1/1	0.94	0.22	113,113,113,113	0
23	MG	A	1789	1/1	0.94	0.09	118,118,118,118	0
23	MG	A	1790	1/1	0.94	0.54	129,129,129,129	0
23	MG	A	1749	1/1	0.95	0.25	99,99,99,99	0
23	MG	A	1614	1/1	0.95	0.14	83,83,83,83	0
23	MG	A	1751	1/1	0.95	0.07	108,108,108,108	0
23	MG	A	1703	1/1	0.95	0.09	109,109,109,109	0
23	MG	A	1754	1/1	0.95	0.18	177,177,177,177	0
23	MG	A	1657	1/1	0.95	0.17	116,116,116,116	0
23	MG	A	1708	1/1	0.95	0.20	135,135,135,135	0
23	MG	A	1846	1/1	0.95	0.12	399,399,399,399	0
23	MG	A	1658	1/1	0.95	0.09	120,120,120,120	0
23	MG	A	1680	1/1	0.95	0.34	104,104,104,104	0
23	MG	A	1643	1/1	0.95	0.08	90,90,90,90	0
23	MG	A	1764	1/1	0.95	0.17	118,118,118,118	0
23	MG	A	1629	1/1	0.95	0.12	138,138,138,138	0
23	MG	A	1766	1/1	0.95	0.11	146,146,146,146	0
23	MG	A	1716	1/1	0.95	0.17	86,86,86,86	0
23	MG	A	1602	1/1	0.95	0.07	144,144,144,144	0
23	MG	A	1742	1/1	0.95	0.10	77,77,77,77	0
23	MG	H	203	1/1	0.95	0.07	124,124,124,124	0
23	MG	A	1686	1/1	0.95	0.13	130,130,130,130	0
23	MG	A	1633	1/1	0.95	0.11	88,88,88,88	0
23	MG	A	1625	1/1	0.95	0.11	179,179,179,179	0
23	MG	M	202	1/1	0.95	0.18	111,111,111,111	0
23	MG	A	1777	1/1	0.95	0.06	485,485,485,485	0
23	MG	A	1652	1/1	0.95	0.08	114,114,114,114	0
23	MG	A	1814	1/1	0.95	0.16	360,360,360,360	0
23	MG	A	1618	1/1	0.95	0.08	108,108,108,108	0
23	MG	A	1780	1/1	0.95	0.11	107,107,107,107	0
23	MG	A	1655	1/1	0.95	0.26	137,137,137,137	0
23	MG	A	1646	1/1	0.96	0.08	99,99,99,99	0
23	MG	A	1647	1/1	0.96	0.07	115,115,115,115	0
23	MG	A	1826	1/1	0.96	0.18	304,304,304,304	0
23	MG	A	1828	1/1	0.96	0.21	289,289,289,289	0
23	MG	A	1733	1/1	0.96	0.11	111,111,111,111	0
23	MG	A	1757	1/1	0.96	0.07	106,106,106,106	0
23	MG	A	1648	1/1	0.96	0.07	227,227,227,227	0
23	MG	A	1736	1/1	0.96	0.10	84,84,84,84	0
23	MG	A	1710	1/1	0.96	0.23	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
23	MG	A	1619	1/1	0.96	0.08	141,141,141,141	0
23	MG	A	1838	1/1	0.96	0.08	126,126,126,126	0
23	MG	A	1839	1/1	0.96	0.09	137,137,137,137	0
23	MG	A	1840	1/1	0.96	0.34	386,386,386,386	0
23	MG	A	1763	1/1	0.96	0.14	93,93,93,93	0
23	MG	A	1791	1/1	0.96	0.10	74,74,74,74	0
23	MG	A	1607	1/1	0.96	0.08	156,156,156,156	0
23	MG	A	1639	1/1	0.96	0.14	116,116,116,116	0
23	MG	A	1687	1/1	0.96	0.08	210,210,210,210	0
23	MG	A	1691	1/1	0.96	0.37	163,163,163,163	0
23	MG	A	1653	1/1	0.96	0.10	145,145,145,145	0
23	MG	A	1854	1/1	0.96	0.24	103,103,103,103	0
23	MG	A	1666	1/1	0.96	0.19	136,136,136,136	0
23	MG	A	1770	1/1	0.96	0.15	108,108,108,108	0
23	MG	A	1641	1/1	0.96	0.07	87,87,87,87	0
23	MG	A	1773	1/1	0.96	0.06	135,135,135,135	0
23	MG	A	1606	1/1	0.96	0.36	96,96,96,96	0
23	MG	A	1617	1/1	0.96	0.07	75,75,75,75	0
23	MG	A	1803	1/1	0.96	0.07	123,123,123,123	0
23	MG	A	1609	1/1	0.96	0.15	108,108,108,108	0
23	MG	A	1807	1/1	0.96	0.21	111,111,111,111	0
23	MG	A	1808	1/1	0.96	0.10	107,107,107,107	0
23	MG	P	101	1/1	0.96	0.17	77,77,77,77	0
23	MG	A	1809	1/1	0.96	0.03	96,96,96,96	0
23	MG	A	1677	1/1	0.96	0.20	97,97,97,97	0
23	MG	A	1813	1/1	0.96	0.08	228,228,228,228	0
23	MG	A	1729	1/1	0.96	0.23	102,102,102,102	0
23	MG	A	1704	1/1	0.96	0.04	105,105,105,105	0
23	MG	A	1812	1/1	0.97	0.10	183,183,183,183	0
23	MG	A	1622	1/1	0.97	0.06	86,86,86,86	0
23	MG	A	1759	1/1	0.97	0.16	96,96,96,96	0
23	MG	A	1851	1/1	0.97	0.06	208,208,208,208	0
23	MG	A	1714	1/1	0.97	0.11	130,130,130,130	0
23	MG	A	1816	1/1	0.97	0.07	282,282,282,282	0
22	SRY	A	1601	40/40	0.97	0.08	85,115,145,148	0
23	MG	A	1615	1/1	0.97	0.09	94,94,94,94	0
23	MG	B	302	1/1	0.97	0.05	89,89,89,89	0
23	MG	A	1824	1/1	0.97	0.10	168,168,168,168	0
23	MG	A	1670	1/1	0.97	0.10	113,113,113,113	0
23	MG	H	201	1/1	0.97	0.09	83,83,83,83	0
23	MG	A	1705	1/1	0.97	0.06	97,97,97,97	0
23	MG	A	1694	1/1	0.97	0.05	95,95,95,95	0

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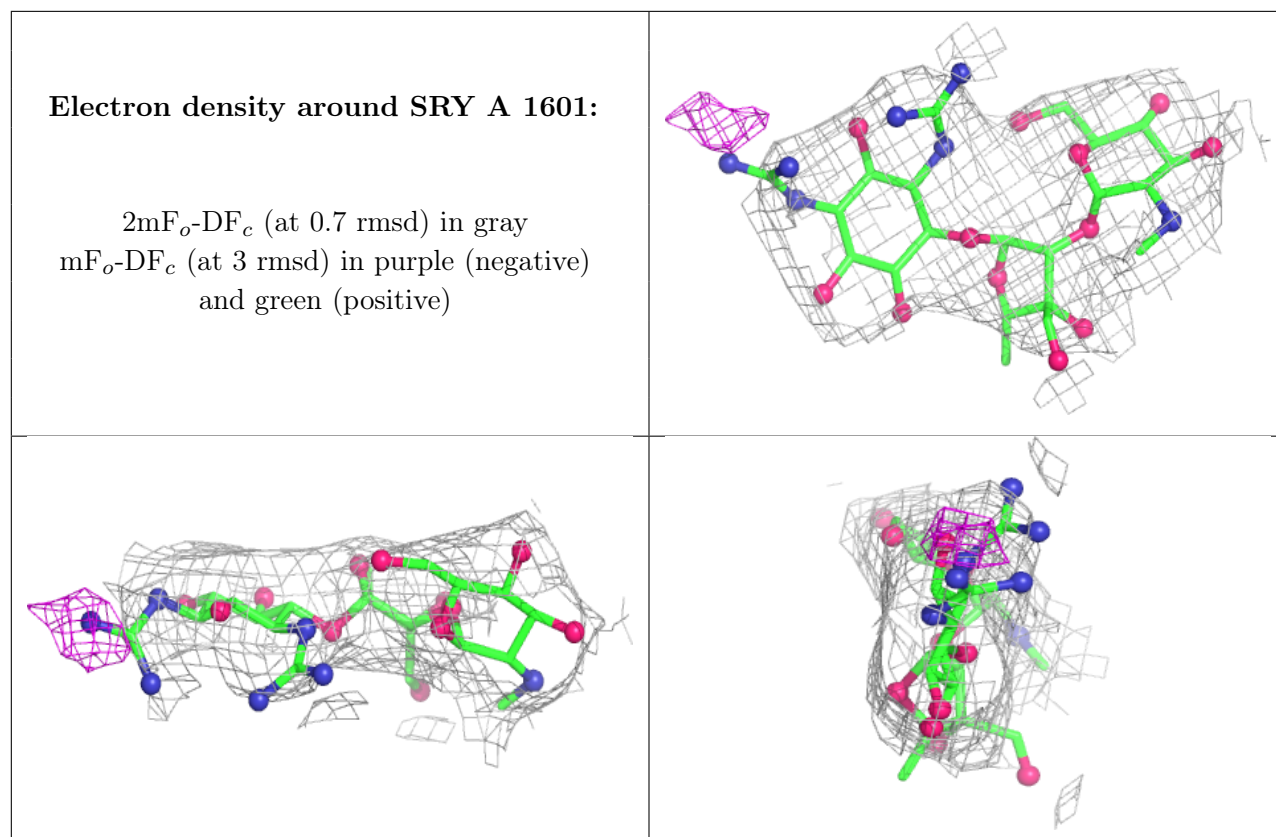
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
23	MG	A	1707	1/1	0.97	0.14	113,113,113,113	0
23	MG	A	1683	1/1	0.97	0.10	159,159,159,159	0
23	MG	A	1752	1/1	0.97	0.06	110,110,110,110	0
23	MG	A	1786	1/1	0.97	0.14	78,78,78,78	0
23	MG	A	1724	1/1	0.97	0.10	71,71,71,71	0
23	MG	A	1611	1/1	0.97	0.05	127,127,127,127	0
23	MG	A	1771	1/1	0.97	0.05	77,77,77,77	0
23	MG	A	1697	1/1	0.97	0.17	145,145,145,145	0
23	MG	A	1621	1/1	0.97	0.15	87,87,87,87	0
23	MG	A	1844	1/1	0.97	0.21	383,383,383,383	0
23	MG	A	1811	1/1	0.97	0.09	87,87,87,87	0
24	ZN	D	301	1/1	0.97	0.18	127,127,127,127	0
23	MG	A	1805	1/1	0.98	0.03	93,93,93,93	0
23	MG	A	1806	1/1	0.98	0.05	88,88,88,88	0
23	MG	A	1675	1/1	0.98	0.09	79,79,79,79	0
23	MG	A	1676	1/1	0.98	0.11	81,81,81,81	0
23	MG	A	1649	1/1	0.98	0.09	162,162,162,162	0
23	MG	A	1636	1/1	0.98	0.12	176,176,176,176	0
23	MG	A	1679	1/1	0.98	0.07	116,116,116,116	0
23	MG	A	1717	1/1	0.98	0.04	106,106,106,106	0
23	MG	A	1613	1/1	0.98	0.13	98,98,98,98	0
23	MG	A	1681	1/1	0.98	0.09	208,208,208,208	0
23	MG	A	1700	1/1	0.98	0.15	107,107,107,107	0
23	MG	A	1701	1/1	0.98	0.28	87,87,87,87	0
23	MG	A	1817	1/1	0.98	0.18	312,312,312,312	0
23	MG	A	1818	1/1	0.98	0.07	266,266,266,266	0
23	MG	A	1620	1/1	0.98	0.09	128,128,128,128	0
23	MG	A	1822	1/1	0.98	0.05	157,157,157,157	0
23	MG	A	1610	1/1	0.98	0.16	129,129,129,129	0
23	MG	A	1669	1/1	0.98	0.07	102,102,102,102	0
23	MG	A	1640	1/1	0.98	0.06	96,96,96,96	0
23	MG	A	1827	1/1	0.98	0.11	200,200,200,200	0
23	MG	J	202	1/1	0.98	0.07	105,105,105,105	0
23	MG	A	1662	1/1	0.98	0.13	141,141,141,141	0
23	MG	A	1830	1/1	0.98	0.12	322,322,322,322	0
23	MG	A	1728	1/1	0.98	0.10	82,82,82,82	0
23	MG	A	1628	1/1	0.98	0.14	171,171,171,171	0
23	MG	A	1689	1/1	0.98	0.04	75,75,75,75	0
23	MG	A	1674	1/1	0.98	0.15	94,94,94,94	0
23	MG	A	1692	1/1	0.98	0.11	170,170,170,170	0
23	MG	A	1711	1/1	0.98	0.12	93,93,93,93	0
23	MG	A	1756	1/1	0.98	0.07	203,203,203,203	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
23	MG	T	202	1/1	0.98	0.17	267,267,267,267	0
23	MG	A	1734	1/1	0.98	0.30	108,108,108,108	0
23	MG	A	1825	1/1	0.99	0.10	272,272,272,272	0
23	MG	A	1630	1/1	0.99	0.08	145,145,145,145	0
23	MG	A	1688	1/1	0.99	0.04	99,99,99,99	0
23	MG	A	1845	1/1	0.99	0.06	159,159,159,159	0
23	MG	A	1631	1/1	0.99	0.09	71,71,71,71	0
23	MG	A	1829	1/1	0.99	0.03	93,93,93,93	0
23	MG	A	1776	1/1	0.99	0.08	299,299,299,299	0
23	MG	A	1831	1/1	0.99	0.08	168,168,168,168	0
23	MG	A	1850	1/1	0.99	0.12	270,270,270,270	0
23	MG	A	1722	1/1	0.99	0.07	71,71,71,71	0
23	MG	A	1690	1/1	0.99	0.13	324,324,324,324	0
23	MG	A	1819	1/1	0.99	0.06	286,286,286,286	0
23	MG	A	1820	1/1	0.99	0.19	313,313,313,313	0
23	MG	A	1612	1/1	0.99	0.04	75,75,75,75	0
23	MG	A	1672	1/1	0.99	0.09	123,123,123,123	0
23	MG	A	1642	1/1	0.99	0.15	105,105,105,105	0
23	MG	A	1605	1/1	0.99	0.04	123,123,123,123	0
23	MG	A	1843	1/1	1.00	0.06	55,55,55,55	0
23	MG	A	1635	1/1	1.00	0.02	62,62,62,62	0
23	MG	A	1842	1/1	1.00	0.04	73,73,73,73	0
24	ZN	N	101	1/1	1.00	0.03	168,168,168,168	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 [i](#)

There are no such residues in this entry.