



Full wwPDB EM Validation Report ⓘ

Dec 29, 2024 – 11:44 PM EST

PDB ID : 7Z34
EMDB ID : EMD-14471
Title : Structure of pre-60S particle bound to DRG1(AFG2).
Authors : Prattes, M.; Grishkovskaya, I.; Bergler, H.; Haselbach, D.
Deposited on : 2022-03-01
Resolution : 3.80 Å(reported)
Based on initial model : 6N8K

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

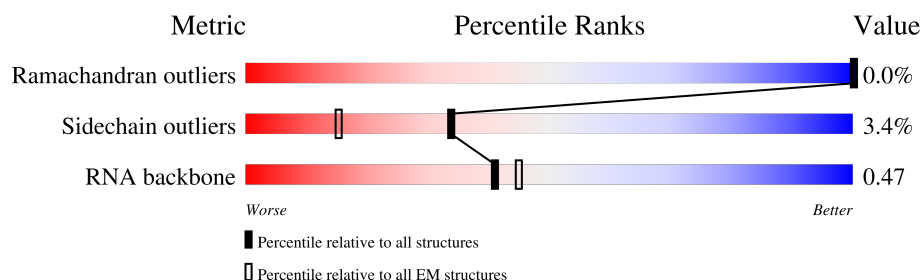
EMDB validation analysis : 0.0.1.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, 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:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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.






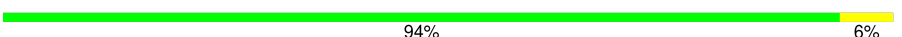
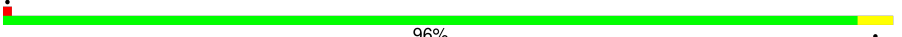





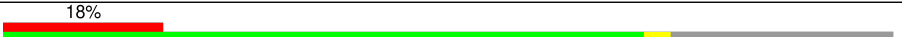


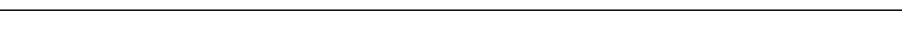
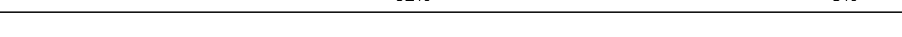
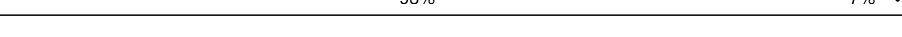
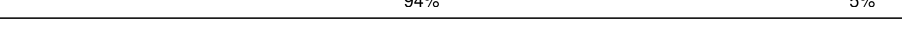
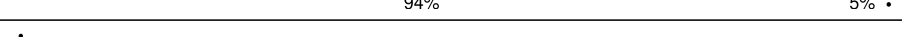
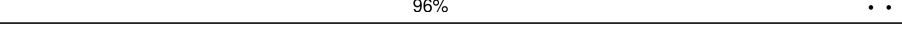
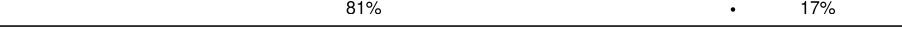

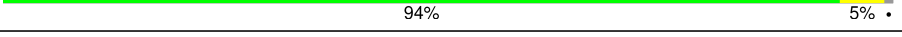
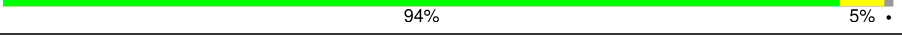

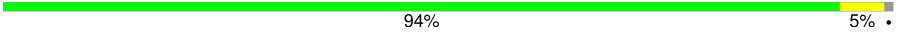
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	Aa	780	
1	m	780	
1	n	780	
1	t	780	
1	w	780	
1	x	780	
2	1	3396	
3	2	121	

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Mol	Chain	Length	Quality of chain
4	3	158	
5	4	593	
6	A	254	
7	B	387	
8	C	362	
9	D	297	
10	E	176	
11	F	244	
12	G	256	
13	H	191	
14	I	166	
15	J	174	
16	K	149	
17	L	199	
18	M	138	
19	N	204	
20	O	199	
21	P	184	
22	Q	186	
23	R	189	
24	S	172	
25	T	160	
26	U	121	
27	V	137	
28	W	236	

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Mol	Chain	Length	Quality of chain
29	X	142	
30	Y	127	
31	Z	136	
32	a	165	
33	b	647	
34	c	105	
35	d	113	
36	e	130	
37	f	107	
38	g	121	
39	h	120	
40	i	100	
41	j	88	
42	k	78	
43	l	51	
44	o	59	
45	p	92	
46	q	106	
47	r	261	
48	u	199	
49	v	518	
50	y	245	
51	z	106	
52	0	19	
53	oC	170	

2 Entry composition [i](#)

There are 55 unique types of molecules in this entry. The entry contains 177847 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called ATPase family gene 2 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Aa	728	Total	C	N	O	S	0	0
			5590	3536	954	1078	22		
1	m	730	Total	C	N	O	S	0	0
			5594	3533	958	1081	22		
1	n	730	Total	C	N	O	S	0	0
			5602	3541	958	1081	22		
1	t	731	Total	C	N	O	S	0	0
			5611	3547	960	1082	22		
1	w	734	Total	C	N	O	S	0	0
			5630	3556	963	1089	22		
1	x	734	Total	C	N	O	S	0	0
			5630	3556	963	1089	22		

- Molecule 2 is a RNA chain called 35S pre-ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	3347	Total	C	N	O	P	0	0
			71573	31964	12868	23394	3347		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 4 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	157	Total	C	N	O	P	0	0
			3333	1491	584	1101	157		

- Molecule 5 is a protein called Probable metalloprotease ARX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	560	Total	C	N	O	S	0	0
			4331	2732	747	837	15		

- Molecule 6 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	245	Total	C	N	O	S	0	0
			1863	1162	376	324	1		

- Molecule 7 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	386	Total	C	N	O	S	0	0
			3082	1956	584	534	8		

- Molecule 8 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	361	Total	C	N	O	S	0	0
			2750	1730	522	495	3		

- Molecule 9 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	273	Total	C	N	O	S	0	0
			2204	1391	382	429	2		

- Molecule 10 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	175	Total	C	N	O	S	0	0
			1401	902	251	247	1		

- Molecule 11 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	222	Total	C	N	O	S	0	0
			1785	1151	324	309	1		

- Molecule 12 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	230	Total	C	N	O	S	0	0
			1798	1149	323	323	3		

- Molecule 13 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	H	188	Total	C	N	O	S	0	0
			1493	948	271	270	4		

- Molecule 14 is a protein called Bud site selection protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	124	Total	C	N	O	S	0	0
			1003	628	186	185	4		

- Molecule 15 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	164	Total	C	N	O	S	0	0
			1312	822	245	242	3		

- Molecule 16 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 17 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	193	Total	C	N	O	S	0	0
			1543	962	315	266			

- Molecule 18 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	137	Total	C	N	O	S	0	0
			1060	678	200	180	2		

- Molecule 19 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	203	Total	C	N	O	S	0	0
			1721	1077	361	282	1		

- Molecule 20 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	197	Total	C	N	O	S	0	0
			1556	1003	289	263	1		

- Molecule 21 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	P	183	Total	C	N	O	0	0
			1443	896	287	260		

- Molecule 22 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	154	Total	C	N	O	S	0	0
			1191	753	231	205	2		

- Molecule 23 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	R	154	Total	C	N	O	0	0
			1241	772	262	207		

- Molecule 24 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S	170	Total	C	N	O	S	0	0
			1425	916	265	241	3		

- Molecule 25 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	T	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 26 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	U	104	Total	C	N	O	0	0
			826	535	136	155		

- Molecule 27 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	V	136	Total	C	N	O	S	0
			1004	628	189	180	7	0

- Molecule 28 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	W	225	Total	C	N	O	S	0
			1810	1148	306	351	5	0

- Molecule 29 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	X	120	Total	C	N	O	S	0
			960	617	168	173	2	0

- Molecule 30 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	Y	126	Total	C	N	O		0
			994	625	192	177		0

- Molecule 31 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	Z	135	Total	C	N	O		0
			1093	710	202	181		0

- Molecule 32 is a protein called 60S ribosomal protein L12-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	a	158	Total	C	N	O	S	0
			1196	750	216	228	2	0

- Molecule 33 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	630	Total	C	N	O	S	0	0
			5087	3185	914	962	26		

- Molecule 34 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 35 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	107	Total	C	N	O	S	0	0
			873	553	165	154	1		

- Molecule 36 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	128	Total	C	N	O	S	0	0
			1029	652	206	170	1		

- Molecule 37 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	f	106	Total	C	N	O	S	0	0
			851	540	165	145	1		

- Molecule 38 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	g	112	Total	C	N	O	S	0	0
			881	546	179	152	4		

- Molecule 39 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	h	119	Total	C	N	O	S	0	0
			970	615	186	168	1		

- Molecule 40 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	i	96	Total	C	N	O	S	0	0
			743	465	148	128	2		

- Molecule 41 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	j	85	Total	C	N	O	S	0	0
			670	408	146	111	5		

- Molecule 42 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	k	77	Total	C	N	O	S	0	0
			613	391	115	107			

- Molecule 43 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	l	50	Total	C	N	O	S	0	0
			437	272	97	66	2		

- Molecule 44 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	o	54	Total	C	N	O	S	0	0
			434	271	94	69			

- Molecule 45 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	p	91	Total	C	N	O	S	0	0
			695	429	138	122	6		

- Molecule 46 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	q	105	Total	C	N	O	S	0	0
			848	534	170	139	5		

- Molecule 47 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	55	Total	C	N	O	S	0	0
			470	291	100	78	1		

- Molecule 48 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	u	149	Total	C	N	O	S	0	0
			1256	788	252	207	9		

- Molecule 49 is a protein called 60S ribosomal export protein NMD3.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	v	245	Total	C	N	O	S	0	0
			1946	1250	329	360	7		

- Molecule 50 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	y	228	Total	C	N	O	S	0	0
			1722	1068	299	349	6		

- Molecule 51 is a protein called UPF0642 protein YBL028C.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	z	55	Total	C	N	O	0	0
			444	273	88	83		

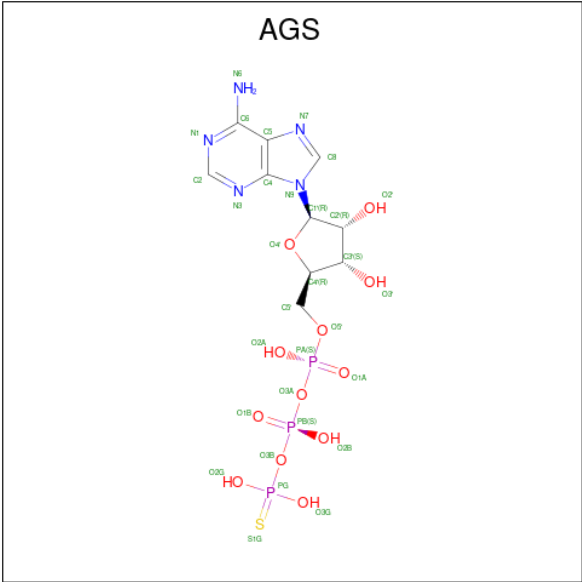
- Molecule 52 is a protein called Unknown peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	0	19	Total	C	N	O	0	0
			96	57	19	20		

- Molecule 53 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	oC	170	Total	C	N	O	0	0
			1021	680	170	171		

- Molecule 54 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (three-letter code: AGS) (formula: C₁₀H₁₆N₅O₁₂P₃S).

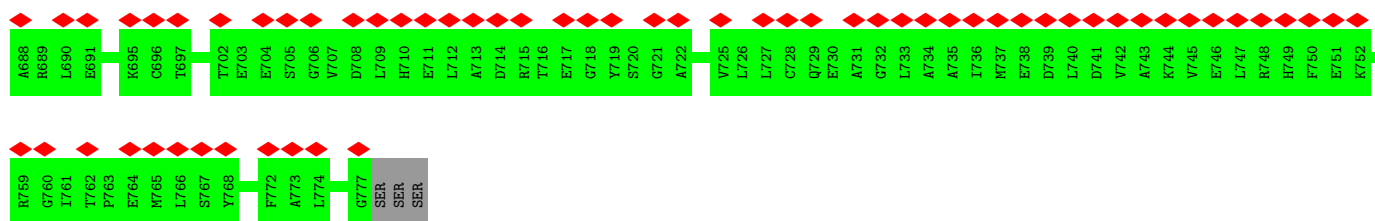


Mol	Chain	Residues	Atoms						AltConf
54	Aa	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
54	Aa	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
54	m	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
54	m	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
54	n	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
54	n	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
54	t	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
54	w	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
54	w	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
54	w	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
54	x	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	

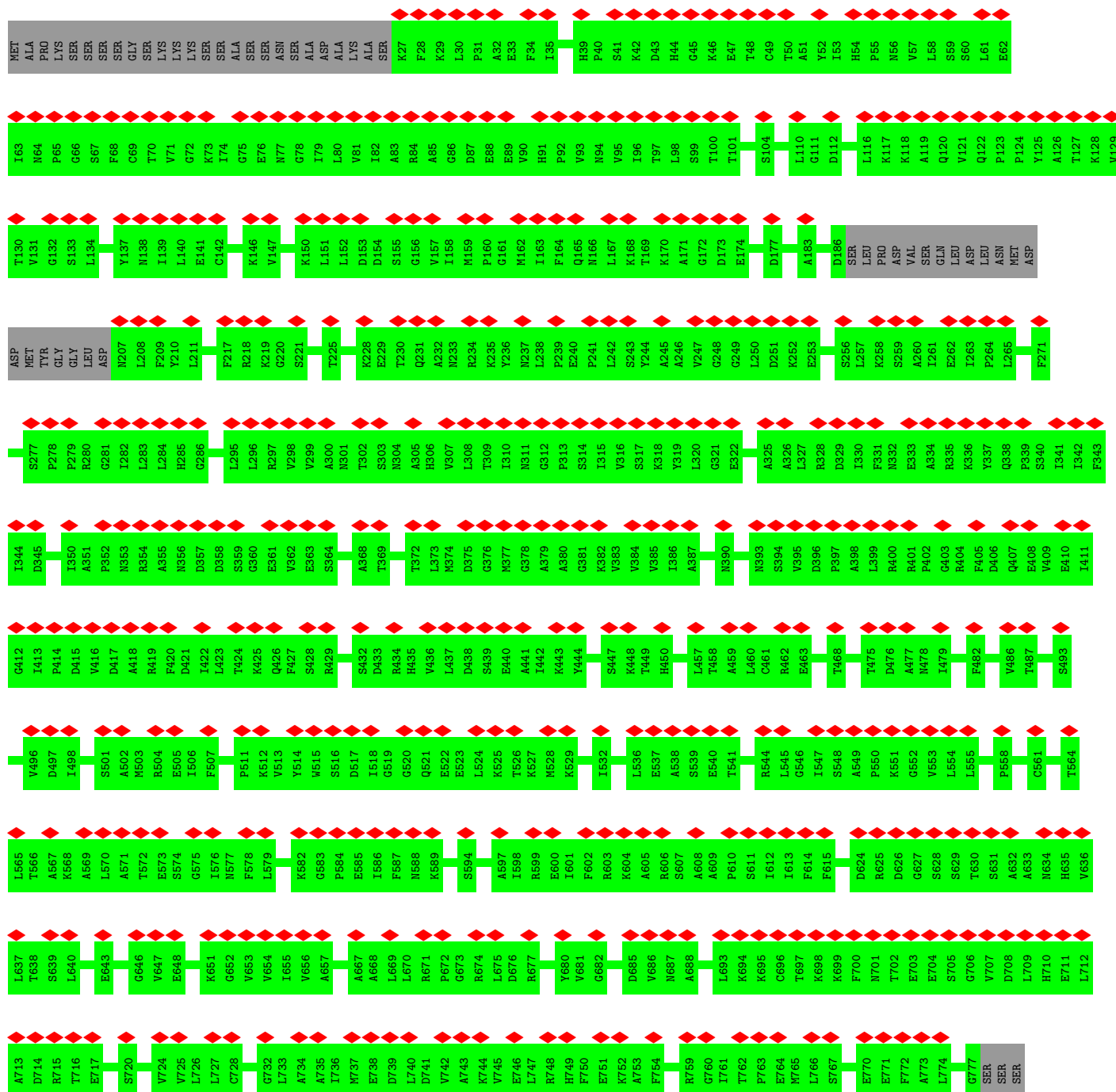
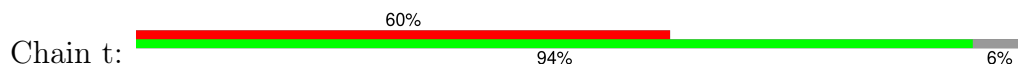
- Molecule 55 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
55	b	1	Total	Mg	0
			1	1	

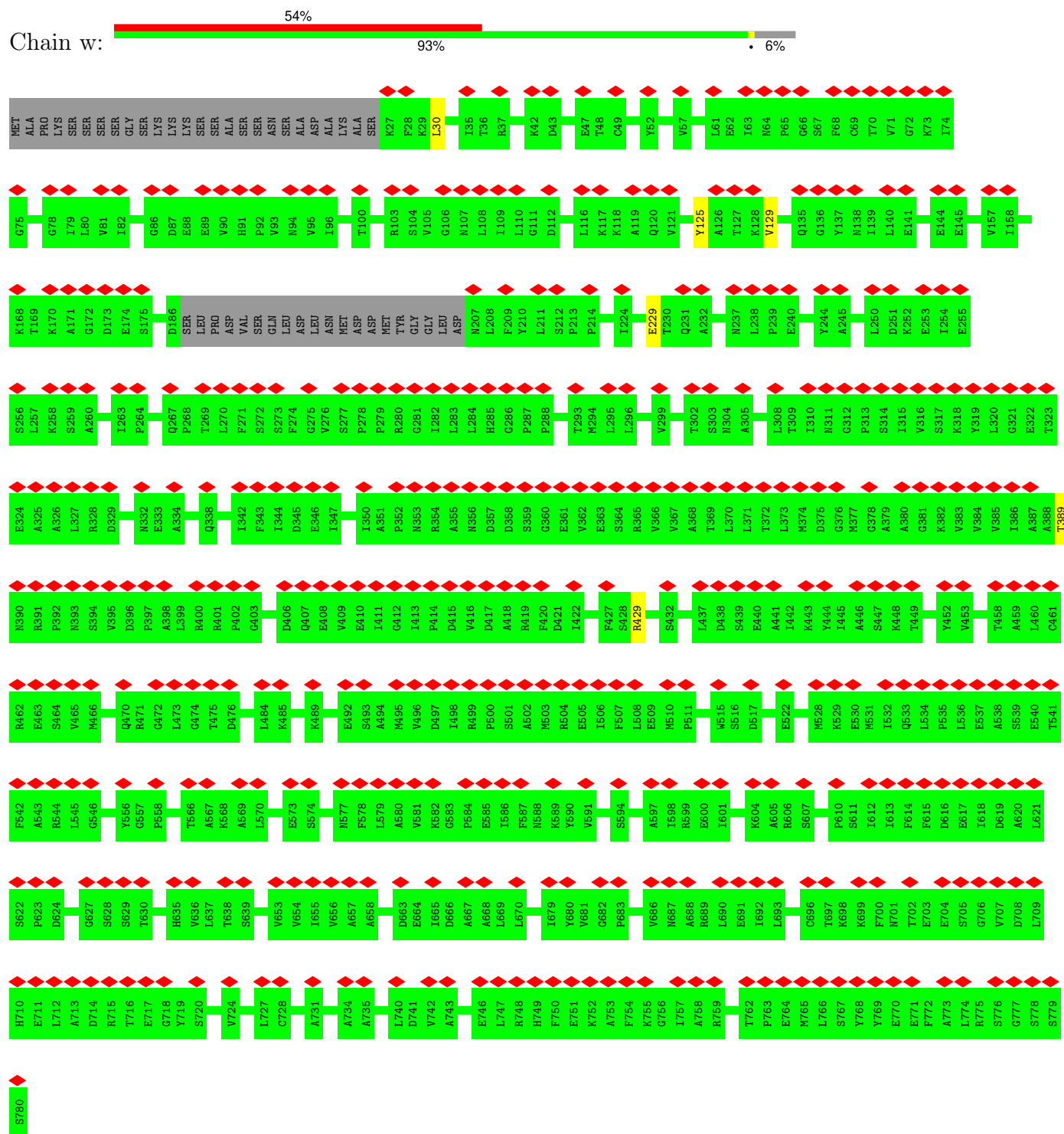




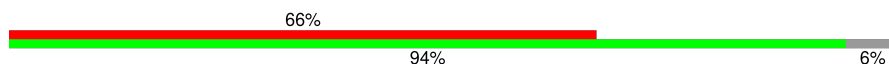
• Molecule 1: ATPase family gene 2 protein



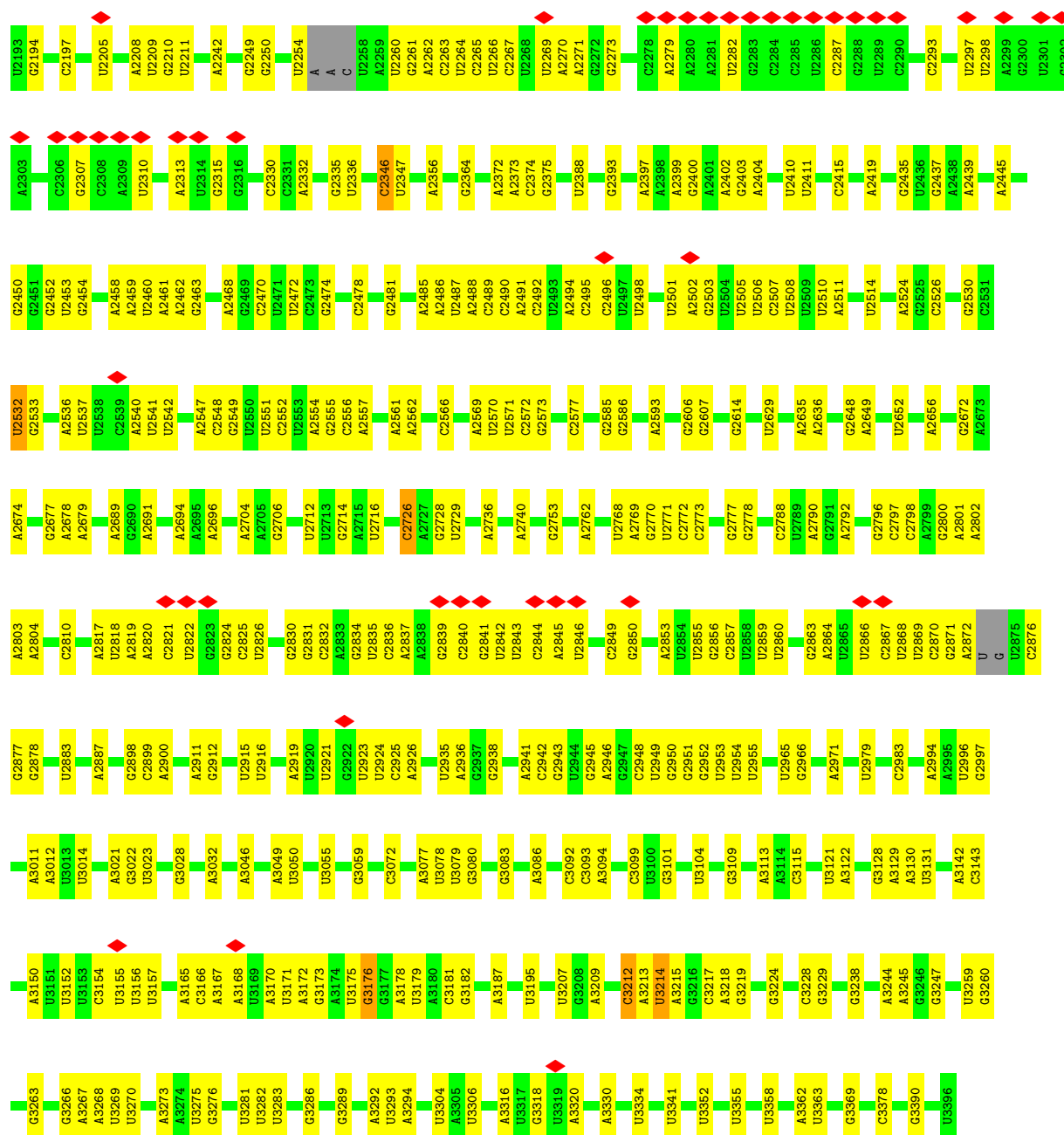
Chain w:




Chain x:

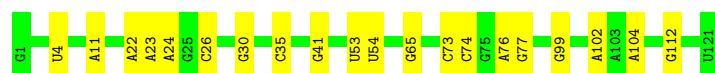


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A2073	G1963	G1796	U1620	C1279	A1180	U1033	A917	G718	U556	C	G251	U152
G2076	C1964	A1797	A1621	C1283	U1181	U1034	A921	U719	A557	C	U252	G156
U2077	U1967	G1808	U1629	A1286	G1186	G1035	G924	A720	U558	U	A253	A157
C2078	G1968	U1630	U1630	A1287	C1192	C1037	A925	G727	U559	G	G269	A165
G2079	G1969	C1631	C1631	A1287	A1193	C1038	G937	A735	G560	C	U270	G170
C2080	U1970	A1638	A1638	G1295	G1194	U1039	G940	A736	U	U	U279	G171
G2083	C1971	A1638	A1638	G1295	A1195	U1040	G941	G737	C	U	A284	G172
C2084	A1972	A1642	A1642	A1303	C1201	U1041	G942	A761	U	G	A295	U177
U2085	C1977	C1644	C1644	G1307	G1206	U1042	U943	G	U	U	U	U
A2086	A1991	U1645	U1645	A1308	G1207	A1047	U944	C765	A589	U	A	U182
C2087	A1995	C1657	C1657	U1309	U1208	A1048	C944	U766	G590	G	U305	U183
A2088	C1996	G1536	G1536	U1315	G1209	A1049	C959	U767	G591	U	A323	U184
A	U1997	U1511	U1511	U1330	U1220	U1050	U960	C768	A592	U	A324	U190
U	C1827	U1511	U1511	A1330	A1221	U1051	C961	U776	C593	A	U	U191
A	U1681	A1539	A1539	G1345	G1222	A1055	G964	U777	U594	G	U329	C192
A	U1681	C1566	C1566	G1345	A1231	A1063	G974	G781	G597	G	C339	U195
A	A1683	A1557	A1557	U1348	C1232	A1064	G974	G785	A598	G	C340	G196
C	A1842	U1567	U1567	A1350	U1235	A1065	G978	A784	G600	A	C346	C200
U	U1688	U1564	U1564	U1351	G1236	G1072	U979	A786	U601	U	G353	G202
U	A1694	G1565	G1565	G1354	G1237	U1081	A980	A801	A602	C	A372	G206
U2010	U1703	A1566	A1566	U1355	C1238	U1082	A988	A806	A607	U	G376	U210
U2011	A1704	U1567	U1567	U1356	C1239	U1083	A998	G815	U612	U	A211	A211
C2012	U1705	U1568	U1568	G1357	U1240	G1087	A1000	A811	A619	U	G212	A213
U2014	G1711	U1570	U1570	G1362	U1241	U1096	C1001	U621	U620	U	A398	U210
G2021	U1716	A1571	A1571	U1366	G1242	U1097	A1002	U492	G493	U	A401	A219
G2022	U1717	G1574	G1574	A1386	A1243	U1098	A1003	C851	G494	U	A402	G220
A2026	U1717	A1575	A1575	G1400	A1244	U1099	U1004	G857	G495	U	A403	A221
C2027	C1725	G1576	G1576	G1417	A1245	U1099	U1008	C861	C515	U	G420	U223
A2029	G1730	U1577	U1577	A1418	G1246	G1097	A1009	U879	A521	U	G421	G229
C2034	A1750	A1580	A1580	A1419	U1247	U1098	G1010	G880	A522	U	A440	U230
A2047	G1751	A1583	A1583	U1430	C1248	U1098	G1011	A849	A523	U	U441	G231
G2048	G1751	A1588	A1588	U1431	U1252	G1104	G1012	U874	A529	U	C439	G234
A2049	U1760	A1589	A1589	G1432	C1254	U1104	G1013	G875	A533	U	A442	A238
C2050	U1763	A1593	A1593	A1433	G1256	U1111	U1014	A876	U534	U	U443	G239
G2052	U1764	C1596	C1596	G1434	C1257	G1117	U1015	U879	G535	U	U446	U240
U2055	U1765	G1599	G1599	C1437	U1258	U1124	C1016	G891	U541	U	U447	G241
G2057	G1766	G1599	G1599	A1446	A1260	G1131	G1017	G907	C546	U	U448	U246
U2059	G1770	A1603	A1603	U1455	G1261	A1143	G1018	G908	A691	U	U449	U449
A2060	C1773	G1604	G1604	G1466	A1262	U1151	G1019	G908	A705	U	U450	G547
C2064	C1774	A1605	A1605	U1481	A1263	G1152	U1022	A914	A709	U	U451	U248
U2065	G1775	U1606	U1606	A1482	G1264	A1153	C1023	A915	G552	U	G452	U249
C2066	G1780	U1607	U1607	G1483	U1265	C1155	G1024					
G2069		G1618	G1618		A1270	A1159	A1025					
					A1271	G1178	A1026					
					C1272		A1027					
							U1028					
							G1029					
							A1030					
							G1031					




● Molecule 3: 5S rRNA

Chain 2:  83% 17%



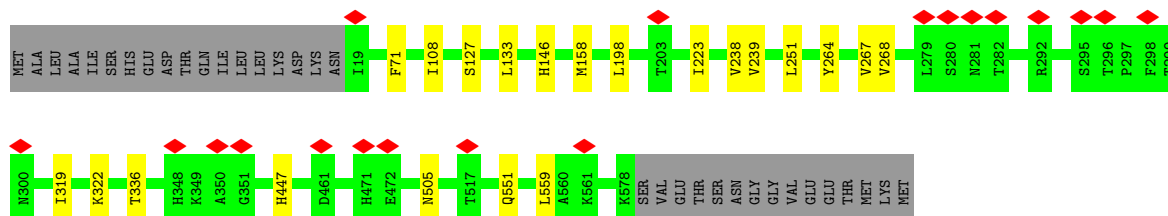
● Molecule 4: 5.8S rRNA

Chain 3:  80% 20%



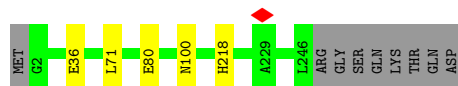
- Molecule 5: Probable metalloprotease ARX1

Chain 4: 91% 6%



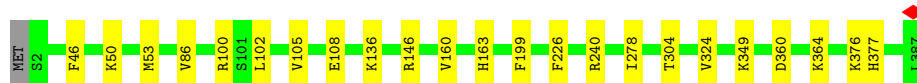
- Molecule 6: 60S ribosomal protein L2-A

Chain A: 94% 6%



- Molecule 7: 60S ribosomal protein L3

Chain B: 94% 6%



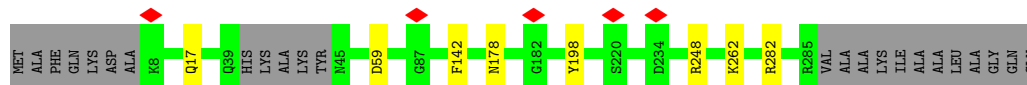
- Molecule 8: 60S ribosomal protein L4-A

Chain C: 96% 6%



- Molecule 9: 60S ribosomal protein L5

Chain D: 89% 8%



- Molecule 10: 60S ribosomal protein L6-A

Chain E: 94% 6%



• Molecule 17: 60S ribosomal protein L13-A

Chain L:  92% 5%

• Molecule 18: 60S ribosomal protein L14-A

Chain M:  93% 7%

• Molecule 19: 60S ribosomal protein L15-A

Chain N:  94% 5%


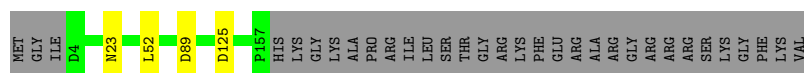
• Molecule 20: 60S ribosomal protein L16-A

Chain O:  94% 5%


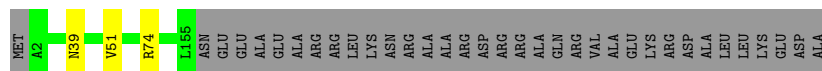
• Molecule 21: 60S ribosomal protein L17-A

Chain P:  96%

• Molecule 22: 60S ribosomal protein L18-A

Chain Q:  81% 17%

• Molecule 23: 60S ribosomal protein L19-A

Chain R:  80% 19%

- Molecule 24: 60S ribosomal protein L20-A

Chain S:  94% 5%




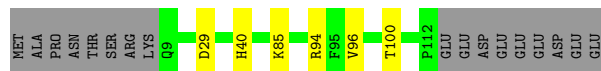
- Molecule 25: 60S ribosomal protein L21-A

Chain T:  94% 5%



- Molecule 26: 60S ribosomal protein L22-A

Chain U:  81% 5% 14%

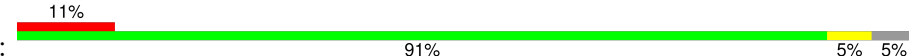


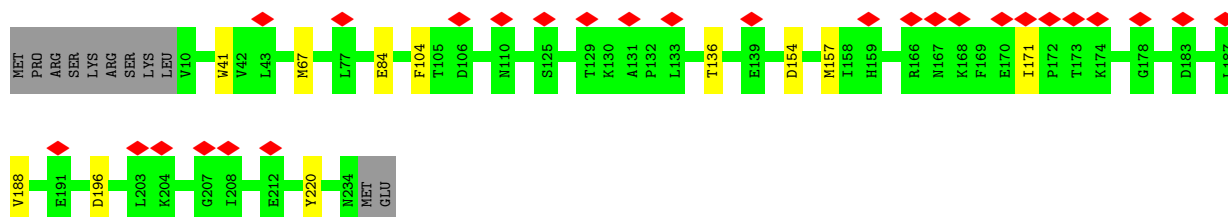
- Molecule 27: 60S ribosomal protein L23-A

Chain V:  94% 5%




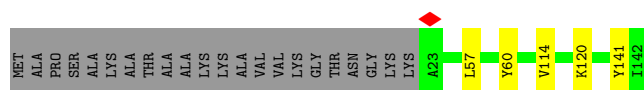
- Molecule 28: Ribosome assembly factor MRT4

Chain W:  11% 91% 5% 5%



- Molecule 29: 60S ribosomal protein L25

Chain X:  81% 15%



- Molecule 30: 60S ribosomal protein L26-A

Chain Y:  96%



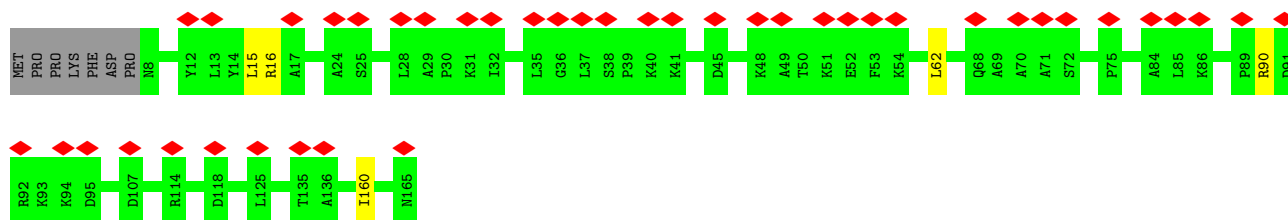
- Molecule 31: 60S ribosomal protein L27-A

Chain Z:  93%

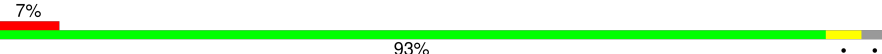


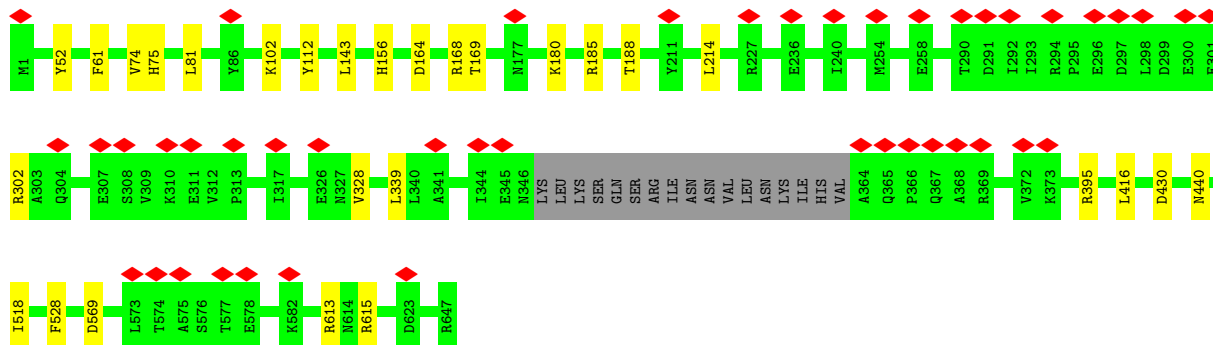
- Molecule 32: 60S ribosomal protein L12-A

Chain a:  25% 93%




- Molecule 33: Nucleolar GTP-binding protein 1

Chain b:  7% 93%



- Molecule 34: 60S ribosomal protein L30

Chain c:  90% 8%



- Molecule 35: 60S ribosomal protein L31-A

Chain d:  90% 5%



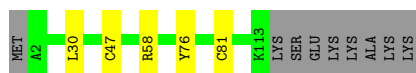
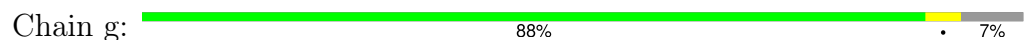
- Molecule 36: 60S ribosomal protein L32



- Molecule 37: 60S ribosomal protein L33-A



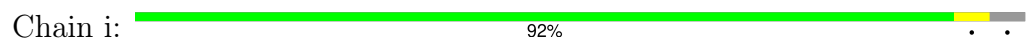
- Molecule 38: 60S ribosomal protein L34-A



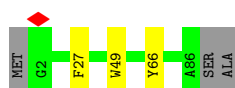
- Molecule 39: 60S ribosomal protein L35-A



- Molecule 40: 60S ribosomal protein L36-A



- Molecule 41: 60S ribosomal protein L37-A




- Molecule 42: 60S ribosomal protein L38

Chain k:  94% 5%




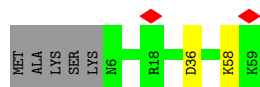
- Molecule 43: 60S ribosomal protein L39

Chain l:  94%



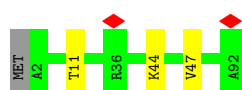
- Molecule 44: 60S ribosomal protein L29

Chain o:  88% 8%



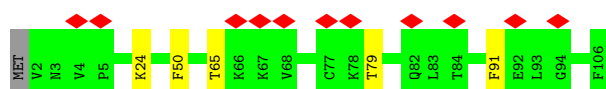
- Molecule 45: 60S ribosomal protein L43-A

Chain p:  96%



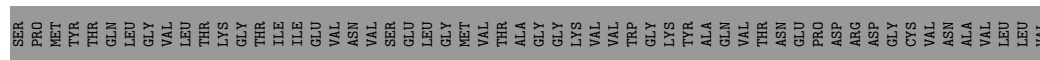
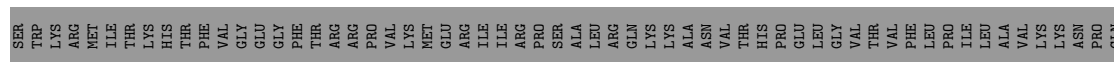
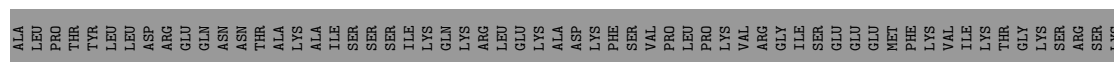
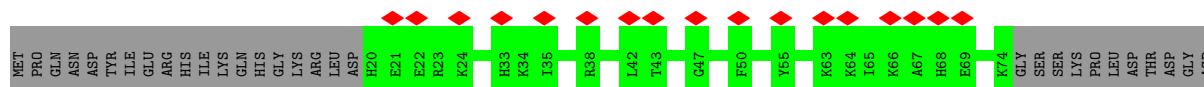
- Molecule 46: 60S ribosomal protein L42-A

Chain q:  10% 94% 5%



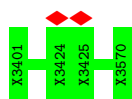
- Molecule 47: Ribosome biogenesis protein NSA2

Chain r:  7% 21% 79%



- Molecule 53: Unknown protein

Chain oC:  100%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1782014	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.047	Depositor
Minimum map value	-0.001	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.039	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	642.0, 642.0, 642.0	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3375, 1.3375, 1.3375	Depositor

5 Model quality

5.1 Standard geometry

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

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	Aa	0.24	0/5688	0.46	0/7700
1	m	0.24	0/5691	0.45	0/7702
1	n	0.24	0/5700	0.45	0/7716
1	t	0.24	0/5709	0.45	0/7727
1	w	0.24	0/5728	0.45	0/7751
1	x	0.24	0/5728	0.46	0/7751
2	1	0.29	0/80102	0.79	30/124881 (0.0%)
3	2	0.26	0/2883	0.77	0/4491
4	3	0.30	0/3724	0.76	0/5798
5	4	0.25	0/4410	0.49	0/5990
6	A	0.26	0/1897	0.55	0/2550
7	B	0.27	0/3153	0.53	0/4239
8	C	0.26	0/2802	0.51	0/3792
9	D	0.26	0/2250	0.50	0/3035
10	E	0.26	0/1425	0.49	0/1912
11	F	0.27	0/1822	0.49	0/2451
12	G	0.26	0/1830	0.48	0/2469
13	H	0.26	0/1514	0.49	0/2039
14	I	0.24	0/1018	0.47	0/1365
15	J	0.24	0/1332	0.53	0/1786
16	K	0.26	0/1204	0.50	0/1612
17	L	0.26	0/1568	0.55	0/2106
18	M	0.25	0/1075	0.50	0/1446
19	N	0.27	0/1758	0.56	0/2354
20	O	0.26	0/1586	0.49	0/2128
21	P	0.26	0/1466	0.53	0/1968
22	Q	0.25	0/1211	0.52	0/1633
23	R	0.24	0/1258	0.56	0/1679
24	S	0.27	0/1460	0.51	0/1962
25	T	0.26	0/1300	0.51	0/1743
26	U	0.26	0/843	0.46	0/1143
27	V	0.27	0/1019	0.52	0/1369

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
28	W	0.25	0/1842	0.48	0/2487
29	X	0.27	0/975	0.49	0/1314
30	Y	0.26	0/1005	0.51	0/1341
31	Z	0.27	0/1119	0.48	0/1497
32	a	0.24	0/1210	0.46	0/1627
33	b	0.25	0/5171	0.50	0/6947
34	c	0.25	0/751	0.45	0/1008
35	d	0.26	0/887	0.51	0/1191
36	e	0.25	0/1050	0.50	0/1406
37	f	0.28	0/869	0.54	0/1168
38	g	0.26	0/891	0.55	0/1191
39	h	0.25	0/979	0.51	0/1301
40	i	0.24	0/749	0.53	0/995
41	j	0.27	0/685	0.56	0/908
42	k	0.25	0/619	0.51	0/826
43	l	0.25	0/444	0.55	0/588
44	o	0.24	0/445	0.51	0/592
45	p	0.25	0/702	0.55	0/934
46	q	0.25	0/861	0.53	0/1136
47	r	0.23	0/476	0.46	0/621
48	u	0.26	0/1278	0.55	0/1699
49	v	0.25	0/1985	0.46	0/2692
50	y	0.25	0/1744	0.51	0/2375
51	z	0.23	0/445	0.46	0/585
All	All	0.27	0/187336	0.66	30/270717 (0.0%)

There are no bond length outliers.

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	1	3212	C	N1-C2-O2	12.89	126.63	118.90
2	1	3212	C	N3-C2-O2	-9.12	115.52	121.90
2	1	1827	C	N3-C2-O2	-8.53	115.93	121.90
2	1	2948	C	N3-C2-O2	-7.82	116.43	121.90
2	1	27	C	N1-C2-O2	7.59	123.45	118.90
2	1	3214	U	C2-N1-C1'	7.35	126.52	117.70
2	1	3176	G	N1-C6-O6	-7.16	115.60	119.90
2	1	3212	C	C2-N1-C1'	7.15	126.66	118.80
2	1	27	C	N3-C2-O2	-7.06	116.96	121.90
2	1	3214	U	N1-C2-O2	6.79	127.55	122.80
2	1	3176	G	C5-C6-O6	6.60	132.56	128.60
2	1	2948	C	N1-C2-O2	6.24	122.64	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	1	3214	U	N3-C2-O2	-6.19	117.87	122.20
2	1	3306	U	C2-N1-C1'	6.10	125.02	117.70
2	1	1618	G	C5-C6-O6	6.07	132.24	128.60
2	1	3212	C	C6-N1-C1'	-6.00	113.60	120.80
2	1	2492	C	N3-C2-O2	-5.59	117.99	121.90
2	1	1032	C	N3-C2-O2	-5.37	118.14	121.90
2	1	1618	G	N1-C6-O6	-5.37	116.68	119.90
2	1	2532	U	N3-C2-O2	-5.36	118.45	122.20
2	1	3306	U	N1-C2-O2	5.34	126.54	122.80
2	1	1711	C	N1-C2-O2	5.33	122.10	118.90
2	1	58	G	N1-C2-N2	-5.22	111.50	116.20
2	1	2263	C	N1-C2-O2	5.20	122.02	118.90
2	1	2346	C	N3-C2-O2	-5.19	118.27	121.90
2	1	940	G	N1-C6-O6	-5.10	116.84	119.90
2	1	3306	U	N3-C2-O2	-5.10	118.63	122.20
2	1	340	C	N1-C2-O2	5.07	121.94	118.90
2	1	2726	C	C2-N1-C1'	5.05	124.36	118.80
2	1	1279	C	C5-C6-N1	5.01	123.50	121.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Aa	724/780 (93%)	680 (94%)	42 (6%)	2 (0%)	37	69
1	m	726/780 (93%)	707 (97%)	17 (2%)	2 (0%)	37	69

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	n	726/780 (93%)	703 (97%)	23 (3%)	0	100	100
1	t	727/780 (93%)	706 (97%)	21 (3%)	0	100	100
1	w	730/780 (94%)	702 (96%)	28 (4%)	0	100	100
1	x	730/780 (94%)	709 (97%)	21 (3%)	0	100	100
5	4	558/593 (94%)	502 (90%)	56 (10%)	0	100	100
6	A	243/254 (96%)	226 (93%)	17 (7%)	0	100	100
7	B	384/387 (99%)	345 (90%)	39 (10%)	0	100	100
8	C	359/362 (99%)	329 (92%)	30 (8%)	0	100	100
9	D	269/297 (91%)	257 (96%)	12 (4%)	0	100	100
10	E	173/176 (98%)	159 (92%)	14 (8%)	0	100	100
11	F	220/244 (90%)	211 (96%)	9 (4%)	0	100	100
12	G	228/256 (89%)	215 (94%)	13 (6%)	0	100	100
13	H	186/191 (97%)	180 (97%)	6 (3%)	0	100	100
14	I	122/166 (74%)	114 (93%)	8 (7%)	0	100	100
15	J	162/174 (93%)	150 (93%)	12 (7%)	0	100	100
16	K	146/149 (98%)	132 (90%)	14 (10%)	0	100	100
17	L	191/199 (96%)	176 (92%)	15 (8%)	0	100	100
18	M	135/138 (98%)	130 (96%)	5 (4%)	0	100	100
19	N	201/204 (98%)	189 (94%)	12 (6%)	0	100	100
20	O	195/199 (98%)	191 (98%)	4 (2%)	0	100	100
21	P	181/184 (98%)	170 (94%)	11 (6%)	0	100	100
22	Q	152/186 (82%)	145 (95%)	7 (5%)	0	100	100
23	R	152/189 (80%)	146 (96%)	6 (4%)	0	100	100
24	S	168/172 (98%)	154 (92%)	14 (8%)	0	100	100
25	T	157/160 (98%)	154 (98%)	3 (2%)	0	100	100
26	U	102/121 (84%)	91 (89%)	11 (11%)	0	100	100
27	V	134/137 (98%)	128 (96%)	6 (4%)	0	100	100
28	W	223/236 (94%)	209 (94%)	14 (6%)	0	100	100
29	X	118/142 (83%)	114 (97%)	4 (3%)	0	100	100
30	Y	124/127 (98%)	119 (96%)	5 (4%)	0	100	100
31	Z	133/136 (98%)	120 (90%)	13 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
32	a	156/165 (94%)	153 (98%)	3 (2%)	0	100	100
33	b	626/647 (97%)	569 (91%)	57 (9%)	0	100	100
34	c	95/105 (90%)	94 (99%)	1 (1%)	0	100	100
35	d	105/113 (93%)	98 (93%)	7 (7%)	0	100	100
36	e	126/130 (97%)	120 (95%)	6 (5%)	0	100	100
37	f	104/107 (97%)	96 (92%)	8 (8%)	0	100	100
38	g	110/121 (91%)	105 (96%)	5 (4%)	0	100	100
39	h	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
40	i	94/100 (94%)	92 (98%)	2 (2%)	0	100	100
41	j	83/88 (94%)	80 (96%)	3 (4%)	0	100	100
42	k	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
43	l	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
44	o	52/59 (88%)	48 (92%)	4 (8%)	0	100	100
45	p	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
46	q	103/106 (97%)	88 (85%)	15 (15%)	0	100	100
47	r	53/261 (20%)	51 (96%)	2 (4%)	0	100	100
48	u	147/199 (74%)	140 (95%)	7 (5%)	0	100	100
49	v	241/518 (46%)	225 (93%)	16 (7%)	0	100	100
50	y	226/245 (92%)	208 (92%)	18 (8%)	0	100	100
51	z	53/106 (50%)	53 (100%)	0	0	100	100
All	All	12482/13870 (90%)	11795 (94%)	683 (6%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	m	563	LYS
1	Aa	589	LYS
1	Aa	702	THR
1	m	707	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Aa	614/657 (94%)	610 (99%)	4 (1%)	81	86
1	m	615/657 (94%)	610 (99%)	5 (1%)	79	84
1	n	615/657 (94%)	610 (99%)	5 (1%)	79	84
1	t	616/657 (94%)	616 (100%)	0	100	100
1	w	619/657 (94%)	613 (99%)	6 (1%)	73	80
1	x	619/657 (94%)	616 (100%)	3 (0%)	86	90
5	4	491/520 (94%)	470 (96%)	21 (4%)	25	49
6	A	188/196 (96%)	183 (97%)	5 (3%)	40	60
7	B	322/323 (100%)	299 (93%)	23 (7%)	12	36
8	C	288/289 (100%)	275 (96%)	13 (4%)	23	47
9	D	230/245 (94%)	222 (96%)	8 (4%)	31	54
10	E	152/153 (99%)	142 (93%)	10 (7%)	14	38
11	F	186/205 (91%)	180 (97%)	6 (3%)	34	56
12	G	189/208 (91%)	179 (95%)	10 (5%)	19	44
13	H	168/171 (98%)	163 (97%)	5 (3%)	36	58
14	I	110/141 (78%)	105 (96%)	5 (4%)	23	47
15	J	142/150 (95%)	138 (97%)	4 (3%)	38	59
16	K	118/119 (99%)	114 (97%)	4 (3%)	32	55
17	L	154/159 (97%)	145 (94%)	9 (6%)	17	42
18	M	108/109 (99%)	99 (92%)	9 (8%)	9	32
19	N	175/176 (99%)	164 (94%)	11 (6%)	15	40
20	O	160/162 (99%)	151 (94%)	9 (6%)	17	43
21	P	145/146 (99%)	139 (96%)	6 (4%)	26	50
22	Q	126/151 (83%)	122 (97%)	4 (3%)	34	56
23	R	127/154 (82%)	124 (98%)	3 (2%)	44	62
24	S	154/156 (99%)	146 (95%)	8 (5%)	19	44
25	T	136/137 (99%)	128 (94%)	8 (6%)	16	41
26	U	91/107 (85%)	85 (93%)	6 (7%)	14	38
27	V	104/105 (99%)	97 (93%)	7 (7%)	13	38
28	W	202/213 (95%)	191 (95%)	11 (5%)	18	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	X	104/118 (88%)	99 (95%)	5 (5%)	21	46
30	Y	109/110 (99%)	105 (96%)	4 (4%)	29	53
31	Z	115/116 (99%)	106 (92%)	9 (8%)	10	34
32	a	129/136 (95%)	124 (96%)	5 (4%)	27	51
33	b	556/573 (97%)	528 (95%)	28 (5%)	20	45
34	c	81/88 (92%)	78 (96%)	3 (4%)	29	53
35	d	94/97 (97%)	89 (95%)	5 (5%)	19	44
36	e	110/111 (99%)	104 (94%)	6 (6%)	18	43
37	f	90/91 (99%)	84 (93%)	6 (7%)	13	38
38	g	95/103 (92%)	90 (95%)	5 (5%)	19	44
39	h	104/105 (99%)	97 (93%)	7 (7%)	13	38
40	i	78/82 (95%)	74 (95%)	4 (5%)	20	45
41	j	69/71 (97%)	66 (96%)	3 (4%)	25	49
42	k	68/69 (99%)	64 (94%)	4 (6%)	16	41
43	l	45/46 (98%)	43 (96%)	2 (4%)	24	48
44	o	43/47 (92%)	41 (95%)	2 (5%)	22	46
45	p	71/72 (99%)	68 (96%)	3 (4%)	25	49
46	q	90/91 (99%)	85 (94%)	5 (6%)	17	43
47	r	48/229 (21%)	48 (100%)	0	100	100
48	u	132/180 (73%)	129 (98%)	3 (2%)	45	63
49	v	220/467 (47%)	216 (98%)	4 (2%)	54	71
50	y	195/211 (92%)	180 (92%)	15 (8%)	10	34
51	z	48/95 (50%)	44 (92%)	4 (8%)	9	32
All	All	10658/11745 (91%)	10298 (97%)	360 (3%)	34	55

All (360) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Aa	603	ARG
1	Aa	716	THR
1	Aa	730	GLU
1	Aa	759	ARG
5	4	71	PHE
5	4	108	ILE

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Mol	Chain	Res	Type
5	4	127	SER
5	4	133	LEU
5	4	146	HIS
5	4	158	MET
5	4	198	LEU
5	4	223	ILE
5	4	238	VAL
5	4	239	VAL
5	4	251	LEU
5	4	264	TYR
5	4	267	VAL
5	4	268	VAL
5	4	319	ILE
5	4	322	LYS
5	4	336	THR
5	4	447	HIS
5	4	505	ASN
5	4	551	GLN
5	4	559	LEU
6	A	36	GLU
6	A	71	LEU
6	A	80	GLU
6	A	100	ASN
6	A	218	HIS
7	B	46	PHE
7	B	50	LYS
7	B	53	MET
7	B	86	VAL
7	B	100	ARG
7	B	102	LEU
7	B	105	VAL
7	B	108	GLU
7	B	136	LYS
7	B	146	ARG
7	B	160	VAL
7	B	163	HIS
7	B	199	PHE
7	B	226	PHE
7	B	240	ARG
7	B	278	ILE
7	B	304	THR
7	B	324	VAL

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Mol	Chain	Res	Type
7	B	349	LYS
7	B	360	ASP
7	B	364	LYS
7	B	376	LYS
7	B	377	HIS
8	C	31	ARG
8	C	108	LYS
8	C	117	GLU
8	C	148	ILE
8	C	156	LEU
8	C	197	ARG
8	C	216	VAL
8	C	238	LEU
8	C	247	PHE
8	C	255	PHE
8	C	279	HIS
8	C	313	LEU
8	C	328	ASN
9	D	17	GLN
9	D	59	ASP
9	D	142	PHE
9	D	178	ASN
9	D	198	TYR
9	D	248	ARG
9	D	262	LYS
9	D	282	ARG
10	E	20	LYS
10	E	31	ARG
10	E	41	ILE
10	E	80	ASN
10	E	84	VAL
10	E	89	THR
10	E	101	PHE
10	E	111	LEU
10	E	128	LYS
10	E	134	ARG
11	F	61	ASN
11	F	75	TYR
11	F	117	VAL
11	F	147	LEU
11	F	191	VAL
11	F	223	PHE

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Mol	Chain	Res	Type
12	G	30	THR
12	G	74	THR
12	G	97	TYR
12	G	133	LYS
12	G	150	LEU
12	G	157	VAL
12	G	161	GLU
12	G	194	THR
12	G	197	VAL
12	G	248	LYS
13	H	53	ILE
13	H	62	ARG
13	H	142	ASP
13	H	152	GLU
13	H	183	HIS
14	I	13	ARG
14	I	19	ASP
14	I	34	LEU
14	I	37	GLN
14	I	60	THR
15	J	80	LEU
15	J	109	HIS
15	J	126	ASP
15	J	156	LYS
16	K	11	HIS
16	K	60	TYR
16	K	63	LYS
16	K	131	SER
17	L	6	ASN
17	L	21	ARG
17	L	37	ASN
17	L	57	VAL
17	L	58	VAL
17	L	116	LEU
17	L	174	ARG
17	L	178	LYS
17	L	188	ARG
18	M	25	LYS
18	M	42	LYS
18	M	44	VAL
18	M	60	LEU
18	M	77	ARG

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Mol	Chain	Res	Type
18	M	112	LEU
18	M	114	ASP
18	M	118	PHE
18	M	125	LYS
19	N	18	VAL
19	N	44	ARG
19	N	62	TYR
19	N	75	VAL
19	N	85	THR
19	N	114	ARG
19	N	135	VAL
19	N	159	ARG
19	N	167	THR
19	N	178	HIS
19	N	188	ARG
20	O	42	ASN
20	O	54	TYR
20	O	96	LYS
20	O	99	LEU
20	O	128	ARG
20	O	129	LEU
20	O	136	THR
20	O	153	VAL
20	O	194	LEU
21	P	22	LEU
21	P	50	GLN
21	P	52	LEU
21	P	64	ASN
21	P	119	VAL
21	P	139	TYR
22	Q	23	ASN
22	Q	52	LEU
22	Q	89	ASP
22	Q	125	ASP
23	R	39	ASN
23	R	51	VAL
23	R	74	ARG
24	S	27	MET
24	S	30	PHE
24	S	61	ILE
24	S	88	HIS
24	S	107	TYR

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Mol	Chain	Res	Type
24	S	118	PHE
24	S	149	LYS
24	S	167	ARG
25	T	7	TYR
25	T	14	MET
25	T	21	LYS
25	T	84	TYR
25	T	98	HIS
25	T	104	GLU
25	T	115	LYS
25	T	136	ARG
26	U	29	ASP
26	U	40	HIS
26	U	85	LYS
26	U	94	ARG
26	U	96	VAL
26	U	100	THR
27	V	25	CYS
27	V	35	TYR
27	V	48	ARG
27	V	54	LEU
27	V	59	MET
27	V	69	LEU
27	V	70	ARG
28	W	41	TRP
28	W	67	MET
28	W	84	GLU
28	W	104	PHE
28	W	136	THR
28	W	154	ASP
28	W	157	MET
28	W	171	ILE
28	W	188	VAL
28	W	196	ASP
28	W	220	TYR
29	X	57	LEU
29	X	60	TYR
29	X	114	VAL
29	X	120	LYS
29	X	141	TYR
30	Y	26	GLN
30	Y	31	LEU

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Mol	Chain	Res	Type
30	Y	109	LEU
30	Y	112	ASP
31	Z	4	PHE
31	Z	14	VAL
31	Z	15	ARG
31	Z	38	PHE
31	Z	43	VAL
31	Z	95	VAL
31	Z	115	LYS
31	Z	122	HIS
31	Z	131	PHE
32	a	15	LEU
32	a	16	ARG
32	a	62	LEU
32	a	90	ARG
32	a	160	ILE
33	b	52	TYR
33	b	61	PHE
33	b	74	VAL
33	b	75	HIS
33	b	81	LEU
33	b	102	LYS
33	b	112	TYR
33	b	143	LEU
33	b	156	HIS
33	b	164	ASP
33	b	168	ARG
33	b	169	THR
33	b	180	LYS
33	b	185	ARG
33	b	188	THR
33	b	214	LEU
33	b	302	ARG
33	b	328	VAL
33	b	339	LEU
33	b	395	ARG
33	b	416	LEU
33	b	430	ASP
33	b	440	ASN
33	b	518	ILE
33	b	528	PHE
33	b	569	ASP

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Mol	Chain	Res	Type
33	b	613	ARG
33	b	615	ARG
34	c	27	TYR
34	c	58	TYR
34	c	86	ARG
35	d	14	ILE
35	d	17	HIS
35	d	37	LYS
35	d	69	TYR
35	d	106	THR
36	e	26	HIS
36	e	55	ILE
36	e	98	HIS
36	e	109	LEU
36	e	115	LEU
36	e	119	VAL
37	f	9	VAL
37	f	14	LEU
37	f	16	TYR
37	f	21	ARG
37	f	23	ASN
37	f	81	VAL
38	g	30	LEU
38	g	47	CYS
38	g	58	ARG
38	g	76	TYR
38	g	81	CYS
39	h	17	LEU
39	h	24	LEU
39	h	28	LEU
39	h	44	ILE
39	h	49	LYS
39	h	55	LEU
39	h	85	THR
40	i	20	MET
40	i	30	LYS
40	i	61	ILE
40	i	86	LYS
41	j	27	PHE
41	j	49	TRP
41	j	66	TYR
42	k	3	ARG

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Mol	Chain	Res	Type
42	k	55	VAL
42	k	65	LEU
42	k	73	LEU
43	l	41	ARG
43	l	42	ARG
1	m	98	LEU
1	m	143	MET
1	m	251	ASP
1	m	680	TYR
1	m	750	PHE
1	n	114	LEU
1	n	283	LEU
1	n	507	PHE
1	n	587	PHE
1	n	669	LEU
44	o	36	ASP
44	o	58	LYS
45	p	11	THR
45	p	44	LYS
45	p	47	VAL
46	q	24	LYS
46	q	50	PHE
46	q	65	THR
46	q	79	THR
46	q	91	PHE
48	u	6	CYS
48	u	9	CYS
48	u	81	TYR
49	v	210	MET
49	v	335	LEU
49	v	379	TYR
49	v	399	LYS
1	w	30	LEU
1	w	125	TYR
1	w	129	VAL
1	w	229	GLU
1	w	389	THR
1	w	429	ARG
1	x	294	MET
1	x	430	MET
1	x	503	MET
50	y	7	PHE

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Mol	Chain	Res	Type
50	y	18	LYS
50	y	23	TYR
50	y	34	PHE
50	y	66	ASN
50	y	68	ARG
50	y	77	THR
50	y	85	ARG
50	y	93	LYS
50	y	128	LEU
50	y	165	THR
50	y	181	LEU
50	y	198	VAL
50	y	205	VAL
50	y	210	THR
51	z	16	VAL
51	z	35	ASP
51	z	43	LYS
51	z	48	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (115) such sidechains are listed below:

Mol	Chain	Res	Type
1	Aa	91	HIS
5	4	36	GLN
5	4	113	ASN
5	4	171	GLN
5	4	188	HIS
5	4	221	GLN
5	4	274	GLN
5	4	348	HIS
5	4	366	GLN
5	4	490	ASN
6	A	86	GLN
6	A	132	ASN
7	B	13	HIS
7	B	165	GLN
7	B	173	GLN
7	B	177	HIS
7	B	198	HIS
8	C	36	HIS
8	C	45	ASN
8	C	48	GLN

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Mol	Chain	Res	Type
8	C	92	ASN
8	C	296	GLN
8	C	320	ASN
8	C	322	GLN
9	D	32	GLN
10	E	28	GLN
11	F	37	ASN
11	F	52	GLN
12	G	240	ASN
13	H	40	HIS
13	H	58	HIS
13	H	96	HIS
13	H	183	HIS
15	J	43	GLN
15	J	47	GLN
15	J	150	ASN
16	K	38	GLN
16	K	39	HIS
16	K	64	GLN
17	L	137	GLN
19	N	57	GLN
19	N	122	ASN
19	N	138	GLN
19	N	156	HIS
20	O	182	ASN
21	P	101	ASN
21	P	116	HIS
23	R	34	GLN
23	R	39	ASN
24	S	65	ASN
24	S	89	ASN
25	T	22	HIS
25	T	58	GLN
25	T	134	GLN
27	V	33	ASN
28	W	44	HIS
28	W	223	ASN
28	W	232	ASN
29	X	91	ASN
32	a	61	GLN
32	a	65	GLN
32	a	100	HIS

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Mol	Chain	Res	Type
32	a	156	ASN
33	b	26	GLN
33	b	72	ASN
33	b	75	HIS
33	b	78	HIS
33	b	124	GLN
33	b	195	GLN
33	b	238	GLN
33	b	406	ASN
33	b	413	ASN
33	b	534	HIS
33	b	546	GLN
34	c	47	ASN
34	c	75	ASN
35	d	57	GLN
36	e	104	ASN
37	f	75	HIS
37	f	106	ASN
38	g	34	HIS
39	h	34	GLN
39	h	113	GLN
41	j	76	ASN
41	j	79	GLN
42	k	28	ASN
42	k	67	GLN
43	l	38	ASN
1	m	231	GLN
1	m	267	GLN
1	m	338	GLN
1	m	729	GLN
1	n	267	GLN
1	n	470	GLN
1	n	521	GLN
1	n	678	HIS
1	n	749	HIS
44	o	7	HIS
44	o	43	HIS
44	o	48	HIS
45	p	34	HIS
46	q	82	GLN
1	t	91	HIS
1	t	635	HIS

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Mol	Chain	Res	Type
1	t	642	ASN
48	u	101	GLN
1	w	91	HIS
1	w	120	GLN
1	w	237	ASN
1	w	311	ASN
1	w	588	ASN
1	x	107	ASN
1	x	306	HIS
1	x	678	HIS
50	y	145	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	1	3342/3396 (98%)	870 (26%)	38 (1%)
3	2	120/121 (99%)	20 (16%)	0
4	3	156/158 (98%)	31 (19%)	0
All	All	3618/3675 (98%)	921 (25%)	38 (1%)

All (921) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	1	4	U
2	1	14	U
2	1	16	A
2	1	22	G
2	1	23	A
2	1	24	G
2	1	25	U
2	1	26	A
2	1	28	C
2	1	30	G
2	1	40	A
2	1	43	A
2	1	46	U
2	1	47	C
2	1	49	A
2	1	57	A
2	1	59	G
2	1	60	A

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Mol	Chain	Res	Type
2	1	65	A
2	1	66	A
2	1	72	C
2	1	74	G
2	1	75	G
2	1	77	A
2	1	92	G
2	1	94	G
2	1	110	G
2	1	111	C
2	1	122	A
2	1	135	C
2	1	136	G
2	1	140	C
2	1	142	C
2	1	150	A
2	1	152	U
2	1	156	G
2	1	157	A
2	1	165	A
2	1	170	G
2	1	172	G
2	1	177	U
2	1	182	U
2	1	184	U
2	1	190	U
2	1	191	U
2	1	192	C
2	1	195	U
2	1	196	G
2	1	200	C
2	1	202	G
2	1	206	G
2	1	210	U
2	1	211	A
2	1	212	G
2	1	213	A
2	1	218	G
2	1	219	A
2	1	220	G
2	1	221	A
2	1	223	U

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Mol	Chain	Res	Type
2	1	229	G
2	1	231	G
2	1	234	G
2	1	238	A
2	1	239	G
2	1	240	U
2	1	242	C
2	1	243	G
2	1	246	U
2	1	247	C
2	1	249	U
2	1	251	G
2	1	253	A
2	1	269	G
2	1	270	U
2	1	279	U
2	1	284	A
2	1	295	A
2	1	305	U
2	1	323	A
2	1	324	A
2	1	329	U
2	1	339	C
2	1	346	C
2	1	353	G
2	1	372	A
2	1	376	G
2	1	398	A
2	1	401	U
2	1	402	A
2	1	403	C
2	1	406	G
2	1	407	A
2	1	420	G
2	1	421	G
2	1	422	A
2	1	424	G
2	1	439	C
2	1	441	U
2	1	442	G
2	1	446	U
2	1	448	U

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Mol	Chain	Res	Type
2	1	449	U
2	1	450	G
2	1	451	U
2	1	452	G
2	1	482	C
2	1	483	G
2	1	484	C
2	1	485	A
2	1	487	U
2	1	488	U
2	1	492	U
2	1	493	G
2	1	494	G
2	1	495	G
2	1	515	C
2	1	521	A
2	1	523	A
2	1	529	A
2	1	533	A
2	1	535	G
2	1	541	U
2	1	546	C
2	1	547	G
2	1	551	A
2	1	552	G
2	1	555	U
2	1	557	A
2	1	559	A
2	1	560	G
2	1	567	G
2	1	573	C
2	1	579	G
2	1	589	A
2	1	590	G
2	1	592	A
2	1	593	C
2	1	594	U
2	1	597	G
2	1	599	C
2	1	600	G
2	1	601	U
2	1	603	A

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Mol	Chain	Res	Type
2	1	607	A
2	1	611	A
2	1	612	U
2	1	620	U
2	1	621	A
2	1	636	C
2	1	645	A
2	1	646	A
2	1	649	A
2	1	667	C
2	1	677	A
2	1	681	U
2	1	683	U
2	1	689	U
2	1	690	A
2	1	691	A
2	1	705	A
2	1	709	A
2	1	717	C
2	1	719	U
2	1	720	A
2	1	727	G
2	1	735	A
2	1	737	G
2	1	761	A
2	1	765	C
2	1	766	U
2	1	767	U
2	1	768	C
2	1	776	U
2	1	777	U
2	1	781	G
2	1	784	A
2	1	785	G
2	1	786	A
2	1	801	A
2	1	806	A
2	1	815	G
2	1	817	A
2	1	830	A
2	1	851	C
2	1	857	G

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Mol	Chain	Res	Type
2	1	861	C
2	1	874	U
2	1	875	G
2	1	876	A
2	1	879	U
2	1	880	G
2	1	884	A
2	1	891	G
2	1	907	G
2	1	908	G
2	1	914	A
2	1	916	G
2	1	917	A
2	1	921	A
2	1	924	G
2	1	925	A
2	1	937	G
2	1	941	G
2	1	943	U
2	1	944	C
2	1	959	C
2	1	960	U
2	1	961	C
2	1	964	G
2	1	974	G
2	1	978	G
2	1	980	A
2	1	998	A
2	1	999	G
2	1	1000	C
2	1	1001	G
2	1	1002	A
2	1	1008	U
2	1	1009	A
2	1	1010	G
2	1	1011	A
2	1	1012	G
2	1	1013	G
2	1	1014	U
2	1	1015	U
2	1	1016	C
2	1	1017	C

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Mol	Chain	Res	Type
2	1	1018	G
2	1	1019	G
2	1	1020	G
2	1	1022	U
2	1	1023	C
2	1	1024	G
2	1	1026	A
2	1	1028	U
2	1	1029	G
2	1	1030	A
2	1	1032	C
2	1	1034	U
2	1	1036	A
2	1	1037	C
2	1	1038	C
2	1	1039	U
2	1	1047	A
2	1	1049	C
2	1	1051	U
2	1	1055	A
2	1	1063	G
2	1	1064	A
2	1	1065	A
2	1	1072	G
2	1	1081	U
2	1	1082	U
2	1	1087	G
2	1	1093	A
2	1	1096	U
2	1	1097	G
2	1	1098	A
2	1	1103	A
2	1	1104	G
2	1	1111	U
2	1	1117	G
2	1	1124	U
2	1	1143	A
2	1	1151	U
2	1	1153	A
2	1	1155	C
2	1	1159	A
2	1	1178	G

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Mol	Chain	Res	Type
2	1	1180	A
2	1	1181	U
2	1	1186	G
2	1	1192	C
2	1	1193	A
2	1	1195	A
2	1	1201	C
2	1	1206	G
2	1	1208	U
2	1	1209	G
2	1	1220	U
2	1	1222	G
2	1	1231	A
2	1	1232	C
2	1	1235	U
2	1	1236	G
2	1	1238	C
2	1	1239	C
2	1	1241	U
2	1	1243	G
2	1	1244	A
2	1	1245	A
2	1	1246	G
2	1	1248	C
2	1	1249	G
2	1	1252	A
2	1	1253	U
2	1	1254	C
2	1	1255	C
2	1	1257	C
2	1	1259	A
2	1	1260	A
2	1	1262	G
2	1	1263	A
2	1	1264	G
2	1	1265	U
2	1	1270	A
2	1	1272	C
2	1	1278	A
2	1	1279	C
2	1	1283	C
2	1	1286	A

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Mol	Chain	Res	Type
2	1	1287	A
2	1	1295	G
2	1	1303	A
2	1	1307	G
2	1	1309	U
2	1	1315	U
2	1	1330	A
2	1	1345	G
2	1	1348	U
2	1	1349	G
2	1	1351	U
2	1	1354	G
2	1	1355	A
2	1	1356	U
2	1	1357	G
2	1	1362	G
2	1	1386	A
2	1	1399	A
2	1	1400	G
2	1	1417	G
2	1	1419	A
2	1	1430	U
2	1	1432	C
2	1	1434	G
2	1	1437	C
2	1	1446	A
2	1	1455	U
2	1	1466	G
2	1	1481	A
2	1	1483	G
2	1	1487	G
2	1	1495	U
2	1	1496	C
2	1	1500	G
2	1	1508	C
2	1	1510	G
2	1	1511	U
2	1	1523	U
2	1	1536	G
2	1	1539	A
2	1	1556	C
2	1	1557	A

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Mol	Chain	Res	Type
2	1	1562	C
2	1	1563	C
2	1	1564	U
2	1	1566	A
2	1	1567	U
2	1	1568	U
2	1	1569	U
2	1	1570	U
2	1	1571	A
2	1	1574	C
2	1	1575	A
2	1	1576	G
2	1	1577	G
2	1	1579	C
2	1	1580	A
2	1	1583	A
2	1	1588	A
2	1	1589	A
2	1	1593	A
2	1	1596	C
2	1	1599	G
2	1	1603	A
2	1	1605	A
2	1	1606	U
2	1	1607	U
2	1	1619	A
2	1	1620	U
2	1	1621	A
2	1	1629	U
2	1	1631	C
2	1	1638	A
2	1	1642	A
2	1	1643	A
2	1	1645	U
2	1	1657	C
2	1	1677	G
2	1	1681	U
2	1	1683	A
2	1	1688	U
2	1	1694	U
2	1	1703	U
2	1	1705	U

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Mol	Chain	Res	Type
2	1	1716	U
2	1	1717	U
2	1	1724	U
2	1	1725	C
2	1	1730	G
2	1	1750	A
2	1	1751	G
2	1	1760	A
2	1	1763	U
2	1	1765	U
2	1	1766	G
2	1	1769	G
2	1	1770	G
2	1	1773	C
2	1	1775	G
2	1	1780	G
2	1	1792	C
2	1	1796	G
2	1	1797	A
2	1	1808	G
2	1	1813	A
2	1	1814	A
2	1	1816	A
2	1	1817	G
2	1	1819	U
2	1	1820	U
2	1	1821	U
2	1	1839	A
2	1	1841	A
2	1	1842	A
2	1	1849	C
2	1	1850	A
2	1	1880	U
2	1	1884	A
2	1	1892	G
2	1	1893	A
2	1	1900	A
2	1	1903	U
2	1	1904	C
2	1	1906	G
2	1	1907	C
2	1	1908	A

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Mol	Chain	Res	Type
2	1	1909	A
2	1	1910	A
2	1	1926	C
2	1	1954	G
2	1	1955	U
2	1	1956	A
2	1	1957	G
2	1	1958	U
2	1	1962	G
2	1	1963	G
2	1	1964	C
2	1	1967	U
2	1	1969	G
2	1	1971	C
2	1	1972	A
2	1	1977	C
2	1	1991	G
2	1	1995	A
2	1	1997	U
2	1	2002	G
2	1	2003	G
2	1	2008	G
2	1	2010	U
2	1	2011	U
2	1	2012	G
2	1	2013	C
2	1	2014	U
2	1	2021	G
2	1	2022	G
2	1	2026	A
2	1	2028	U
2	1	2029	A
2	1	2047	A
2	1	2048	G
2	1	2050	C
2	1	2055	U
2	1	2056	U
2	1	2057	G
2	1	2058	G
2	1	2060	A
2	1	2064	C
2	1	2066	C

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Mol	Chain	Res	Type
2	1	2069	G
2	1	2072	G
2	1	2076	G
2	1	2077	U
2	1	2078	C
2	1	2079	G
2	1	2080	C
2	1	2083	G
2	1	2084	C
2	1	2085	U
2	1	2086	A
2	1	2087	C
2	1	2088	A
2	1	2101	C
2	1	2102	U
2	1	2107	A
2	1	2111	G
2	1	2112	U
2	1	2113	A
2	1	2116	G
2	1	2119	A
2	1	2121	G
2	1	2122	G
2	1	2131	A
2	1	2139	A
2	1	2142	A
2	1	2149	A
2	1	2158	A
2	1	2160	G
2	1	2170	U
2	1	2180	G
2	1	2192	C
2	1	2194	G
2	1	2197	C
2	1	2205	U
2	1	2208	A
2	1	2209	U
2	1	2210	G
2	1	2211	U
2	1	2242	A
2	1	2250	G
2	1	2254	U

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Mol	Chain	Res	Type
2	1	2260	U
2	1	2261	G
2	1	2262	A
2	1	2265	C
2	1	2267	C
2	1	2269	U
2	1	2270	A
2	1	2271	A
2	1	2273	G
2	1	2279	A
2	1	2282	U
2	1	2287	C
2	1	2293	C
2	1	2297	U
2	1	2298	U
2	1	2307	G
2	1	2310	U
2	1	2313	A
2	1	2315	G
2	1	2330	C
2	1	2332	A
2	1	2335	G
2	1	2336	U
2	1	2346	C
2	1	2347	U
2	1	2356	A
2	1	2364	G
2	1	2372	A
2	1	2373	A
2	1	2374	C
2	1	2375	G
2	1	2388	U
2	1	2393	G
2	1	2397	A
2	1	2399	A
2	1	2400	G
2	1	2402	A
2	1	2403	G
2	1	2404	A
2	1	2410	U
2	1	2411	U
2	1	2415	C

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Mol	Chain	Res	Type
2	1	2419	A
2	1	2435	G
2	1	2437	G
2	1	2439	A
2	1	2445	A
2	1	2450	G
2	1	2452	G
2	1	2453	U
2	1	2454	G
2	1	2458	A
2	1	2459	A
2	1	2460	U
2	1	2461	A
2	1	2462	A
2	1	2463	G
2	1	2468	A
2	1	2470	C
2	1	2472	U
2	1	2474	G
2	1	2478	C
2	1	2481	G
2	1	2485	A
2	1	2486	A
2	1	2487	U
2	1	2488	A
2	1	2489	C
2	1	2490	C
2	1	2491	A
2	1	2494	A
2	1	2495	C
2	1	2496	C
2	1	2498	U
2	1	2502	A
2	1	2503	G
2	1	2505	U
2	1	2506	U
2	1	2507	C
2	1	2508	U
2	1	2510	U
2	1	2511	A
2	1	2514	U
2	1	2524	A

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Mol	Chain	Res	Type
2	1	2526	C
2	1	2530	G
2	1	2532	U
2	1	2533	G
2	1	2536	A
2	1	2537	U
2	1	2540	A
2	1	2541	U
2	1	2542	U
2	1	2548	C
2	1	2549	G
2	1	2551	U
2	1	2552	C
2	1	2554	A
2	1	2555	G
2	1	2556	C
2	1	2557	A
2	1	2561	A
2	1	2562	A
2	1	2566	C
2	1	2569	A
2	1	2570	U
2	1	2571	U
2	1	2572	C
2	1	2573	G
2	1	2577	C
2	1	2585	G
2	1	2586	G
2	1	2593	A
2	1	2606	G
2	1	2607	G
2	1	2614	G
2	1	2629	U
2	1	2635	A
2	1	2636	A
2	1	2648	G
2	1	2649	A
2	1	2652	U
2	1	2656	A
2	1	2672	G
2	1	2674	A
2	1	2677	G

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Mol	Chain	Res	Type
2	1	2678	A
2	1	2679	A
2	1	2689	A
2	1	2691	A
2	1	2694	A
2	1	2696	A
2	1	2704	A
2	1	2706	G
2	1	2712	U
2	1	2714	G
2	1	2716	U
2	1	2726	C
2	1	2728	G
2	1	2729	U
2	1	2736	A
2	1	2740	A
2	1	2753	G
2	1	2762	A
2	1	2768	U
2	1	2769	A
2	1	2770	G
2	1	2771	U
2	1	2772	C
2	1	2773	C
2	1	2777	G
2	1	2778	G
2	1	2788	C
2	1	2790	A
2	1	2792	A
2	1	2796	G
2	1	2797	C
2	1	2798	C
2	1	2800	G
2	1	2801	A
2	1	2802	A
2	1	2803	A
2	1	2804	A
2	1	2810	C
2	1	2817	A
2	1	2818	U
2	1	2819	A
2	1	2820	A

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Mol	Chain	Res	Type
2	1	2821	C
2	1	2822	U
2	1	2824	G
2	1	2825	C
2	1	2826	U
2	1	2830	G
2	1	2831	G
2	1	2832	C
2	1	2834	G
2	1	2835	U
2	1	2836	C
2	1	2837	A
2	1	2839	G
2	1	2840	C
2	1	2841	G
2	1	2842	U
2	1	2843	U
2	1	2844	C
2	1	2845	A
2	1	2846	U
2	1	2849	C
2	1	2850	G
2	1	2853	A
2	1	2855	U
2	1	2856	G
2	1	2857	C
2	1	2859	U
2	1	2860	U
2	1	2863	G
2	1	2864	A
2	1	2867	C
2	1	2868	U
2	1	2869	U
2	1	2870	C
2	1	2871	G
2	1	2872	A
2	1	2876	C
2	1	2877	G
2	1	2878	G
2	1	2883	U
2	1	2887	A
2	1	2898	G

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Mol	Chain	Res	Type
2	1	2899	C
2	1	2900	A
2	1	2911	A
2	1	2912	G
2	1	2915	U
2	1	2916	U
2	1	2919	A
2	1	2921	U
2	1	2923	U
2	1	2924	U
2	1	2925	C
2	1	2926	A
2	1	2935	U
2	1	2936	A
2	1	2938	G
2	1	2941	A
2	1	2942	C
2	1	2943	G
2	1	2945	G
2	1	2946	A
2	1	2949	U
2	1	2950	G
2	1	2951	G
2	1	2952	G
2	1	2953	U
2	1	2954	U
2	1	2955	U
2	1	2966	G
2	1	2971	A
2	1	2979	U
2	1	2983	C
2	1	2994	A
2	1	2996	U
2	1	2997	G
2	1	3011	A
2	1	3012	A
2	1	3014	U
2	1	3021	A
2	1	3022	G
2	1	3023	U
2	1	3028	G
2	1	3032	A

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Mol	Chain	Res	Type
2	1	3046	A
2	1	3049	A
2	1	3050	U
2	1	3055	U
2	1	3059	G
2	1	3072	C
2	1	3077	A
2	1	3079	U
2	1	3080	G
2	1	3083	G
2	1	3086	A
2	1	3092	C
2	1	3093	C
2	1	3094	A
2	1	3099	C
2	1	3101	G
2	1	3104	U
2	1	3109	G
2	1	3113	A
2	1	3115	C
2	1	3122	A
2	1	3128	G
2	1	3129	A
2	1	3130	A
2	1	3131	U
2	1	3142	A
2	1	3143	C
2	1	3150	A
2	1	3152	U
2	1	3154	C
2	1	3155	U
2	1	3156	U
2	1	3157	U
2	1	3165	A
2	1	3166	C
2	1	3167	A
2	1	3168	A
2	1	3170	A
2	1	3171	U
2	1	3172	A
2	1	3173	G
2	1	3175	U

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Mol	Chain	Res	Type
2	1	3176	G
2	1	3178	A
2	1	3179	U
2	1	3181	C
2	1	3182	G
2	1	3187	A
2	1	3195	U
2	1	3207	U
2	1	3209	A
2	1	3212	C
2	1	3213	A
2	1	3214	U
2	1	3215	A
2	1	3217	C
2	1	3218	A
2	1	3219	G
2	1	3224	G
2	1	3229	G
2	1	3238	G
2	1	3244	A
2	1	3245	A
2	1	3247	G
2	1	3259	U
2	1	3260	G
2	1	3263	G
2	1	3266	G
2	1	3267	A
2	1	3268	A
2	1	3270	U
2	1	3273	A
2	1	3275	U
2	1	3276	G
2	1	3281	U
2	1	3282	U
2	1	3283	U
2	1	3286	G
2	1	3289	G
2	1	3293	U
2	1	3294	A
2	1	3304	U
2	1	3316	A
2	1	3318	G

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Mol	Chain	Res	Type
2	1	3320	A
2	1	3330	A
2	1	3334	U
2	1	3341	U
2	1	3352	U
2	1	3355	U
2	1	3358	U
2	1	3362	A
2	1	3363	U
2	1	3369	G
2	1	3378	C
2	1	3390	G
3	2	4	U
3	2	11	A
3	2	22	A
3	2	23	A
3	2	24	A
3	2	26	C
3	2	30	G
3	2	35	C
3	2	41	G
3	2	53	U
3	2	54	U
3	2	65	G
3	2	73	C
3	2	74	C
3	2	76	A
3	2	77	G
3	2	99	G
3	2	102	A
3	2	104	A
3	2	112	G
4	3	2	A
4	3	16	G
4	3	25	G
4	3	34	U
4	3	35	C
4	3	39	G
4	3	46	G
4	3	49	G
4	3	51	G
4	3	59	A

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Mol	Chain	Res	Type
4	3	62	C
4	3	63	G
4	3	72	A
4	3	80	A
4	3	82	U
4	3	83	C
4	3	86	U
4	3	87	G
4	3	88	A
4	3	91	C
4	3	95	G
4	3	97	A
4	3	98	U
4	3	104	A
4	3	106	C
4	3	111	A
4	3	113	U
4	3	125	U
4	3	126	A
4	3	148	G
4	3	155	A

All (38) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	1	421	G
2	1	448	U
2	1	493	G
2	1	599	C
2	1	619	A
2	1	916	G
2	1	998	A
2	1	1027	A
2	1	1038	C
2	1	1064	A
2	1	1097	G
2	1	1243	G
2	1	1494	U
2	1	1576	G
2	1	1815	U
2	1	1816	A
2	1	1953	G

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Mol	Chain	Res	Type
2	1	2012	G
2	1	2056	U
2	1	2101	C
2	1	2209	U
2	1	2249	G
2	1	2264	U
2	1	2266	U
2	1	2346	C
2	1	2403	G
2	1	2501	U
2	1	2541	U
2	1	2547	A
2	1	2845	A
2	1	2866	U
2	1	2945	G
2	1	2965	U
2	1	3078	U
2	1	3121	U
2	1	3228	C
2	1	3269	U
2	1	3292	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 1 is monoatomic - leaving 11 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
54	AGS	Aa	902	-	28,33,33	0.74	1 (3%)	31,52,52	0.98	2 (6%)
54	AGS	w	903	-	28,33,33	0.73	1 (3%)	31,52,52	0.93	2 (6%)
54	AGS	n	901	-	28,33,33	0.72	1 (3%)	31,52,52	0.97	2 (6%)
54	AGS	x	901	-	28,33,33	0.73	1 (3%)	31,52,52	1.06	3 (9%)
54	AGS	Aa	901	-	28,33,33	0.72	1 (3%)	31,52,52	0.95	2 (6%)
54	AGS	n	902	-	28,33,33	0.74	1 (3%)	31,52,52	0.95	2 (6%)
54	AGS	w	902	-	28,33,33	0.73	1 (3%)	31,52,52	0.97	2 (6%)
54	AGS	m	902	-	28,33,33	0.74	1 (3%)	31,52,52	0.93	2 (6%)
54	AGS	t	801	-	28,33,33	0.73	1 (3%)	31,52,52	0.95	2 (6%)
54	AGS	m	901	-	28,33,33	0.73	1 (3%)	31,52,52	0.94	2 (6%)
54	AGS	w	901	-	28,33,33	0.72	1 (3%)	31,52,52	0.95	2 (6%)

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
54	AGS	Aa	902	-	-	1/17/38/38	0/3/3/3
54	AGS	w	903	-	-	4/17/38/38	0/3/3/3
54	AGS	n	901	-	-	5/17/38/38	0/3/3/3
54	AGS	x	901	-	-	2/17/38/38	0/3/3/3
54	AGS	Aa	901	-	-	3/17/38/38	0/3/3/3
54	AGS	n	902	-	-	4/17/38/38	0/3/3/3
54	AGS	w	902	-	-	3/17/38/38	0/3/3/3
54	AGS	m	902	-	-	2/17/38/38	0/3/3/3
54	AGS	t	801	-	-	6/17/38/38	0/3/3/3
54	AGS	m	901	-	-	4/17/38/38	0/3/3/3
54	AGS	w	901	-	-	7/17/38/38	0/3/3/3

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	m	902	AGS	PG-S1G	2.17	1.95	1.90
54	w	902	AGS	PG-S1G	2.17	1.95	1.90
54	n	902	AGS	PG-S1G	2.16	1.95	1.90
54	x	901	AGS	PG-S1G	2.16	1.95	1.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	Aa	901	AGS	PG-S1G	2.15	1.95	1.90
54	Aa	902	AGS	PG-S1G	2.15	1.95	1.90
54	n	901	AGS	PG-S1G	2.15	1.95	1.90
54	w	901	AGS	PG-S1G	2.15	1.95	1.90
54	t	801	AGS	PG-S1G	2.14	1.95	1.90
54	m	901	AGS	PG-S1G	2.12	1.95	1.90
54	w	903	AGS	PG-S1G	2.12	1.95	1.90

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	w	902	AGS	PB-O3B-PG	-3.73	119.53	133.17
54	w	901	AGS	PB-O3B-PG	-3.63	119.90	133.17
54	n	902	AGS	PB-O3B-PG	-3.55	120.16	133.17
54	n	901	AGS	PB-O3B-PG	-3.55	120.19	133.17
54	x	901	AGS	PB-O3B-PG	-3.53	120.23	133.17
54	t	801	AGS	PB-O3B-PG	-3.47	120.46	133.17
54	Aa	902	AGS	PB-O3B-PG	-3.45	120.53	133.17
54	m	902	AGS	PB-O3B-PG	-3.45	120.53	133.17
54	Aa	901	AGS	PB-O3B-PG	-3.41	120.71	133.17
54	m	901	AGS	PB-O3B-PG	-3.39	120.78	133.17
54	w	903	AGS	PB-O3B-PG	-3.34	120.96	133.17
54	x	901	AGS	C4'-O4'-C1'	-2.79	107.37	109.92
54	t	801	AGS	C5-C6-N6	2.31	123.83	120.31
54	w	903	AGS	C5-C6-N6	2.31	123.83	120.31
54	n	901	AGS	C5-C6-N6	2.30	123.82	120.31
54	w	901	AGS	C5-C6-N6	2.30	123.82	120.31
54	w	902	AGS	C5-C6-N6	2.30	123.81	120.31
54	x	901	AGS	C5-C6-N6	2.30	123.81	120.31
54	m	902	AGS	C5-C6-N6	2.30	123.81	120.31
54	Aa	901	AGS	C5-C6-N6	2.29	123.81	120.31
54	Aa	902	AGS	C5-C6-N6	2.29	123.81	120.31
54	m	901	AGS	C5-C6-N6	2.29	123.80	120.31
54	n	902	AGS	C5-C6-N6	2.28	123.78	120.31

There are no chirality outliers.

All (41) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
54	m	902	AGS	PB-O3B-PG-O3G
54	n	901	AGS	PB-O3B-PG-O2G
54	n	901	AGS	PB-O3B-PG-O3G

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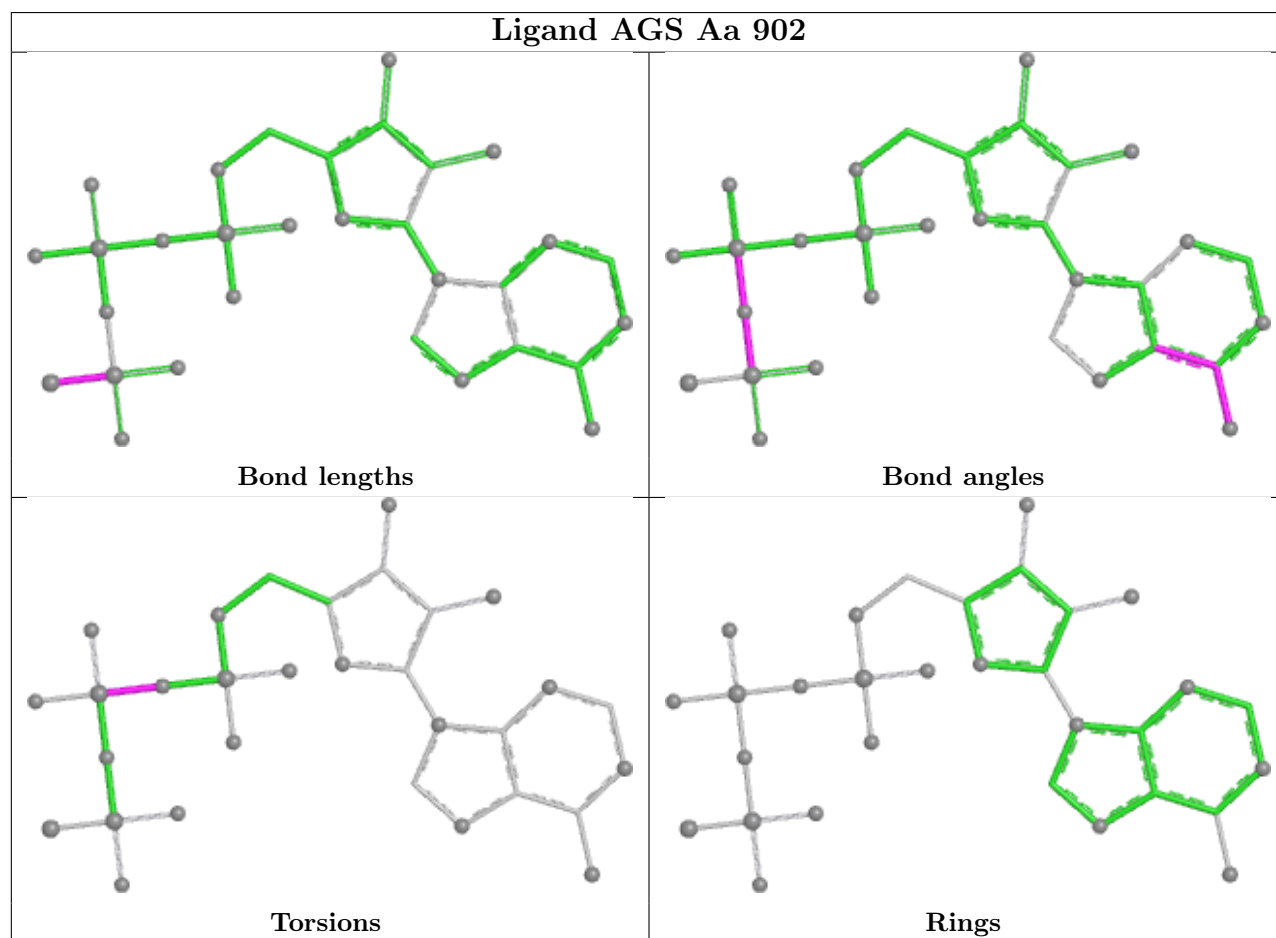
Mol	Chain	Res	Type	Atoms
54	n	902	AGS	C5'-O5'-PA-O2A
54	t	801	AGS	PB-O3B-PG-O2G
54	t	801	AGS	PB-O3B-PG-O3G
54	t	801	AGS	C5'-O5'-PA-O3A
54	w	901	AGS	PB-O3B-PG-O2G
54	w	901	AGS	PB-O3B-PG-O3G
54	w	901	AGS	C5'-O5'-PA-O1A
54	w	901	AGS	C5'-O5'-PA-O3A
54	w	903	AGS	C5'-O5'-PA-O1A
54	w	903	AGS	C5'-O5'-PA-O3A
54	w	901	AGS	O4'-C4'-C5'-O5'
54	w	903	AGS	O4'-C4'-C5'-O5'
54	t	801	AGS	C3'-C4'-C5'-O5'
54	w	903	AGS	C3'-C4'-C5'-O5'
54	w	901	AGS	C3'-C4'-C5'-O5'
54	Aa	901	AGS	C3'-C4'-C5'-O5'
54	x	901	AGS	O4'-C4'-C5'-O5'
54	t	801	AGS	O4'-C4'-C5'-O5'
54	n	901	AGS	C4'-C5'-O5'-PA
54	n	901	AGS	C5'-O5'-PA-O1A
54	n	902	AGS	C5'-O5'-PA-O1A
54	n	902	AGS	C5'-O5'-PA-O3A
54	t	801	AGS	C5'-O5'-PA-O1A
54	w	901	AGS	C5'-O5'-PA-O2A
54	w	902	AGS	C5'-O5'-PA-O1A
54	w	902	AGS	C5'-O5'-PA-O2A
54	w	902	AGS	C5'-O5'-PA-O3A
54	m	901	AGS	C4'-C5'-O5'-PA
54	m	901	AGS	PA-O3A-PB-O2B
54	x	901	AGS	C3'-C4'-C5'-O5'
54	Aa	901	AGS	PA-O3A-PB-O1B
54	m	902	AGS	PB-O3B-PG-O2G
54	Aa	901	AGS	PA-O3A-PB-O3B
54	Aa	902	AGS	PA-O3A-PB-O2B
54	m	901	AGS	PA-O3A-PB-O1B
54	m	901	AGS	O4'-C4'-C5'-O5'
54	n	902	AGS	O4'-C4'-C5'-O5'
54	n	901	AGS	O4'-C4'-C5'-O5'

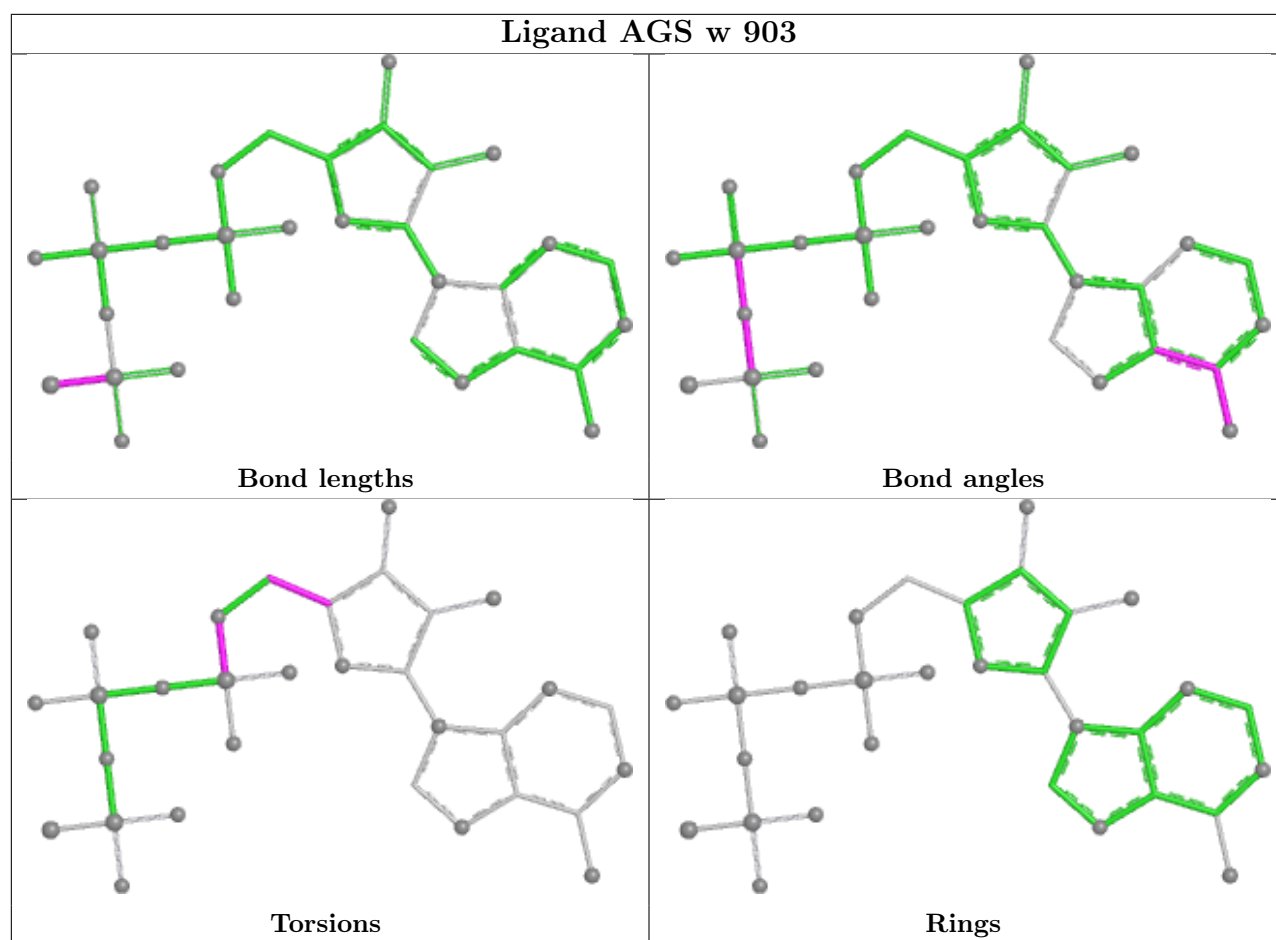
There are no ring outliers.

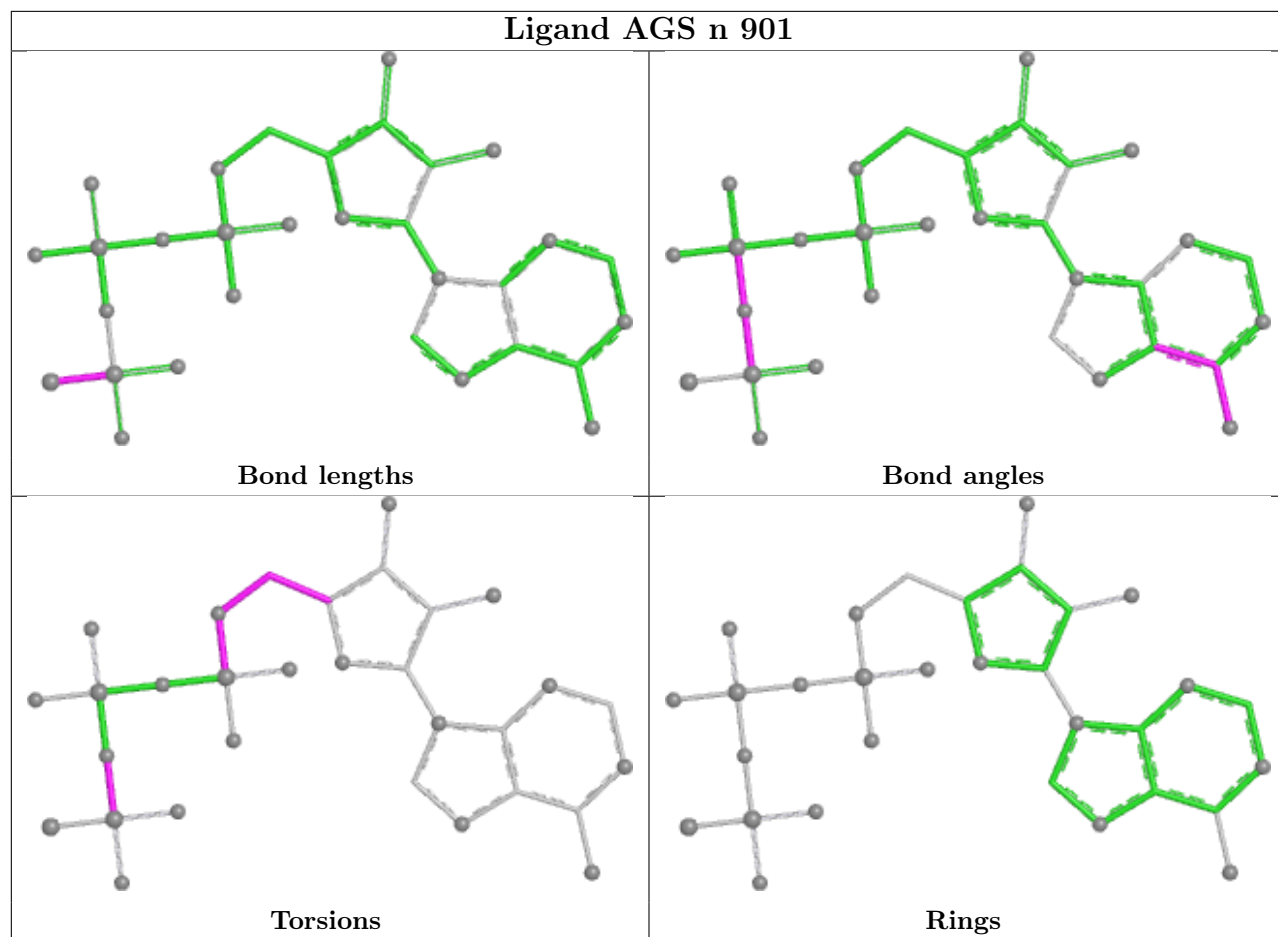
No monomer is involved in short contacts.

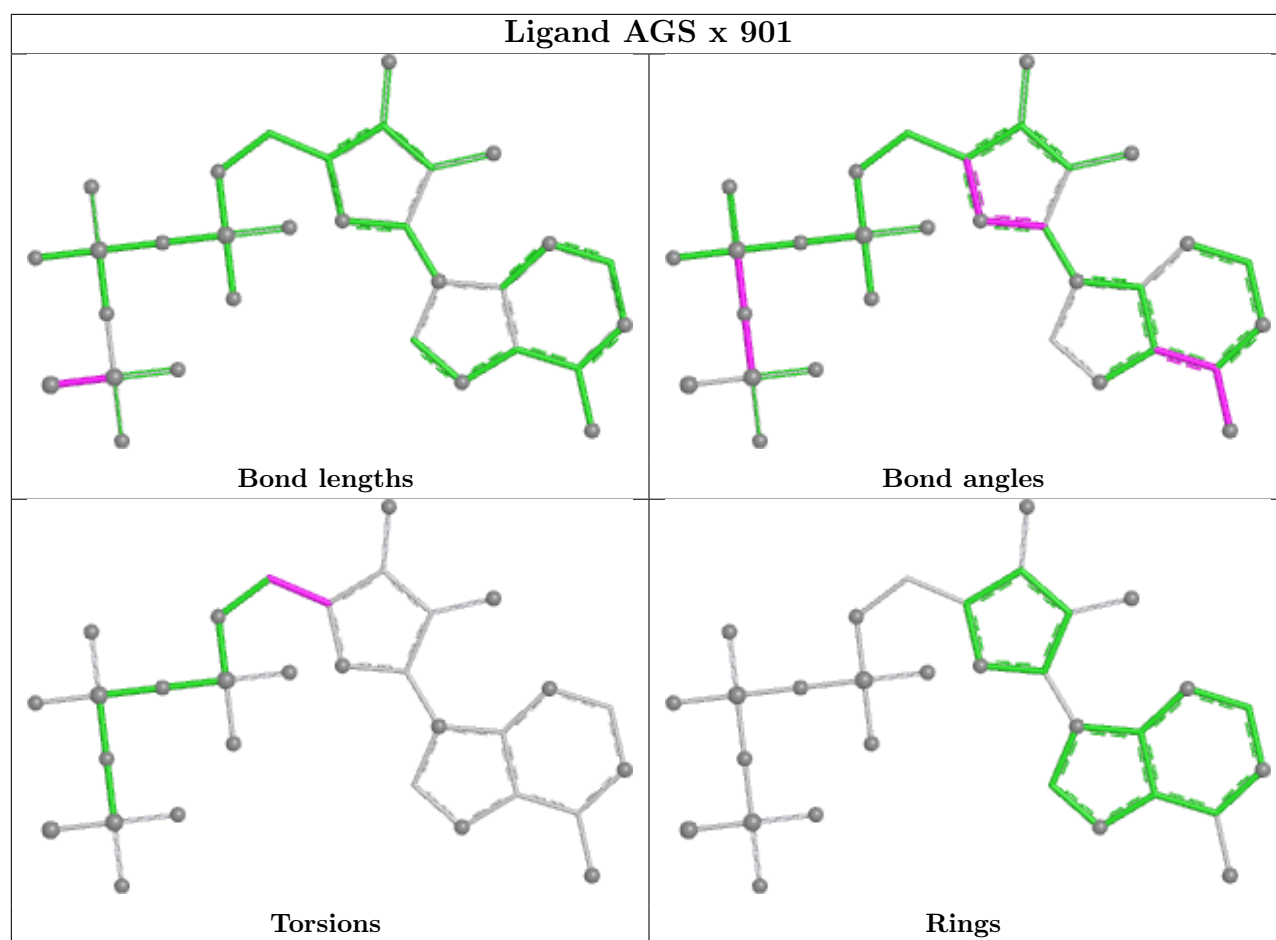
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

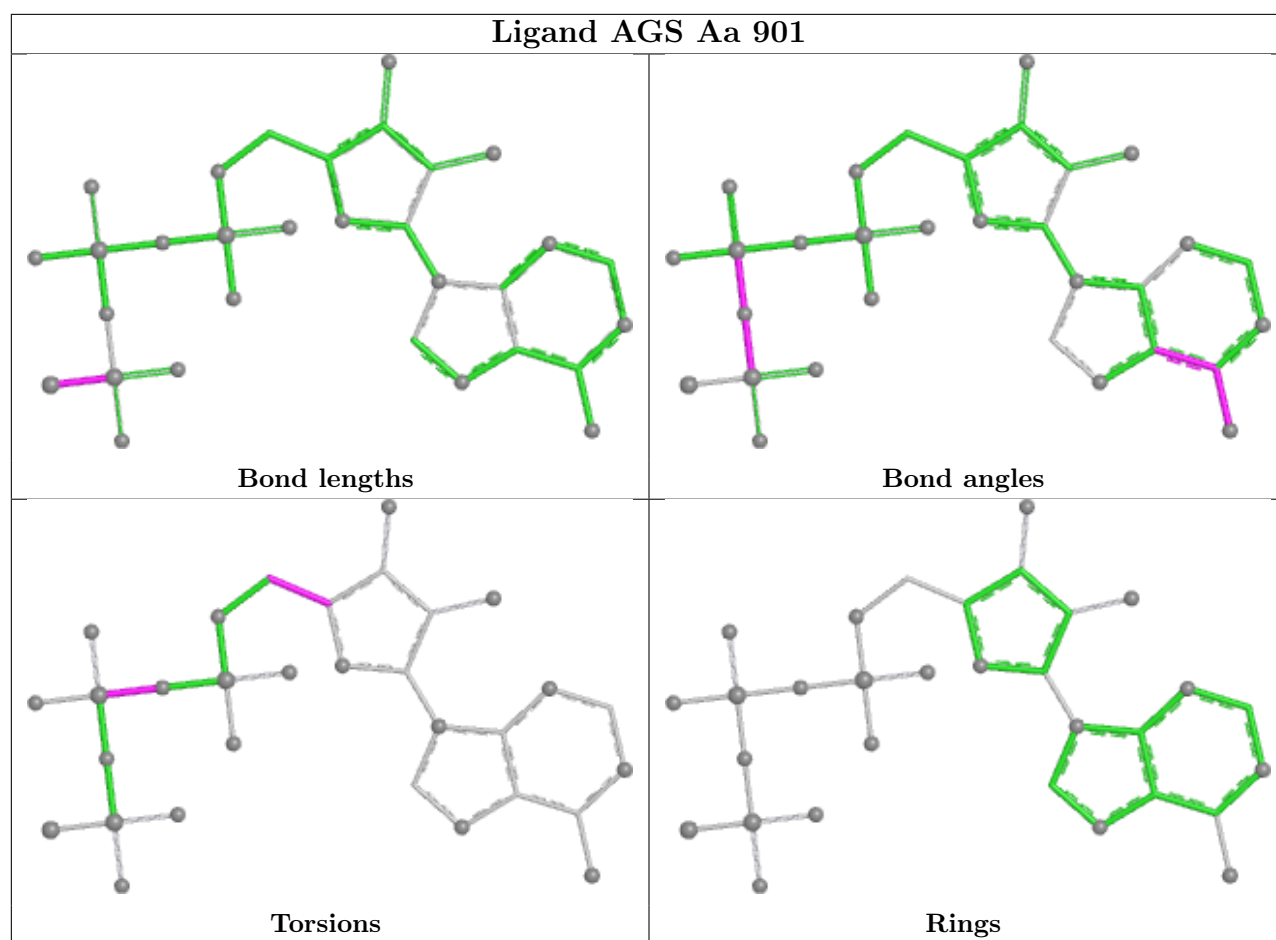
bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

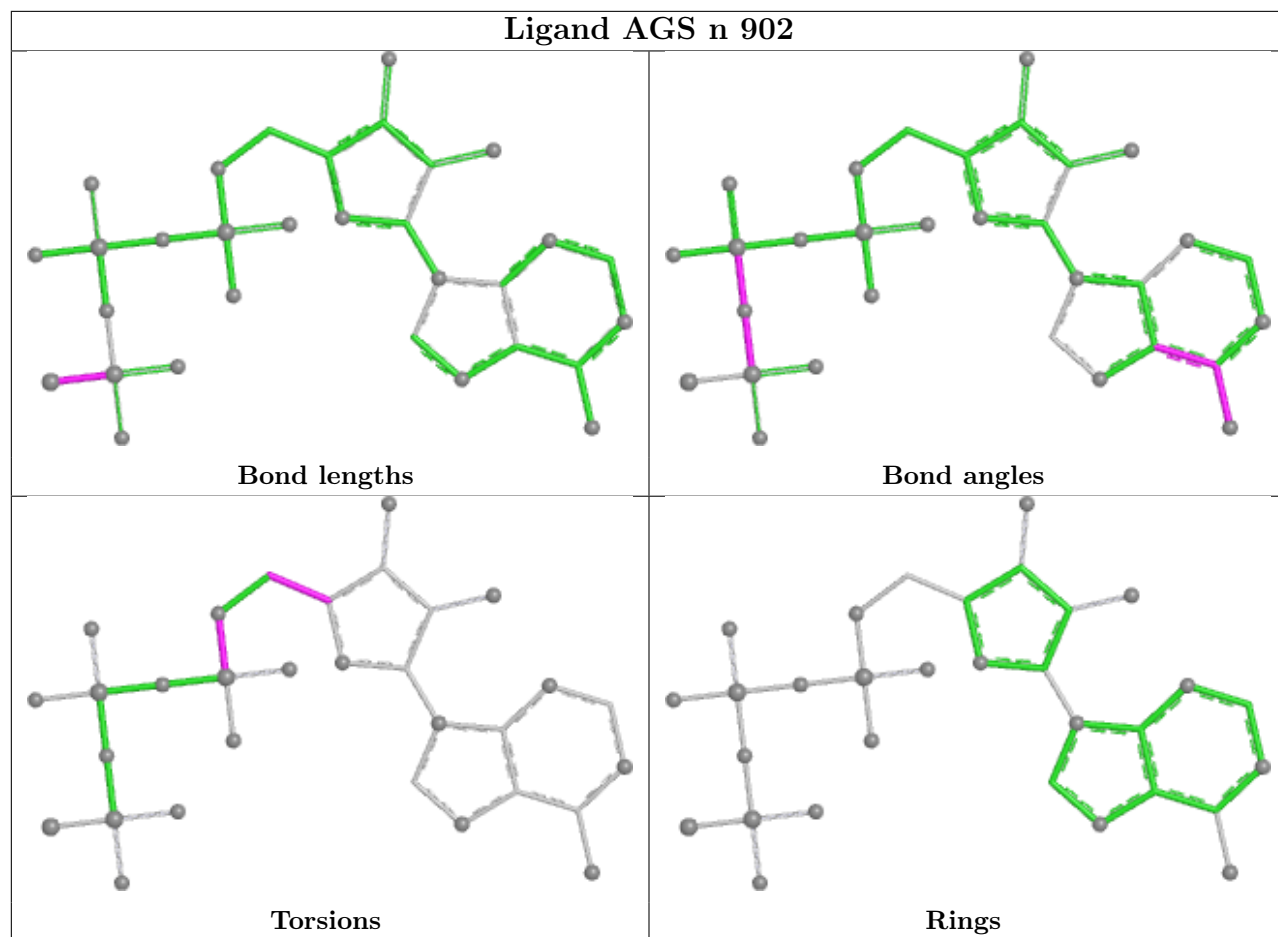


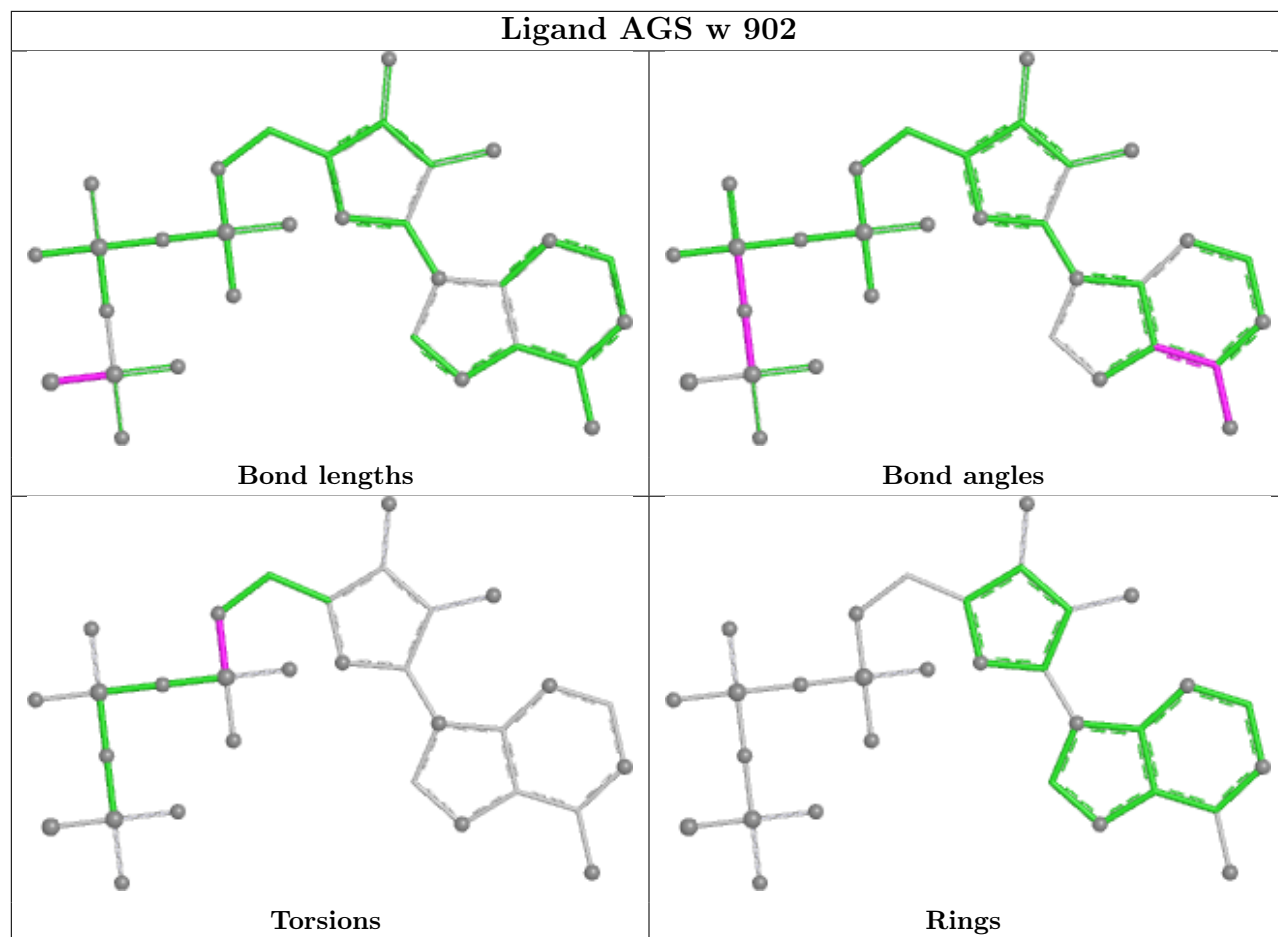


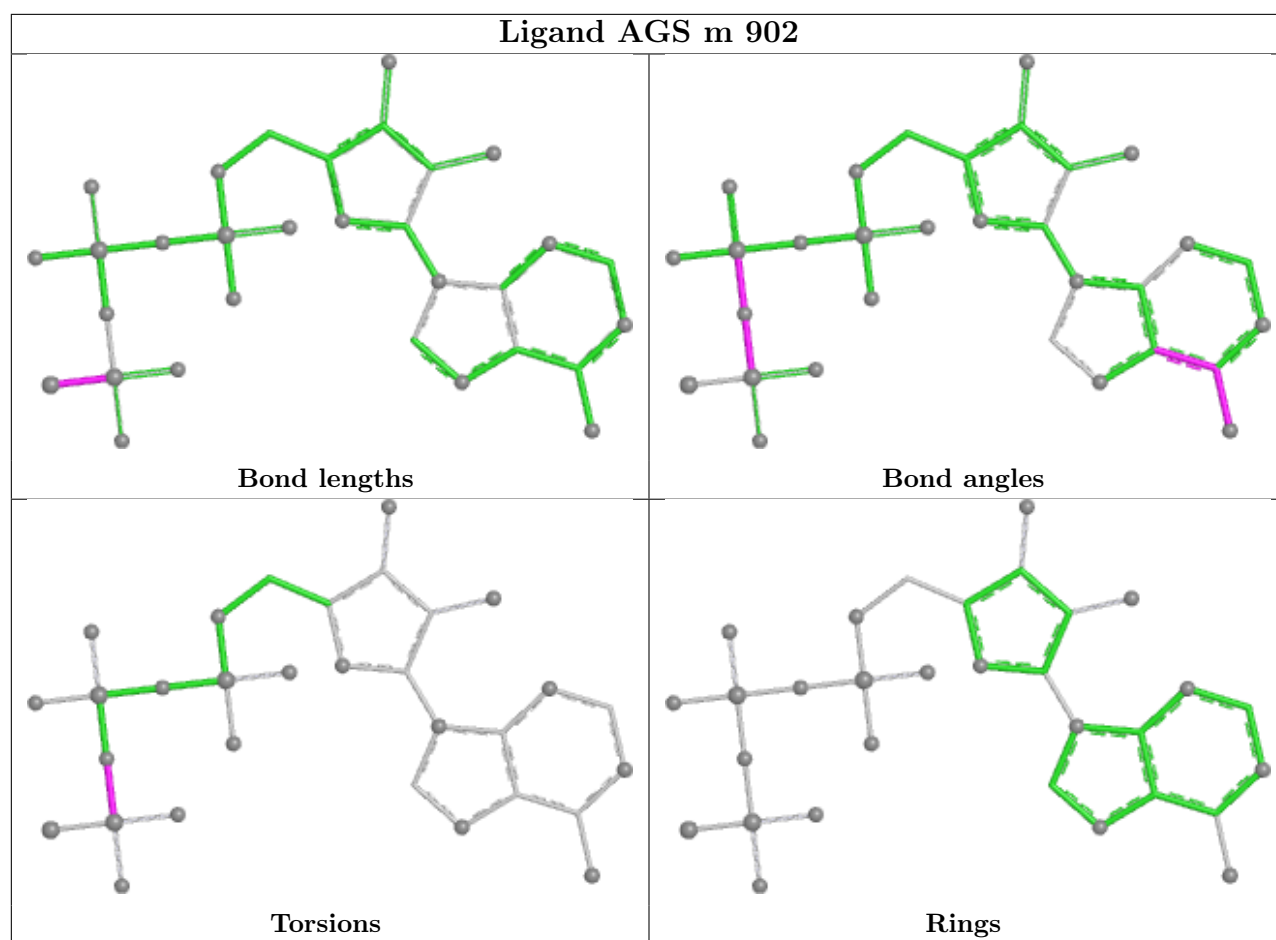


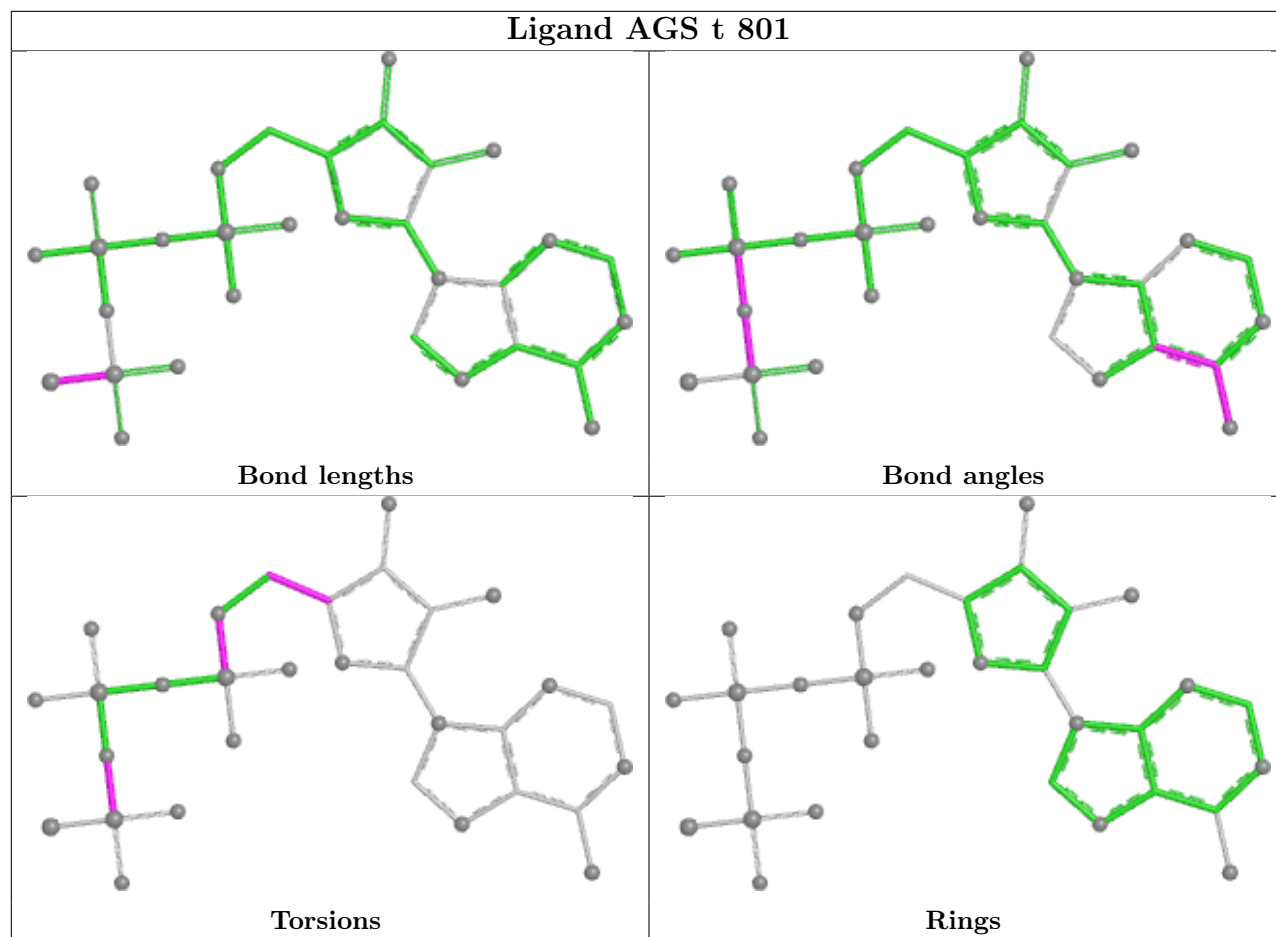


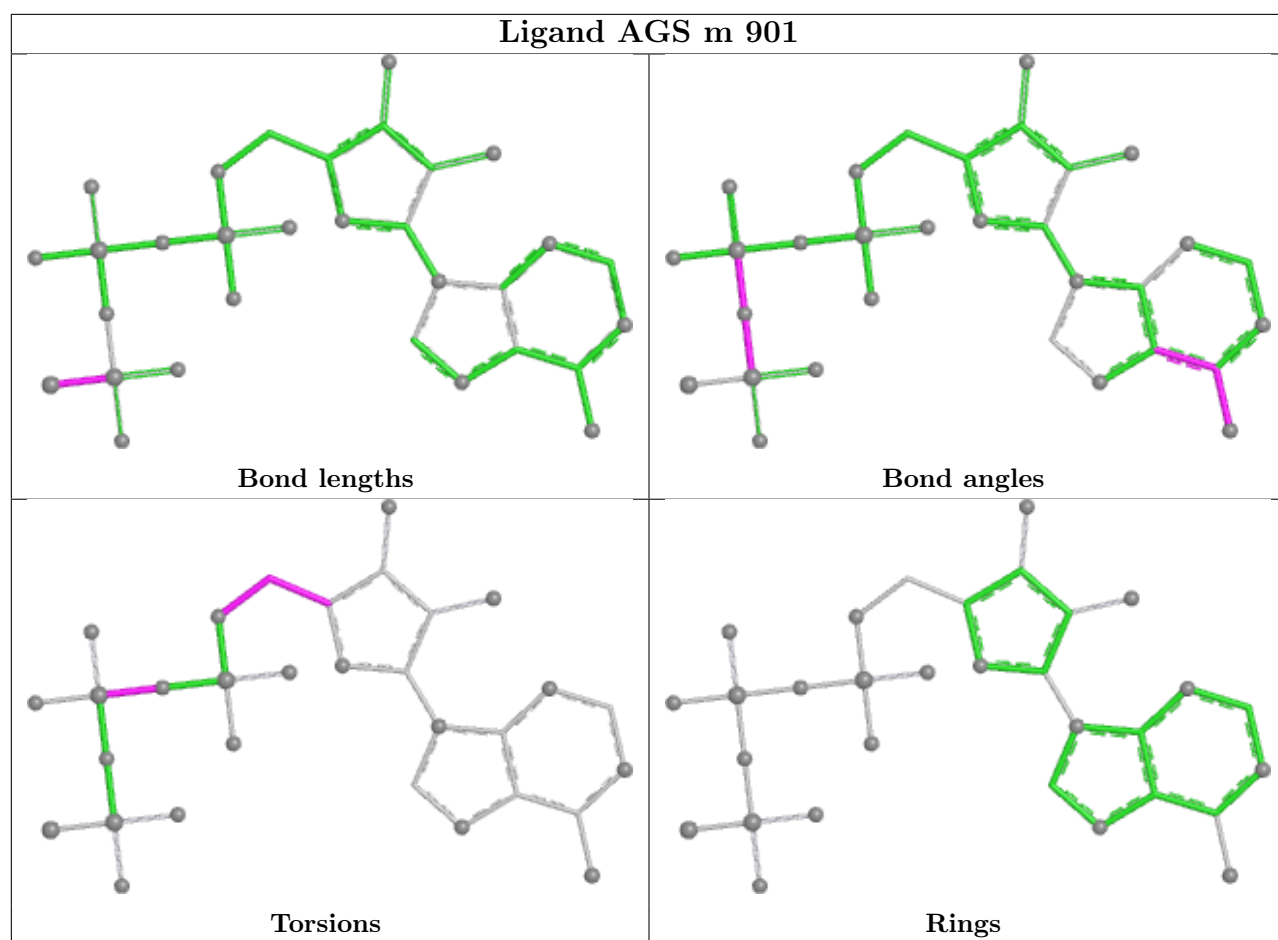


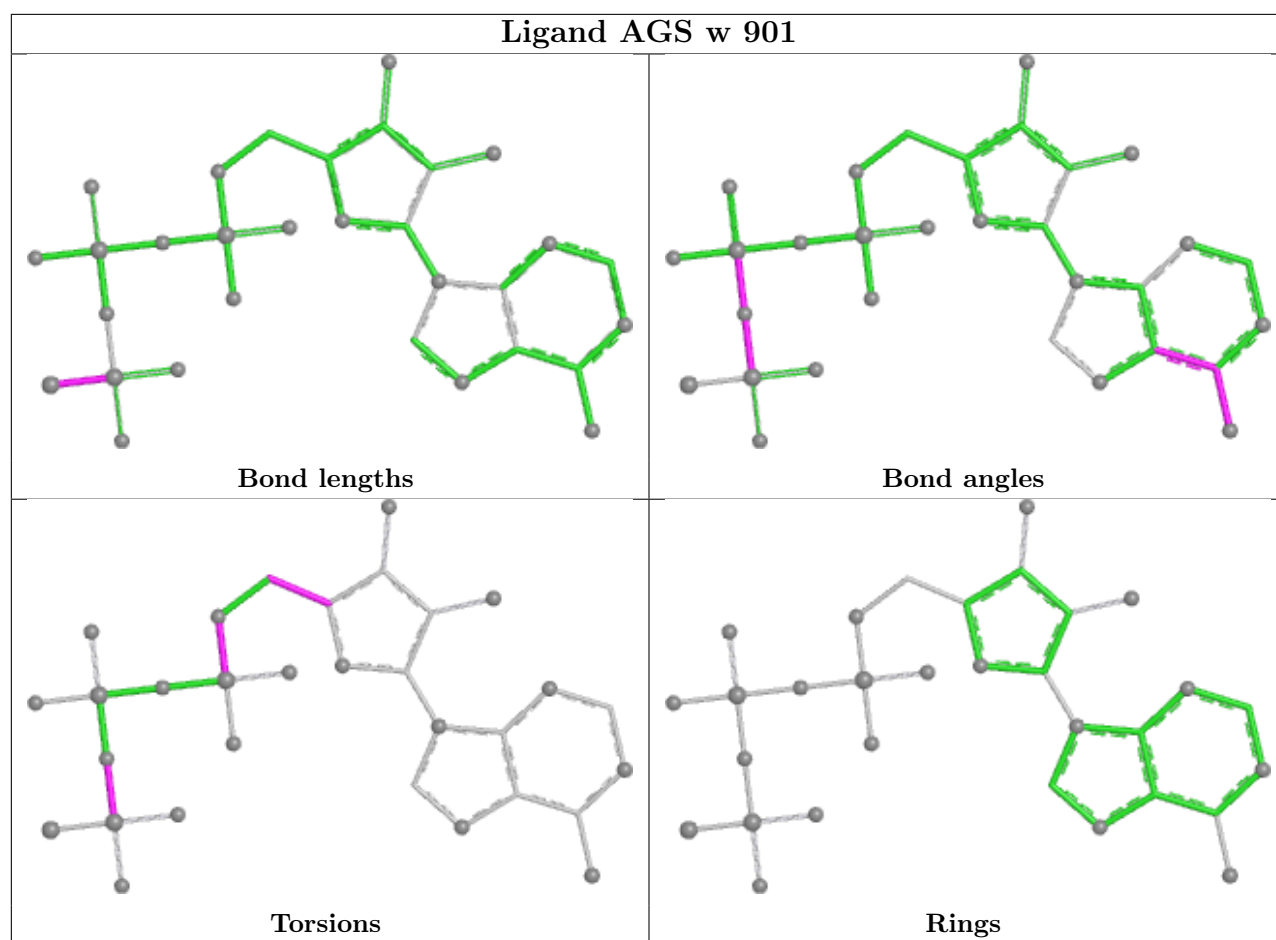












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

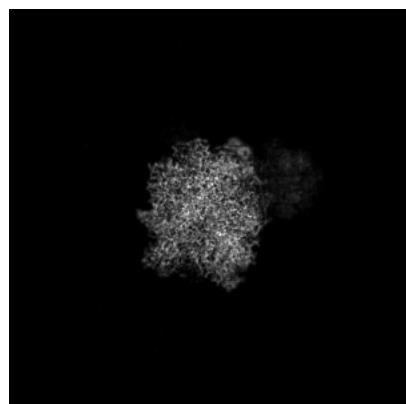
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14471. These allow visual inspection of the internal detail of the map and identification of artifacts.

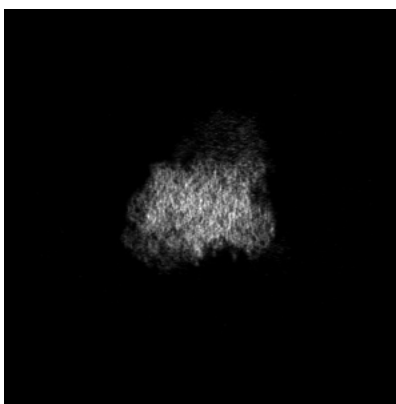
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

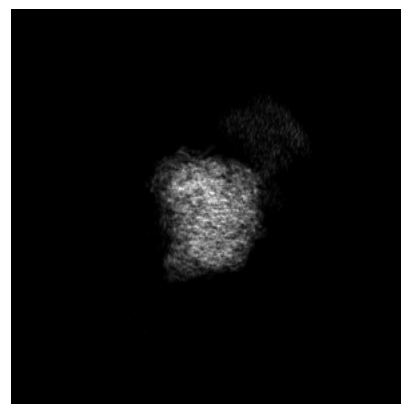
6.1.1 Primary map



X

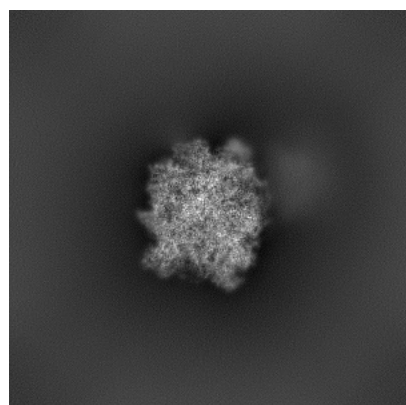


Y

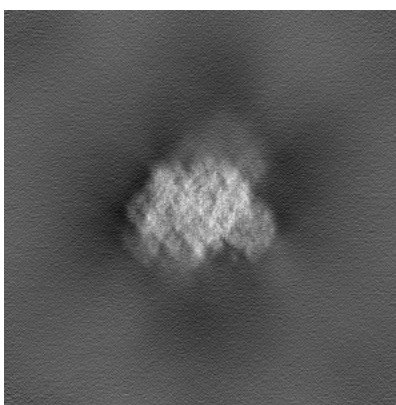


Z

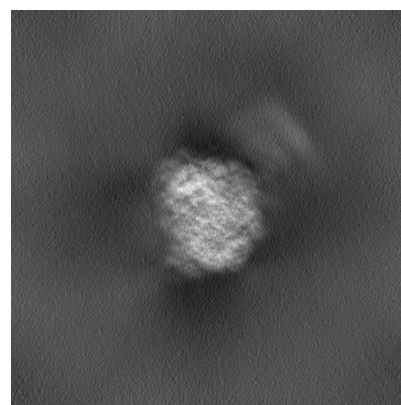
6.1.2 Raw map



X



Y



Z

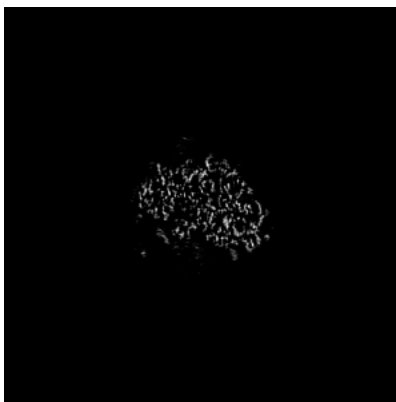
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 240

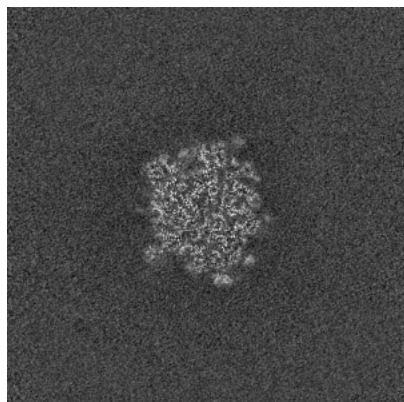


Y Index: 240

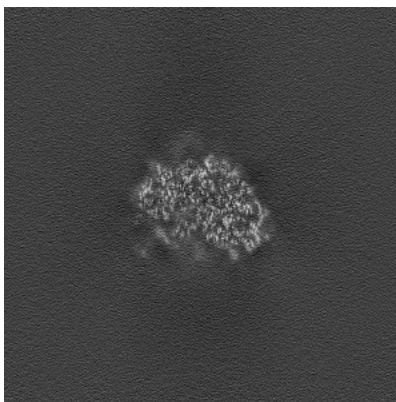


Z Index: 240

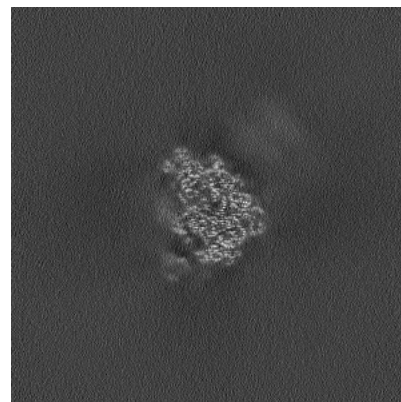
6.2.2 Raw map



X Index: 240



Y Index: 240



Z Index: 240

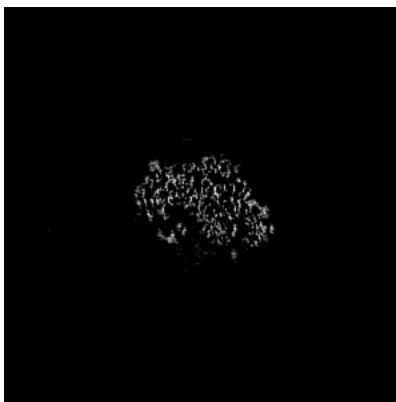
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

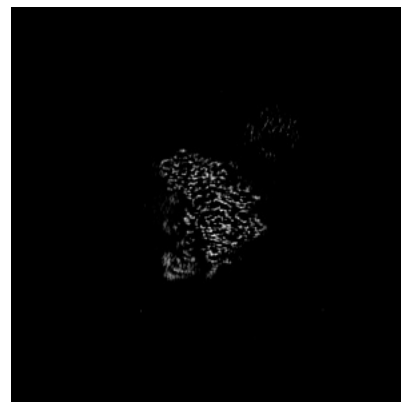
6.3.1 Primary map



X Index: 241

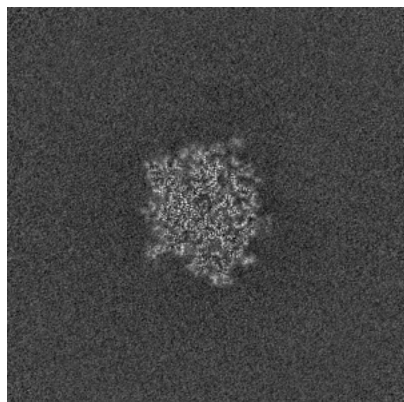


Y Index: 237

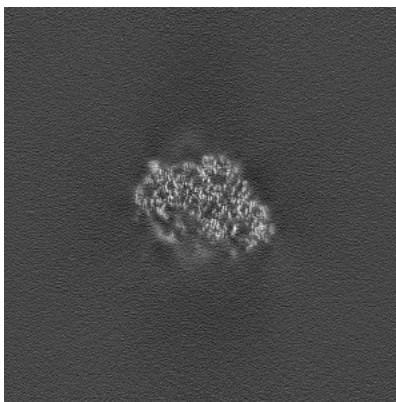


Z Index: 235

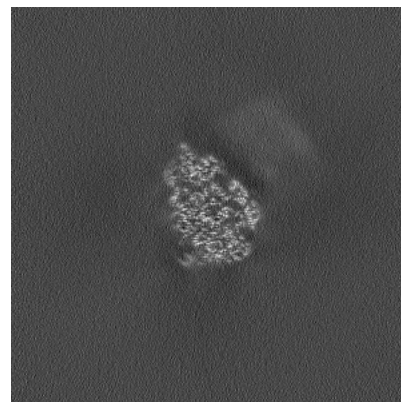
6.3.2 Raw map



X Index: 243



Y Index: 236

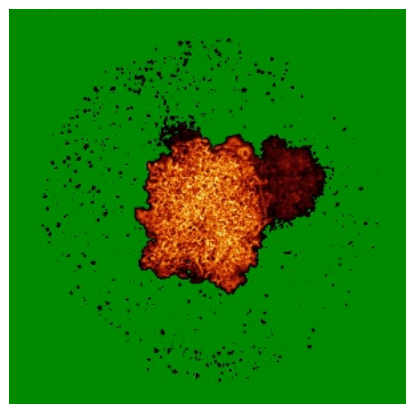


Z Index: 254

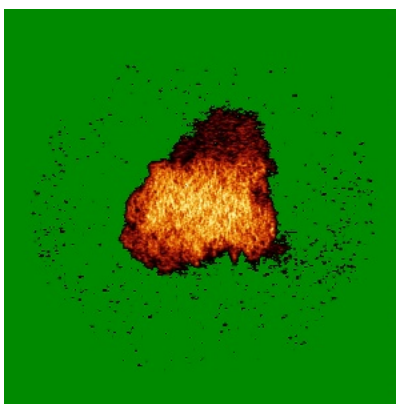
The images above show the largest variance slices of the map in three orthogonal directions.

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

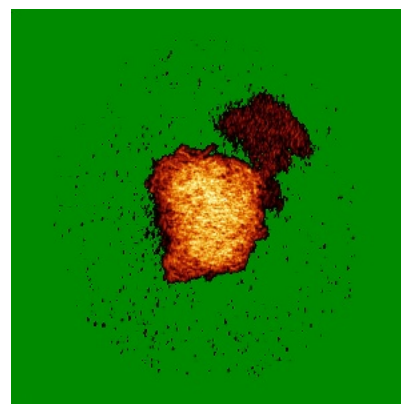
6.4.1 Primary map



X

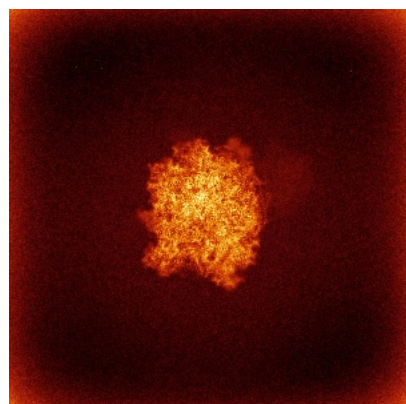


Y

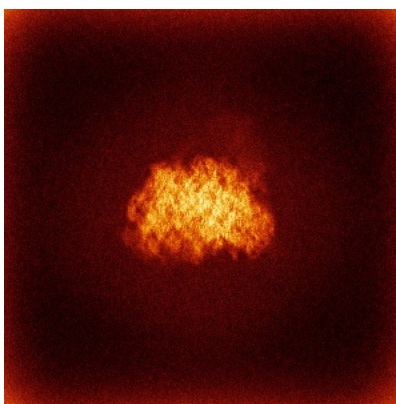


Z

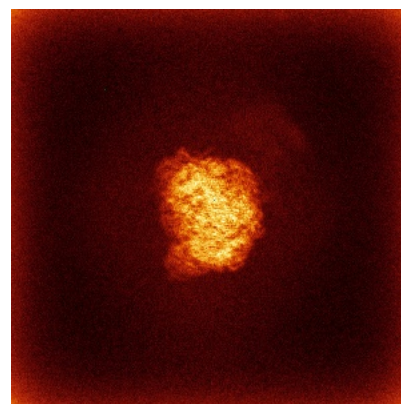
6.4.2 Raw map



X



Y

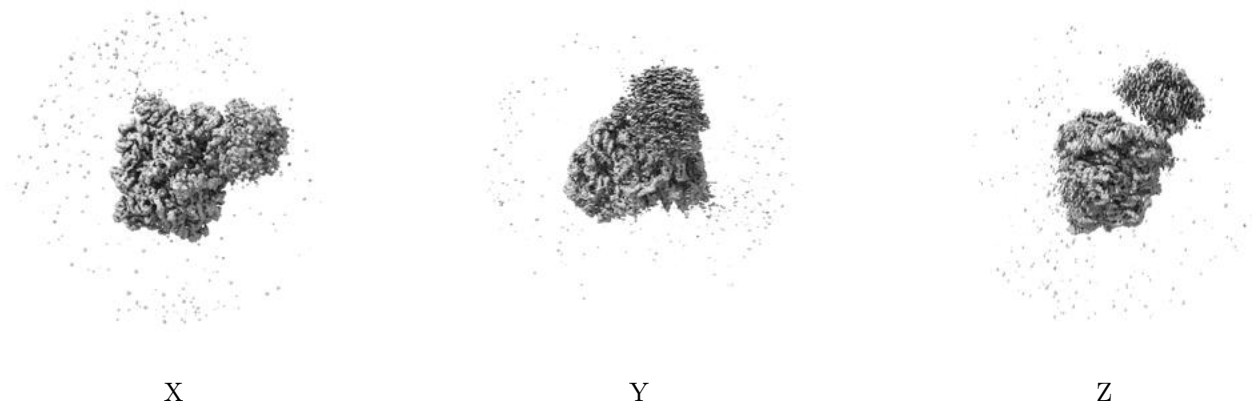


Z

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

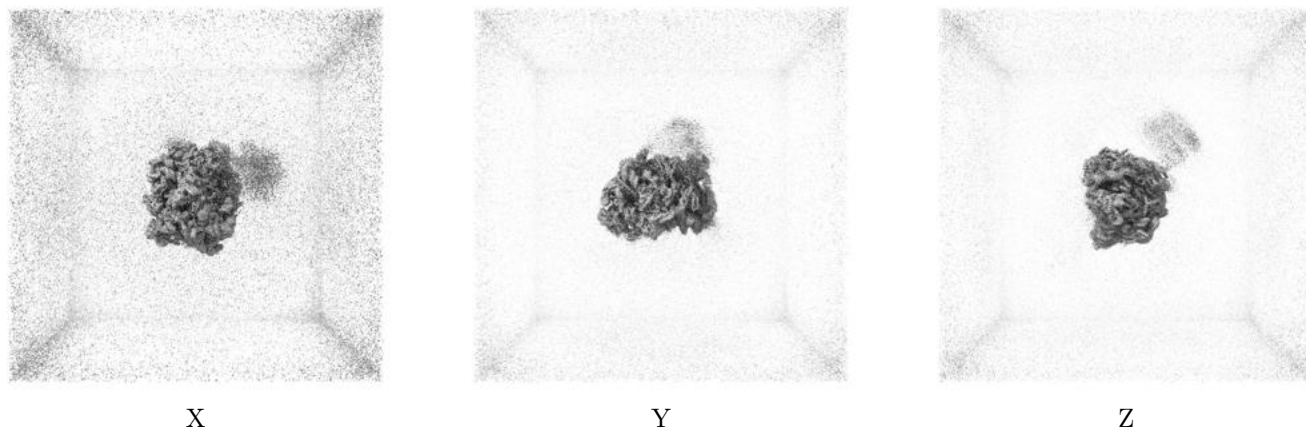
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

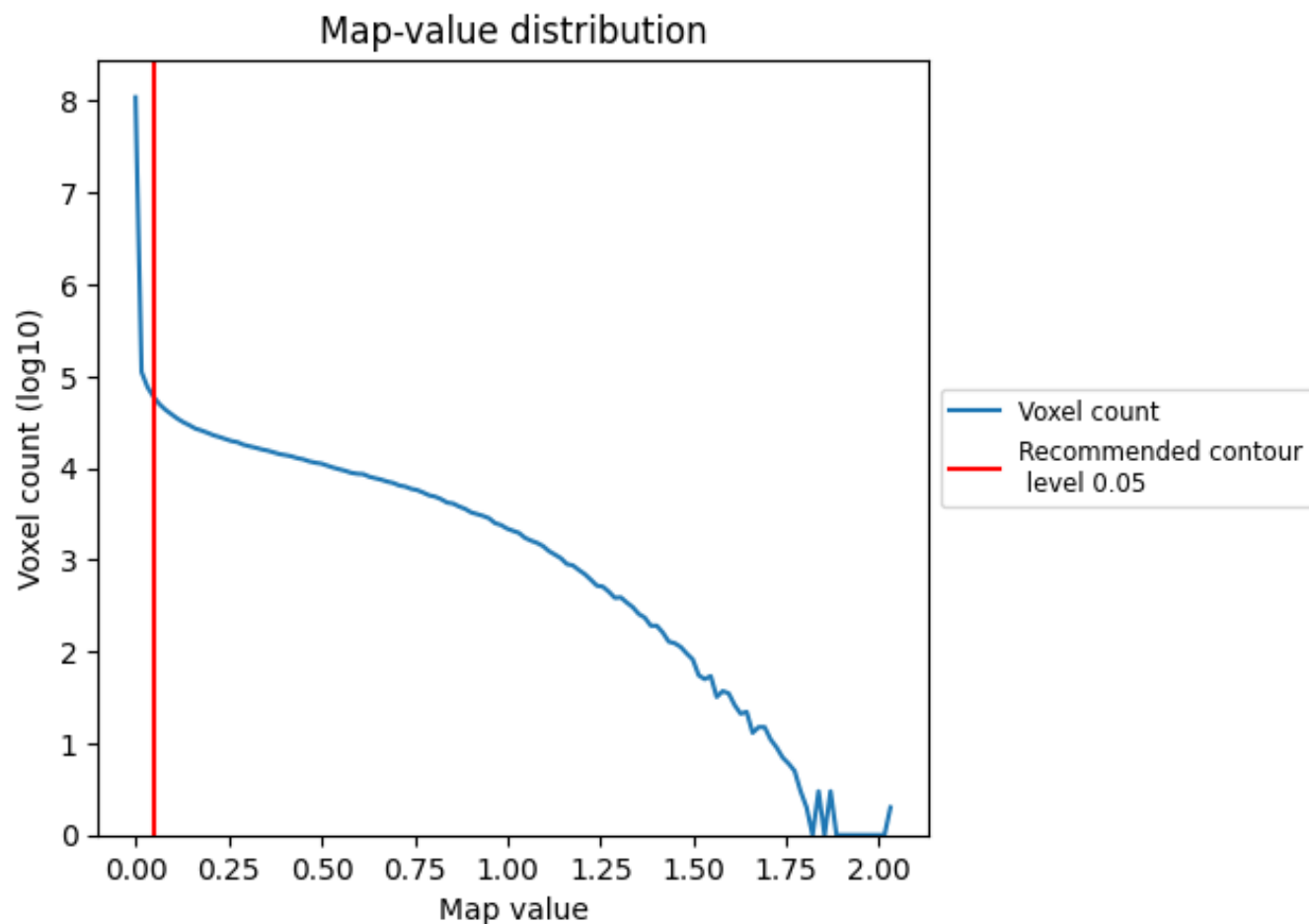
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

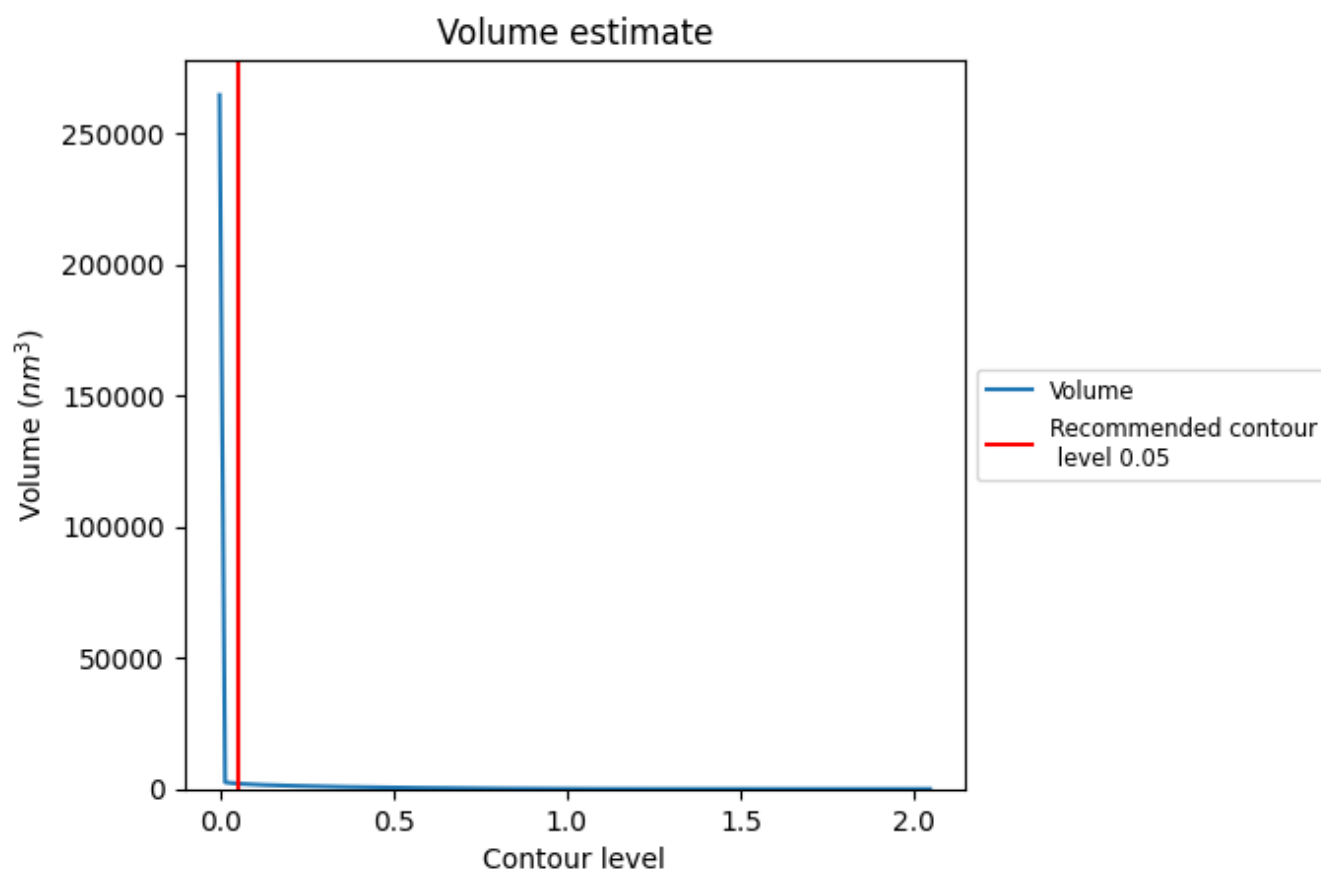
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

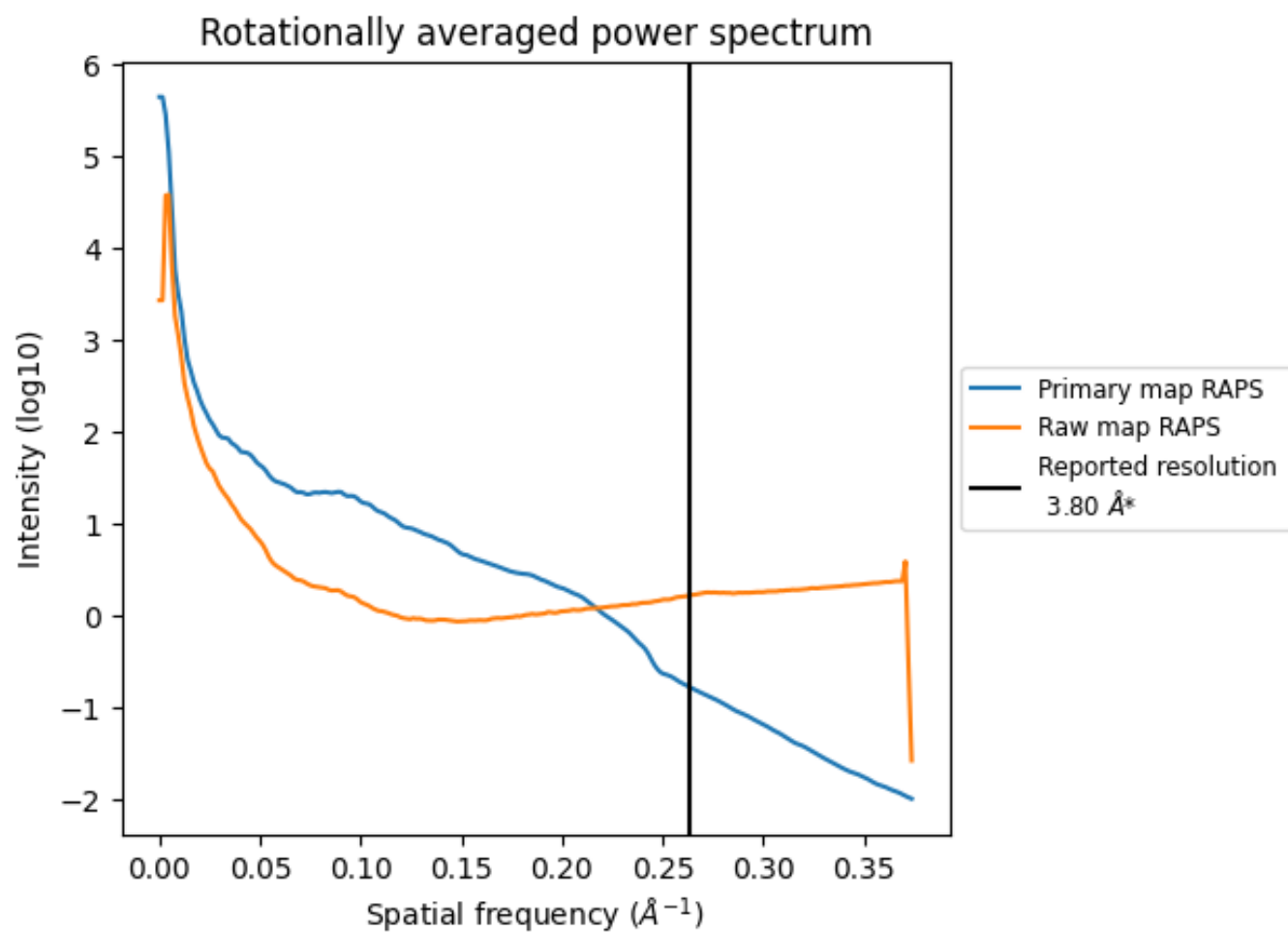
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2056 nm³; this corresponds to an approximate mass of 1857 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

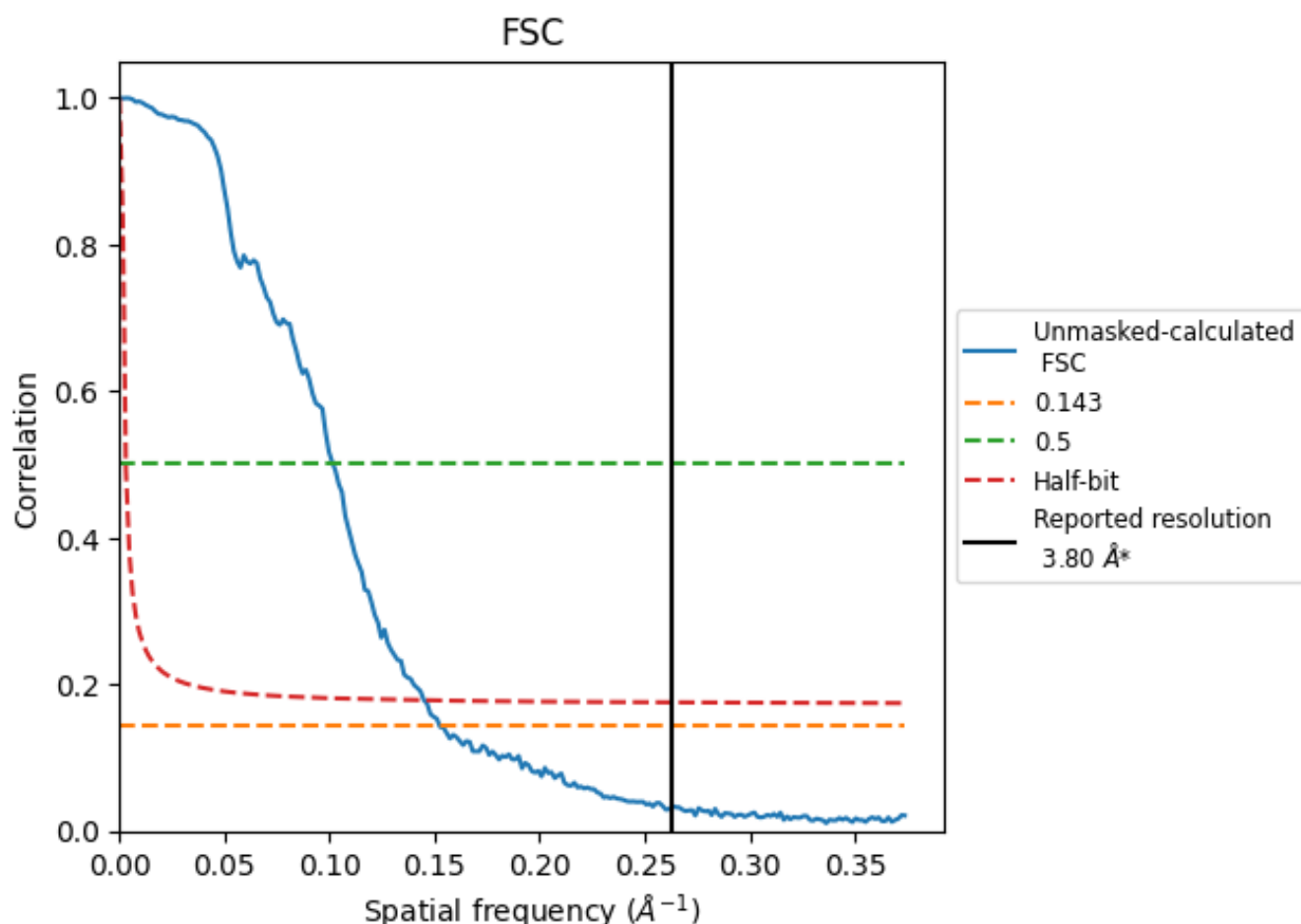


*Reported resolution corresponds to spatial frequency of 0.263 \AA^{-1}

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.263 \AA^{-1}

8.2 Resolution estimates [i](#)

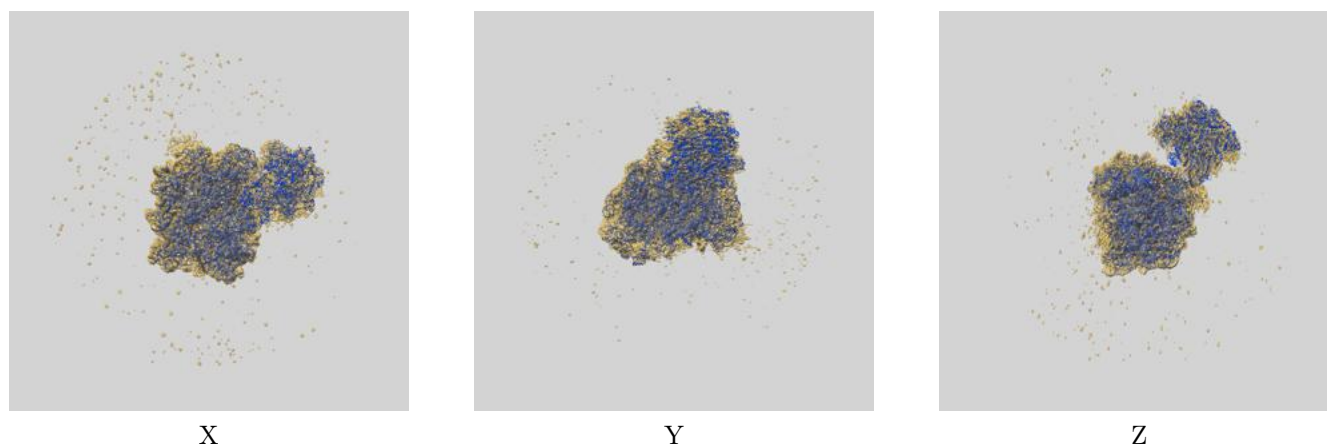
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.56	9.83	6.90

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.56 differs from the reported value 3.8 by more than 10 %

9 Map-model fit [i](#)

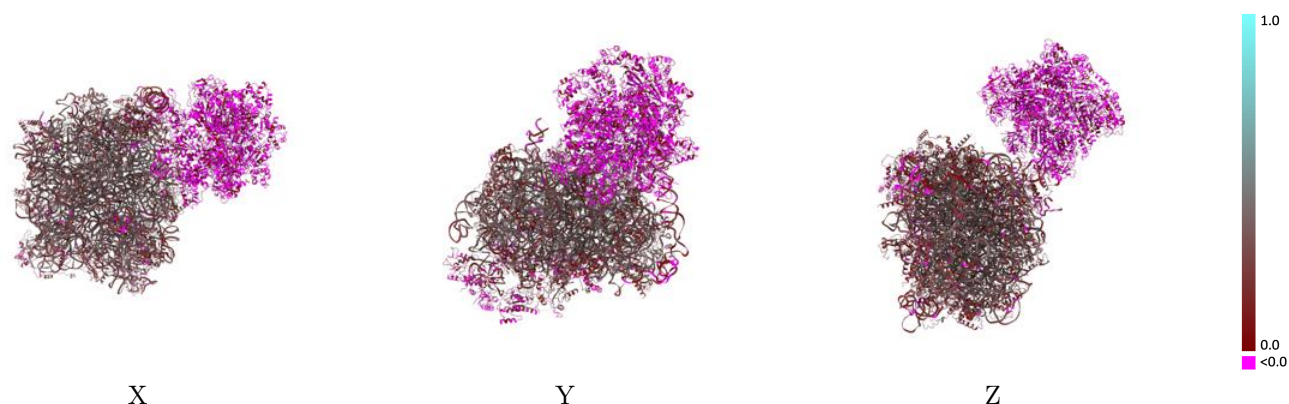
This section contains information regarding the fit between EMDB map EMD-14471 and PDB model 7Z34. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)



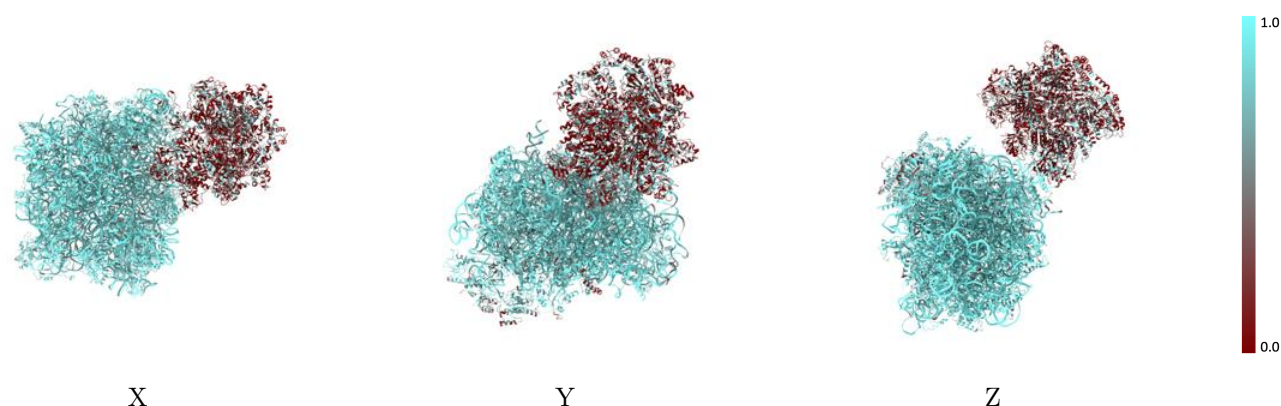
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



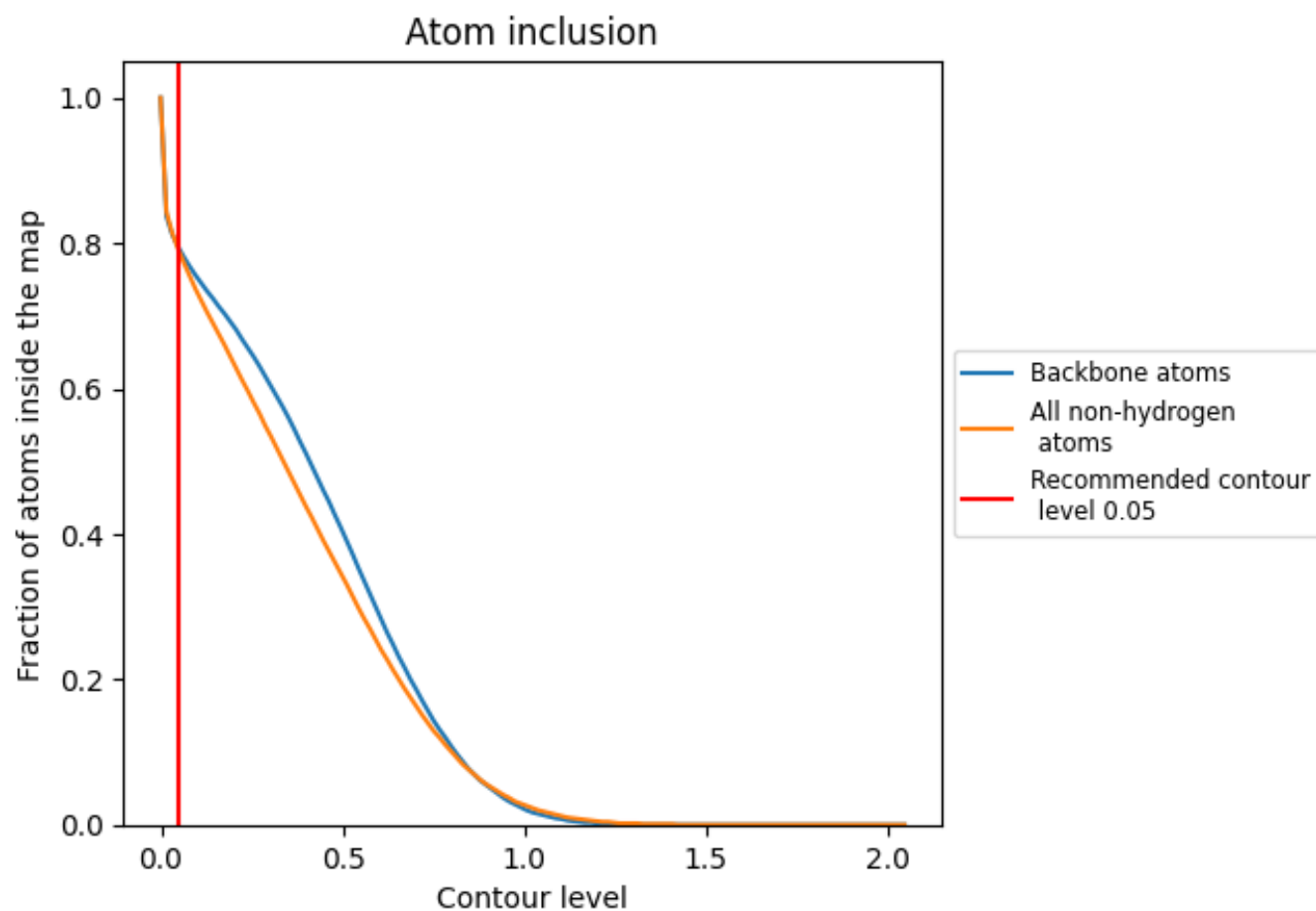
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 79% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

















































The table lists the average atom inclusion at the recommended contour level (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7880	 0.2270
0	 0.2810	 0.0450
1	 0.9430	 0.3120
2	 0.9590	 0.3070
3	 0.9770	 0.3520
4	 0.8610	 0.2430
A	 0.8920	 0.3020
Aa	 0.1900	 -0.0320
B	 0.9010	 0.3070
C	 0.9040	 0.3030
D	 0.8520	 0.2130
E	 0.8710	 0.2760
F	 0.9050	 0.2810
G	 0.8930	 0.2610
H	 0.8970	 0.2800
I	 0.6590	 0.1650
J	 0.8450	 0.2000
K	 0.8960	 0.3040
L	 0.9040	 0.3000
M	 0.8740	 0.2670
N	 0.8910	 0.3110
O	 0.8970	 0.2890
P	 0.8680	 0.2840
Q	 0.8870	 0.2900
R	 0.8780	 0.2610
S	 0.8840	 0.3010
T	 0.8850	 0.2880
U	 0.8990	 0.2720
V	 0.8870	 0.2950
W	 0.7970	 0.1140
X	 0.8790	 0.3020
Y	 0.8920	 0.3040
Z	 0.8760	 0.2510
a	 0.6300	 0.0470
b	 0.7880	 0.1820



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Chain	Atom inclusion	Q-score
c	 0.8840	 0.2590
d	 0.8500	 0.2850
e	 0.8980	 0.3200
f	 0.9070	 0.3350
g	 0.8620	 0.2720
h	 0.8890	 0.2880
i	 0.8690	 0.2390
j	 0.9180	 0.3350
k	 0.8630	 0.2390
l	 0.8800	 0.2800
m	 0.2600	 -0.0330
n	 0.2820	 -0.0240
o	 0.8630	 0.2480
oC	 0.9470	 0.2780
p	 0.8720	 0.2350
q	 0.7740	 0.1850
r	 0.5150	 0.0500
t	 0.3220	 -0.0230
u	 0.8770	 0.2460
v	 0.8090	 0.2320
w	 0.3860	 0.0020
x	 0.2680	 -0.0230
y	 0.8940	 0.2390
z	 0.8890	 0.2650