



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Mar 2, 2017 – 12:43 pm GMT

PDB ID : 4V6K
EMDB ID: : EMD-1849
Title : Structural insights into cognate vs. near-cognate discrimination during decoding.
Authors : Agirrezabala, X.; Schreiner, E.; Trabuco, L.G.; Lei, J.; Ortiz-Meoz, R.F.; Schulten, K.; Green, R.; Frank, J.
Deposited on : 2011-01-07
Resolution : 8.25 Å (reported)
Based on PDB ID : 2I2V

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB entry.

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

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : recalc29047

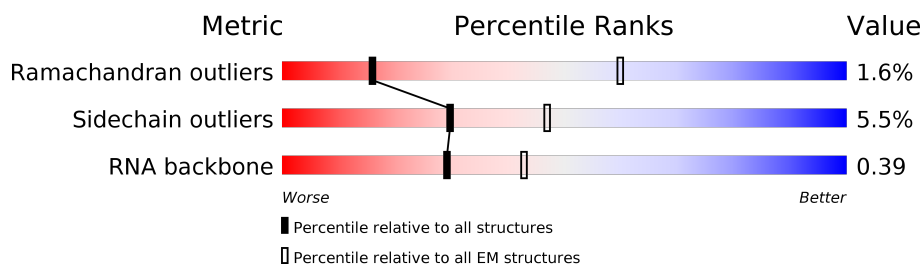
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 8.25 Å.

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



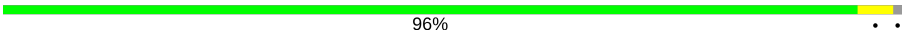
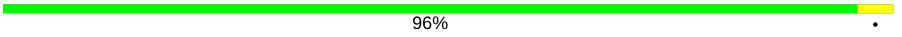

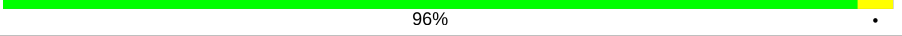
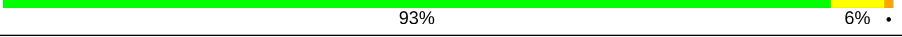
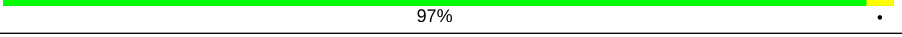


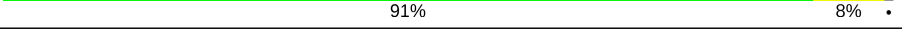

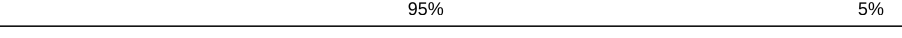
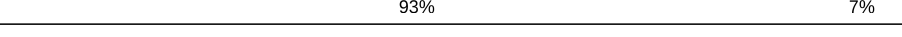
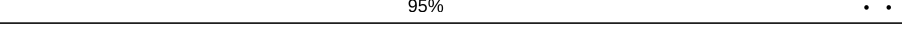
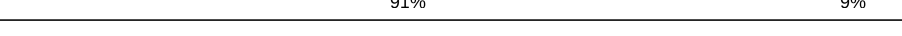
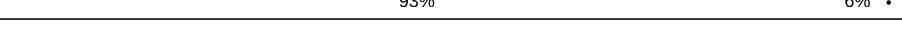
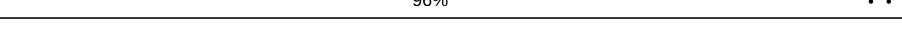
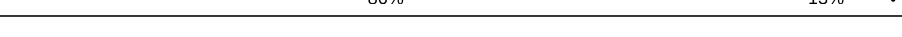

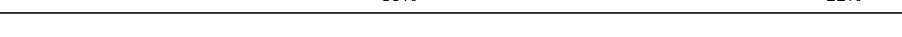
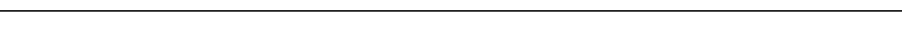

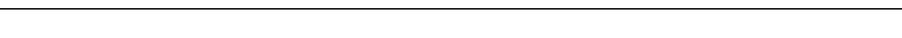
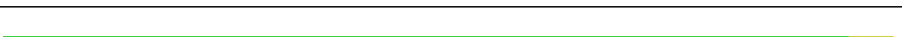
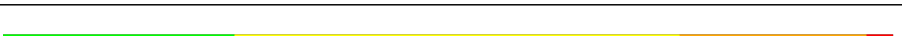

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	AA	120	
2	AB	2904	
3	AC	234	
4	AD	273	
5	AE	209	
6	AF	201	
7	AG	179	
8	AH	177	
9	AI	149	



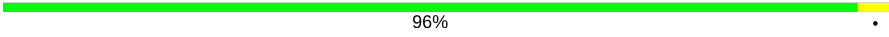

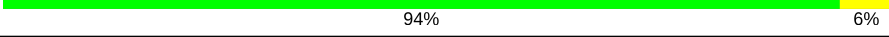
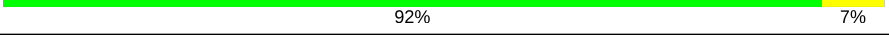
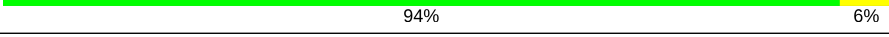
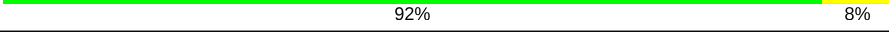
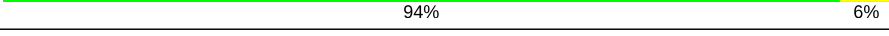
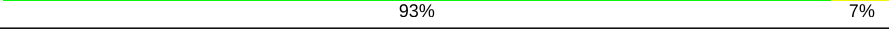
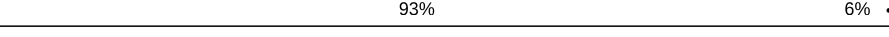


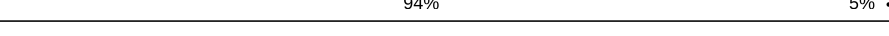
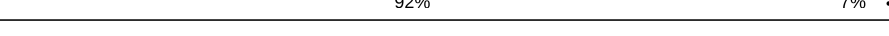
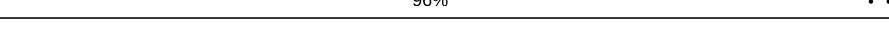

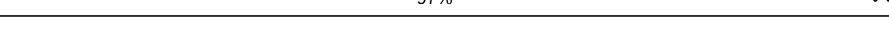
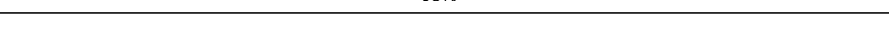
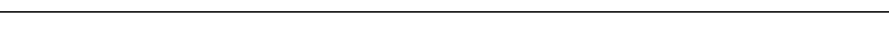
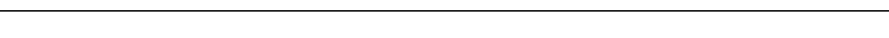
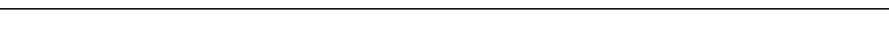
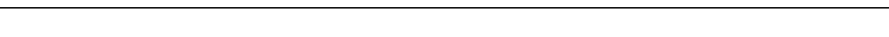

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Mol	Chain	Length	Quality of chain
10	AJ	142	 96% . .
11	AK	142	 96% .
12	AL	123	 90% 10%
13	AM	144	 96% .
14	AN	136	 93% 6% .
15	AO	127	 97% .
16	AP	117	 93% 7%
17	AQ	115	 90% 8% . .
18	AR	118	 91% 8% .
19	AS	103	 90% 10%
20	AT	110	 95% 5%
21	AU	100	 93% 7%
22	AV	104	 95% . .
23	AW	94	 91% 9%
24	AX	85	 93% 6% .
25	AY	78	 96% . .
26	AZ	63	 86% 13% .
27	Aa	59	 92% 7% .
28	Ab	70	 89% 11%
29	Ac	57	 88% 11% .
30	Ad	55	 93% 5% .
31	Ae	46	 87% 13%
32	Af	65	 95% . .
33	Ag	38	 95% 5%
34	BA	1542	 26% 50% 21% .

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Mol	Chain	Length	Quality of chain
35	BB	76	
35	BE	76	
36	BC	393	
37	BD	24	
38	BF	241	
39	BG	233	
40	BH	206	
41	BI	167	
42	BJ	135	
43	BK	179	
44	BL	130	
45	BM	130	
46	BN	103	
47	BO	129	
48	BP	124	
49	BQ	118	
50	BR	101	
51	BS	89	
52	BT	82	
53	BU	84	
54	BV	75	
55	BW	92	
56	BX	87	
57	BY	71	

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 153634 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called ribosomal RNA 5S.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	120	Total	C	N	O	P	0	0
			2566	1144	468	835	119		

- Molecule 2 is a RNA chain called ribosomal RNA 23S.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	2904	Total	C	N	O	P	0	0
			62351	27824	11469	20155	2903		

- Molecule 3 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	234	Total	C	N	O	S	0	0
			1733	1081	315	330	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AD	272	Total	C	N	O	S	0	0
			2092	1294	425	366	7		

- Molecule 5 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AE	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 6 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AF	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 7 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	178	Total	C	N	O	S	0	0
			1420	905	251	258	6		

- Molecule 8 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AH	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 9 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AI	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 10 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AJ	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 11 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AK	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 12 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AL	123	Total	C	N	O	S	0	0
			947	593	181	167	6		

- Molecule 13 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AM	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 14 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 15 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AO	127	Total	C	N	O	S	0	0
			1008	621	204	178	5		

- Molecule 16 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AP	117	Total	C	N	O	S	0	0
			900	557	179	163	1		

- Molecule 17 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AQ	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 18 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AR	117	Total	C	N	O		0	0
			947	604	192	151			

- Molecule 19 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AS	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 20 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AT	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 21 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AU	100	Total	C	N	O	S	0	0
			787	496	146	143	2		

- Molecule 22 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	103	Total	C	N	O	S	0	0
			789	498	148	143			

- Molecule 23 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AW	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 24 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AX	84	Total	C	N	O	S	0	0
			634	391	129	113	1		

- Molecule 25 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AY	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 26 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AZ	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 27 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Aa	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 28 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Ab	70	Total	C	N	O	S	0	0
			549	339	104	100	6		

- Molecule 29 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Ac	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 30 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Ad	54	Total	C	N	O	S	0	0
			441	284	81	76			

- Molecule 31 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Ae	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 32 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Af	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 33 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ag	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 34 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BA	1542	Total	C	N	O	P	0	0
			33089	14767	6064	10717	1541		

- Molecule 35 is a RNA chain called A/T-site tRNA Phe.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	BB	76	Total	C	N	O	P	S	0	0
			1635	735	291	532	75	2		
35	BE	76	Total	C	N	O	P	S	0	0
			1635	735	291	532	75	2		

- Molecule 36 is a protein called Elongation factor Tu 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BC	393	Total	C	N	O	S	0	0
			3036	1918	523	582	13		

- Molecule 37 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BD	24	Total	C	N	O	P	0	0
			495	222	68	181	24		

- Molecule 38 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BF	240	Total	C	N	O	S	0	0
			1872	1180	332	352	8		

- Molecule 39 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BG	232	Total	C	N	O	S	0	0
			1822	1149	346	323	4		

- Molecule 40 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BH	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 41 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BI	166	Total	C	N	O	S	0	0
			1225	761	232	226	6		

- Molecule 42 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BJ	135	Total	C	N	O	S	0	0
			1101	677	198	219	7		

- Molecule 43 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BK	178	Total	C	N	O	S	0	0
			1400	874	269	253	4		

- Molecule 44 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BL	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 45 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BM	129	Total	C	N	O	S	0	0
			1036	642	208	183	3		

- Molecule 46 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BN	103	Total	C	N	O	S	0	0
			825	514	158	151	2		

- Molecule 47 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BO	128	Total	C	N	O	S	0	0
			965	595	196	171	3		

- Molecule 48 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BP	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 49 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BQ	117	Total	C	N	O	S	0	0
			910	564	183	160	3		

- Molecule 50 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BR	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 51 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BS	88	Total	C	N	O	S	0	0
			716	440	146	129	1		

- Molecule 52 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BT	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 53 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BU	83	Total	C	N	O	S	0	0
			672	425	124	120	3		

- Molecule 54 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BV	74	Total	C	N	O	S	0	0
			626	395	123	107	1		

- Molecule 55 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BW	91	Total	C	N	O	S	0	0
			727	464	139	122	2		

- Molecule 56 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BX	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

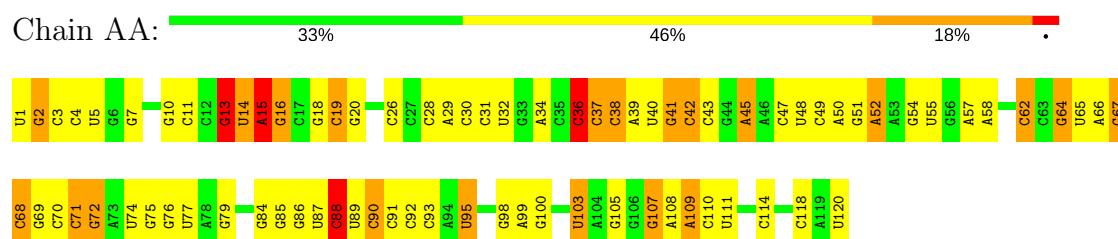
- Molecule 57 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BY	70	Total	C	N	O	S	0	0
			590	366	125	98	1		

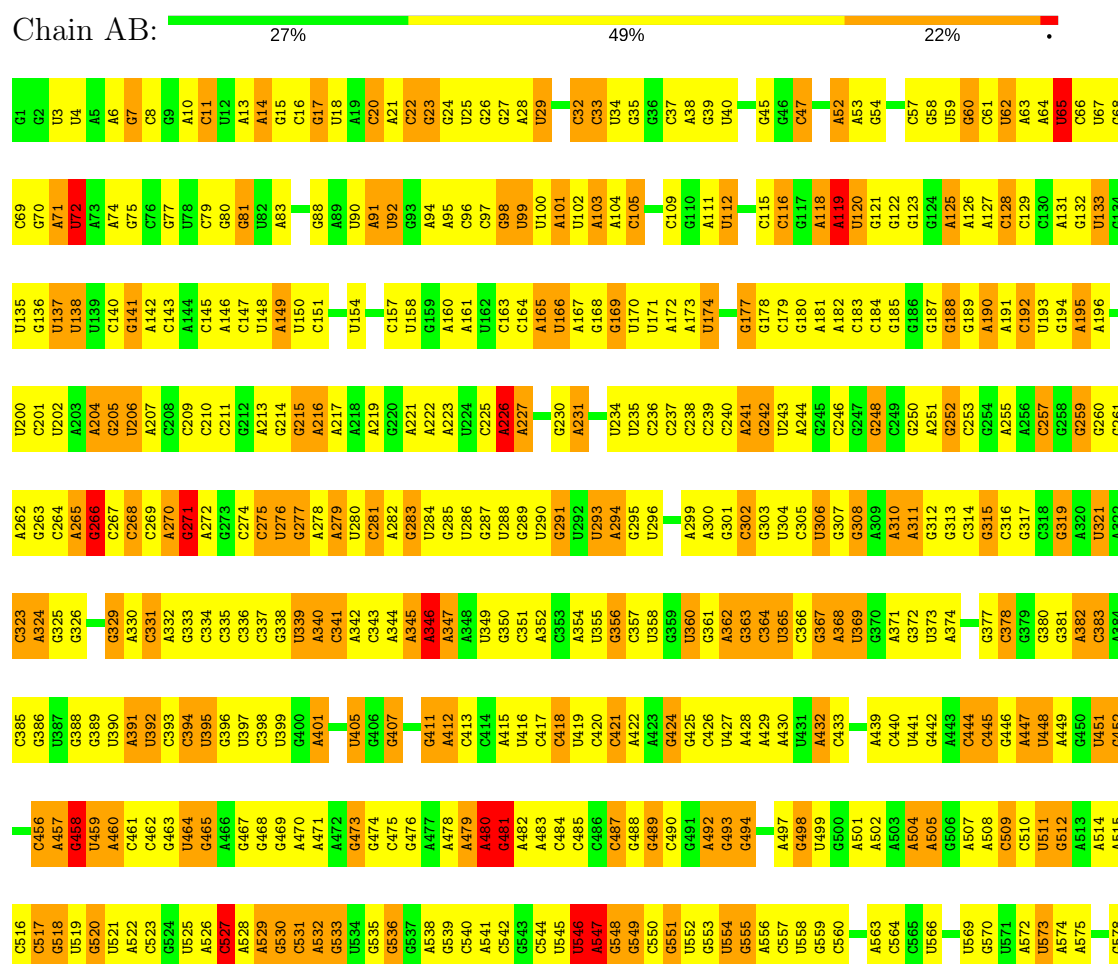
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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. 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. 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: ribosomal RNA 5S

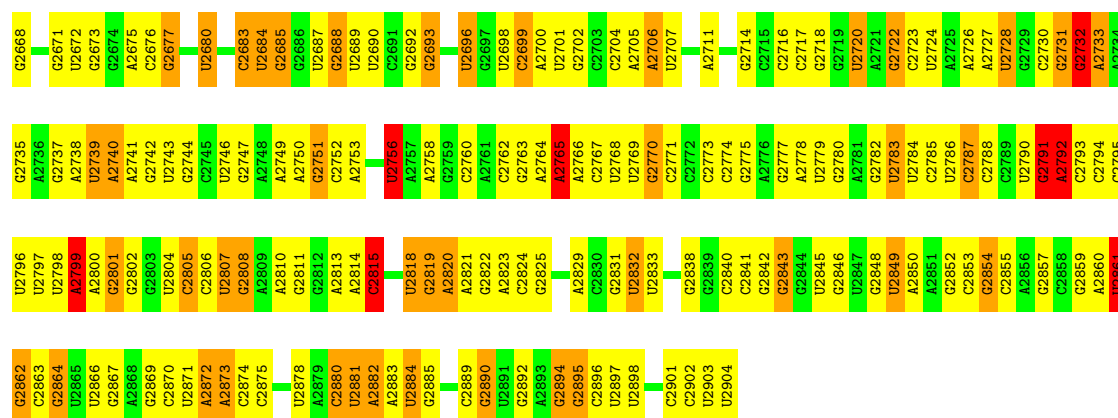


• Molecule 2: ribosomal RNA 23S



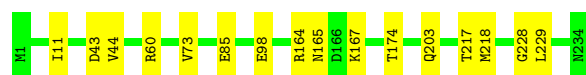
U1554	G1491	C1357	G1220	U1159	U1094	A1029	G966	C902	U714	G648	G579
G1492	G1492	G1358	C1221	G1160	A1095	U1033	U967	C903	A715	G649	U580
C1558	G1423	A1359	G1222	C1161	A1096	G1034	C968	U906	A716	G650	C581
U1559	G1424	G1360	G1223	G1162	U1097	G1035	C969	G907	C717	G651	A582
G1560	G1425	G1361	G1224	G1163	A1098	U1036	U970	C908	A718	A583	G583
C1561	G1426	C1362	G1225	G1164	G1099	G1036	G971	A909	C719	A584	C584
A1427	A1427	C1363	A1226	A1165	C1100	G1037	A972	A910	U720	A585	G585
C1499	A1433	G1364	G1227	G1166	U1101	G1038	A973	A911	A721	G656	A586
U1563	A1434	A1365	G1228	C1167	C1102	A1039	G974	A912	A722	U587	C587
C1564	G1435	A1366	C1229	U1174	A1103	A1040	A975	C912	C723	U588	U589
C1565	G1436	G1367	G1230	A1175	G1104	G1041	G976	U913	G724	U589	A590
A1566	G1437	G1368	U1231	G1171	U1105	G1042	G977	C914	G725	C660	A591
G1567	A1504	G1369	G1232	G1172	G1106	U1045	G978	C915	G726	A661	U591
G1568	A1505	A1302	C1233	U1173	G1107	C1046	A979	C916	A727	G662	A592
A1569	U1506	G1303	U1234	U1174	U1108	A1046	A980	A917	G728	G663	U593
A1570	C1507	A1304	G1235	A1175	C1109	A1047	A981	A918	U729	G664	U594
A1571	U1508	A1372	G1236	U1176	A1048	A1048	C982	U919	A730	U665	C595
A1572	A1509	G1374	A1237	G1177	G1110	C1049	A983	A920	C731	U666	U596
A1573	G1510	U1375	G1238	G1178	G1112	U1052	A984	C921	C732	U667	G597
C1574	G1511	A1376	U1241	G1179	U1113	C1053	C987	C922	G733	A668	U598
C1575	C1512	G1377	A1242	U1180	C1114	G1054	A988	G923	A734	G669	A599
U1576	G1513	A1378	G1243	U1181	G1115	A1055	A989	A925	U741	A670	G600
C1577	G1514	U1379	C1244	G1182	G1116	G1056	G990	A926	A742	C671	C601
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A1580	U1520	A1384	U1255	G1185	U1119	U1059	C992	G930	A739	G674	G604
G1581	G1521	A1385	G1256	G1186	G1120	U1060	C993	U931	U740	A675	U607
A1583	A1522	G1386	U1257	G1187	C1121	U1061	A994	U932	A741	A676	A608
U1584	G1523	G1389	U1258	U1188	G1122	G1062	A995	A933	A742	C678	A609
C1585	G1524	U1390	U1259	U1189	G1123	G1063	G997	U934	U744	U681	C611
A1586	U1525	U1391	G1261	G1190	G1124	C1064	C998	C935	C809	G681	G612
C1587	G1526	A1392	G1262	U1191	G1125	U1065	U999	A936	U747	G682	A613
U1588	G1527	A1393	U1263	G1192	U1126	U1066	A1000	G937	A748	U683	A614
G1589	A1528	U1394	U1264	A1194	U1130	A1067	A1001	G938	U749	G684	U615
A1590	G1529	G1395	C1265	G1195	U1131	G1068	G1002	A941	A750	A685	A616
A1591	G1530	U1396	A1266	C1196	U1132	A1069	G1003	G942	A751	U686	G617
C1592	C1531	U1397	U1267	G1197	A1133	A1070	U1004	A943	A752	C687	G618
A1593	U1532	C1398	G1268	U1198	G1134	G1071	C1005	A944	A753	U688	G619
C1594	U1533	G1399	U1269	U1199	C1135	A1072	C1006	C945	A756	A689	G622
A1596	A1534	U1400	G1270	U1201	G1136	A1073	C1007	C946	G757	G690	C623
A1597	G1535	U1401	A1268	U1202	G1137	G1074	C1008	A947	U758	C692	C624
C1598	G1536	A1402	G1271	G1203	U1138	C1075	A1010	C948	G759	A693	A627
U1599	G1537	C1403	A1272	U1204	G1139	U1076	G1011	G949	U760	U694	G630
C1600	G1538	U1404	A1273	A1205	C1140	A1077	U1012	C950	G763	G695	A631
A1603	U1539	G1343	A1275	G1206	U1141	U1078	C1013	C951	A764	G696	A632
C1604	G1540	U1344	G1276	C1207	A1142	A1079	A1014	G952	C765	G697	G633
C1605	U1541	G1408	G1277	C1208	A1143	A1080	U1015	G953	U826	U700	G636
C1606	U1542	U1409	C1278	U1209	A1144	U1081	G1016	G954	U827	G701	A637
U1607	G1543	A1347	G1279	G1210	C1145	U1082	G1017	C957	U828	U702	A638
A1608	A1544	U1481	G1280	C1211	U1146	U1083	U1018	C958	U767	U703	G639
A1609	G1545	G1482	G1281	G1212	A1147	A1084	U1019	U958	G768	U704	A640
A1610	U1546	C1414	U1282	A1213	U1148	A1085	G831	A959	U769	G705	A641
A1611	A1547	U1415	G1283	A1214	G1150	G1087	U832	A960	G770	A706	U642
C1612	U1548	G1416	A1284	G1215	A1151	A1088	A833	C961	C771	U710	A643
U1613	C1550	C1417	A1285	G1216	G1152	G1023	C962	U963	U772	G711	A644
A1614	A1551	U1418	A1286	U1217	C1153	G1024	G1025	U964	U773	G712	U645
U1615	U1552	G1419	G1287	G1218	U1154	A1027	A1026	A900	G774	U713	U646
A1616	A1553	A1420	G1288	U1219	G1155	G1093	A1028	C965	G776		G647

C2606	U2473	U2401	A2335	U2272	C2207	U2137	U2074	U2011	U1883	C1822	G1755	U1692	G1619
C2538	U2474	U2402	A2336	A2273	C2208	G2138	U2075	G2012	G1884	U1825	A1751	U1693	G1620
C2539	C2337	C2403	G2337	C2275	A2211	U2139	U2076	A2015	A1885	U1826	U1758	C1694	U1621
C2540	C2338	U2404	C2338	C2276	U2212	G2140	U2077	U2016	U1886	G1826	G1761	G1695	U1622
G2543	C2339	G2405	C2339	G2277	U2213	C2145	C2078	U2017	C1887	U1827	A1762	G1696	G1623
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C2480	U2343	U2408	U2344	G2279	C2215	A2147	U2081	A2019	A1893	A1829	U1765	A1700	G1627
C2481	U2344		U2345	G2280			U2082	A2020	A1890	G1830	G1764	A1701	G1628
C2482	A2411		A2346	A2281	G2218	C2150	C2083	C2021	G1891	G1831	U1765	G1702	G1629
G2485	G2414		G2347	G2282	U2219		C2084	U2022	A1960	G1766	G1767	G1703	A1630
	G2415		U2348	C2283	U2220	G2156	U2085	C2023	C1893	C1832	G1768	G1704	G1631
	C2416		G2349	A2284	G2221	G1157	U2086	G2024	C1894	U1834	U1769	A1705	A1632
	C2417		C2350	C2285	C2222	A2158	G2087	C2025	C1895	G1835	U1769	C1706	
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	A2419		A2352	A2287	G2224	C2160	C2089	G2027	A1899	C1838	C1774	U1708	C1639
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				G2290	A2227	A2163	U2082	U2030	A1969	U1841	U1777	A1711	G1642
	U2423			U2291	G2228	C2164	G2083	A2031	A1970	G1842	U1778		G1643
	C2424			U2292	U2229		U2094	G2032	U1971	C1843	U1779	U1714	G1644
	A2425			G2293	G2230	A2168	A2097	U2033	G1906	C1844	U1780	G1715	G1645
	A2426			G2294		C2169	U2098	U2034	G1907	G1845	U1781	U1716	C1646
	C2427			C2295		A2170	U2099	G2035	C1908	G1846	U1782	A1717	U1647
				U2296		A2171	U2099	C2036	C1909	A1847	A1783	G1718	U1648
	G2428			G2233	G2234	U2172			A1912	A1848	A1784	G1719	G1649
	G2429			G2235		A2173		U2039	A1912	G1849	A1785	U1720	
	A2430			U2236		C2174		G2040	A1913	G1850	A1786	G1721	A1652
	A2431			G2237		C2175		U2041	A1914	G1851	A1787	U1722	G1653
	A2432			G2238		A2176		A2042	G1915	U1852	C1788	G1723	A1654
	A2433			C2239		C2177		C2043	A1916	A1853	A1789	G1724	A1655
	A2434			U2240		C2178		C2044	U1917	A1854	C1790	U1725	G1656
				A2241		C2179		C2045	A1918	U1855	A1791	U1726	G1657
						U2180		G2046	A1919	G1856	G1727	C1658	
				A2244		U2181		C2047	C1920	G1857		C1728	
						U2182		G2048	G1921		U1796	U1729	G1663
				C2248		A2183		G2049	U1859	A1858	G1797	G1730	G1664
				U2249		A2184		C2050	G1924	G1860	U1798	G1731	A1664
				G2250		U2185		A2051	C1925	G1861	G1799	G1732	A1665
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				G2252		U2187		A2052	U1927	G1863	A1801	G1734	
				G2253		U2188		G2053	A1928	U1864	A1802	A1735	C1670
				G2254		U2189		A2054	A1929	U1865	A1803	U1736	U1671
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				G2256		A2191		G2056	U1931	G1867	A1805	G1738	G1673
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				G2258		G2193		A2058	G1933	G1869	G1807	G1740	G1675
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				C2261		C2196		A2062	A1936	A1872	A1810	G1743	A1678
				U2262		U2197		C2063	A1937	G1873	G1811		A1679
				G2263		A2198		C2064	A1938	C1874	A1812	U1746	U1680
				C2264		A2199		C2065	U1939	G1875	G1813	U1747	
				U2265		C2200		C2066	U1940	A1876		C1748	C1685
				A2266		G2201		G2067	C1941	G1877	G1816	A1750	C1686
				G2267		U2202		U2068	C1942	A1878	G1817	G1750	C1687
				A2268		U2203			U1943	C1879	U1818	U1751	U1688
				G2269		G2204			U1946	U1880	A1819	C1752	U1689
				A2270		A2205			U1947	U1881	U1820		A1690
				G2271		C2206			C2010	U1882	A1821		C1691



• Molecule 3: 50S ribosomal protein L1

Chain AC: 93% 7%



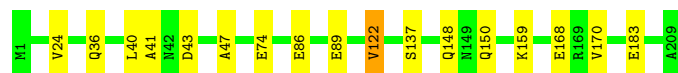
• Molecule 4: 50S ribosomal protein L2

Chain AD: 92% 7%



• Molecule 5: 50S ribosomal protein L3

Chain AE: 92% 8%



• Molecule 6: 50S ribosomal protein L4

Chain AF: 95% 5%



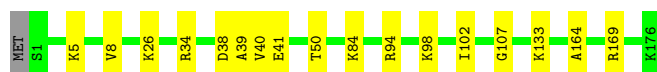
• Molecule 7: 50S ribosomal protein L5

Chain AG: 92% 7% ..



• Molecule 8: 50S ribosomal protein L6

Chain AH: 90% 10% .



- Molecule 9: 50S ribosomal protein L9

Chain AI: 90% 9% .



- Molecule 10: 50S ribosomal protein L11

Chain AJ: 96% . .



- Molecule 11: 50S ribosomal protein L13

Chain AK: 96% .



- Molecule 12: 50S ribosomal protein L14

Chain AL: 90% 10%



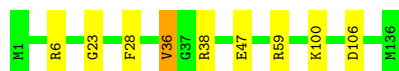
- Molecule 13: 50S ribosomal protein L15

Chain AM: 96% .



- Molecule 14: 50S ribosomal protein L16

Chain AN: 93% 6% .

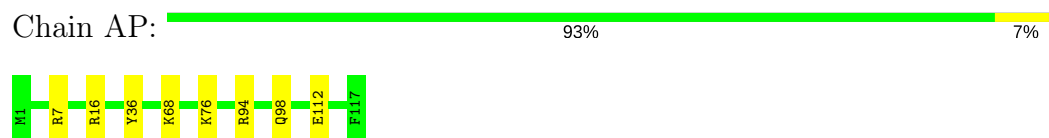


- Molecule 15: 50S ribosomal protein L17

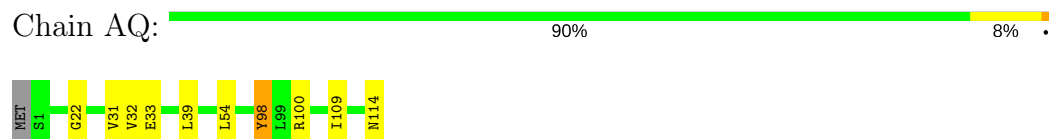
Chain AO: 97% .



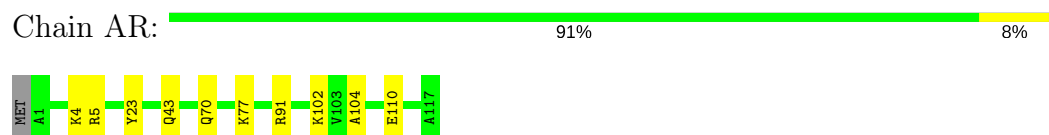
- Molecule 16: 50S ribosomal protein L18



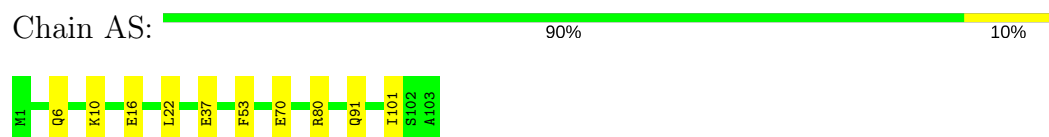
- Molecule 17: 50S ribosomal protein L19



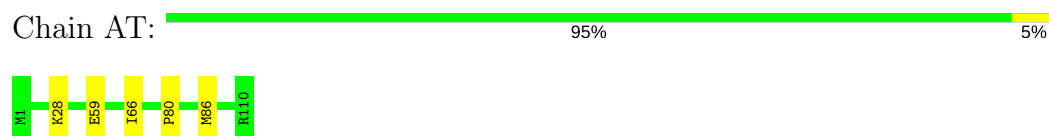
- Molecule 18: 50S ribosomal protein L20



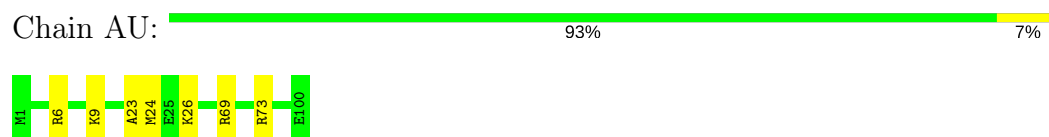
- Molecule 19: 50S ribosomal protein L21



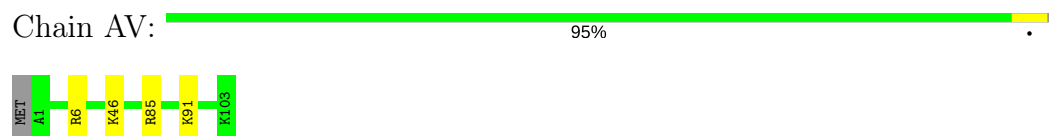
- Molecule 20: 50S ribosomal protein L22



- Molecule 21: 50S ribosomal protein L23



- Molecule 22: 50S ribosomal protein L24



- Molecule 23: 50S ribosomal protein L25

Chain AW:  91% 9%



- Molecule 24: 50S ribosomal protein L27

Chain AX:  93% 6%




- Molecule 25: 50S ribosomal protein L28

Chain AY:  96%



- Molecule 26: 50S ribosomal protein L29

Chain AZ:  86% 13%



- Molecule 27: 50S ribosomal protein L30

Chain Aa:  92% 7%




- Molecule 28: 50S ribosomal protein L31

Chain Ab:  89% 11%



- Molecule 29: 50S ribosomal protein L32

Chain Ac:  88% 11%

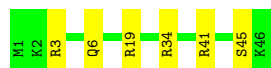
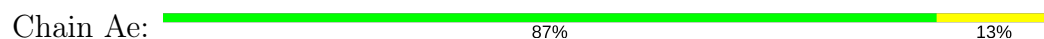


- Molecule 30: 50S ribosomal protein L33

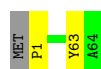
Chain Ad:  93% 5%



- Molecule 31: 50S ribosomal protein L34



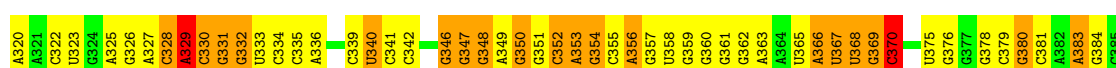
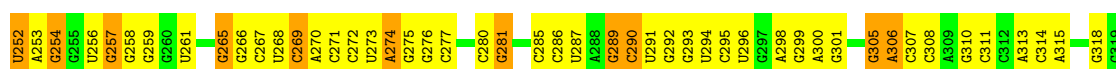
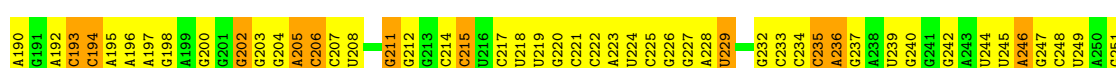
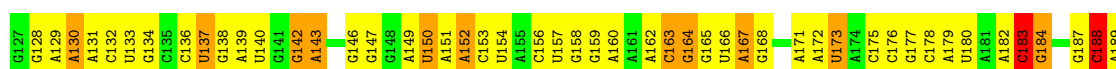
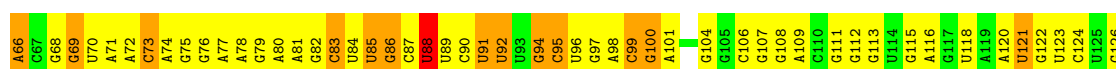
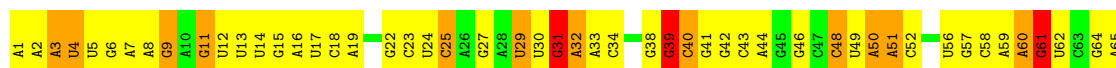
- Molecule 32: 50S ribosomal protein L35



- Molecule 33: 50S ribosomal protein L36

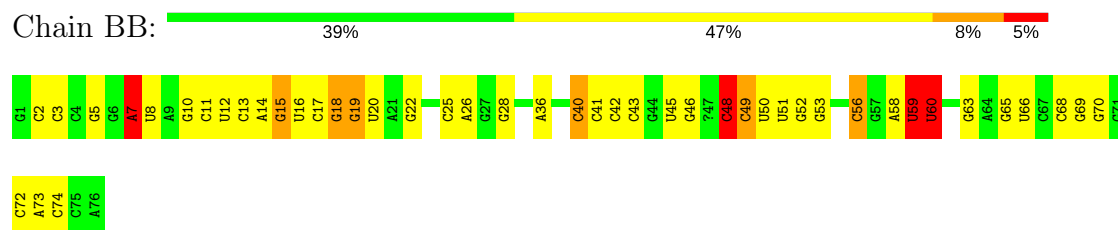


- Molecule 34: 16S ribosomal RNA

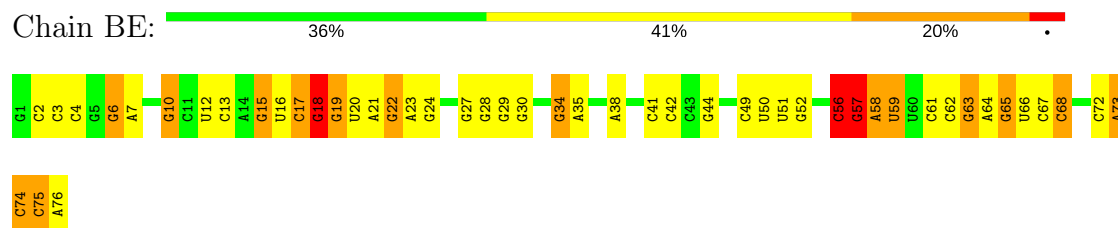


G1501	G1438	G1366	U1301	C1230	C1162	G1099	A1036	G971	A907	G844	C779	A718	C651	G584	G517
A1502	G1439	G1371	C1302	G1231	A1163	C1100	C1037	C372	A908	A845	A780	C719	U652	G585	C518
A1503	U1440	G1372	C1303	U1232	G1164	A1101	G1038	A975	A909	G846	A781	G720	U653	C586	C519
G1504	A1441	G1373	G1304	G1233	U1165	C1102	G1039	G976	C910	G847	A782	G721	G654	G587	A520
G1505	G1442	G1374	G1305	C1234	G1166	C1103	U1041	G977	U911	C848	C783	G722	G655	G588	G521
G1506	G1443	A1374	A1306	U1235	A1167	G1104	G1041	A978	C912	G849	G786	U723	G658	U589	C522
G1507	U1444	A1375	U1307	G1236	U1168	A1105	A1042	A979	A913	U850	G787	G724	U659	U590	A523
G1508	U1445	U1376	G1308	U1240	A1169	G1106	G1043	C979	A914	G851	A787	G725	C660	U591	G524
C1510	A1446	U1377	G1309	G1241	A1170	C1107	A1044	C980	A915	G852	U788	G726	G661	G592	C525
G1511	C1447	C1378	G1310	G1242	A1171	G1108	C1045	U981	U916	U855	U789	G727	U662	U593	G526
G1512	A1448	G1379	A1311	C1243	U1172	C1109	A1046	U982	G917	U856	A790	G728	U663	U594	G527
A1513	U1449	U1380	G1312	G1244	U1173	A1110	G1047	A983	A918	C856	G791	A729	G664	A595	C528
G1514	C1450	U1381	U1313	G1245	G1174	A1111	G1048	C984	A919	C857	A792	G730	G665	A596	G529
U1515	U1451	C1382	C1314	C1249	A1176	G1115	U1049	C985	U920	G858	U793	G731	G668	C597	G530
G1517	G1452	G1383	G1315	A1250	G1177	U1116	G1050	U986	U921	G859	A794	G732	G669	U598	U531
C1520	C1453	C1384	G1316	G1255	G1178	U1116	C1051	C987	C922	A860	C795	G733	G670	C599	A532
C1521	G1454	G1385	C1317	U1256	A1179	U1117	U1052	U988	A923	G861	C796	G734	G671	A600	A533
U1522	G1455	A1318	A1257	A1256	A1180	U1118	G1053	U989	G928	U863	C797	G735	G672	G601	C536
U1527	G1457	C1388	C1320	G1288	G1182	C1120	U1056	U991	G929	A864	U798	G736	A673	U603	G537
G1528	G1458	U1321	U1321	C1259	U1183	U1121	U1057	U992	C930	A865	U801	C738	G674	U604	G538
G1529	C1459	G1390	C1322	G1260	G1184	U1122	G1058	A994	C932	C866	A802	C739	A675	A539	G539
G1530	C1460	U1391	G1323	G1261	G1185	U1123	G1059	C995	G933	C867	G803	U740	A676	A607	G540
A1531	G1461	G1392	C1262	C1262	A1189	G1124	U1061	C996	G934	C868	U804	G741	U677	A608	G541
U1532	U1462	U1326	C1263	C1263	U1189	U1125	U1062	A996	C935	G869	C805	G742	U678	A609	G542
C1533	U1463	C1327	U1264	U1264	G1190	U1126	C1063	U997	A935	U870	C806	A743	G682	U543	G543
A1534	U1464	C1328	C1265	C1265	A1191	G1127	G1064	C998	C936	U871	G809	G744	G682	C612	G544
C1535	A1465	C1329	G1266	G1266	U1192	C1128	U1065	C999	A937	A872	C810	G745	G683	C613	C545
C1536	C1466	U1398	C1267	G1193	G1193	C1129	A1066	A1000	A938	A873	C811	A746	U684	C614	A546
U1537	C1467	C1399	A1333	G1268	A1196	G1131	A1067	C1001	G939	G874	G812	A747	G685	A547	G547
C1538	A1468	C1400	G1334	A1269	G1197	C1132	G1068	G1002	C940	U875	U813	G748	U686	C618	G548
U1539	C1469	G1401	U1335	G1270	A1197	G1133	C1069	G1003	G941	C876	U814	A749	A887	U619	C549
U1540	U1470	C1402	C1396	G1271	G1198	G1134	U1070	A1004	G942	G877	A814	C750	G688	C620	G550
A1541	U1471	G1403	G1337	G1272	C1200	U1135	C1071	A1005	U943	G880	A815	U751	C689	A621	U551
A1542	U1474	A1339	A1339	C1273	U1201	C1136	U1072	U1007	G945	C881	A816	G752	G691	A622	C556
G1475	G1475	A1340	A1340	G1276	U1202	C1137	G1073	U1008	A946	C882	C817	A753	U692	C623	G557
A1476	A1476	U1341	U1341	C1277	C1203	G1138	U1074	U1009	G951	C883	G818	C754	G693	C624	G558
U1477	C1342	G1342	G1342	G1278	A1204	G1139	U1075	U1010	C948	U884	U820	C756	G694	U625	A559
U1478	U1478	G1343	G1343	G1279	U1205	C1140	U1076	G952	C949	C885	G821	U757	A695	G628	G562
C1479	A1413	U1344	U1344	C1281	G1206	G1141	G1077	A1014	U950	G886	U822	C758	A696	C631	A563
U1480	U1414	U1345	U1345	C1282	U1212	G1142	U1078	U1015	G952	C887	C823	A759	U697	U632	C564
U1481	G1415	A1346	A1346	U1213	A1213	G1143	A1080	G1016	U955	C888	G824	G760	G698	G633	U565
G1482	G1416	G1347	G1347	C1283	C1214	G1144	A1081	U1017	U956	C889	U827	U762	G700	U636	G566
A1483	G1417	U1351	U1351	C1284	G1215	C1147	A1082	U1018	U957	U891	U828	G763	U701	C637	G567
C1484	U1418	C1352	C1352	G1285	G1216	U1148	U1083	A1019	U958	A892	C829	C764	A702	U638	G568
U1424	U1424	G1353	G1353	A1288	C1217	C1149	U1085	G1020	A958	C893	G830	G765	G703	G639	G569
G1425	U1425	U1354	U1354	A1289	C1218	C1150	U1086	A1021	A959	C894	G833	A768	A704	G640	G570
G1426	G1426	G1355	G1355	G1290	A1219	A1151	U1087	A1022	U960	C896	U834	G769	G705	U641	A572
G1489	G1489	G1356	G1356	U1291	G1220	A1152	U1089	U1025	U961	C897	U835	C770	C708	A642	A573
U1490	U1490	A1357	A1357	G1292	G1221	G1153	U1090	G1026	C962	C898	U836	G771	G709	C643	C576
G1491	A1430	U1358	U1358	C1293	G1222	G1154	U1091	G1027	A964	C899	G837	U772	G710	U644	G577
A1492	A1492	C1359	C1359	G1294	C1223	A1155	A1092	C1028	A965	A900	G838	G773	G711	G645	G578
A1493	G1432	A1360	A1360	U1295	U1224	G1156	A1093	C1028	G966	A901	C839	G774	A712	G646	C579
G1494	G1433	G1361	G1361	C1296	A1225	A1157	G1094	U1095	G967	G902	C840	G775	G713	C647	A579
U1495	A1434	A1362	A1362	G1297	C1226	C1158	U1095	G1032	C968	G903	C841	G776	G714	A648	C582
G1496	G1435	U1363	U1363	U1298	A1227	U1159	C1096	G1033	A968	U904	C842	A777	A715	A649	G583
G1497	U1436	U1364	U1364	C1228	C1228	G1160	C1097	U905	A969	U904	C843	G778	G716	G650	
G1498	G1437	G1365	G1365	G1300	A1229	C1161	C1098	A1035	C970	A906	U843	G778			

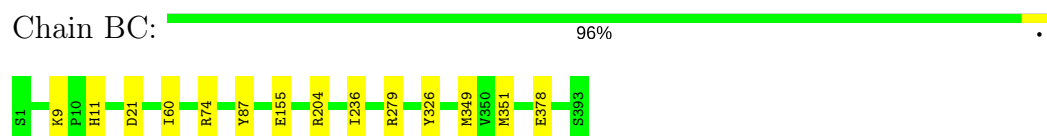
● Molecule 35: A/T-site tRNA Phe



- Molecule 35: A/T-site tRNA Phe



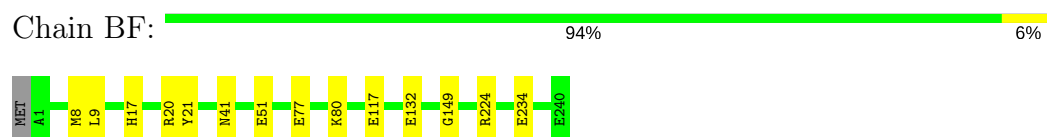
- Molecule 36: Elongation factor Tu 2



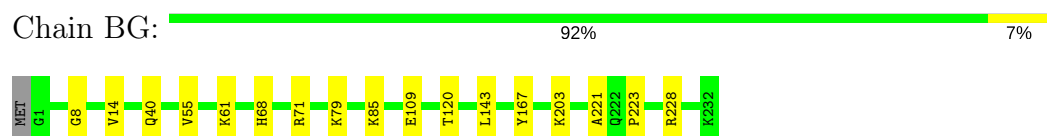
- Molecule 37: mRNA



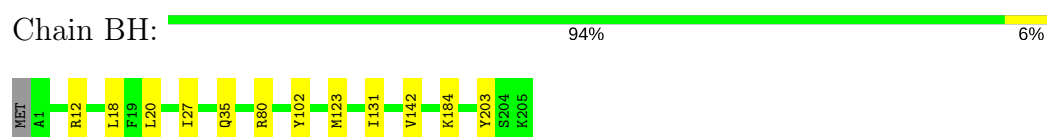
- Molecule 38: 30S ribosomal protein S2



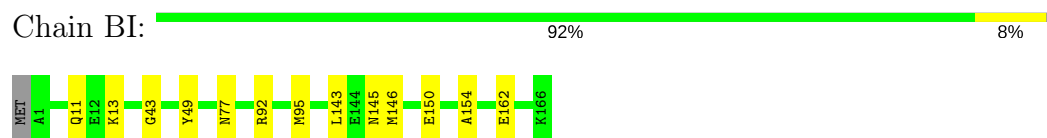
- Molecule 39: 30S ribosomal protein S3



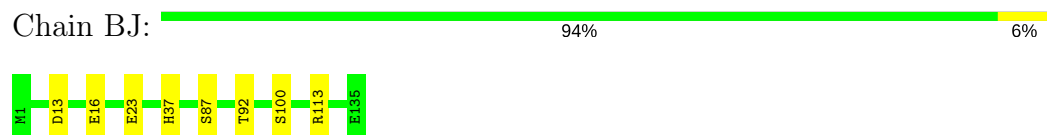
- Molecule 40: 30S ribosomal protein S4



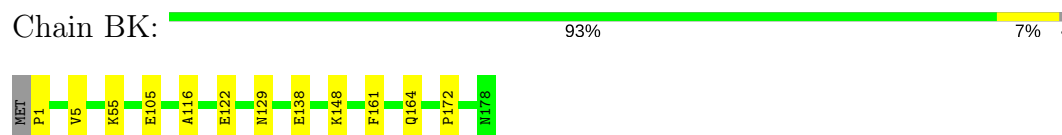
- Molecule 41: 30S ribosomal protein S5



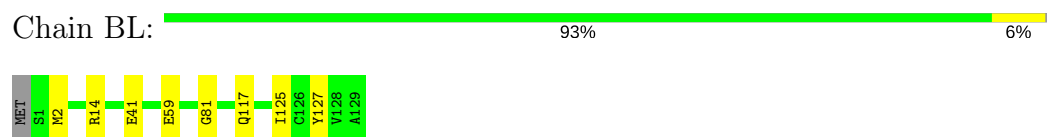
- Molecule 42: 30S ribosomal protein S6



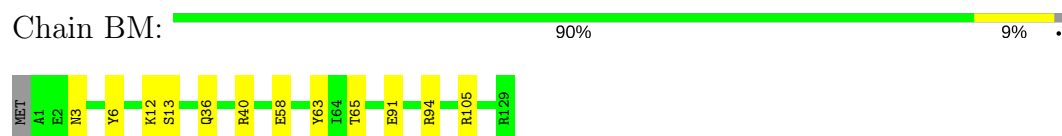
- Molecule 43: 30S ribosomal protein S7



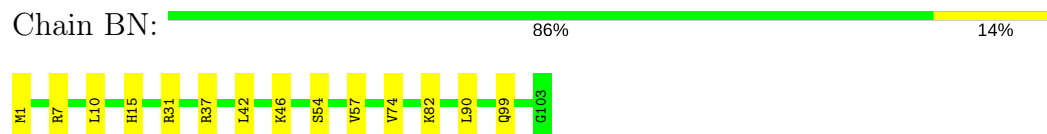
- Molecule 44: 30S ribosomal protein S8



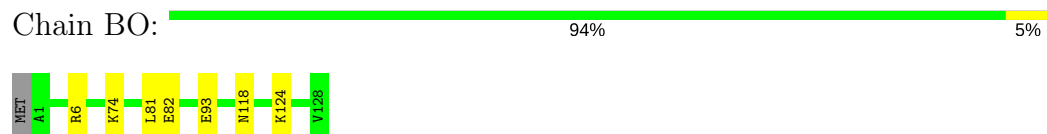
- Molecule 45: 30S ribosomal protein S9



- Molecule 46: 30S ribosomal protein S10



- Molecule 47: 30S ribosomal protein S11



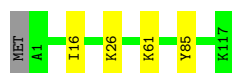
- Molecule 48: 30S ribosomal protein S12

Chain BP:  92% 7% .




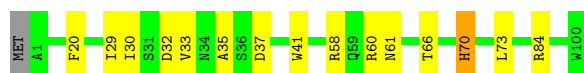
- Molecule 49: 30S ribosomal protein S13

Chain BQ:  96% ..



- Molecule 50: 30S ribosomal protein S14

Chain BR:  84% 14% ..



- Molecule 51: 30S ribosomal protein S15

Chain BS:  97% ..



- Molecule 52: 30S ribosomal protein S16

Chain BT:  98% .




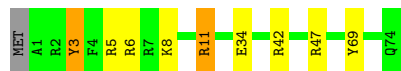
- Molecule 53: 30S ribosomal protein S17

Chain BU:  96% ..



- Molecule 54: 30S ribosomal protein S18

Chain BV:  87% 9% ..



- Molecule 55: 30S ribosomal protein S19

Chain BW:  92% 5% ..



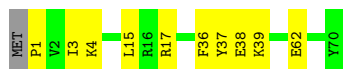
- Molecule 56: 30S ribosomal protein S20

Chain BX: 97% ..



- Molecule 57: 30S ribosomal protein S21

Chain BY: 85% 14% .



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	Not provided	Depositor
Microscope	Not provided	Depositor
Voltage (kV)	Not provided	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	Not provided	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 3TD, 5MU, CH, OMG, OMU, MA6, MIA, OMC, 1MG, H2U, 2MA, 6MZ, 2MG, 5MC, UR3, 4OC, 4SU, 7MG, 3AU, PSU

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 >2	RMSZ	# Z >2
1	AA	1.18	0/2869	2.04	104/4474 (2.3%)
10	AJ	0.57	0/1046	0.92	0/1410
11	AK	0.63	0/1152	0.99	0/1551
12	AL	0.57	0/956	1.00	0/1279
13	AM	0.60	0/1062	1.01	0/1413
14	AN	0.63	0/1093	1.05	1/1460 (0.1%)
15	AO	0.61	0/1021	1.03	0/1364
16	AP	0.60	0/910	1.00	0/1219
17	AQ	0.61	0/929	1.06	0/1242
18	AR	0.67	0/960	1.02	1/1278 (0.1%)
19	AS	0.62	0/829	1.01	0/1107
2	AB	1.17	0/69257	1.96	2261/108040 (2.1%)
20	AT	0.52	0/864	0.96	0/1156
21	AU	0.55	0/794	0.99	0/1060
22	AV	0.56	0/797	1.03	0/1062
23	AW	0.60	0/766	0.97	0/1025
24	AX	0.64	0/642	1.09	0/848
25	AY	0.64	0/635	1.06	0/848
26	AZ	0.56	0/510	1.10	1/677 (0.1%)
27	Aa	0.54	0/453	0.98	0/605
28	Ab	0.63	0/559	1.17	2/745 (0.3%)
29	Ac	0.59	0/450	1.05	0/599
3	AC	0.56	0/1748	0.96	1/2355 (0.0%)
30	Ad	0.61	0/448	1.00	0/594
31	Ae	0.63	0/380	1.11	1/498 (0.2%)
32	Af	0.58	0/513	1.01	1/676 (0.1%)
33	Ag	0.53	0/303	1.00	0/397
34	BA	1.17	1/36769 (0.0%)	1.96	1171/57354 (2.0%)
35	BB	1.23	0/1580	1.96	45/2459 (1.8%)
35	BE	1.20	0/1580	2.05	59/2459 (2.4%)
36	BC	0.61	0/3092	0.96	1/4183 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
37	BD	1.30	0/548	1.88	16/848 (1.9%)
38	BF	0.60	0/1904	1.00	0/2565
39	BG	0.60	0/1852	1.04	0/2490
4	AD	0.60	0/2131	1.07	1/2863 (0.0%)
40	BH	0.63	0/1665	1.02	0/2227
41	BI	0.56	0/1239	1.00	1/1664 (0.1%)
42	BJ	0.61	0/1121	1.05	0/1509
43	BK	0.62	0/1422	1.04	1/1908 (0.1%)
44	BL	0.58	0/989	0.97	0/1326
45	BM	0.65	0/1048	1.03	0/1394
46	BN	0.59	0/835	1.08	0/1127
47	BO	0.61	0/982	1.00	0/1323
48	BP	0.61	0/969	1.09	0/1300
49	BQ	0.57	0/919	1.01	0/1226
5	AE	0.58	0/1586	1.02	0/2134
50	BR	0.63	0/817	1.14	1/1088 (0.1%)
51	BS	0.58	0/724	1.00	1/966 (0.1%)
52	BT	0.63	0/659	1.04	0/884
53	BU	0.58	0/681	0.99	0/913
54	BV	0.71	0/637	1.06	0/851
55	BW	0.60	0/744	1.02	3/995 (0.3%)
56	BX	0.55	0/676	0.91	0/895
57	BY	0.69	0/598	1.17	1/792 (0.1%)
6	AF	0.57	0/1571	0.99	0/2113
7	AG	0.65	0/1444	1.10	4/1937 (0.2%)
8	AH	0.59	0/1343	1.02	0/1816
9	AI	0.57	0/1122	1.01	1/1515 (0.1%)
All	All	1.03	1/165193 (0.0%)	1.75	3679/246106 (1.5%)

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	AA	0	27
11	AK	0	2
15	AO	0	1
17	AQ	0	1
18	AR	0	1
2	AB	0	821
28	Ab	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
3	AC	0	2
30	Ad	0	1
31	Ae	0	2
34	BA	0	473
35	BB	0	12
35	BE	0	15
37	BD	0	4
38	BF	0	1
39	BG	0	2
40	BH	0	2
41	BI	0	3
42	BJ	0	1
43	BK	0	2
45	BM	0	2
47	BO	0	1
48	BP	0	1
5	AE	0	3
50	BR	0	1
54	BV	0	1
55	BW	0	1
57	BY	0	3
6	AF	0	1
8	AH	0	2
9	AI	0	2
All	All	0	1392

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	BA	1535	C	P-O5'	5.14	1.64	1.59

The worst 5 of 3679 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	13	G	O4'-C1'-N9	15.20	120.36	108.20
2	AB	736	C	O4'-C1'-N1	14.43	119.74	108.20
34	BA	465	A	O4'-C1'-N9	13.60	119.08	108.20
2	AB	2832	U	O4'-C1'-N1	12.97	118.58	108.20
34	BA	1152	A	O4'-C1'-N9	12.96	118.57	108.20

There are no chirality outliers.

5 of 1392 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	13	G	Sidechain
1	AA	14	U	Sidechain
1	AA	15	A	Sidechain
1	AA	2	G	Sidechain
1	AA	7	G	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	AA	2566	0	1302	0	0
2	AB	62351	0	31387	0	0
3	AC	1733	0	1824	0	0
4	AD	2092	0	2170	0	0
5	AE	1565	0	1616	0	0
6	AF	1552	0	1619	0	0
7	AG	1420	0	1460	0	0
8	AH	1323	0	1374	0	0
9	AI	1111	0	1148	0	0
10	AJ	1032	0	1088	0	0
11	AK	1129	0	1162	0	0
12	AL	947	0	1023	0	0
13	AM	1053	0	1129	0	0
14	AN	1074	0	1157	0	0
15	AO	1008	0	1045	0	0
16	AP	900	0	935	0	0
17	AQ	917	0	965	0	0
18	AR	947	0	1022	0	0
19	AS	816	0	839	0	0
20	AT	857	0	922	0	0
21	AU	787	0	846	0	0
22	AV	789	0	847	0	0
23	AW	753	0	780	0	0
24	AX	634	0	656	0	0
25	AY	625	0	655	0	0
26	AZ	509	0	543	0	0
27	Aa	449	0	491	0	0
28	Ab	549	0	552	0	0
29	Ac	444	0	461	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	Ad	441	0	485	0	0
31	Ae	377	0	418	0	0
32	Af	504	0	574	0	0
33	Ag	302	0	343	0	0
34	BA	33089	0	16678	0	0
35	BB	1635	0	849	0	0
35	BE	1635	0	849	0	0
36	BC	3036	0	3052	0	0
37	BD	495	0	249	0	0
38	BF	1872	0	1885	0	0
39	BG	1822	0	1913	0	0
40	BH	1643	0	1710	0	0
41	BI	1225	0	1273	0	0
42	BJ	1101	0	1050	0	0
43	BK	1400	0	1449	0	0
44	BL	979	0	1034	0	0
45	BM	1036	0	1084	0	0
46	BN	825	0	865	0	0
47	BO	965	0	997	0	0
48	BP	955	0	1019	0	0
49	BQ	910	0	981	0	0
50	BR	805	0	847	0	0
51	BS	716	0	742	0	0
52	BT	649	0	666	0	0
53	BU	672	0	716	0	0
54	BV	626	0	651	0	0
55	BW	727	0	769	0	0
56	BX	670	0	722	0	0
57	BY	590	0	631	0	0
All	All	153634	0	105519	0	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). Clashscore could not be calculated for this entry.

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	AC	232/234 (99%)	204 (88%)	25 (11%)	3 (1%)	14	56
4	AD	270/273 (99%)	239 (88%)	23 (8%)	8 (3%)	5	37
5	AE	207/209 (99%)	186 (90%)	15 (7%)	6 (3%)	5	38
6	AF	199/201 (99%)	182 (92%)	14 (7%)	3 (2%)	12	53
7	AG	176/179 (98%)	147 (84%)	27 (15%)	2 (1%)	17	60
8	AH	174/177 (98%)	163 (94%)	8 (5%)	3 (2%)	11	50
9	AI	147/149 (99%)	126 (86%)	16 (11%)	5 (3%)	4	35
10	AJ	139/142 (98%)	123 (88%)	15 (11%)	1 (1%)	25	68
11	AK	140/142 (99%)	132 (94%)	8 (6%)	0	100	100
12	AL	121/123 (98%)	106 (88%)	13 (11%)	2 (2%)	11	50
13	AM	142/144 (99%)	125 (88%)	15 (11%)	2 (1%)	13	54
14	AN	134/136 (98%)	122 (91%)	9 (7%)	3 (2%)	8	44
15	AO	125/127 (98%)	117 (94%)	7 (6%)	1 (1%)	22	67
16	AP	115/117 (98%)	104 (90%)	10 (9%)	1 (1%)	20	63
17	AQ	112/115 (97%)	100 (89%)	10 (9%)	2 (2%)	10	49
18	AR	115/118 (98%)	110 (96%)	4 (4%)	1 (1%)	20	63
19	AS	101/103 (98%)	91 (90%)	6 (6%)	4 (4%)	3	31
20	AT	108/110 (98%)	98 (91%)	9 (8%)	1 (1%)	20	63
21	AU	98/100 (98%)	85 (87%)	11 (11%)	2 (2%)	9	46
22	AV	101/104 (97%)	89 (88%)	11 (11%)	1 (1%)	18	61
23	AW	92/94 (98%)	85 (92%)	5 (5%)	2 (2%)	8	44
24	AX	82/85 (96%)	67 (82%)	12 (15%)	3 (4%)	4	33
25	AY	75/78 (96%)	64 (85%)	9 (12%)	2 (3%)	6	40
26	AZ	61/63 (97%)	49 (80%)	9 (15%)	3 (5%)	2	27
27	Aa	56/59 (95%)	54 (96%)	1 (2%)	1 (2%)	10	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	Ab	68/70 (97%)	57 (84%)	10 (15%)	1 (2%)	12	53
29	Ac	54/57 (95%)	47 (87%)	5 (9%)	2 (4%)	4	33
30	Ad	52/55 (94%)	45 (86%)	7 (14%)	0	100	100
31	Ae	44/46 (96%)	40 (91%)	4 (9%)	0	100	100
32	Af	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
33	Ag	36/38 (95%)	32 (89%)	3 (8%)	1 (3%)	6	39
36	BC	391/393 (100%)	368 (94%)	20 (5%)	3 (1%)	22	67
38	BF	238/241 (99%)	215 (90%)	20 (8%)	3 (1%)	14	56
39	BG	230/233 (99%)	211 (92%)	17 (7%)	2 (1%)	20	63
40	BH	203/206 (98%)	191 (94%)	10 (5%)	2 (1%)	18	61
41	BI	164/167 (98%)	144 (88%)	17 (10%)	3 (2%)	10	49
42	BJ	133/135 (98%)	128 (96%)	3 (2%)	2 (2%)	12	53
43	BK	176/179 (98%)	160 (91%)	14 (8%)	2 (1%)	17	60
44	BL	127/130 (98%)	117 (92%)	8 (6%)	2 (2%)	11	51
45	BM	127/130 (98%)	111 (87%)	14 (11%)	2 (2%)	11	51
46	BN	101/103 (98%)	86 (85%)	11 (11%)	4 (4%)	3	31
47	BO	126/129 (98%)	113 (90%)	11 (9%)	2 (2%)	11	51
48	BP	121/124 (98%)	104 (86%)	12 (10%)	5 (4%)	3	30
49	BQ	115/118 (98%)	108 (94%)	7 (6%)	0	100	100
50	BR	98/101 (97%)	83 (85%)	8 (8%)	7 (7%)	1	19
51	BS	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
52	BT	80/82 (98%)	79 (99%)	1 (1%)	0	100	100
53	BU	81/84 (96%)	73 (90%)	8 (10%)	0	100	100
54	BV	72/75 (96%)	65 (90%)	5 (7%)	2 (3%)	6	39
55	BW	89/92 (97%)	80 (90%)	9 (10%)	0	100	100
56	BX	84/87 (97%)	78 (93%)	6 (7%)	0	100	100
57	BY	68/71 (96%)	60 (88%)	7 (10%)	1 (2%)	12	53
All	All	6548/6682 (98%)	5904 (90%)	536 (8%)	108 (2%)	16	51

5 of 108 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	AD	260	LYS

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Mol	Chain	Res	Type
5	AE	122	VAL
5	AE	150	GLN
5	AE	170	VAL
9	AI	23	ALA

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	AC	181/181 (100%)	171 (94%)	10 (6%)	25	58
4	AD	217/218 (100%)	204 (94%)	13 (6%)	22	55
5	AE	164/164 (100%)	154 (94%)	10 (6%)	22	55
6	AF	165/165 (100%)	158 (96%)	7 (4%)	34	64
7	AG	149/150 (99%)	138 (93%)	11 (7%)	16	48
8	AH	137/138 (99%)	125 (91%)	12 (9%)	12	39
9	AI	114/114 (100%)	106 (93%)	8 (7%)	18	50
10	AJ	109/110 (99%)	105 (96%)	4 (4%)	39	68
11	AK	116/116 (100%)	113 (97%)	3 (3%)	51	75
12	AL	104/104 (100%)	94 (90%)	10 (10%)	10	35
13	AM	103/103 (100%)	99 (96%)	4 (4%)	37	66
14	AN	109/109 (100%)	103 (94%)	6 (6%)	25	58
15	AO	103/103 (100%)	101 (98%)	2 (2%)	62	82
16	AP	87/87 (100%)	80 (92%)	7 (8%)	14	45
17	AQ	99/100 (99%)	91 (92%)	8 (8%)	14	44
18	AR	89/90 (99%)	82 (92%)	7 (8%)	14	45
19	AS	84/84 (100%)	78 (93%)	6 (7%)	17	49
20	AT	93/93 (100%)	89 (96%)	4 (4%)	33	64
21	AU	84/84 (100%)	79 (94%)	5 (6%)	22	55
22	AV	84/85 (99%)	81 (96%)	3 (4%)	40	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	AW	78/78 (100%)	72 (92%)	6 (8%)	15	47
24	AX	62/63 (98%)	60 (97%)	2 (3%)	44	71
25	AY	67/68 (98%)	67 (100%)	0	100	100
26	AZ	55/55 (100%)	49 (89%)	6 (11%)	7	30
27	Aa	48/49 (98%)	45 (94%)	3 (6%)	21	53
28	Ab	62/62 (100%)	58 (94%)	4 (6%)	20	52
29	Ac	47/48 (98%)	43 (92%)	4 (8%)	12	42
30	Ad	48/49 (98%)	46 (96%)	2 (4%)	34	64
31	Ae	38/38 (100%)	35 (92%)	3 (8%)	14	45
32	Af	51/52 (98%)	50 (98%)	1 (2%)	60	82
33	Ag	34/34 (100%)	33 (97%)	1 (3%)	48	73
36	BC	326/326 (100%)	316 (97%)	10 (3%)	45	71
38	BF	198/199 (100%)	188 (95%)	10 (5%)	28	60
39	BG	189/190 (100%)	176 (93%)	13 (7%)	18	51
40	BH	172/173 (99%)	164 (95%)	8 (5%)	30	62
41	BI	125/126 (99%)	118 (94%)	7 (6%)	25	57
42	BJ	116/116 (100%)	111 (96%)	5 (4%)	33	64
43	BK	146/147 (99%)	139 (95%)	7 (5%)	30	61
44	BL	104/105 (99%)	98 (94%)	6 (6%)	23	56
45	BM	106/107 (99%)	98 (92%)	8 (8%)	16	48
46	BN	90/90 (100%)	80 (89%)	10 (11%)	7	29
47	BO	98/99 (99%)	94 (96%)	4 (4%)	35	65
48	BP	103/104 (99%)	100 (97%)	3 (3%)	48	73
49	BQ	95/96 (99%)	91 (96%)	4 (4%)	34	64
50	BR	83/84 (99%)	76 (92%)	7 (8%)	13	43
51	BS	76/77 (99%)	75 (99%)	1 (1%)	73	87
52	BT	65/65 (100%)	63 (97%)	2 (3%)	45	71
53	BU	77/78 (99%)	75 (97%)	2 (3%)	51	75
54	BV	64/65 (98%)	56 (88%)	8 (12%)	5	26
55	BW	78/79 (99%)	74 (95%)	4 (5%)	28	60
56	BX	65/66 (98%)	63 (97%)	2 (3%)	45	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	BY	60/61 (98%)	55 (92%)	5 (8%)	13	43
All	All	5417/5447 (99%)	5119 (94%)	298 (6%)	30	58

5 of 298 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
21	AU	24	MET
30	Ad	34	GLU
52	BT	5	ARG
22	AV	85	ARG
26	AZ	30	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	119/120 (99%)	15 (12%)	0
2	AB	2898/2904 (99%)	396 (13%)	0
34	BA	1538/1542 (99%)	192 (12%)	0
35	BB	73/76 (96%)	12 (16%)	0
35	BE	73/76 (96%)	12 (16%)	0
37	BD	23/24 (95%)	4 (17%)	0
All	All	4724/4742 (99%)	631 (13%)	0

5 of 631 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	10	G
1	AA	13	G
1	AA	15	A
1	AA	16	G
1	AA	36	C

There are no RNA pucker outliers to report.

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

55 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
2	6MZ	AB	1618	2	18,25,26	1.00	1 (5%)	16,36,39	1.47	2 (12%)
2	2MG	AB	1835	2	19,26,27	1.36	1 (5%)	20,38,41	2.31	4 (20%)
2	PSU	AB	1911	2	16,21,22	1.40	2 (12%)	20,30,33	6.13	6 (30%)
2	3TD	AB	1915	2	16,22,23	1.08	1 (6%)	19,32,35	1.85	5 (26%)
2	PSU	AB	1917	2	16,21,22	1.45	2 (12%)	20,30,33	6.15	6 (30%)
2	5MU	AB	1939	2	14,22,23	1.34	2 (14%)	16,32,35	4.22	4 (25%)
2	5MC	AB	1962	2	15,22,23	1.08	1 (6%)	17,32,35	1.13	3 (17%)
2	6MZ	AB	2030	2	18,25,26	0.99	1 (5%)	16,36,39	1.60	4 (25%)
2	7MG	AB	2069	2	20,26,27	2.29	4 (20%)	22,39,42	2.03	2 (9%)
2	OMG	AB	2251	2	18,26,27	1.38	3 (16%)	22,38,41	2.32	3 (13%)
2	2MG	AB	2445	2	19,26,27	1.42	3 (15%)	20,38,41	2.29	4 (20%)
2	H2U	AB	2449	2	17,21,22	0.91	1 (5%)	21,30,33	0.89	1 (4%)
2	PSU	AB	2457	2	16,21,22	1.38	2 (12%)	20,30,33	6.09	8 (40%)
2	OMC	AB	2498	2	15,22,23	0.94	0	19,31,34	1.10	1 (5%)
2	2MA	AB	2503	2	18,25,26	1.18	3 (16%)	17,37,40	1.38	1 (5%)
2	PSU	AB	2504	2	16,21,22	1.50	3 (18%)	20,30,33	6.06	7 (35%)
2	OMU	AB	2552	2	14,22,23	1.38	2 (14%)	18,31,34	3.44	4 (22%)
2	CH	AB	2575	2	15,21,22	0.96	1 (6%)	16,30,33	1.18	2 (12%)
2	PSU	AB	2580	2	16,21,22	1.43	2 (12%)	20,30,33	5.94	6 (30%)
2	PSU	AB	2605	2	16,21,22	1.42	2 (12%)	20,30,33	6.16	7 (35%)
2	1MG	AB	745	2	18,26,27	1.13	2 (11%)	18,39,42	1.62	2 (11%)
2	PSU	AB	746	2	16,21,22	1.42	2 (12%)	20,30,33	6.09	8 (40%)
2	5MU	AB	747	2	14,22,23	1.24	1 (7%)	16,32,35	4.15	5 (31%)
2	PSU	AB	955	2	16,21,22	1.36	2 (12%)	20,30,33	6.13	6 (30%)
34	2MG	BA	1207	34	19,26,27	1.40	3 (15%)	20,38,41	2.42	3 (15%)
34	4OC	BA	1402	34	16,23,24	1.12	2 (12%)	19,32,35	1.22	2 (10%)
34	5MC	BA	1407	34	15,22,23	1.16	2 (13%)	17,32,35	0.93	1 (5%)
34	UR3	BA	1498	34	14,22,23	1.05	1 (7%)	16,32,35	1.12	1 (6%)
34	2MG	BA	1516	34	19,26,27	1.37	3 (15%)	20,38,41	2.49	4 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
34	MA6	BA	1518	34	16,26,27	0.95	1 (6%)	18,38,41	1.12	1 (5%)
34	MA6	BA	1519	34	16,26,27	0.89	1 (6%)	18,38,41	1.57	3 (16%)
34	PSU	BA	516	34	16,21,22	1.34	1 (6%)	20,30,33	6.03	7 (35%)
34	7MG	BA	527	34	20,26,27	2.25	3 (15%)	22,39,42	2.22	4 (18%)
34	2MG	BA	966	34	19,26,27	1.31	2 (10%)	20,38,41	2.88	9 (45%)
34	5MC	BA	967	34	15,22,23	1.13	2 (13%)	17,32,35	0.77	0
35	H2U	BB	16	35	17,21,22	0.97	1 (5%)	21,30,33	1.18	2 (9%)
35	H2U	BB	20	35	17,21,22	0.94	1 (5%)	21,30,33	0.98	1 (4%)
35	PSU	BB	32	35	16,21,22	1.40	2 (12%)	20,30,33	6.03	7 (35%)
35	MIA	BB	37	35	23,31,32	1.17	5 (21%)	25,44,47	1.72	4 (16%)
35	PSU	BB	39	35	16,21,22	1.29	1 (6%)	20,30,33	6.16	7 (35%)
35	7MG	BB	46	35	20,26,27	2.27	3 (15%)	22,39,42	2.29	3 (13%)
35	3AU	BB	47	-	13,28,29	0.95	0	13,40,43	0.89	0
35	5MU	BB	54	35	14,22,23	1.29	2 (14%)	16,32,35	4.04	3 (18%)
35	PSU	BB	55	35	16,21,22	1.32	2 (12%)	20,30,33	6.00	6 (30%)
35	4SU	BB	8	35	14,21,22	1.21	2 (14%)	15,30,33	2.26	2 (13%)
35	H2U	BE	16	35	17,21,22	1.01	1 (5%)	21,30,33	0.96	1 (4%)
35	H2U	BE	20	35	17,21,22	0.99	1 (5%)	21,30,33	1.25	2 (9%)
35	PSU	BE	32	35	16,21,22	1.40	2 (12%)	20,30,33	6.01	7 (35%)
35	MIA	BE	37	35	23,31,32	1.18	5 (21%)	25,44,47	1.48	4 (16%)
35	PSU	BE	39	35	16,21,22	1.38	2 (12%)	20,30,33	6.06	6 (30%)
35	7MG	BE	46	35	20,26,27	2.30	5 (25%)	22,39,42	2.10	2 (9%)
35	3AU	BE	47	-	13,28,29	0.99	0	13,40,43	2.20	3 (23%)
35	5MU	BE	54	35	14,22,23	1.36	2 (14%)	16,32,35	4.18	3 (18%)
35	PSU	BE	55	35	16,21,22	1.44	2 (12%)	20,30,33	6.00	5 (25%)
35	4SU	BE	8	35	14,21,22	1.19	1 (7%)	15,30,33	2.56	6 (40%)

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
2	6MZ	AB	1618	2	-	0/5/27/28	0/3/3/3
2	2MG	AB	1835	2	-	0/5/27/28	0/3/3/3
2	PSU	AB	1911	2	-	0/7/25/26	0/2/2/2
2	3TD	AB	1915	2	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PSU	AB	1917	2	-	0/7/25/26	0/2/2/2
2	5MU	AB	1939	2	-	0/3/25/26	0/2/2/2
2	5MC	AB	1962	2	-	0/3/25/26	0/2/2/2
2	6MZ	AB	2030	2	-	0/5/27/28	0/3/3/3
2	7MG	AB	2069	2	-	0/7/37/38	0/3/3/3
2	OMG	AB	2251	2	-	0/5/27/28	0/3/3/3
2	2MG	AB	2445	2	-	0/5/27/28	0/3/3/3
2	H2U	AB	2449	2	-	0/7/38/39	0/2/2/2
2	PSU	AB	2457	2	-	0/7/25/26	0/2/2/2
2	OMC	AB	2498	2	-	0/5/27/28	0/2/2/2
2	2MA	AB	2503	2	-	0/3/25/26	0/3/3/3
2	PSU	AB	2504	2	-	0/7/25/26	0/2/2/2
2	OMU	AB	2552	2	-	0/5/27/28	0/2/2/2
2	CH	AB	2575	2	-	0/3/25/26	0/2/2/2
2	PSU	AB	2580	2	-	0/7/25/26	0/2/2/2
2	PSU	AB	2605	2	-	0/7/25/26	0/2/2/2
2	1MG	AB	745	2	-	0/3/25/26	0/3/3/3
2	PSU	AB	746	2	-	0/7/25/26	0/2/2/2
2	5MU	AB	747	2	-	0/3/25/26	0/2/2/2
2	PSU	AB	955	2	-	0/7/25/26	0/2/2/2
34	2MG	BA	1207	34	-	0/5/27/28	0/3/3/3
34	4OC	BA	1402	34	-	0/7/29/30	0/2/2/2
34	5MC	BA	1407	34	-	0/3/25/26	0/2/2/2
34	UR3	BA	1498	34	-	0/3/25/26	0/2/2/2
34	2MG	BA	1516	34	-	0/5/27/28	0/3/3/3
34	MA6	BA	1518	34	-	0/7/29/30	0/3/3/3
34	MA6	BA	1519	34	-	0/7/29/30	0/3/3/3
34	PSU	BA	516	34	-	0/7/25/26	0/2/2/2
34	7MG	BA	527	34	-	0/7/37/38	0/3/3/3
34	2MG	BA	966	34	-	0/5/27/28	0/3/3/3
34	5MC	BA	967	34	-	0/3/25/26	0/2/2/2
35	H2U	BB	16	35	-	0/7/38/39	0/2/2/2
35	H2U	BB	20	35	-	0/7/38/39	0/2/2/2
35	PSU	BB	32	35	-	0/7/25/26	0/2/2/2
35	MIA	BB	37	35	-	0/11/33/34	0/3/3/3
35	PSU	BB	39	35	-	0/7/25/26	0/2/2/2
35	7MG	BB	46	35	-	0/7/37/38	0/3/3/3
35	3AU	BB	47	-	-	0/8/34/35	0/2/2/2
35	5MU	BB	54	35	-	0/3/25/26	0/2/2/2
35	PSU	BB	55	35	-	0/7/25/26	0/2/2/2
35	4SU	BB	8	35	-	0/3/25/26	0/2/2/2
35	H2U	BE	16	35	-	0/7/38/39	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
35	H2U	BE	20	35	-	0/7/38/39	0/2/2/2
35	PSU	BE	32	35	-	0/7/25/26	0/2/2/2
35	MIA	BE	37	35	-	0/11/33/34	0/3/3/3
35	PSU	BE	39	35	-	0/7/25/26	0/2/2/2
35	7MG	BE	46	35	-	0/7/37/38	0/3/3/3
35	3AU	BE	47	-	-	0/8/34/35	0/2/2/2
35	5MU	BE	54	35	-	0/3/25/26	0/2/2/2
35	PSU	BE	55	35	-	0/7/25/26	0/2/2/2
35	4SU	BE	8	35	-	0/3/25/26	0/2/2/2

The worst 5 of 105 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	BB	46	7MG	C8-N9	-7.95	1.33	1.45
2	AB	2069	7MG	C8-N9	-7.91	1.34	1.45
35	BE	46	7MG	C8-N9	-7.89	1.34	1.45
34	BA	527	7MG	C8-N9	-7.84	1.34	1.45
2	AB	2069	7MG	C8-N7	-2.86	1.30	1.43

The worst 5 of 210 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AB	1917	PSU	N1-C2-N3	-19.60	114.30	128.40
2	AB	1911	PSU	N1-C2-N3	-19.35	114.49	128.40
2	AB	2605	PSU	N1-C2-N3	-19.24	114.56	128.40
35	BB	39	PSU	N1-C2-N3	-19.23	114.57	128.40
35	BE	55	PSU	N1-C2-N3	-19.15	114.63	128.40

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.