



wwPDB EM Validation Summary Report ⓘ

Jun 23, 2026 – 11:14 PM EDT

PDB ID : 7UVY / pdb_00007uvy
EMDB ID : EMD-26820
Title : A. baumannii ribosome-Streptothricin-D complex: 70S with P-site tRNA
Authors : Morgan, C.E.; Yu, E.W.
Deposited on : 2022-05-02
Resolution : 2.39 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

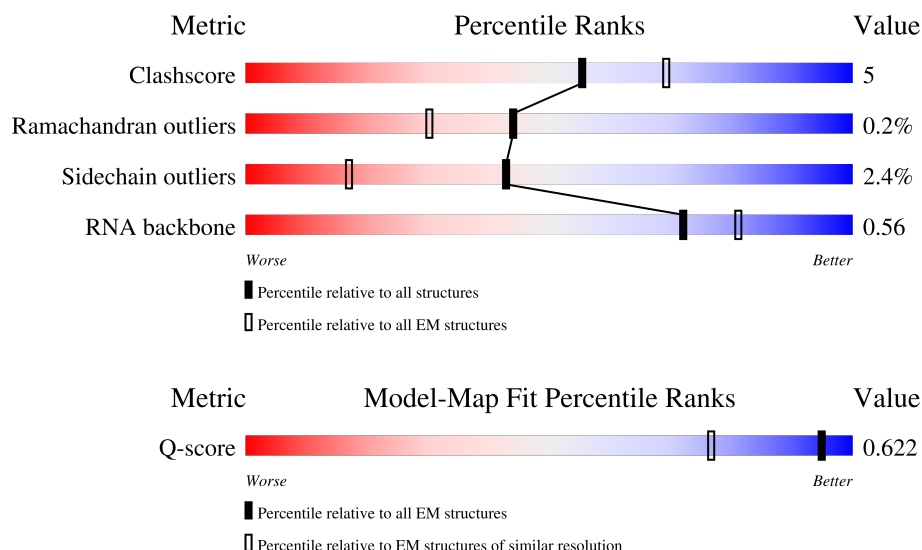
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.39 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	4884 (1.90 - 2.89)

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	0	51	
2	1	44	
3	2	64	

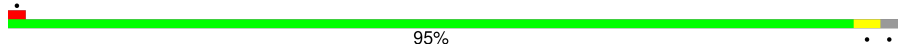
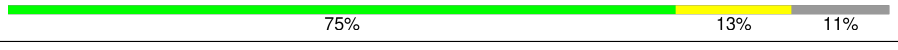
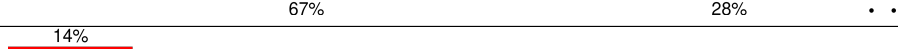
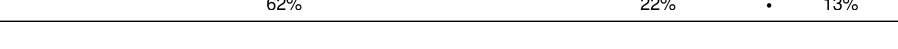
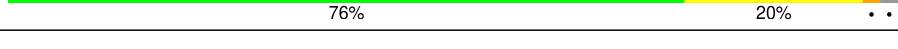
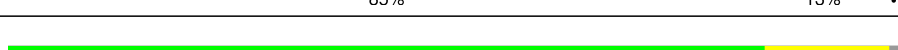
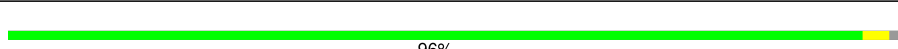
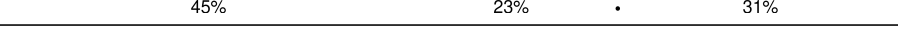
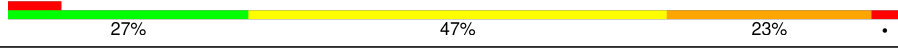
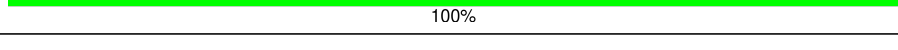
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Mol	Chain	Length	Quality of chain
4	3	38	
5	A	2918	
6	B	115	
7	C	274	
8	D	212	
9	E	200	
10	F	178	
11	G	177	
12	H	148	
13	I	142	
14	J	122	
15	K	146	
16	L	137	
17	M	125	
18	N	116	
19	O	122	
20	P	119	
21	Q	103	
22	R	109	
23	S	106	
24	T	105	
25	U	98	
26	V	85	
27	W	78	
28	X	65	

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Mol	Chain	Length	Quality of chain
29	Y	58	
30	Z	61	
31	a	1544	
32	b	250	
33	c	250	
34	d	208	
35	e	165	
36	f	127	
37	g	156	
38	h	131	
39	i	128	
40	j	103	
41	k	128	
42	l	124	
43	m	118	
44	n	101	
45	o	89	
46	p	101	
47	q	85	
48	r	75	
49	s	91	
50	t	88	
51	u	71	
52	v	77	
53	w	3	

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 138881 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 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	51	Total	C	N	O	S	0	0
			427	274	77	73	3		

- Molecule 2 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	44	Total	C	N	O	S	0	0
			363	222	85	54	2		

- Molecule 3 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	63	Total	C	N	O	S	0	0
			509	319	110	76	4		

- Molecule 4 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	38	Total	C	N	O	S	0	0
			295	179	64	48	4		

- Molecule 5 is a RNA chain called 23s ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	2724	Total	C	N	O	P	0	0
			58438	26086	10700	18928	2724		

- Molecule 6 is a RNA chain called 5s ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	115	Total	C	N	O	P	0	0
			2450	1095	440	800	115		

- Molecule 7 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	272	Total	C	N	O	S	0	0
			2111	1302	436	365	8		

- Molecule 8 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	211	Total	C	N	O	S	0	0
			1572	972	297	300	3		

- Molecule 9 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E	200	Total	C	N	O	S	0	0
			1516	952	281	278	5		

- Molecule 10 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	174	Total	C	N	O	S	0	0
			1370	871	243	248	8		

- Molecule 11 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	G	174	Total	C	N	O	S	0	0
			1318	832	236	249	1		

- Molecule 12 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	H	60	Total	C	N	O	S	0	0
			458	287	84	86	1		

- Molecule 13 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	I	142	Total	C	N	O	S	0	0
			1125	718	200	203	4		

- Molecule 14 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	J	122	Total	C	N	O	S	0	0
			946	592	180	169	5		

- Molecule 15 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	K	144	Total	C	N	O		0	0
			1071	663	213	195			

- Molecule 16 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L	137	Total	C	N	O	S	0	0
			1087	687	210	185	5		

- Molecule 17 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	119	Total	C	N	O	S	0	0
			942	590	186	163	3		

- Molecule 18 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N	116	Total	C	N	O	S	0	0
			873	537	176	158	2		

- Molecule 19 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	O	117	Total	C	N	O		0	0
			919	578	177	164			

- Molecule 20 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	117	Total	C	N	O	S	0	0
			934	589	197	146	2		

- Molecule 21 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Q	103	Total	C	N	O	S	0	0
			807	506	155	143	3		

- Molecule 22 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	R	109	Total	C	N	O	S	0	0
			826	514	158	150	4		

- Molecule 23 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	91	Total	C	N	O	S	0	0
			710	452	128	129	1		

- Molecule 24 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T	103	Total	C	N	O		0	0
			766	476	142	148			

- Molecule 25 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	U	97	Total	C	N	O	S	0	0
			760	477	143	139	1		

- Molecule 26 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	V	76	Total	C	N	O	S	0	0
			577	358	111	106	2		

- Molecule 27 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	W	77	Total	C	N	O	S	0	0
			632	395	130	105	2		

- Molecule 28 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	X	60	Total	C	N	O	S	0	0
			486	302	93	90	1		

- Molecule 29 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	57	Total	C	N	O	S	0	0
			455	281	87	84	3		

- Molecule 30 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Z	54	Total	C	N	O	S	0	0
			447	265	100	81	1		

- Molecule 31 is a RNA chain called 16s Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	a	1528	Total	C	N	O	P	0	0
			32782	14631	5994	10630	1527		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	1007	U	C	conflict	GB 1211343212
a	1034	C	U	conflict	GB 1211343212

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	b	225	Total	C	N	O	S	0	0
			1769	1110	328	325	6		

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c	215	Total	C	N	O	S	0	0
			1690	1065	318	299	8		

- Molecule 34 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	207	Total	C	N	O	S	0	0
			1631	1017	313	299	2		

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	155	Total	C	N	O	S	0	0
			1129	700	217	207	5		

- Molecule 36 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f	104	Total	C	N	O	S	0	0
			867	546	158	159	4		

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	136	Total	C	N	O	S	0	0
			1073	671	201	194	7		

- Molecule 38 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	130	Total	C	N	O	S	0	0
			985	615	177	187	6		

- Molecule 39 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	126	Total	C	N	O	S	0	0
			991	618	197	175	1		

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	100	Total	C	N	O	S	0	0
			801	500	150	148	3		

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	117	Total	C	N	O	S	0	0
			862	535	167	159	1		

- Molecule 42 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l	122	Total	C	N	O	S	0	0
			945	580	193	167	5		

- Molecule 43 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	m	115	Total	C	N	O	S	0	0
			903	558	184	158	3		

- Molecule 44 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	n	100	Total	C	N	O	S	0	0
			792	493	158	137	4		

- Molecule 45 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	88	Total	C	N	O	S	0	0
			705	434	144	126	1		

- Molecule 46 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	p	82	Total	C	N	O	S	0	0
			644	403	128	112	1		

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	q	79	Total	C	N	O	S	0	0
			621	390	116	114	1		

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	r	52	Total	C	N	O	0	0
			426	273	74	79		

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	s	82	Total	C	N	O	S	0	0
			646	412	125	107	2		

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	t	86	Total	C	N	O	S	0	0
			663	409	139	113	2		

- Molecule 51 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	u	63	Total	C	N	O	S	0	0
			522	327	105	89	1		

- Molecule 52 is a RNA chain called tRNA-met.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	v	77	Total	C	N	O	P	S	0	0
			1636	733	291	535	76	1		

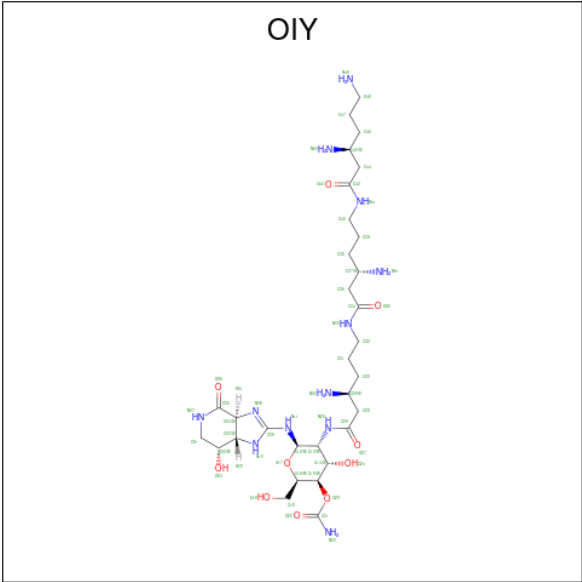
- Molecule 53 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	w	3	Total	C	N	O	P	0	0
			65	29	12	21	3		

- Molecule 54 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
54	3	1	Total	Zn	0
			1	1	

- Molecule 55 is Streptothricin D (CCD ID: OIY) (formula: C₃₁H₅₈N₁₂O₁₀) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
55	A	1	Total	C	N	O	0
			40	22	9	9	
55	A	1	Total	C	N	O	0
			47	27	10	10	
55	A	1	Total	C	N	O	0
			53	31	12	10	
55	A	1	Total	C	N	O	0
			53	31	12	10	
55	A	1	Total	C	N	O	0
			35	19	8	8	
55	A	1	Total	C	N	O	0
			44	25	10	9	
55	N	1	Total	C	N	O	0
			35	19	8	8	
55	W	1	Total	C	N	O	0
			53	31	12	10	
55	a	1	Total	C	N	O	0
			35	19	8	8	
55	a	1	Total	C	N	O	0
			53	31	12	10	
55	a	1	Total	C	N	O	0
			53	31	12	10	
55	a	1	Total	C	N	O	0
			35	19	8	8	

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	A	1	Total 1	Mg 1	0

- Molecule 57 is water.

Mol	Chain	Residues	Atoms		AltConf
57	A	4	Total 4	O 4	0
57	R	1	Total 1	O 1	0

3 Residue-property plots

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

- Molecule 1: 50S ribosomal protein L33

Chain 0:  84% 16%



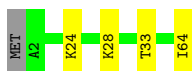
- Molecule 2: 50S ribosomal protein L34

Chain 1:  100%

There are no outlier residues recorded for this chain.

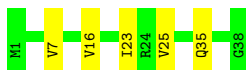
- Molecule 3: 50S ribosomal protein L35

Chain 2:  92% 6%



- Molecule 4: 50S ribosomal protein L36

Chain 3:  87% 13%

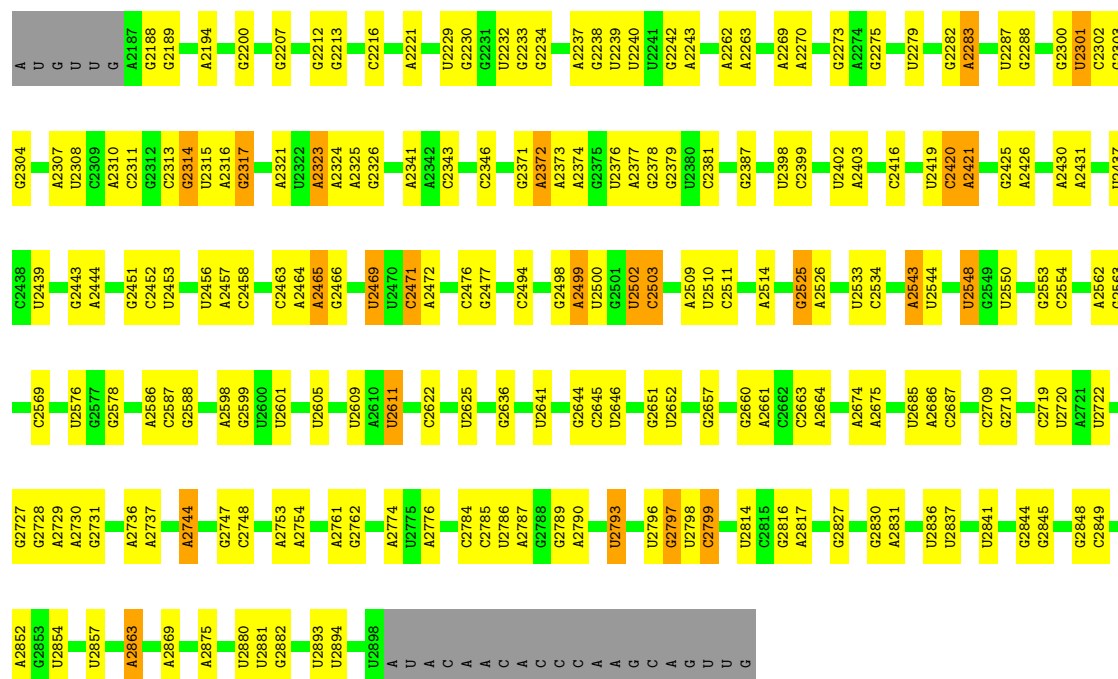


- Molecule 5: 23s ribosomal RNA

Chain A:  67% 24% 7%

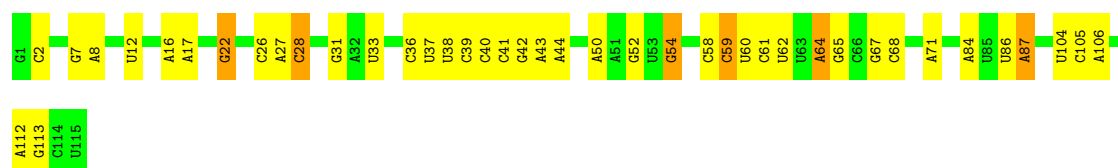


U2035	A1892	G1752	C1575	U1481	A1360	A1166	C	G855	U712	G575	A411	A280
C2039	A1897	G1760	A1577	U1483	G1363	U1170	A	G856	A713	U578	C412	A251
A2048	G1902	A1769	A1578	U1484	G1363	U1171	C	G857	A714	C579	C413	U284
C2051	U1907	A1776	G1579	U1485	U1374	U1173	C	G862	C715	A580	A414	U285
G2052	A1908	A1776	C1580	U1488	A1376	U1174	U	C863	A716	G581	C419	U286
A2056	A1909	U1786	U1581	A1489	A1378	G1179	U	U868	A719	U591	U418	G287
G2057	A1910	A1786	C1582	A1490	A1379	G1179	A	U869	A720	U592	C423	U288
A2058	C1910	A1787	U1583	U1491	A1380	A998	A	U870	C721	C593	G424	G289
C2059	3TD1911	A1788	A1585	U1492	A1381	C1004	A	C874	G727	A594	U418	G290
G2060	A1912	A1790	C1494	C1493	U1382	G1182	G	U	A728	G595	C435	U292
C2061	U1913	C1791	C1503	C1494	U1391	G1185	A	A	G740	U596	C455	G297
C2062	A1914	U1792	U1504	C1598	C1394	G1186	A	G	U741	A597	A456	G304
G2063	A1915	C1793	C1598	A1905	A1395	G1187	G	G	U745	A601	G464	G304
A2064	A1923	U1794	G1605	U1509	G1406	U1193	C	G	A762	U605	U308	U308
G2065	A1924	C1796	A1606	G1510	U1407	C1195	C	G	G773	A606	G465	G309
A2066	G1925	A1797	U1616	A1511	U1411	G1243	U	U	G774	A607	U309	U309
C2067	G1926	A1798	A1616	A1512	C1412	U1244	A	C	U611	U611	A478	A478
G2068	A1934	A1799	A1630	A1513	G1413	G1245	U	A	A612	A612	A479	A479
C2069	A1934	A1805	A1630	U1514	G1413	G1245	U	C	G774	A612	A481	A481
U2070	U1942	A1806	G1634	U1519	A1414	A1248	C	C	G774	G618	A482	A482
U2071	C1943	G1807	A1635	A1520	A1414	A1249	C	C	A780	U618	A482	A482
U2082	U1951	C1812	C1644	G1521	A1422	U1250	U	C	A781	A625	G492	G492
G2083	U1952	C1812	U1645	G1522	C1423	G1251	C	G	G783	A625	G493	G493
C2089	C1953	A1825	U1646	A1523	G1424	G1251	A	A	G783	G633	G494	G494
U2092	C1954	U1826	G1647	A1524	G1425	G1251	C	C	C794	G633	G495	G495
G2093	U1959	G1827	C1654	U1527	A1426	G1266	C	U	U795	A635	A347	A347
U2094	C1963	C1829	U1655	U1529	G1427	C1268	A	U	U795	G636	A348	A348
C2095	U1966	C1833	C1656	A1530	A1428	C1268	A	A	G803	U637	A504	A504
G2096	U1967	A1843	U1657	U1530	A1428	C1268	C	C	C810	U638	G511	G511
C2097	G1968	G1845	G1672	C1531	U1433	A1297	A	A	U811	U643	G521	G521
C2098	U1978	A1849	G1680	U1532	A1434	A1297	A	A	C812	U643	G522	G522
G2099	G1983	A1850	U1681	U1533	A1435	A1311	C	C	A817	G649	G629	G629
U2100	U1987	A1854	U1682	U1534	A1439	G1312	G	G	U825	U651	C530	C530
C2101	U1989	G1865	C1724	G1534	G1440	U1313	A	A	U826	U655	A531	A531
A2102	U2018	A1867	U1725	U1535	C1441	C1314	G	G	U826	U655	G532	G532
G2103	C2019	A1868	C1726	G1536	C1442	C1315	G	G	U830	U656	U533	U533
C2104	G2020	G1869	G1727	C1537	U1443	A1316	U	U	A831	C669	U544	U544
A2105	U2022	A1872	U1728	A1538	G1447	C1318	C	C	G832	C670	C545	C545
C2106	A2026	U1879	U1729	U1539	U1448	G1319	U	U	A675	A675	G546	G546
G2107	C2027	U1880	C1731	G1540	U1455	U1320	C	C	U838	U684	G548	G548
C2108	U2028	A1881	U1733	G1541	G1462	U1324	A	A	G843	A554	A554	A554
A2109	A2029	A1885	G1735	U1542	A1463	C1344	U	U	A844	A687	A561	A561
G2110	G2034	A1886	G1736	A1543	A1464	C1345	A	A	U846	U688	C391	C391
U2111	U2034	A1886	G1749	G1544	A1465	C1346	C	C	A847	A691	G395	G395
C2112	U2034	A1886	G1749	G1544	A1465	C1346	C	C	C848	G698	U571	U571
U2113	U2034	A1886	G1749	G1544	A1465	C1346	C	C	U851	U701	A572	A572
C2114	U2034	A1886	G1749	G1544	A1465	C1346	C	C	G854	G702	U574	U574



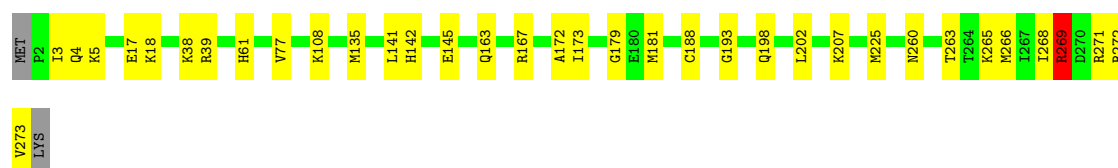
- Molecule 6: 5s ribosomal RNA

Chain B: 63% 31% 5%



- Molecule 7: 50S ribosomal protein L2

Chain C: 86% 12%



- Molecule 8: 50S ribosomal protein L3

Chain D: 89% 10%



- Molecule 9: 50S ribosomal protein L4

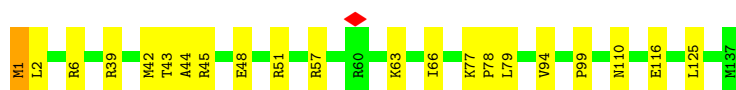
Chain E: 92% 8%

Chain K:  86% 13%



- Molecule 16: 50S ribosomal protein L16

Chain L:  85% 15%



- Molecule 17: 50S ribosomal protein L17

Chain M:  92% 5%



- Molecule 18: 50S ribosomal protein L18

Chain N:  83% 17%



- Molecule 19: 50S ribosomal protein L19

Chain O:  84% 11%



- Molecule 20: 50S ribosomal protein L20

Chain P:  92% 6%



- Molecule 21: 50S ribosomal protein L21

Chain Q:  84% 16%



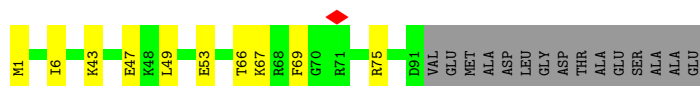
- Molecule 22: 50S ribosomal protein L22

Chain R:  89% 11%



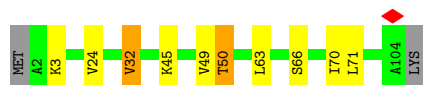
- Molecule 23: 50S ribosomal protein L23

Chain S:  76% 9% 14%



- Molecule 24: 50S ribosomal protein L24

Chain T:  89% 8% . .



- Molecule 25: 50S ribosomal protein L25

Chain U:  92% 7% .



- Molecule 26: 50S ribosomal protein L27

Chain V:  85% 5% 11%



- Molecule 27: 50S ribosomal protein L28

Chain W:  85% 14% .

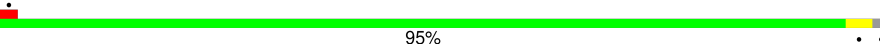


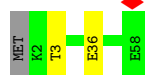
- Molecule 28: 50S ribosomal protein L29

Chain X:  69% 23% 8%



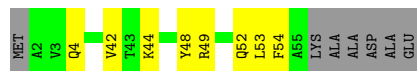
- Molecule 29: 50S ribosomal protein L30

Chain Y:  95%



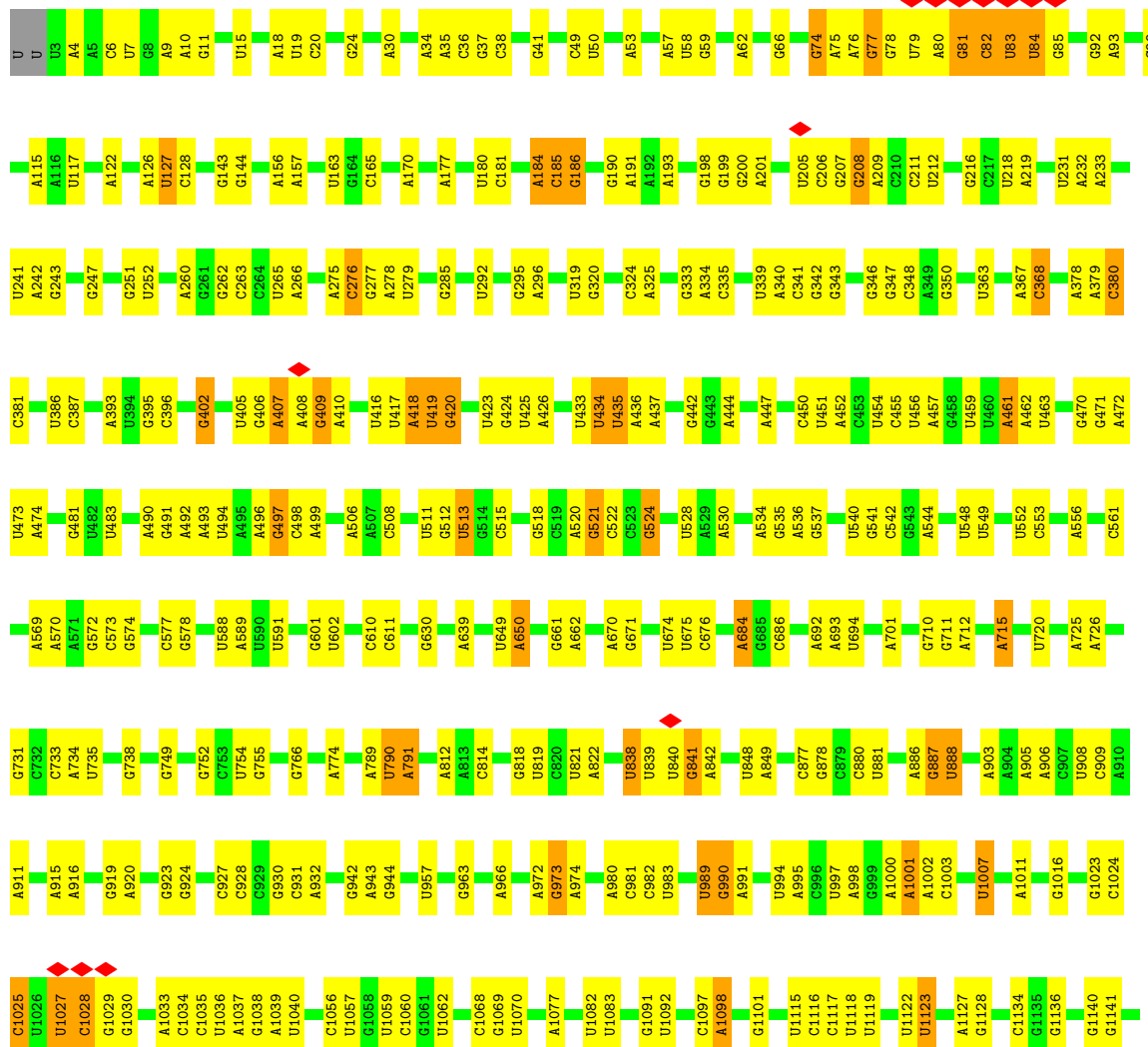
- Molecule 30: 50S ribosomal protein L32

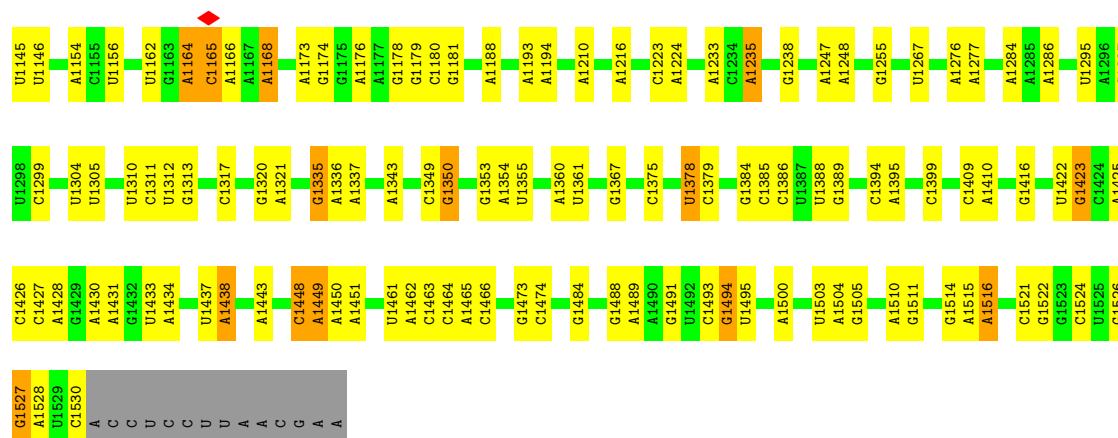
Chain Z:  75% 13% 11%



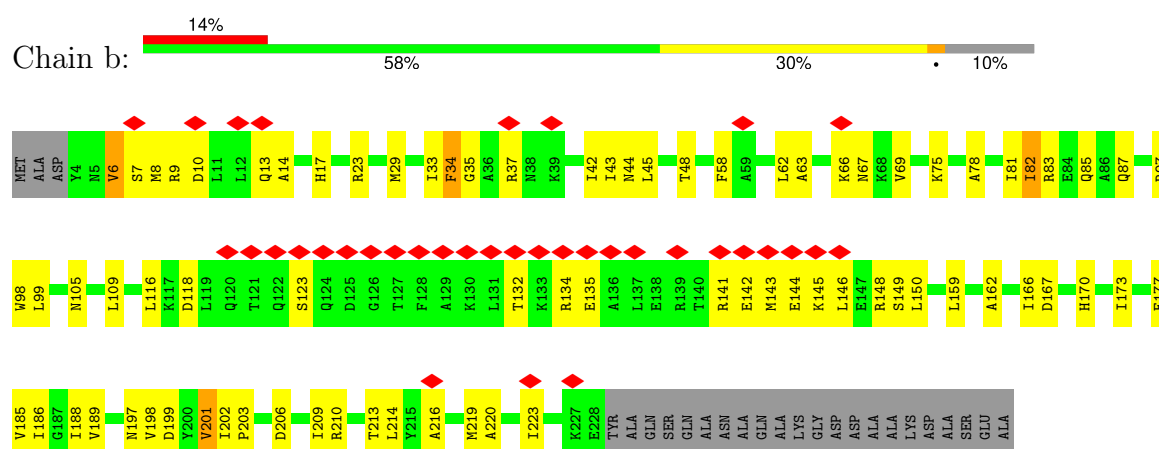
- Molecule 31: 16s Ribosomal RNA

Chain a:  67% 28%

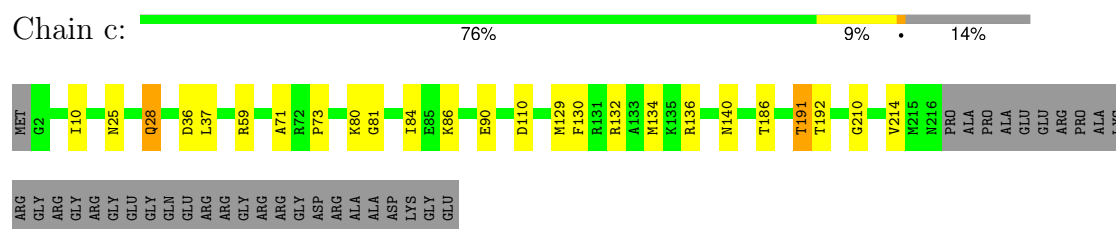




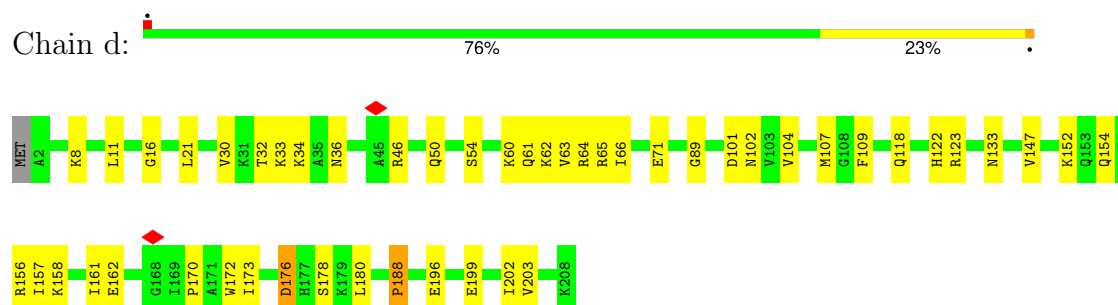
• Molecule 32: 30S ribosomal protein S2



• Molecule 33: 30S ribosomal protein S3

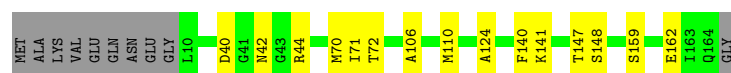


• Molecule 34: 30S ribosomal protein S4



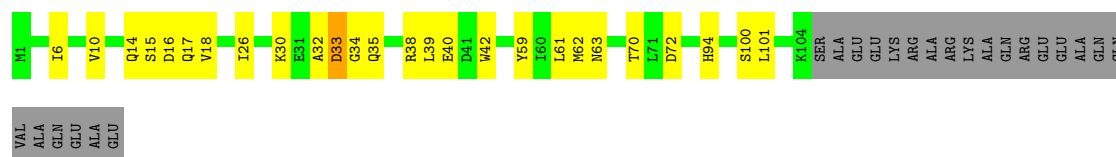
• Molecule 35: 30S ribosomal protein S5

Chain e: 



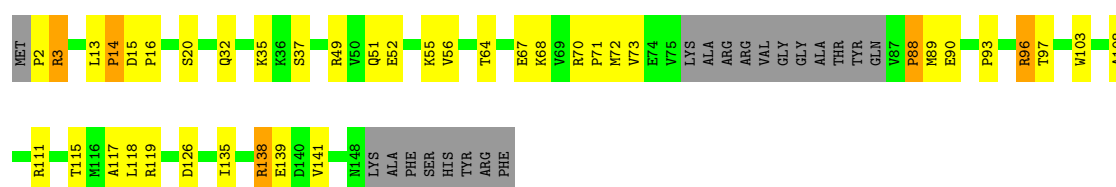
- Molecule 36: 30S ribosomal protein S6

Chain f: 



- Molecule 37: 30S ribosomal protein S7

Chain g: 



- Molecule 38: 30S ribosomal protein S8

Chain h: 



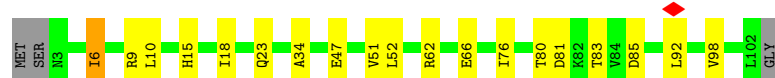
- Molecule 39: 30S ribosomal protein S9

Chain i: 



- Molecule 40: 30S ribosomal protein S10

Chain j: 



- Molecule 41: 30S ribosomal protein S11

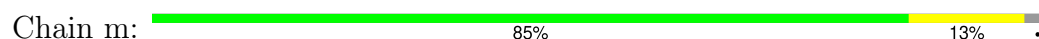
Chain k: 



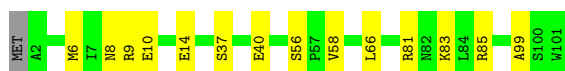
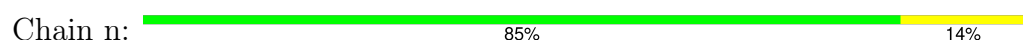
- Molecule 42: 30S ribosomal protein S12



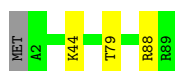
- Molecule 43: 30S ribosomal protein S13



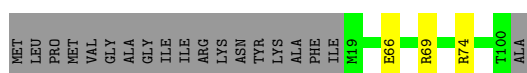
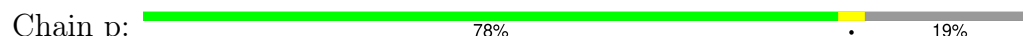
- Molecule 44: 30S ribosomal protein S14



- Molecule 45: 30S ribosomal protein S15



- Molecule 46: 30S ribosomal protein S16



- Molecule 47: 30S ribosomal protein S17

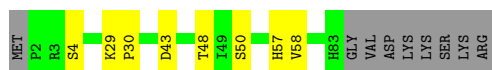
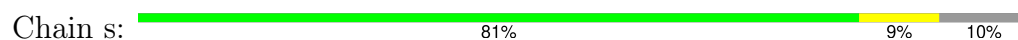


- Molecule 48: 30S ribosomal protein S18

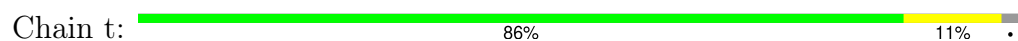




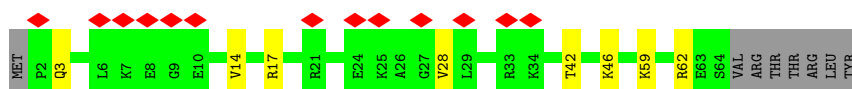
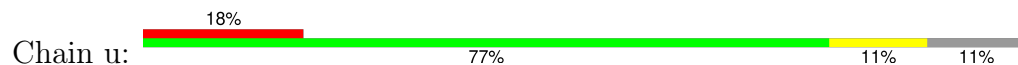
- Molecule 49: 30S ribosomal protein S19



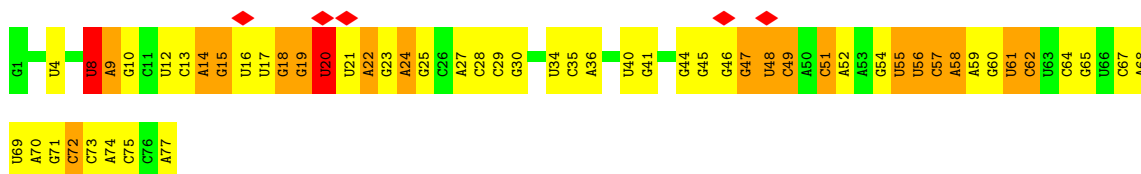
- Molecule 50: 30S ribosomal protein S20



- Molecule 51: 30S ribosomal protein S21



- Molecule 52: tRNA-met



- Molecule 53: mRNA



There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	144189	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 ($e^-/\text{\AA}^2$)	36	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.869	Depositor
Minimum map value	-0.032	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.08	Depositor
Map size (Å)	460.80002, 460.80002, 460.80002	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.72, 0.72, 0.72	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.16	0/434	0.34	0/573
2	1	0.15	0/367	0.34	0/481
3	2	0.16	0/515	0.40	0/678
4	3	0.17	0/296	0.39	0/389
5	A	0.19	0/65086	0.33	0/101513
6	B	0.15	0/2739	0.29	0/4266
7	C	0.23	0/2152	0.46	0/2891
8	D	0.18	0/1590	0.38	0/2142
9	E	0.18	0/1537	0.40	0/2073
10	F	0.19	0/1390	0.52	0/1863
11	G	0.18	0/1337	0.44	0/1807
12	H	0.18	0/461	0.51	0/616
13	I	0.17	0/1151	0.40	0/1551
14	J	0.17	0/956	0.39	0/1286
15	K	0.16	0/1079	0.34	0/1439
16	L	0.17	0/1104	0.40	0/1475
17	M	0.17	0/956	0.39	0/1282
18	N	0.15	0/881	0.44	0/1177
19	O	0.17	0/931	0.39	0/1249
20	P	0.19	0/947	0.36	0/1262
21	Q	0.17	0/818	0.36	0/1094
22	R	0.17	0/831	0.34	0/1113
23	S	0.15	0/716	0.36	0/957
24	T	0.14	0/770	0.34	0/1034
25	U	0.16	0/770	0.38	0/1036
26	V	0.17	0/585	0.39	0/783
27	W	0.16	0/642	0.36	0/856
28	X	0.16	0/487	0.38	0/646
29	Y	0.17	0/460	0.32	0/614
30	Z	0.15	0/453	0.32	0/604
31	a	0.17	0/36476	0.31	0/56895

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	b	0.18	0/1799	0.41	0/2429
33	c	0.17	0/1714	0.40	0/2304
34	d	0.19	0/1653	0.48	1/2213 (0.0%)
35	e	0.17	0/1141	0.38	0/1537
36	f	0.17	0/882	0.43	0/1189
37	g	0.23	0/1087	0.59	1/1456 (0.1%)
38	h	0.16	0/993	0.36	0/1331
39	i	0.18	0/1002	0.42	0/1339
40	j	0.19	0/811	0.50	0/1096
41	k	0.18	0/878	0.44	0/1189
42	l	0.18	0/958	0.42	0/1284
43	m	0.18	0/913	0.48	2/1226 (0.2%)
44	n	0.19	0/803	0.36	0/1071
45	o	0.17	0/715	0.33	0/958
46	p	0.15	0/655	0.37	0/879
47	q	0.16	0/628	0.40	0/847
48	r	0.18	0/432	0.44	0/583
49	s	0.17	0/664	0.35	0/897
50	t	0.18	0/669	0.32	0/892
51	u	0.13	0/528	0.33	0/697
52	v	0.17	0/1739	0.31	0/2709
53	w	0.10	0/72	0.16	0/110
All	All	0.18	0/149653	0.34	4/223881 (0.0%)

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
7	C	0	1
21	Q	0	1
All	All	0	2

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	g	14	PRO	CA-N-CD	-6.40	103.04	112.00
43	m	64	PRO	CA-C-N	-6.04	115.25	122.44
43	m	64	PRO	C-N-CA	-6.04	115.25	122.44
34	d	188	PRO	CA-N-CD	-5.21	104.71	112.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	C	269	ARG	Sidechain
21	Q	51	ALA	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	427	0	462	8	0
2	1	363	0	401	0	0
3	2	509	0	566	3	0
4	3	295	0	326	3	0
5	A	58438	0	29389	332	0
6	B	2450	0	1241	16	0
7	C	2111	0	2176	37	0
8	D	1572	0	1610	13	0
9	E	1516	0	1569	8	0
10	F	1370	0	1420	55	0
11	G	1318	0	1373	28	0
12	H	458	0	480	9	0
13	I	1125	0	1148	5	0
14	J	946	0	1007	3	0
15	K	1071	0	1141	10	0
16	L	1087	0	1162	15	0
17	M	942	0	987	1	0
18	N	873	0	917	11	0
19	O	919	0	973	12	0
20	P	934	0	997	5	0
21	Q	807	0	842	8	0
22	R	826	0	894	9	0
23	S	710	0	768	7	0
24	T	766	0	816	4	0
25	U	760	0	783	3	0
26	V	577	0	580	3	0
27	W	632	0	667	7	0
28	X	486	0	528	9	0

Continued on next page...

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	Y	455	0	476	0	0
30	Z	447	0	435	6	0
31	a	32782	0	16508	256	0
32	b	1769	0	1787	54	0
33	c	1690	0	1774	13	0
34	d	1631	0	1691	34	0
35	e	1129	0	1174	10	0
36	f	867	0	868	15	0
37	g	1073	0	1118	28	0
38	h	985	0	1047	11	0
39	i	991	0	1048	8	0
40	j	801	0	832	12	0
41	k	862	0	877	19	0
42	l	945	0	998	22	0
43	m	903	0	962	8	0
44	n	792	0	833	13	0
45	o	705	0	712	2	0
46	p	644	0	655	2	0
47	q	621	0	665	8	0
48	r	426	0	447	9	0
49	s	646	0	663	4	0
50	t	663	0	715	8	0
51	u	522	0	565	5	0
52	v	1636	0	835	44	0
53	w	65	0	33	0	0
54	3	1	0	0	0	0
55	A	272	0	0	4	0
55	N	35	0	0	1	0
55	W	53	0	0	2	0
55	a	176	0	0	1	0
56	A	1	0	0	0	0
57	A	4	0	0	0	0
57	R	1	0	0	0	0
All	All	138881	0	92941	1135	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 1135 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:1036:A:N6	5:A:1113:G:H1	1.44	1.14
7:C:269:ARG:HH11	7:C:269:ARG:HB3	1.09	1.08
52:v:27:A:N6	52:v:45:G:H1	1.51	1.08
31:a:75:A:N6	31:a:92:G:H1	1.59	0.97
31:a:74:G:H1	31:a:93:A:H61	0.99	0.97

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	49/51 (96%)	49 (100%)	0	0	100	100
2	1	42/44 (96%)	42 (100%)	0	0	100	100
3	2	61/64 (95%)	58 (95%)	3 (5%)	0	100	100
4	3	36/38 (95%)	36 (100%)	0	0	100	100
7	C	270/274 (98%)	262 (97%)	8 (3%)	0	100	100
8	D	209/212 (99%)	200 (96%)	9 (4%)	0	100	100
9	E	198/200 (99%)	197 (100%)	1 (0%)	0	100	100
10	F	172/178 (97%)	157 (91%)	12 (7%)	3 (2%)	7	10
11	G	172/177 (97%)	166 (96%)	5 (3%)	1 (1%)	21	32
12	H	58/148 (39%)	55 (95%)	3 (5%)	0	100	100
13	I	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
14	J	120/122 (98%)	119 (99%)	1 (1%)	0	100	100
15	K	142/146 (97%)	139 (98%)	3 (2%)	0	100	100
16	L	135/137 (98%)	130 (96%)	4 (3%)	1 (1%)	18	28
17	M	117/125 (94%)	113 (97%)	4 (3%)	0	100	100
18	N	114/116 (98%)	110 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	O	115/122 (94%)	114 (99%)	1 (1%)	0	100	100
20	P	115/119 (97%)	115 (100%)	0	0	100	100
21	Q	101/103 (98%)	98 (97%)	2 (2%)	1 (1%)	12	20
22	R	107/109 (98%)	107 (100%)	0	0	100	100
23	S	89/106 (84%)	87 (98%)	2 (2%)	0	100	100
24	T	101/105 (96%)	97 (96%)	4 (4%)	0	100	100
25	U	95/98 (97%)	92 (97%)	3 (3%)	0	100	100
26	V	74/85 (87%)	73 (99%)	1 (1%)	0	100	100
27	W	75/78 (96%)	75 (100%)	0	0	100	100
28	X	58/65 (89%)	58 (100%)	0	0	100	100
29	Y	55/58 (95%)	54 (98%)	1 (2%)	0	100	100
30	Z	52/61 (85%)	51 (98%)	1 (2%)	0	100	100
32	b	223/250 (89%)	213 (96%)	8 (4%)	2 (1%)	14	22
33	c	213/250 (85%)	206 (97%)	7 (3%)	0	100	100
34	d	205/208 (99%)	200 (98%)	5 (2%)	0	100	100
35	e	153/165 (93%)	151 (99%)	2 (1%)	0	100	100
36	f	102/127 (80%)	99 (97%)	2 (2%)	1 (1%)	12	20
37	g	132/156 (85%)	123 (93%)	7 (5%)	2 (2%)	8	12
38	h	128/131 (98%)	126 (98%)	2 (2%)	0	100	100
39	i	124/128 (97%)	121 (98%)	3 (2%)	0	100	100
40	j	98/103 (95%)	96 (98%)	2 (2%)	0	100	100
41	k	115/128 (90%)	111 (96%)	4 (4%)	0	100	100
42	l	120/124 (97%)	114 (95%)	6 (5%)	0	100	100
43	m	113/118 (96%)	109 (96%)	4 (4%)	0	100	100
44	n	98/101 (97%)	94 (96%)	4 (4%)	0	100	100
45	o	86/89 (97%)	85 (99%)	1 (1%)	0	100	100
46	p	80/101 (79%)	79 (99%)	1 (1%)	0	100	100
47	q	77/85 (91%)	75 (97%)	2 (3%)	0	100	100
48	r	50/75 (67%)	49 (98%)	1 (2%)	0	100	100
49	s	80/91 (88%)	79 (99%)	1 (1%)	0	100	100
50	t	84/88 (96%)	84 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	u	61/71 (86%)	60 (98%)	1 (2%)	0	100	100
All	All	5414/5872 (92%)	5265 (97%)	138 (2%)	11 (0%)	44	58

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	F	137	VAL
32	b	8	MET
36	f	33	ASP
37	g	88	PRO
37	g	3	ARG

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	0	47/47 (100%)	46 (98%)	1 (2%)	47	69
2	1	36/36 (100%)	36 (100%)	0	100	100
3	2	52/53 (98%)	51 (98%)	1 (2%)	50	71
4	3	33/33 (100%)	32 (97%)	1 (3%)	36	58
7	C	218/220 (99%)	216 (99%)	2 (1%)	70	85
8	D	166/167 (99%)	164 (99%)	2 (1%)	63	81
9	E	155/155 (100%)	150 (97%)	5 (3%)	34	56
10	F	144/147 (98%)	137 (95%)	7 (5%)	22	39
11	G	139/142 (98%)	131 (94%)	8 (6%)	18	32
12	H	45/112 (40%)	45 (100%)	0	100	100
13	I	118/118 (100%)	115 (98%)	3 (2%)	42	64
14	J	103/103 (100%)	101 (98%)	2 (2%)	50	71
15	K	106/108 (98%)	102 (96%)	4 (4%)	29	49
16	L	113/113 (100%)	111 (98%)	2 (2%)	51	73
17	M	96/101 (95%)	93 (97%)	3 (3%)	35	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	N	85/85 (100%)	83 (98%)	2 (2%)	43	65
19	O	99/102 (97%)	98 (99%)	1 (1%)	68	84
20	P	85/86 (99%)	85 (100%)	0	100	100
21	Q	84/84 (100%)	83 (99%)	1 (1%)	63	81
22	R	88/88 (100%)	86 (98%)	2 (2%)	44	66
23	S	77/87 (88%)	76 (99%)	1 (1%)	61	80
24	T	83/85 (98%)	77 (93%)	6 (7%)	13	23
25	U	79/80 (99%)	78 (99%)	1 (1%)	61	80
26	V	59/64 (92%)	59 (100%)	0	100	100
27	W	69/70 (99%)	69 (100%)	0	100	100
28	X	53/56 (95%)	52 (98%)	1 (2%)	50	71
29	Y	53/54 (98%)	51 (96%)	2 (4%)	29	49
30	Z	46/50 (92%)	46 (100%)	0	100	100
32	b	185/200 (92%)	176 (95%)	9 (5%)	22	39
33	c	175/198 (88%)	171 (98%)	4 (2%)	44	66
34	d	170/171 (99%)	168 (99%)	2 (1%)	63	81
35	e	113/120 (94%)	113 (100%)	0	100	100
36	f	94/111 (85%)	91 (97%)	3 (3%)	34	56
37	g	113/128 (88%)	108 (96%)	5 (4%)	25	43
38	h	108/109 (99%)	106 (98%)	2 (2%)	50	71
39	i	99/100 (99%)	97 (98%)	2 (2%)	48	70
40	j	89/91 (98%)	86 (97%)	3 (3%)	32	54
41	k	88/98 (90%)	85 (97%)	3 (3%)	32	54
42	l	104/106 (98%)	99 (95%)	5 (5%)	23	40
43	m	95/98 (97%)	94 (99%)	1 (1%)	65	82
44	n	81/82 (99%)	81 (100%)	0	100	100
45	o	71/72 (99%)	70 (99%)	1 (1%)	59	79
46	p	63/77 (82%)	63 (100%)	0	100	100
47	q	71/76 (93%)	67 (94%)	4 (6%)	19	33
48	r	46/66 (70%)	44 (96%)	2 (4%)	26	44
49	s	70/78 (90%)	68 (97%)	2 (3%)	37	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
50	t	65/67 (97%)	64 (98%)	1 (2%)	57 77
51	u	54/62 (87%)	53 (98%)	1 (2%)	50 71
All	All	4485/4756 (94%)	4377 (98%)	108 (2%)	43 65

5 of 108 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	Y	36	GLU
34	d	30	VAL
47	q	30	VAL
32	b	23	ARG
32	b	201	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
42	l	96	HIS
45	o	48	HIS
51	u	43	GLN
24	T	38	ASN
20	P	44	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
31	a	1527/1544 (98%)	207 (13%)	0
5	A	2720/2918 (93%)	379 (13%)	19 (0%)
52	v	76/77 (98%)	28 (36%)	0
53	w	2/3 (66%)	0	0
6	B	114/115 (99%)	21 (18%)	1 (0%)
All	All	4439/4657 (95%)	635 (14%)	20 (0%)

5 of 635 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	A	22	G
5	A	50	G
5	A	53	G
5	A	67	G

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Mol	Chain	Res	Type
5	A	78	A

5 of 20 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	A	1187	G
5	A	2443	G
6	B	86	U
5	A	2502	U
5	A	424	G

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

28 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	$\# Z > 2$
31	7MG	a	524	31	23,26,27	1.09	1 (4%)	27,39,42	0.89	2 (7%)
31	PSU	a	513	31	18,21,22	1.10	1 (5%)	21,30,33	1.85	5 (23%)
31	4OC	a	1399	31	20,23,24	3.13	8 (40%)	25,32,35	0.99	1 (4%)
5	PSU	A	1913	5	18,21,22	1.13	1 (5%)	21,30,33	1.87	4 (19%)
52	5MU	v	55	52	19,22,23	0.41	0	27,32,35	0.61	0
5	PSU	A	2576	5	18,21,22	1.10	2 (11%)	21,30,33	1.98	5 (23%)
31	2MG	a	1204	31	23,26,27	0.45	0	33,38,41	0.53	0
52	4SU	v	8	52	18,21,22	4.40	8 (44%)	25,30,33	2.23	4 (16%)
5	OMG	A	2247	5,52	23,26,27	0.50	0	32,38,41	0.45	0
5	PSU	A	2500	5	18,21,22	1.07	1 (5%)	21,30,33	1.85	4 (19%)
5	PSU	A	2601	5	18,21,22	1.05	1 (5%)	21,30,33	1.84	3 (14%)
5	3TD	A	1911	5	19,22,23	4.39	6 (31%)	23,32,35	1.73	3 (13%)
52	PSU	v	56	52	18,21,22	1.16	1 (5%)	21,30,33	1.88	5 (23%)
5	6MZ	A	2026	5	22,25,26	2.54	4 (18%)	29,36,39	3.27	10 (34%)
31	UR3	a	1495	31	19,22,23	2.86	7 (36%)	26,32,35	1.61	3 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
52	H2U	v	20	52	18,21,22	0.52	0	19,30,33	0.98	1 (5%)
5	7MG	A	2065	5	23,26,27	1.07	1 (4%)	27,39,42	0.94	2 (7%)
5	PSU	A	1907	5	18,21,22	1.12	1 (5%)	21,30,33	1.86	4 (19%)
31	MA6	a	1516	31	23,26,27	1.42	4 (17%)	33,38,41	3.28	13 (39%)
5	PSU	A	2453	5	18,21,22	1.08	1 (5%)	21,30,33	1.92	5 (23%)
5	5MU	A	1935	5	19,22,23	0.45	0	27,32,35	0.52	0
5	OMU	A	2548	5	19,22,23	3.03	8 (42%)	25,31,34	1.83	5 (20%)
5	2MA	A	2499	5	22,25,26	3.89	9 (40%)	32,37,40	2.62	10 (31%)
31	2MG	a	963	31	23,26,27	0.47	0	33,38,41	0.55	0
31	5MC	a	964	31	19,22,23	0.55	0	26,32,35	0.60	0
5	2MG	A	2441	5	23,26,27	0.50	0	33,38,41	0.46	0
5	PSU	A	952	5	18,21,22	1.07	1 (5%)	21,30,33	1.91	4 (19%)
31	MA6	a	1515	31	23,26,27	1.43	4 (17%)	33,38,41	3.20	12 (36%)

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
31	7MG	a	524	31	-	2/7/37/38	0/3/3/3
31	PSU	a	513	31	-	0/7/25/26	0/2/2/2
31	4OC	a	1399	31	-	1/9/29/30	0/2/2/2
5	PSU	A	1913	5	-	0/7/25/26	0/2/2/2
52	5MU	v	55	52	-	3/7/25/26	0/2/2/2
5	PSU	A	2576	5	-	0/7/25/26	0/2/2/2
31	2MG	a	1204	31	-	0/9/27/28	0/3/3/3
52	4SU	v	8	52	-	2/7/25/26	0/2/2/2
5	OMG	A	2247	5,52	-	0/9/27/28	0/3/3/3
5	PSU	A	2500	5	-	1/7/25/26	0/2/2/2
5	PSU	A	2601	5	-	0/7/25/26	0/2/2/2
5	3TD	A	1911	5	-	2/7/25/26	0/2/2/2
52	PSU	v	56	52	-	4/7/25/26	0/2/2/2
5	6MZ	A	2026	5	-	2/9/27/28	0/3/3/3
31	UR3	a	1495	31	-	0/7/25/26	0/2/2/2
52	H2U	v	20	52	-	3/7/38/39	0/2/2/2
5	7MG	A	2065	5	-	0/7/37/38	0/3/3/3
5	PSU	A	1907	5	-	0/7/25/26	0/2/2/2
31	MA6	a	1516	31	-	0/11/29/30	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PSU	A	2453	5	-	0/7/25/26	0/2/2/2
5	5MU	A	1935	5	-	0/7/25/26	0/2/2/2
5	OMU	A	2548	5	-	0/9/27/28	0/2/2/2
5	2MA	A	2499	5	-	2/7/25/26	0/3/3/3
31	2MG	a	963	31	-	0/9/27/28	0/3/3/3
31	5MC	a	964	31	-	0/7/25/26	0/2/2/2
5	2MG	A	2441	5	-	0/9/27/28	0/3/3/3
5	PSU	A	952	5	-	0/7/25/26	0/2/2/2
31	MA6	a	1515	31	-	0/11/29/30	0/3/3/3

The worst 5 of 70 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1911	3TD	C6-C5	13.15	1.49	1.35
5	A	2499	2MA	C4-N3	11.85	1.49	1.34
5	A	1911	3TD	C2-N1	10.57	1.50	1.37
5	A	2026	6MZ	C6-N6	10.16	1.45	1.34
52	v	8	4SU	C2-N1	9.42	1.53	1.38

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	a	1516	MA6	N1-C6-N6	-11.95	102.29	116.86
31	a	1515	MA6	N1-C6-N6	-11.40	102.97	116.86
5	A	2026	6MZ	C4-N9-C1'	-8.87	105.88	126.63
5	A	2026	6MZ	C1'-N9-C8	8.86	146.76	127.09
31	a	1516	MA6	C5-C6-N6	8.01	138.01	125.33

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
52	v	8	4SU	O4'-C4'-C5'-O5'
52	v	55	5MU	C3'-C4'-C5'-O5'
52	v	55	5MU	O4'-C4'-C5'-O5'
52	v	56	PSU	O4'-C1'-C5-C4
52	v	56	PSU	O4'-C1'-C5-C6

There are no ring outliers.

7 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
31	a	513	PSU	1	0
52	v	55	5MU	1	0
52	v	8	4SU	1	0
52	v	56	PSU	2	0
5	A	2026	6MZ	1	0
52	v	20	H2U	3	0
5	A	2548	OMU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 2 are monoatomic - leaving 12 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
55	OIY	a	1603	-	54,55,55	1.80	11 (20%)	55,74,74	1.61	8 (14%)
55	OIY	a	1601	-	36,37,55	1.34	6 (16%)	37,52,74	1.69	4 (10%)
55	OIY	A	3005	-	36,37,55	1.34	6 (16%)	37,52,74	1.98	6 (16%)
55	OIY	W	101	-	54,55,55	1.80	11 (20%)	55,74,74	1.61	8 (14%)
55	OIY	a	1604	-	36,37,55	1.30	6 (16%)	37,52,74	1.79	5 (13%)
55	OIY	A	3006	-	45,46,55	1.67	9 (20%)	46,63,74	1.57	6 (13%)
55	OIY	A	3003	-	54,55,55	1.80	11 (20%)	55,74,74	1.51	7 (12%)
55	OIY	A	3001	-	41,42,55	1.66	9 (21%)	43,58,74	1.64	6 (13%)
55	OIY	N	201	-	36,37,55	1.36	6 (16%)	37,52,74	1.66	5 (13%)
55	OIY	A	3002	-	48,49,55	1.84	12 (25%)	50,67,74	1.91	9 (18%)
55	OIY	a	1602	-	54,55,55	1.79	10 (18%)	55,74,74	1.53	8 (14%)
55	OIY	A	3004	-	54,55,55	1.77	10 (18%)	55,74,74	1.56	6 (10%)

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
55	OIY	a	1603	-	-	7/44/89/89	0/3/3/3
55	OIY	a	1601	-	-	3/22/67/89	0/3/3/3
55	OIY	A	3005	-	-	7/22/67/89	0/3/3/3
55	OIY	W	101	-	-	11/44/89/89	0/3/3/3
55	OIY	a	1604	-	-	3/22/67/89	0/3/3/3
55	OIY	A	3006	-	-	14/33/78/89	0/3/3/3
55	OIY	A	3003	-	-	17/44/89/89	0/3/3/3
55	OIY	A	3001	-	-	5/28/73/89	0/3/3/3
55	OIY	N	201	-	-	4/22/67/89	0/3/3/3
55	OIY	A	3002	-	-	15/36/81/89	0/3/3/3
55	OIY	a	1602	-	-	13/44/89/89	0/3/3/3
55	OIY	A	3004	-	-	12/44/89/89	0/3/3/3

The worst 5 of 107 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	A	3002	OIY	C34-N33	6.90	1.49	1.33
55	a	1602	OIY	C34-N33	6.77	1.49	1.33
55	A	3006	OIY	C34-N33	6.71	1.49	1.33
55	a	1603	OIY	C34-N33	6.70	1.49	1.33
55	W	101	OIY	C34-N33	6.70	1.49	1.33

The worst 5 of 78 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	a	1604	OIY	C02-C01-N07	8.06	118.04	109.83
55	A	3002	OIY	C02-C01-N07	7.72	117.69	109.83
55	W	101	OIY	C02-C01-N07	7.65	117.63	109.83
55	a	1601	OIY	C02-C01-N07	7.48	117.45	109.83
55	A	3001	OIY	C02-C01-N07	7.39	117.36	109.83

There are no chirality outliers.

5 of 111 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
55	A	3002	OIY	C28-C29-C30-C31

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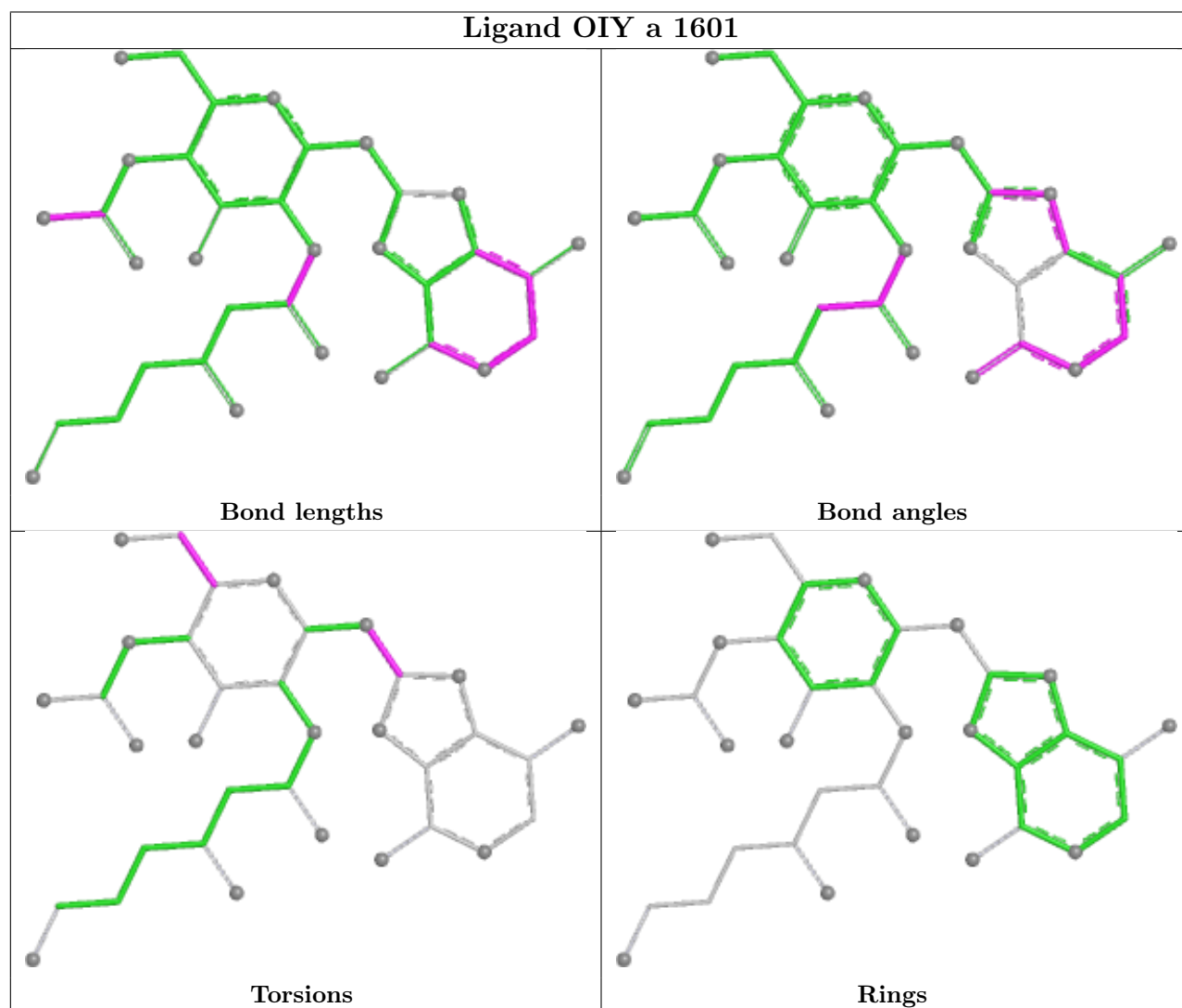
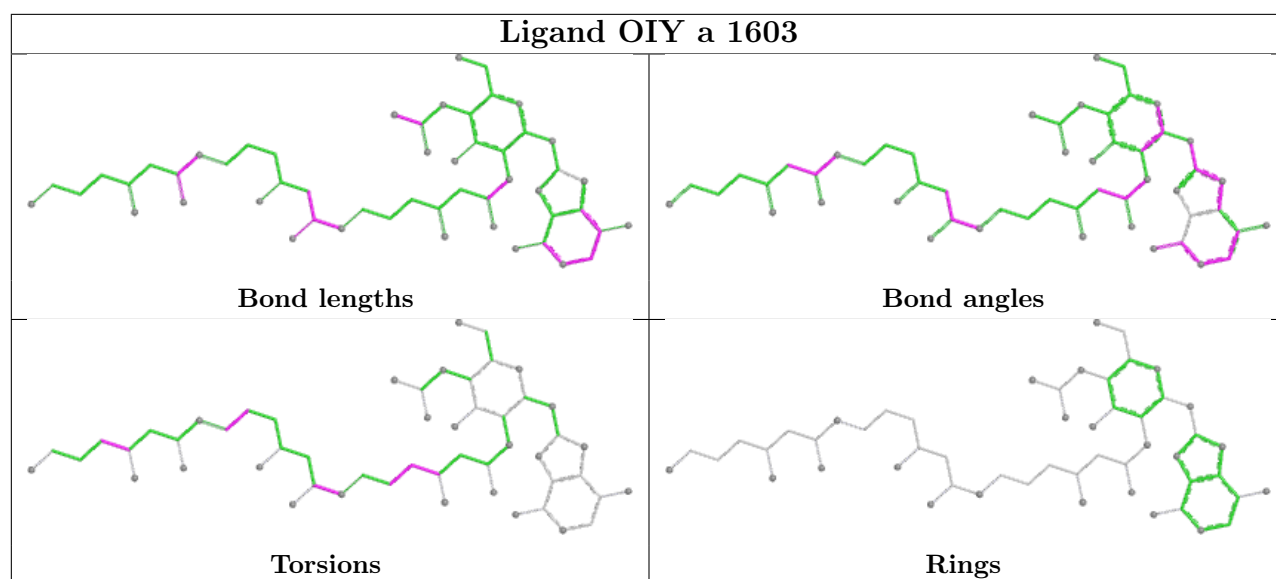
Mol	Chain	Res	Type	Atoms
55	A	3002	OIY	N52-C29-C30-C31
55	A	3002	OIY	C36-C37-C38-C39
55	A	3002	OIY	N51-C37-C38-C39
55	A	3003	OIY	C12-C13-N25-C26

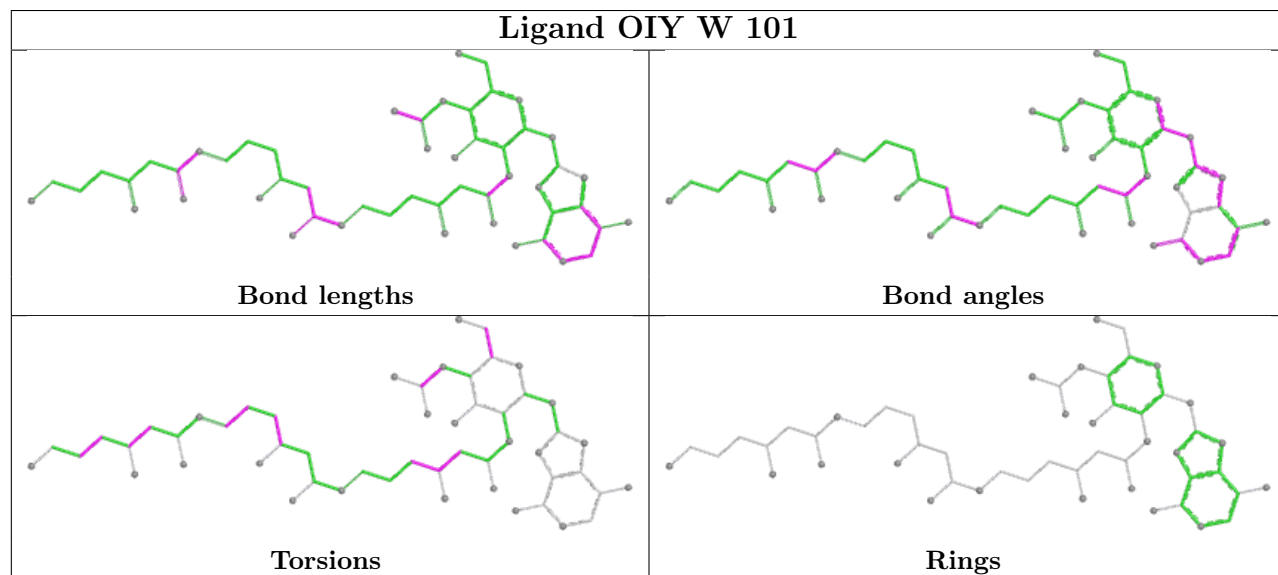
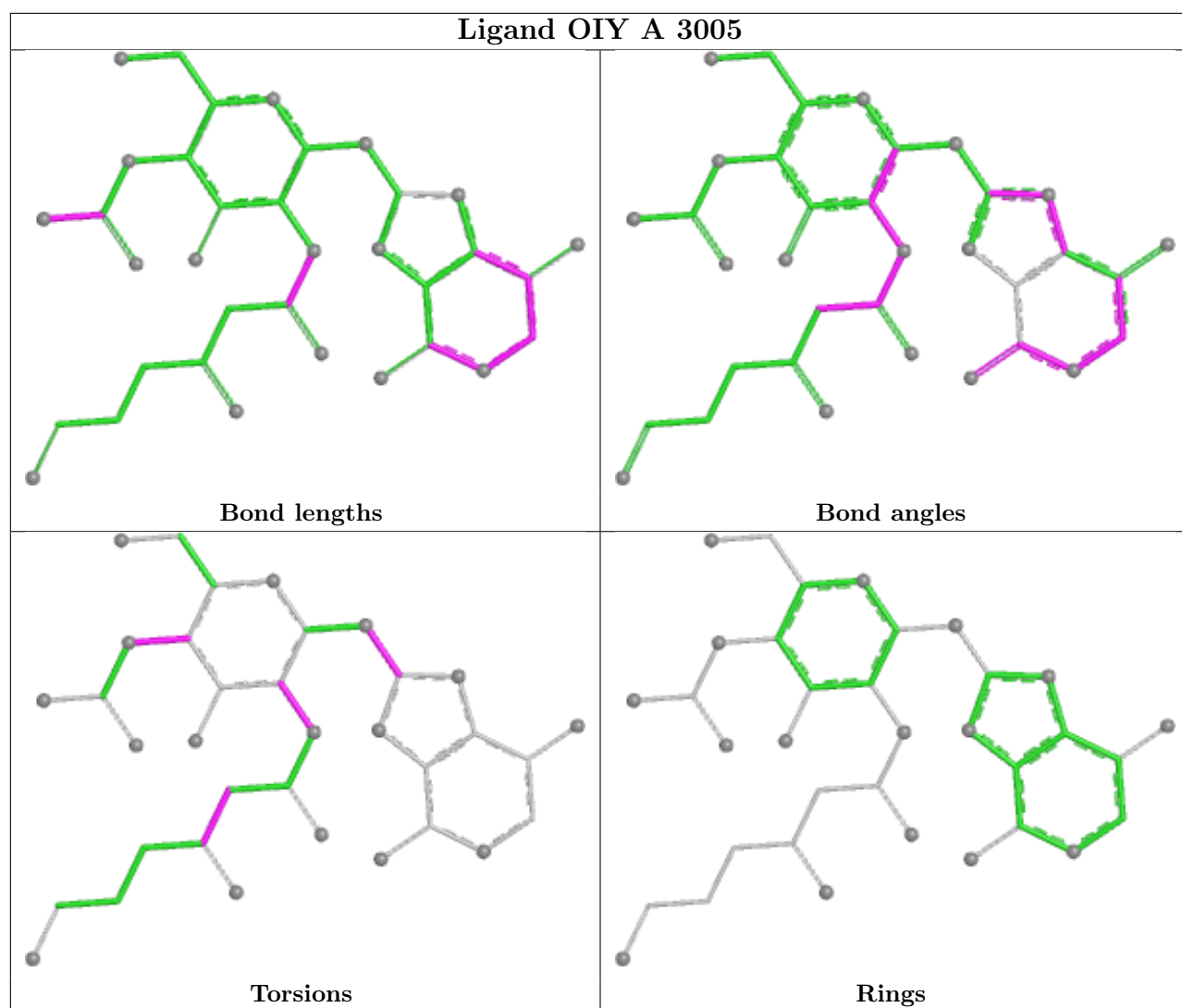
There are no ring outliers.

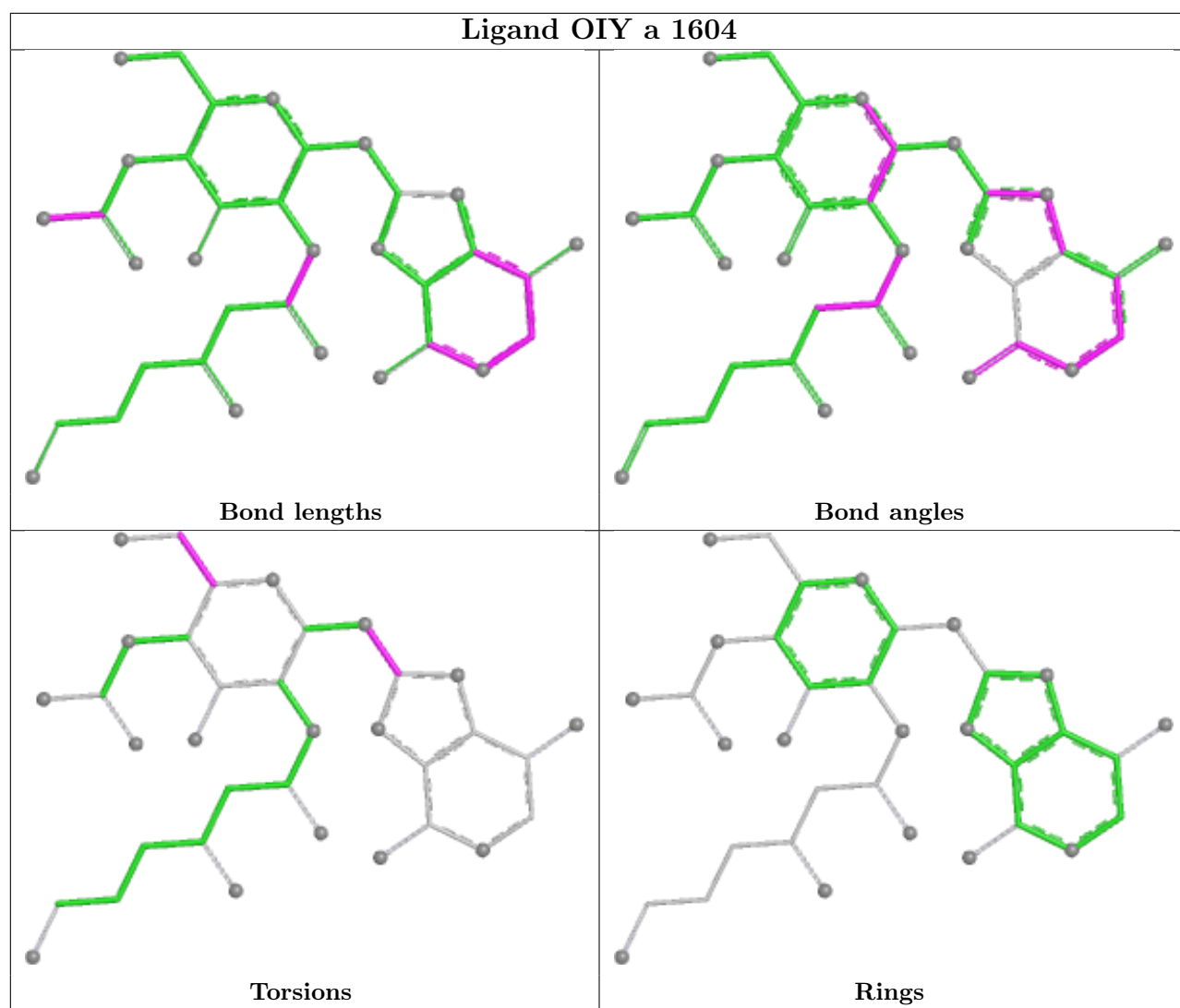
7 monomers are involved in 8 short contacts:

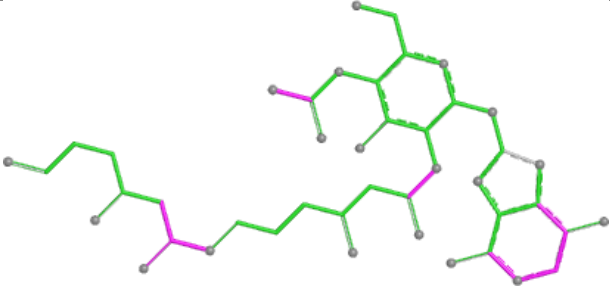
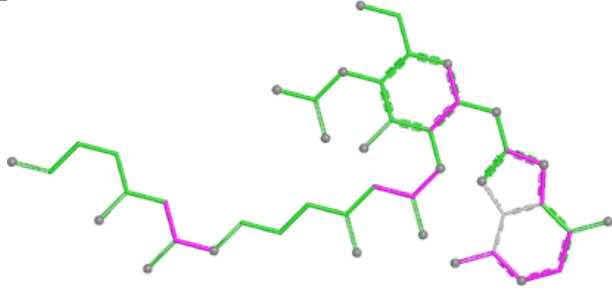
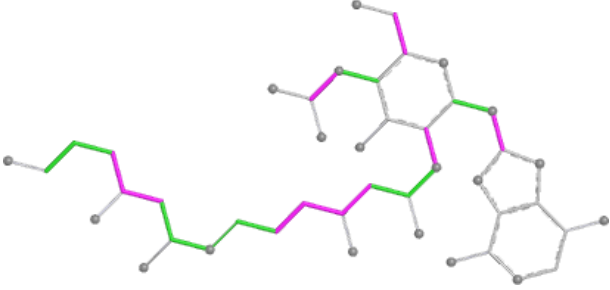
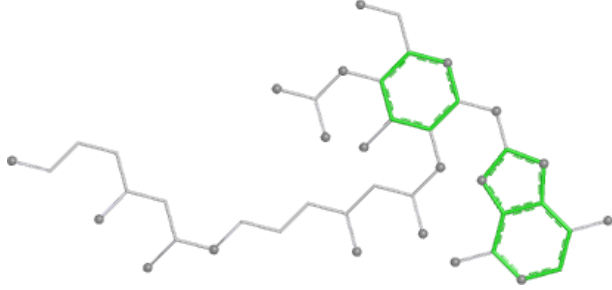
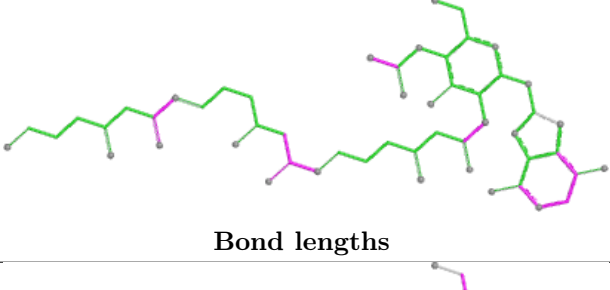
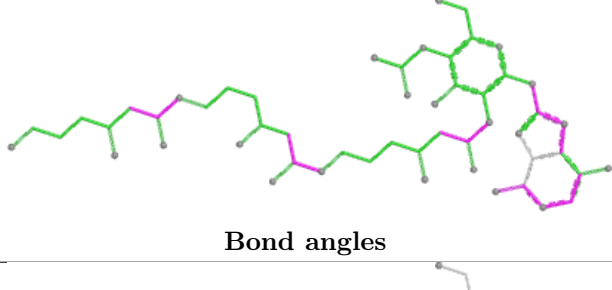
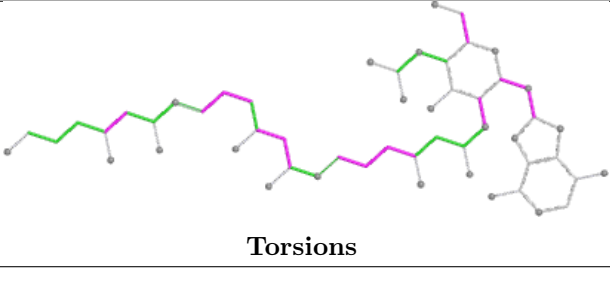
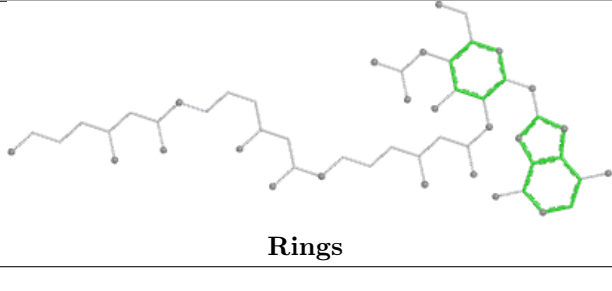
Mol	Chain	Res	Type	Clashes	Symm-Clashes
55	A	3005	OIY	1	0
55	W	101	OIY	2	0
55	A	3006	OIY	1	0
55	N	201	OIY	1	0
55	A	3002	OIY	1	0
55	a	1602	OIY	1	0
55	A	3004	OIY	1	0

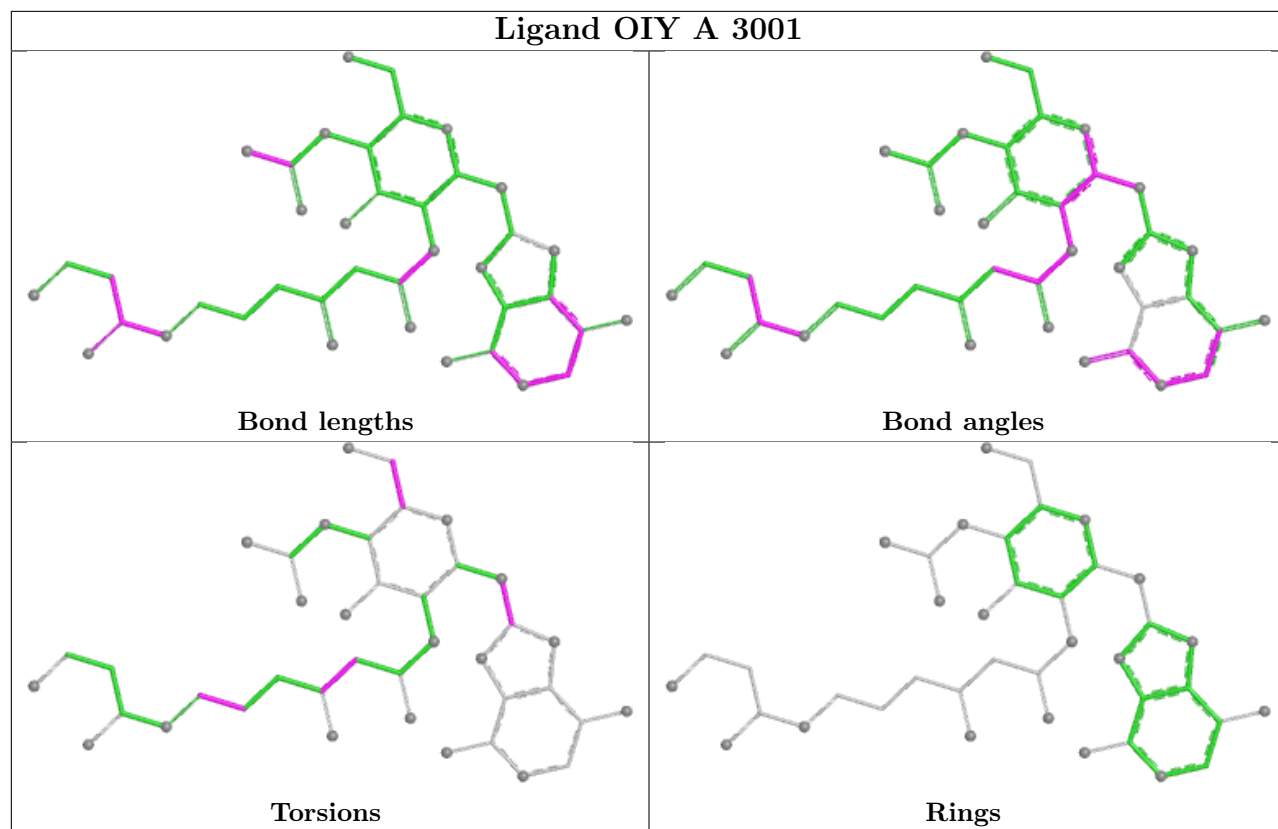
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

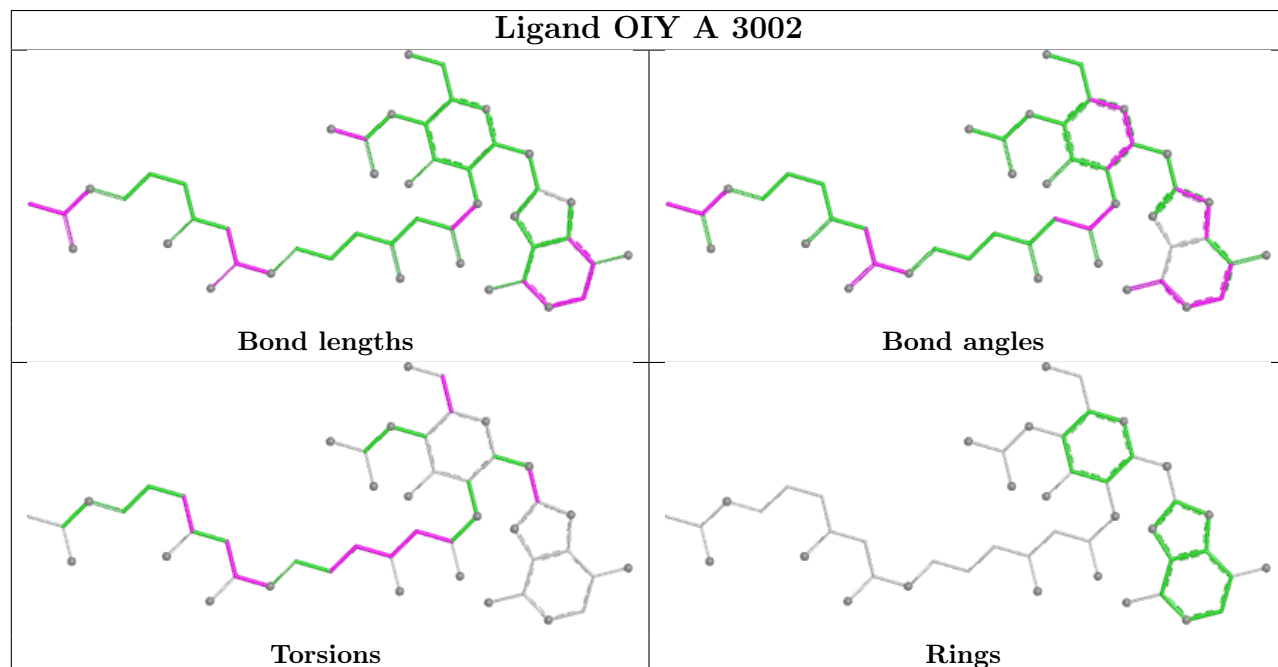
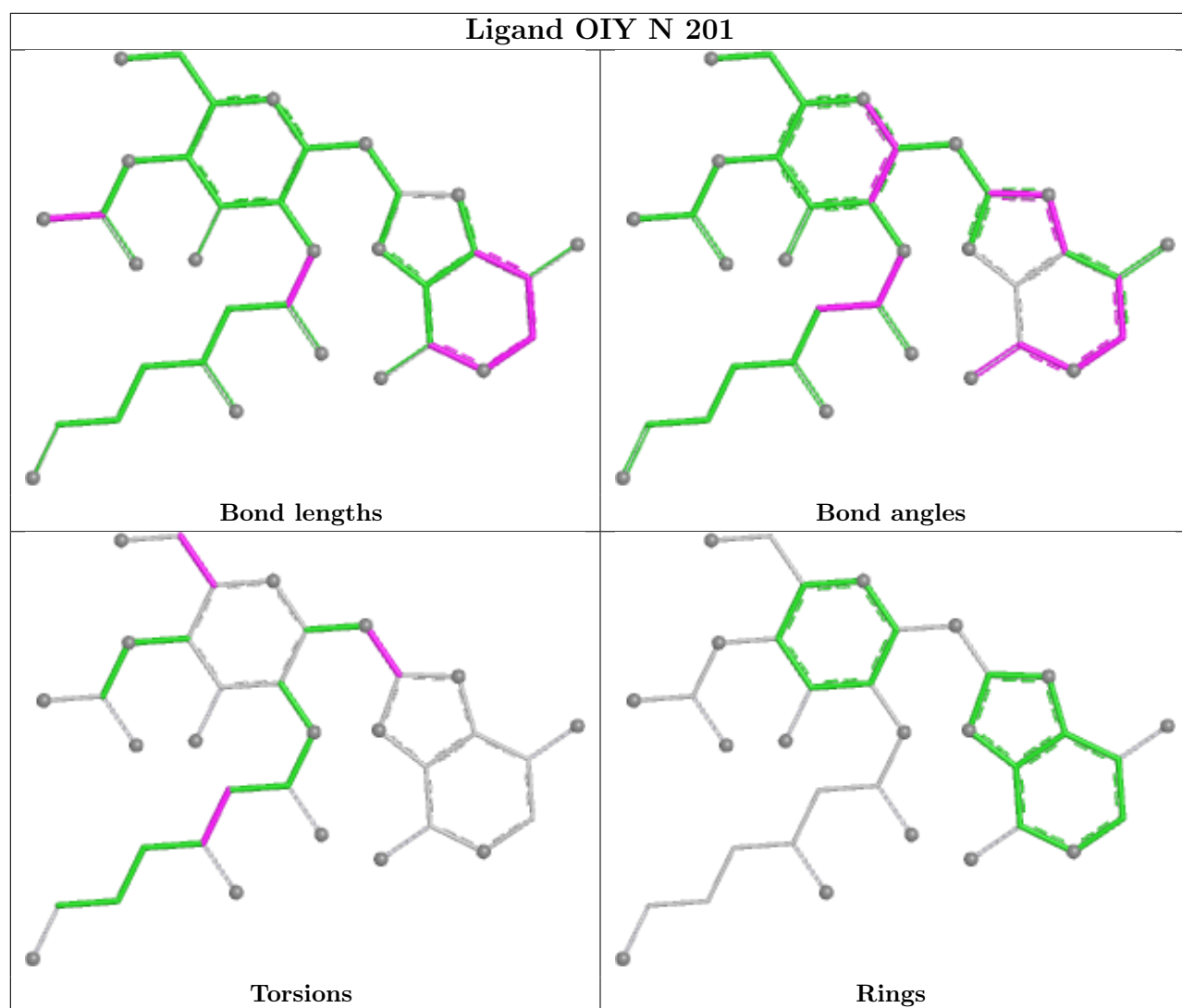


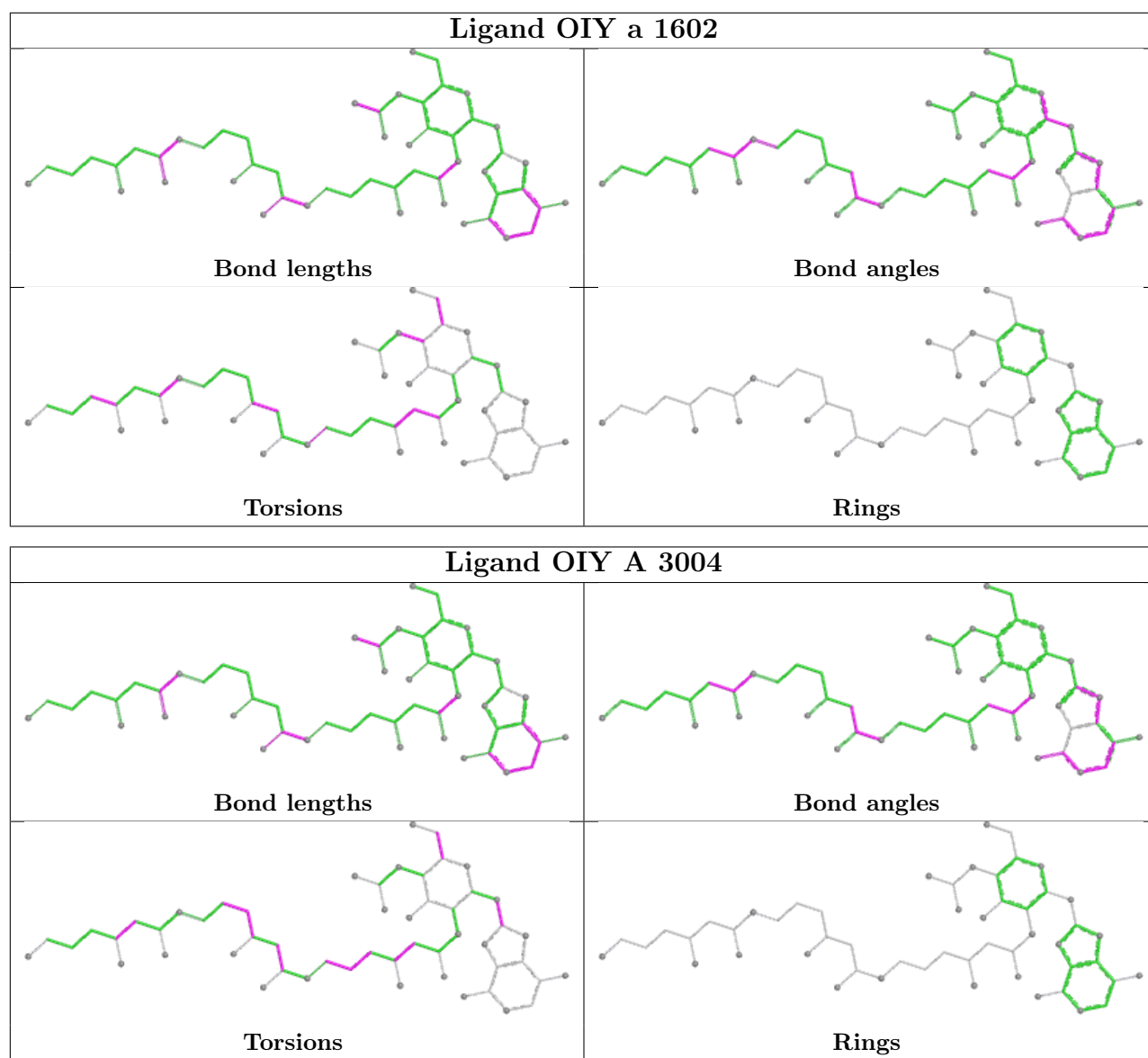




Ligand OIY A 3006	
 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand OIY A 3003	
 Bond lengths	 Bond angles
 Torsions	 Rings







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.

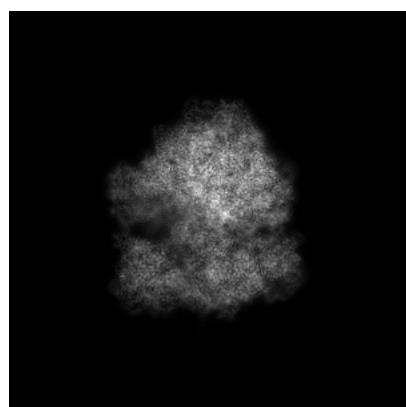
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26820. These allow visual inspection of the internal detail of the map and identification of artifacts.

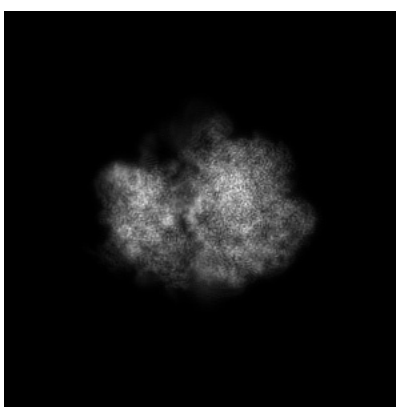
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

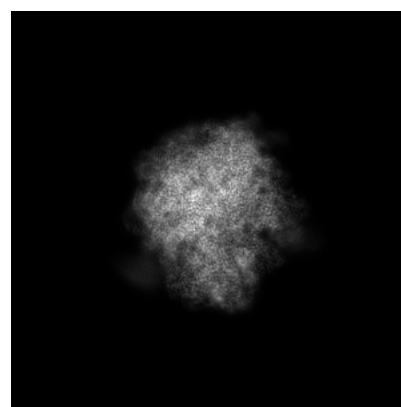
6.1.1 Primary map



X



Y

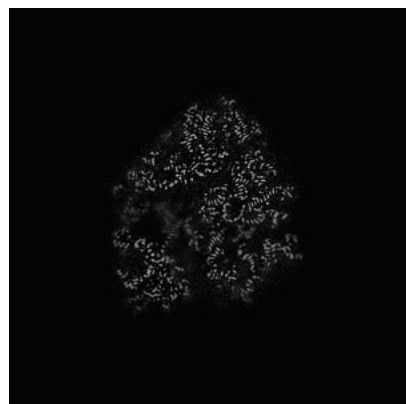


Z

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

6.2 Central slices [i](#)

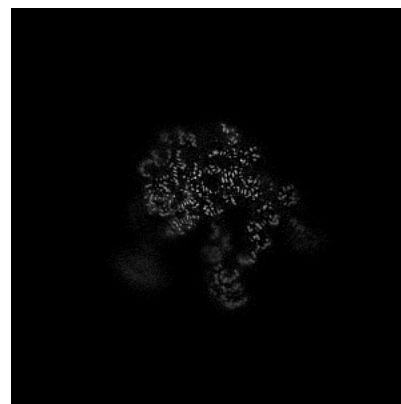
6.2.1 Primary map



X Index: 320



Y Index: 320

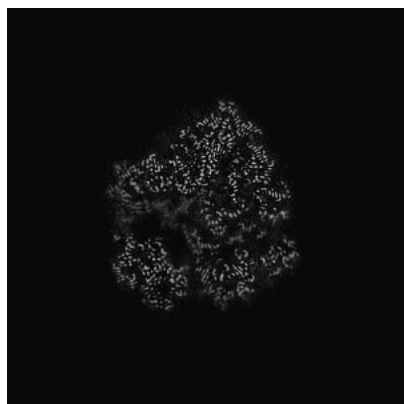


Z Index: 320

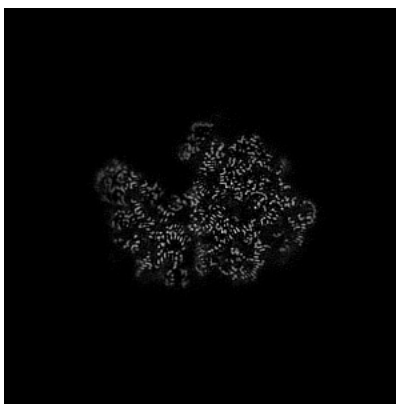
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

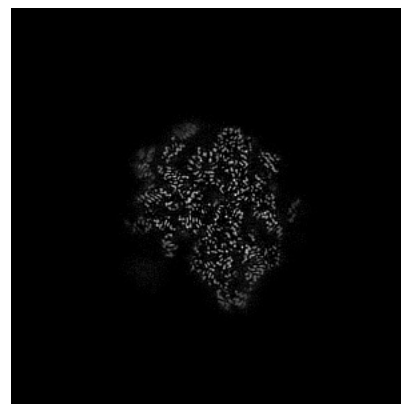
6.3.1 Primary map



X Index: 329



Y Index: 341

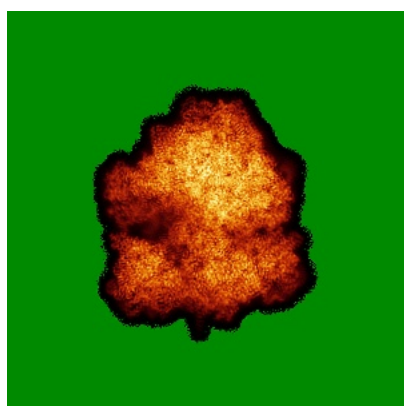


Z Index: 364

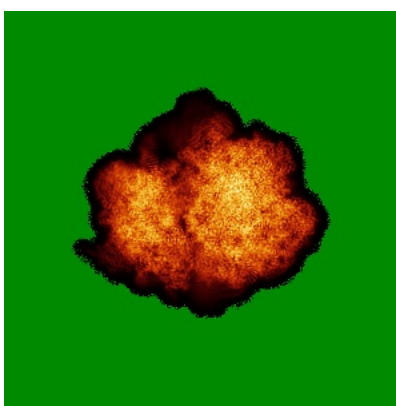
The images above show the largest variance slices of the map in three orthogonal directions.

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

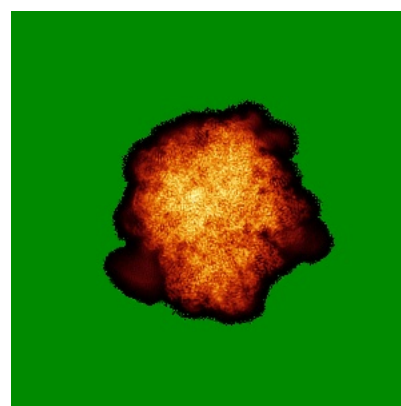
6.4.1 Primary map



X



Y

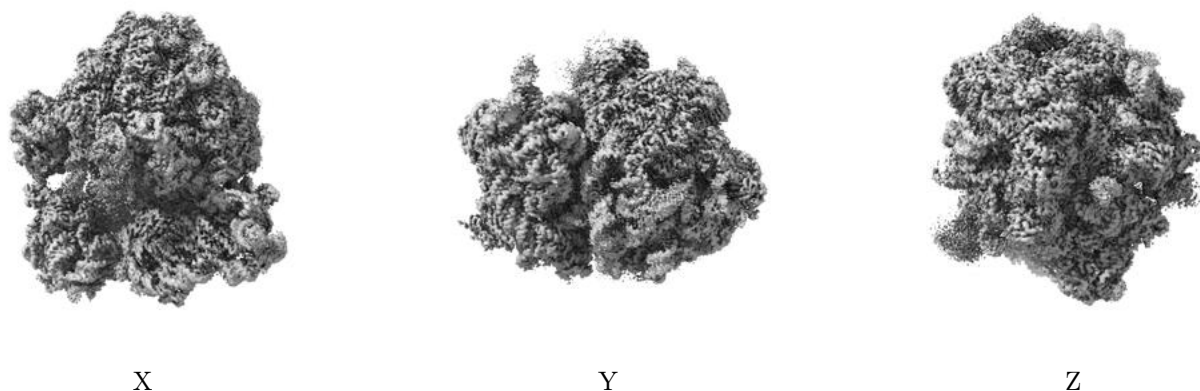


Z

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 0.08. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

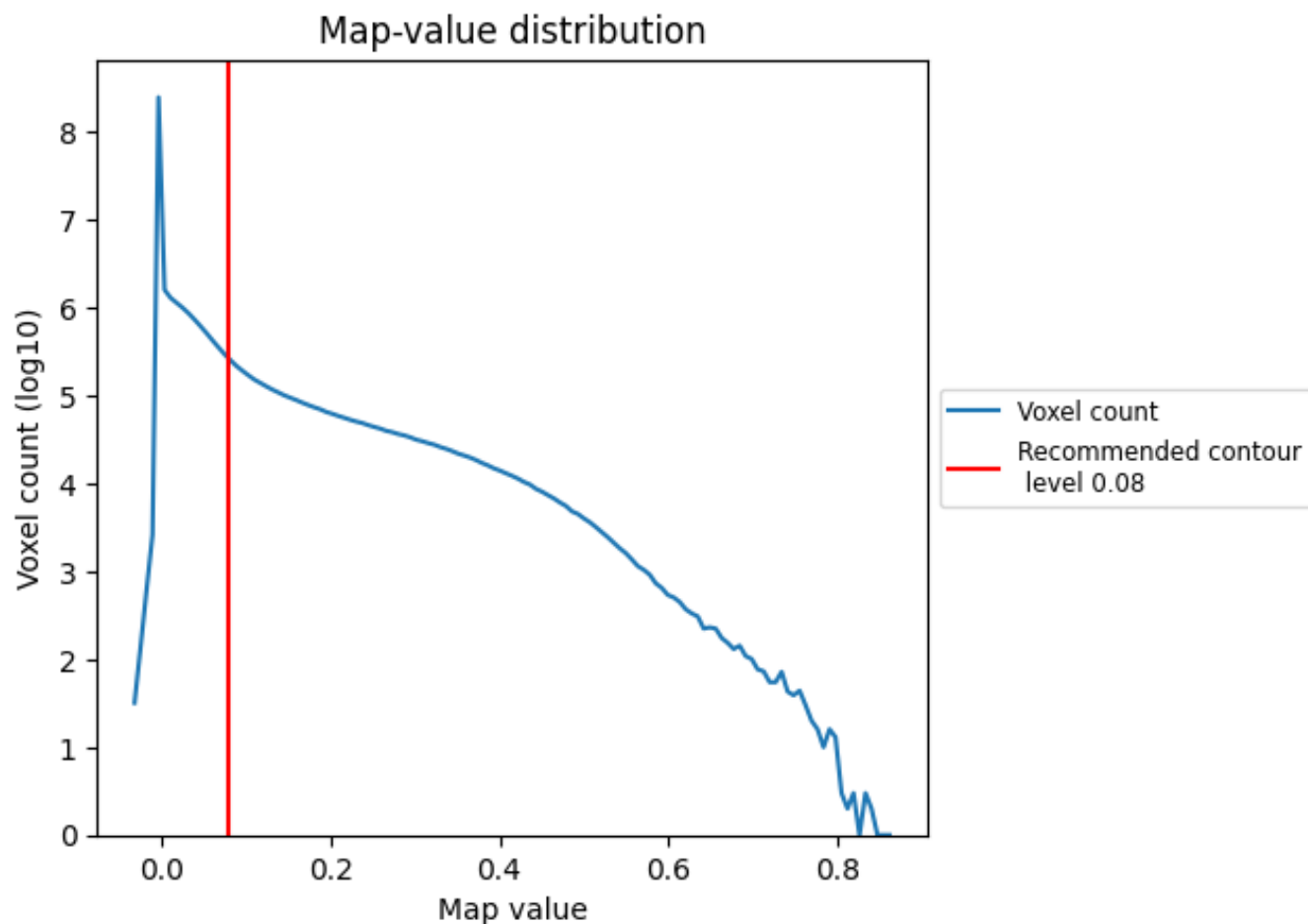
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

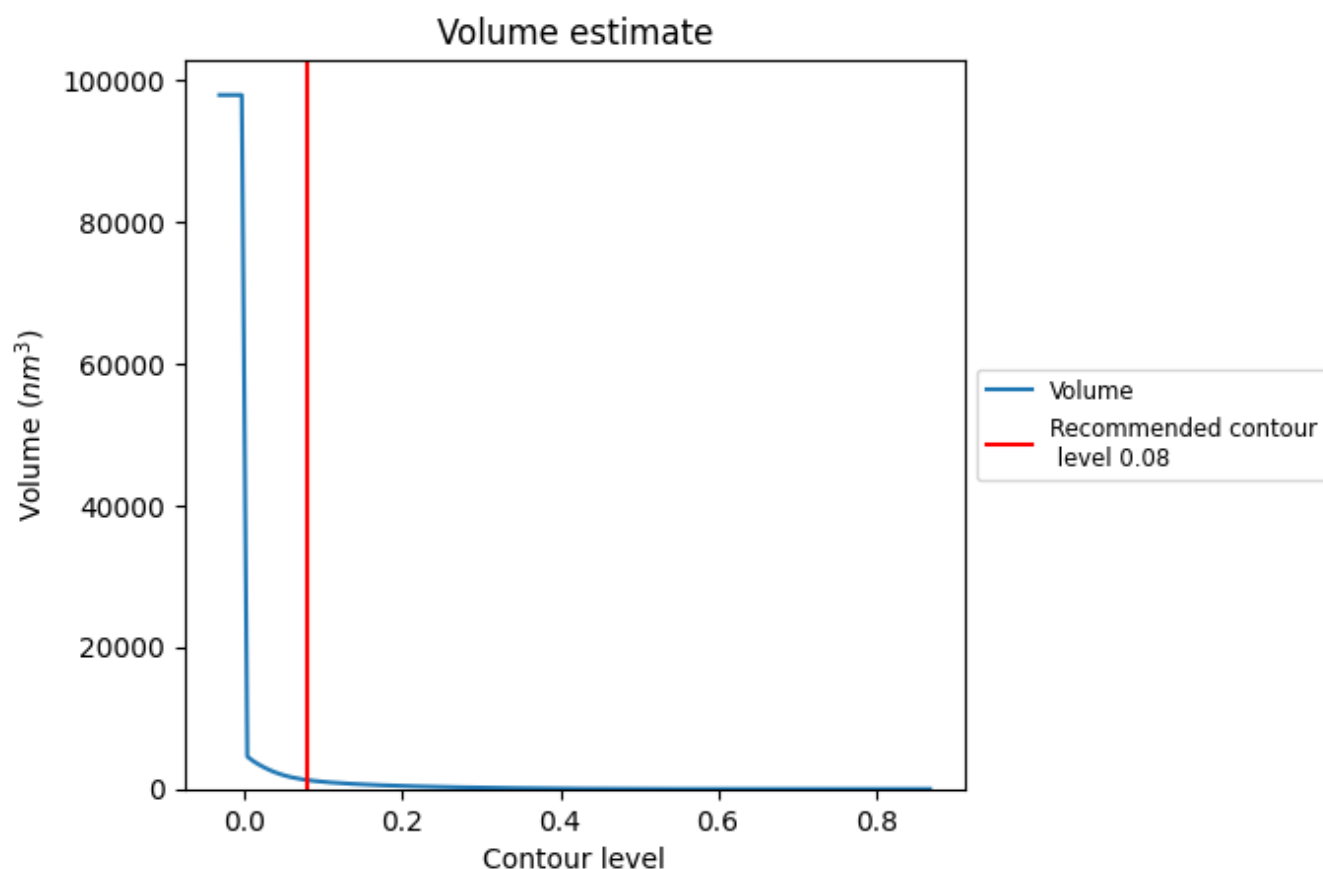
This section contains the results of statistical analysis of the map.

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.

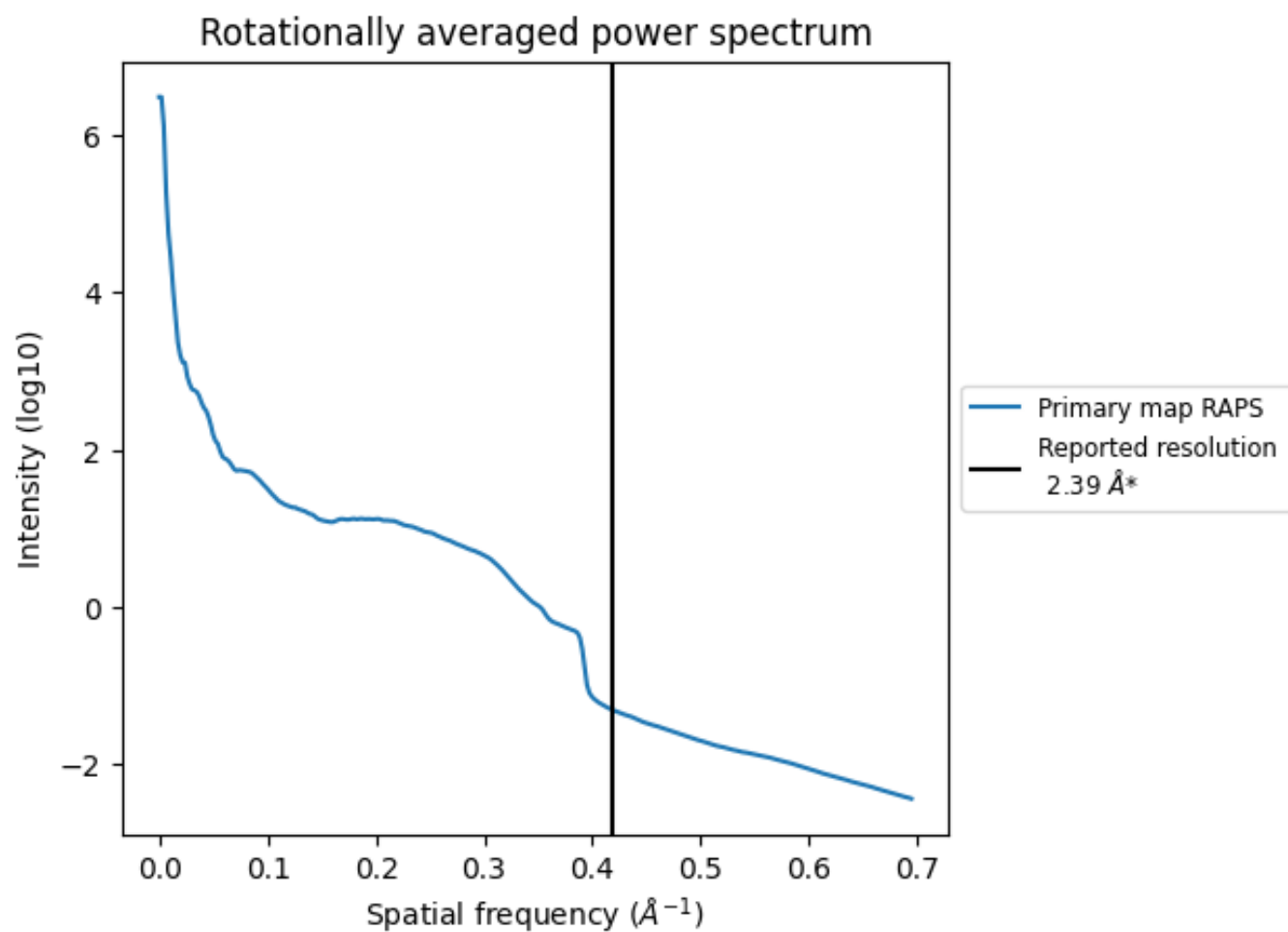
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1240 nm^3 ; this corresponds to an approximate mass of 1120 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 0.418 Å⁻¹

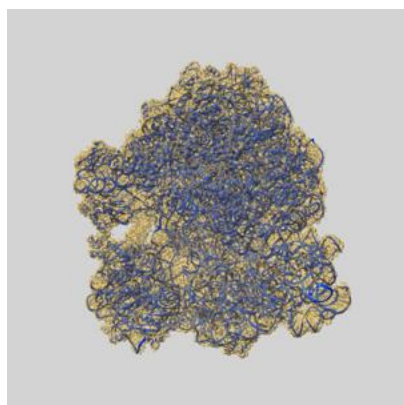
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

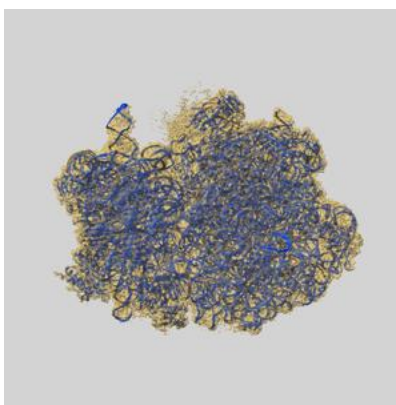
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-26820 and PDB model 7UVY. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

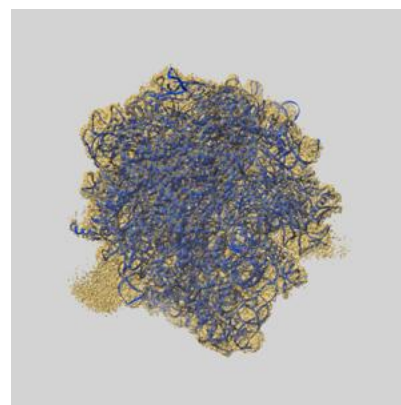
9.1 Map-model overlay [i](#)



X



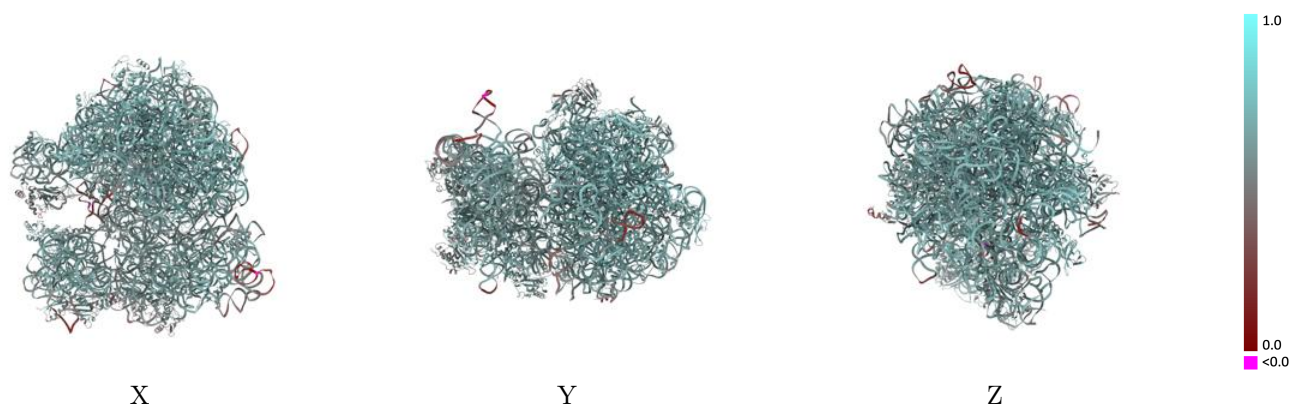
Y



Z

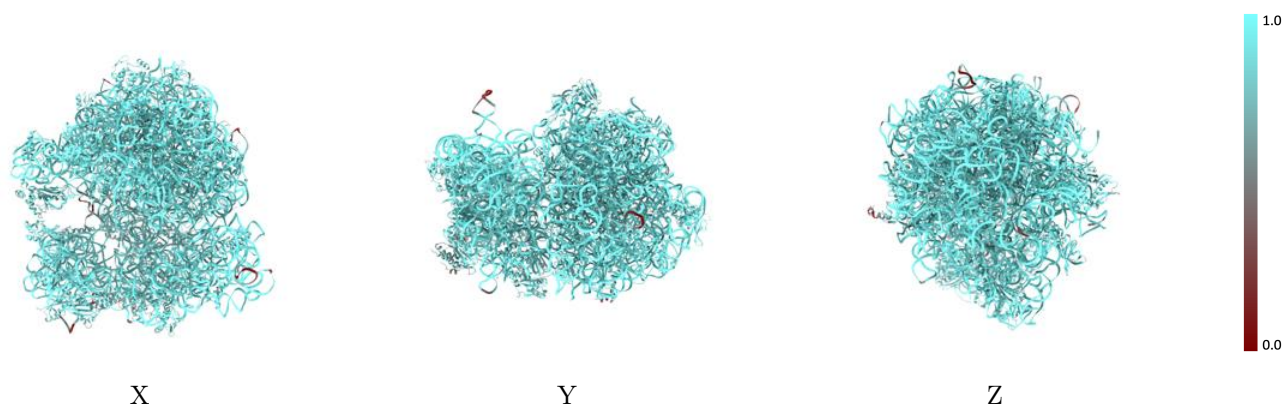
The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



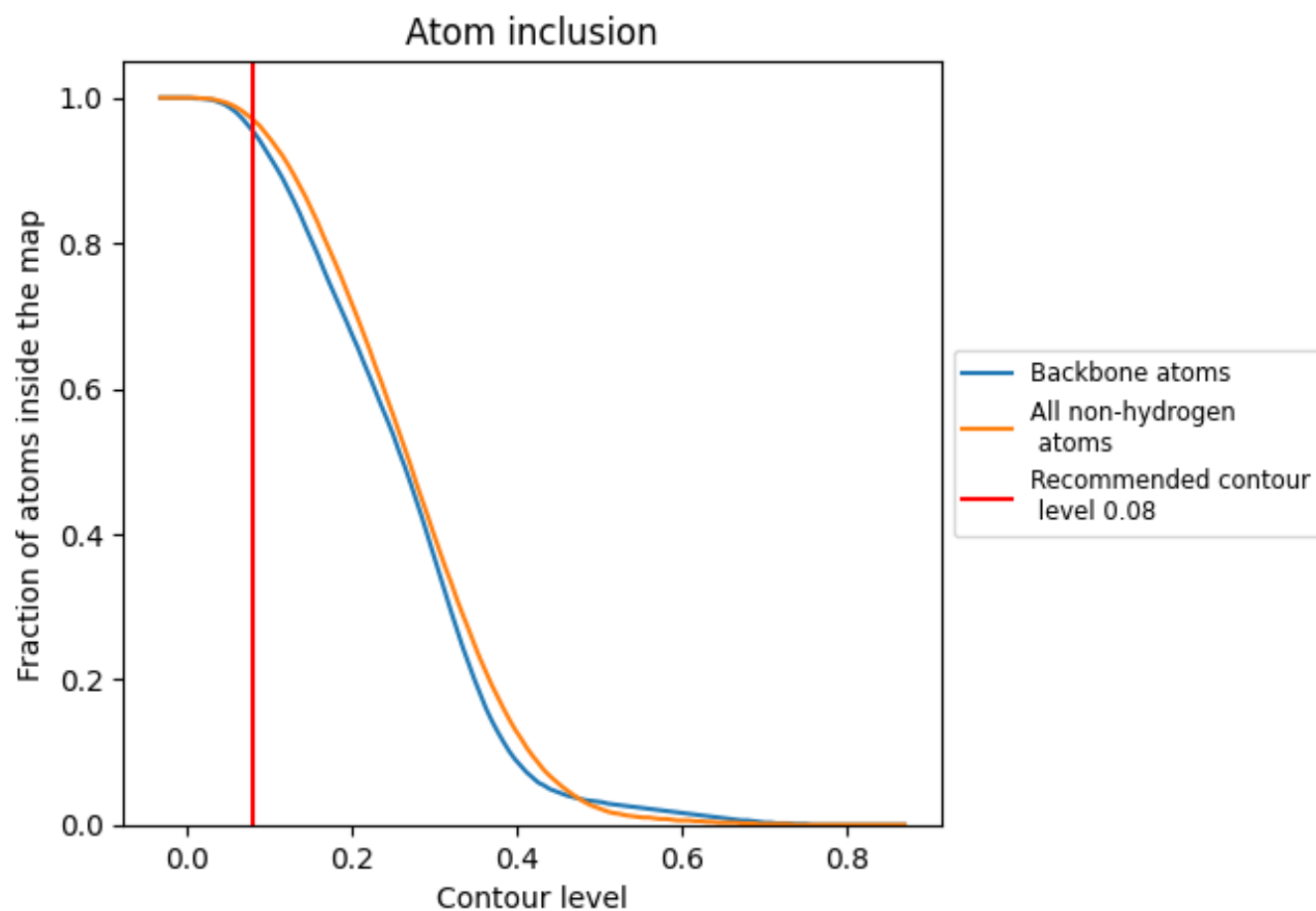
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.08).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 97% 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 (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9700	 0.6220
0	 0.9260	 0.6420
1	 0.9880	 0.6980
2	 0.9960	 0.6850
3	 0.9830	 0.6550
A	 0.9900	 0.6450
B	 0.9960	 0.5940
C	 0.9850	 0.6670
D	 0.9820	 0.6790
E	 0.9740	 0.6600
F	 0.8410	 0.4750
G	 0.9170	 0.5690
H	 0.7110	 0.4750
I	 0.9860	 0.6760
J	 0.9770	 0.6620
K	 0.9830	 0.6710
L	 0.9730	 0.6600
M	 0.9950	 0.6880
N	 0.9610	 0.6060
O	 0.9770	 0.6530
P	 0.9970	 0.6900
Q	 0.9750	 0.6670
R	 0.9830	 0.6770
S	 0.9570	 0.6430
T	 0.9340	 0.6100
U	 0.9520	 0.6390
V	 0.9890	 0.6800
W	 0.9640	 0.6650
X	 0.9330	 0.5970
Y	 0.9710	 0.6680
Z	 0.9740	 0.6690
a	 0.9820	 0.6000
b	 0.6790	 0.4810
c	 0.9460	 0.6130
d	 0.9040	 0.5220



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Chain	Atom inclusion	Q-score
e	 0.9790	 0.6290
f	 0.9220	 0.5780
g	 0.8590	 0.5340
h	 0.9770	 0.6360
i	 0.9720	 0.6300
j	 0.9190	 0.6030
k	 0.9360	 0.5770
l	 0.9230	 0.6050
m	 0.9610	 0.6190
n	 0.9580	 0.6280
o	 0.9770	 0.6320
p	 0.9730	 0.6220
q	 0.9640	 0.6020
r	 0.9660	 0.6090
s	 0.9780	 0.6340
t	 0.9800	 0.6130
u	 0.6910	 0.5320
v	 0.8140	 0.4220
w	 0.9850	 0.6120