



Full wwPDB EM Validation Report ⓘ

Jul 1, 2025 – 05:53 pm BST

PDB ID : 9GXX / pdb_00009gxx
EMDB ID : EMD-51679
Title : 70S ribosome with doublet-decoding tRNA^{Ser3} bound to A-site GCA codon
Authors : Krishnaswamy, S.; Larsson, D.S.D.; Selmer, M.
Deposited on : 2024-10-01
Resolution : 2.61 Å (reported)
Based on initial models : 8CGJ, 8CF1, 8CGK, 7K00

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.dev118
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0rc1
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) : 2.44

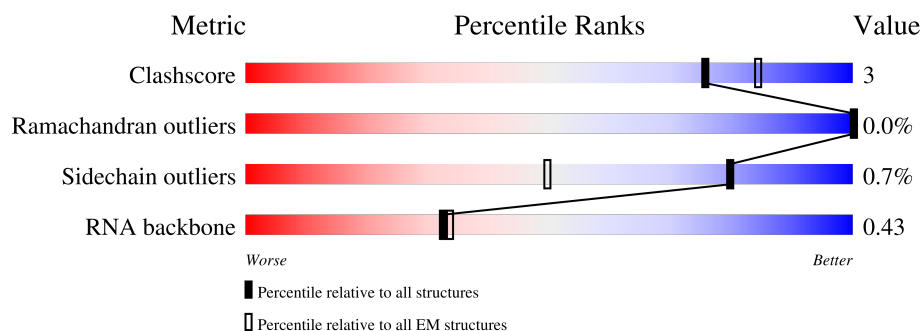
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.61 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.



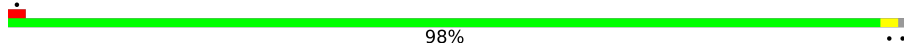
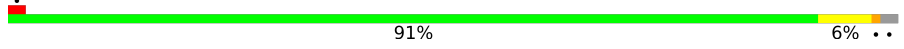


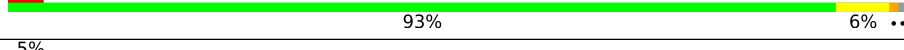
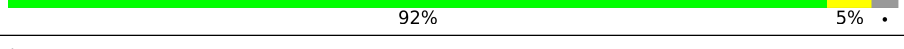
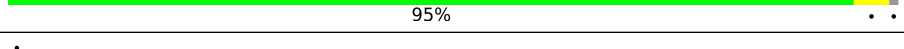
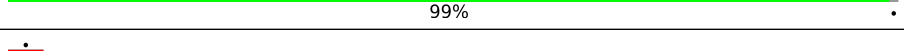
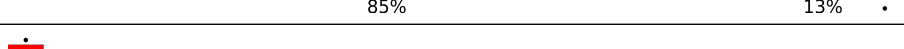
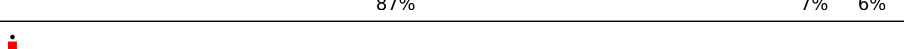
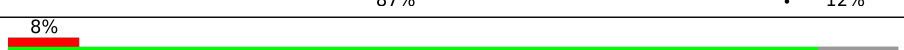
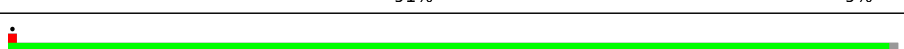
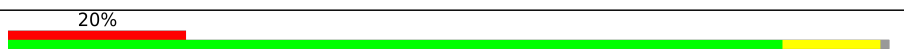
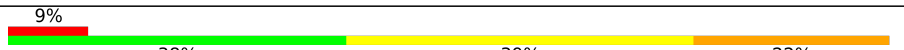
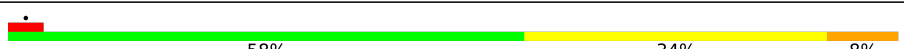

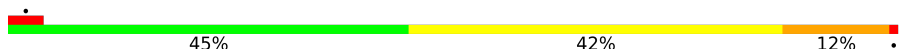


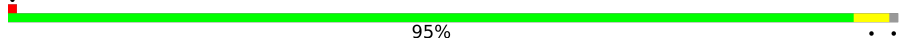
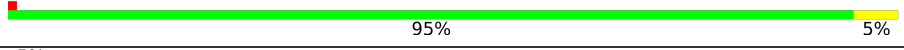
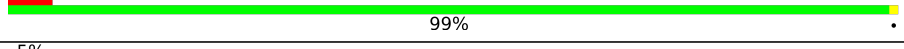

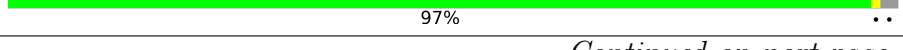

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	A	1542	
2	B	241	
3	C	233	
4	D	206	
5	E	167	
6	F	135	
7	G	179	


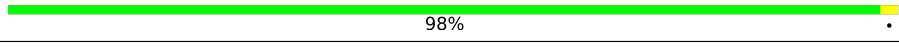
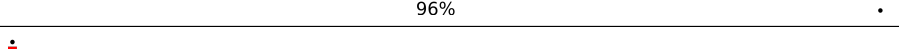
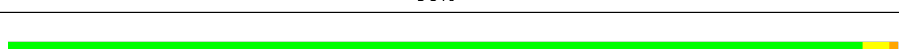
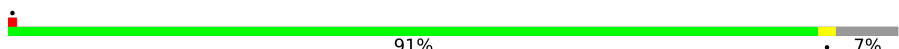

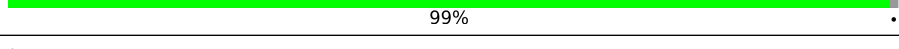
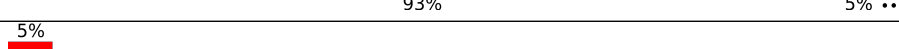
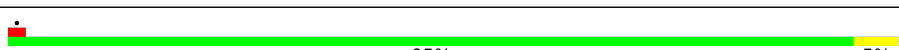

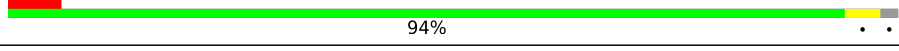
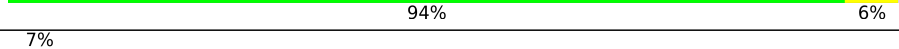
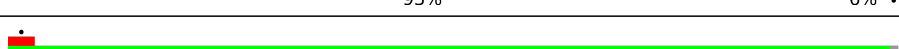
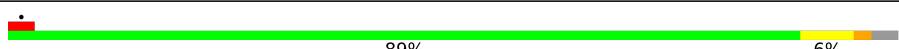
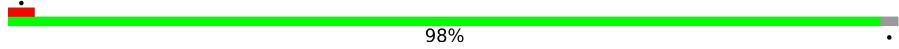
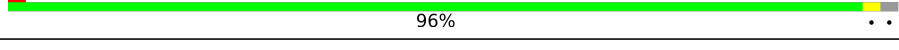
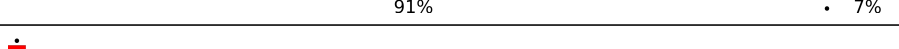







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Mol	Chain	Length	Quality of chain
8	H	130	
9	I	130	
10	J	103	
11	K	129	
12	L	124	
13	M	118	
14	N	101	
15	O	89	
16	P	82	
17	Q	84	
18	R	75	
19	S	92	
20	T	87	
21	U	71	
22	V	76	
22	Z	76	
23	X	24	
24	Y	93	
25	a	2904	
26	b	120	
27	c	273	
28	d	209	
29	e	201	
30	f	179	
31	g	177	

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Mol	Chain	Length	Quality of chain
32	h	149	
33	i	142	
34	j	123	
35	k	144	
36	l	136	
37	m	127	
38	n	117	
39	o	115	
40	p	118	
41	q	103	
42	r	110	
43	s	100	
44	t	104	
45	u	94	
46	v	85	
47	w	78	
48	x	63	
49	y	59	
50	z	57	
51	0	55	
52	1	46	
53	2	65	
54	3	38	
55	4	70	

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 144033 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1520	Total	C	N	O	P	0	0
			32634	14562	5991	10561	1520		

- Molecule 2 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	224	Total	C	N	O	S	0	0
			1753	1109	315	321	8		

- Molecule 3 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 4 is a protein called Small ribosomal subunit protein uS4.

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

- Molecule 5 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 6 is a protein called Small ribosomal subunit protein bS6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	103	Total	C	N	O	S	0	0
			839	530	151	151	7		

- Molecule 7 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	153	Total	C	N	O	S	0	0
			1203	750	231	218	4		

- Molecule 8 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 9 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 10 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 11 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	117	Total	C	N	O	S	0	0
			877	540	173	161	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	119	IAS	ASN	conflict	UNP P0A7R9

- Molecule 12 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 13 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	115	Total	C	N	O	S	0	0
			891	552	179	157	3		

- Molecule 14 is a protein called Small ribosomal subunit protein uS14.

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

- Molecule 15 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 16 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	81	Total	C	N	O	S	0	0
			643	403	127	112	1		

- Molecule 17 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	79	Total	C	N	O	S	0	0
			641	406	120	112	3		

- Molecule 18 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	66	Total	C	N	O	S	0	0
			544	345	102	96	1		

- Molecule 19 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	84	Total	C	N	O	S	0	0
			668	427	127	112	2		

- Molecule 20 is a protein called Small ribosomal subunit protein bS20.

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

- Molecule 21 is a protein called Small ribosomal subunit protein bS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 22 is a RNA chain called tRNA(fMet).

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	76	Total	C	N	O	P	0	0
			1623	723	294	530	76		
22	Z	76	Total	C	N	O	P	0	0
			1623	723	294	530	76		

- Molecule 23 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	11	Total	C	N	O	P	0	0
			240	108	50	71	11		

- Molecule 24 is a RNA chain called tRNA(Ser3).

Mol	Chain	Residues	Atoms					AltConf	Trace	
24	Y	93	Total	C	N	O	P	S	0	0
			2000	893	365	648	92	2		

- Molecule 25 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	a	2753	Total	C	N	O	P	2	0
			59172	26403	10905	19109	2755		

- Molecule 26 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	b	119	Total	C	N	O	P	0	0
			2549	1135	466	829	119		

- Molecule 27 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	c	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 28 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	d	209	Total	C	N	O	S	0	0
			1566	980	288	294	4		

- Molecule 29 is a protein called Large ribosomal subunit protein uL4.

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

- Molecule 30 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	f	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 31 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	g	173	Total	C	N	O	S	0	0
			1295	814	237	242	2		

- Molecule 32 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	h	41	Total	C	N	O	S	0	0
			303	194	54	54	1		

- Molecule 33 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 34 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	j	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 35 is a protein called Large ribosomal subunit protein uL15.

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

- Molecule 36 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	l	136	Total	C	N	O	S	0	0
			1075	686	205	177	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
l	82	MS6	MET	conflict	UNP P0ADY7

- Molecule 37 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	m	118	Total	C	N	O	S	0	0
			945	585	194	161	5		

- Molecule 38 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	n	116	Total	C	N	O		0	0
			892	552	178	162			

- Molecule 39 is a protein called Large ribosomal subunit protein bL19.

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

- Molecule 40 is a protein called Large ribosomal subunit protein bL20.

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

- Molecule 41 is a protein called Large ribosomal subunit protein bL21.

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

- Molecule 42 is a protein called Large ribosomal subunit protein uL22.

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

- Molecule 43 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 44 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	t	102	Total	C	N	O	0	0
			779	492	146	141		

- Molecule 45 is a protein called Large ribosomal subunit protein bL25.

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

- Molecule 46 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	v	84	Total	C	N	O	S	0	0
			628	388	126	113	1		

- Molecule 47 is a protein called Large ribosomal subunit protein bL28.

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

- Molecule 48 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	x	61	Total	C	N	O	S	0	0
			495	305	97	92	1		

- Molecule 49 is a protein called Large ribosomal subunit protein uL30.

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

- Molecule 50 is a protein called Large ribosomal subunit protein bL32.

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

- Molecule 51 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	0	51	Total	C	N	O	0	0
			417	269	76	72		

- Molecule 52 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	1	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 53 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	2	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 54 is a protein called Large ribosomal subunit protein bL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	3	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

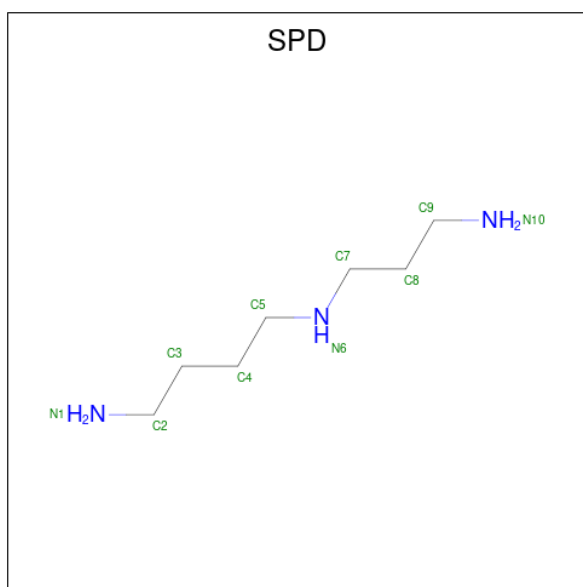
- Molecule 55 is a protein called Large ribosomal subunit protein bL31A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	4	60	Total	C	N	O	S	0	0
			480	299	90	85	6		

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

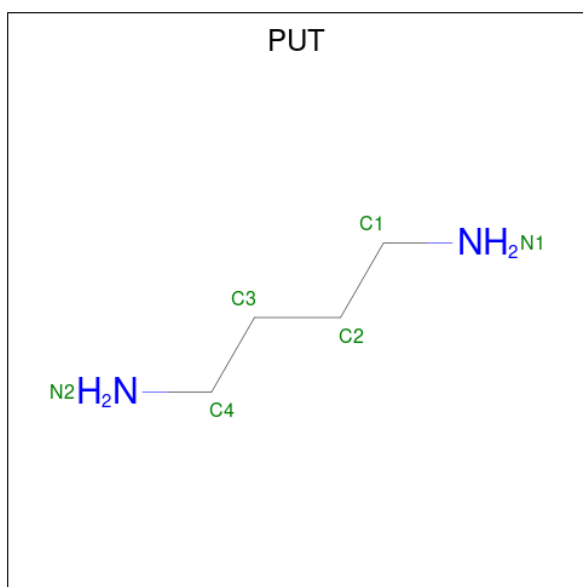
Mol	Chain	Residues	Atoms		AltConf
56	A	87	Total	Mg	0
			87	87	
56	Y	4	Total	Mg	0
			4	4	
56	a	187	Total	Mg	0
			187	187	
56	b	5	Total	Mg	0
			5	5	
56	c	1	Total	Mg	0
			1	1	
56	d	2	Total	Mg	0
			2	2	
56	m	1	Total	Mg	0
			1	1	
56	z	1	Total	Mg	0
			1	1	

- Molecule 57 is SPERMIDINE (CCD ID: SPD) (formula: C₇H₁₉N₃).



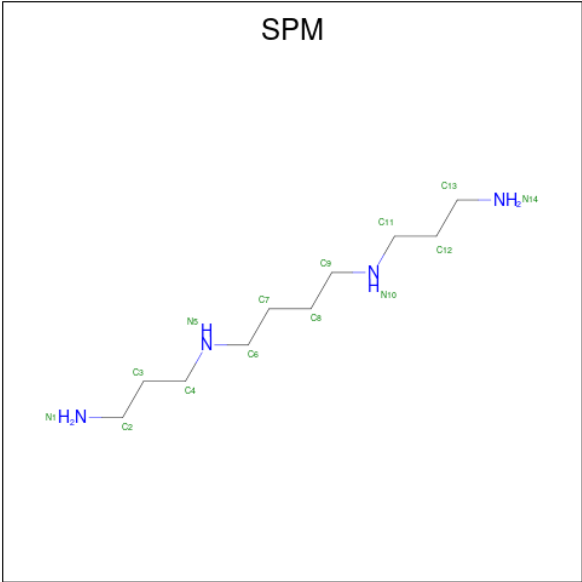
Mol	Chain	Residues	Atoms			AltConf
57	A	1	Total	C	N	0
			10	7	3	
57	a	1	Total	C	N	0
			10	7	3	
57	a	1	Total	C	N	0
			10	7	3	
57	a	1	Total	C	N	0
			10	7	3	
57	a	1	Total	C	N	0
			10	7	3	
57	a	1	Total	C	N	0
			10	7	3	

- Molecule 58 is 1,4-DIAMINOBTANE (CCD ID: PUT) (formula: C₄H₁₂N₂).



Mol	Chain	Residues	Atoms			AltConf
58	A	1	Total	C	N	0
			6	4	2	
58	a	1	Total	C	N	0
			6	4	2	
58	a	1	Total	C	N	0
			6	4	2	
58	a	1	Total	C	N	0
			6	4	2	
58	a	1	Total	C	N	0
			6	4	2	
58	a	1	Total	C	N	0
			6	4	2	

- Molecule 59 is SPERMINE (CCD ID: SPM) (formula: C₁₀H₂₆N₄).



Mol	Chain	Residues	Atoms			AltConf
59	a	1	Total	C	N	0
			14	10	4	

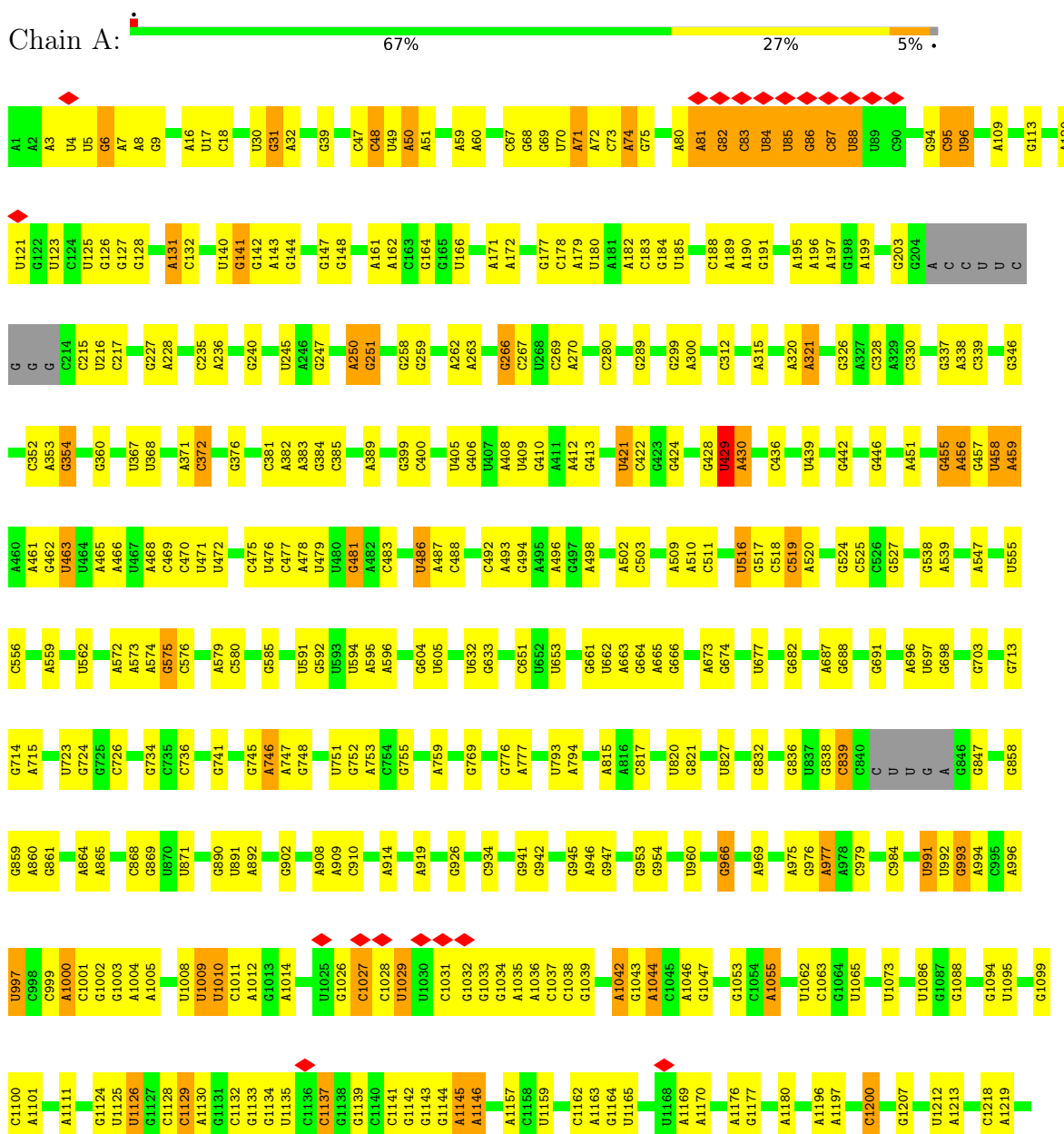
- Molecule 60 is ZINC ION (CCD ID: ZN) (formula: Zn).

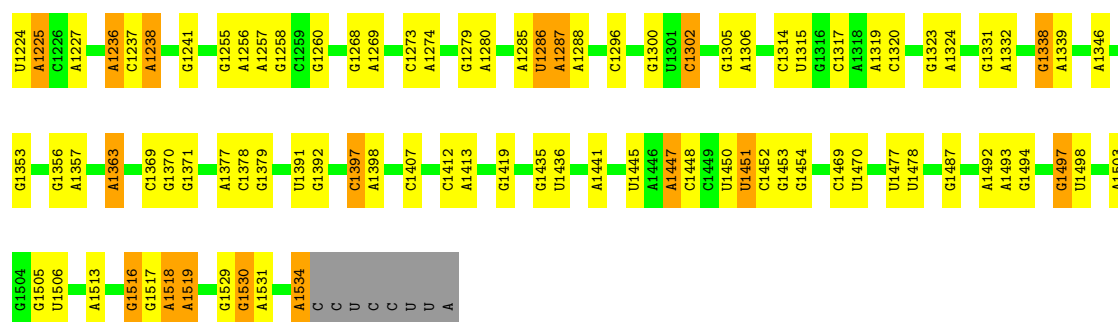
Mol	Chain	Residues	Atoms		AltConf
60	3	1	Total	Zn	0
			1	1	
60	4	1	Total	Zn	0
			1	1	

3 Residue-property plots

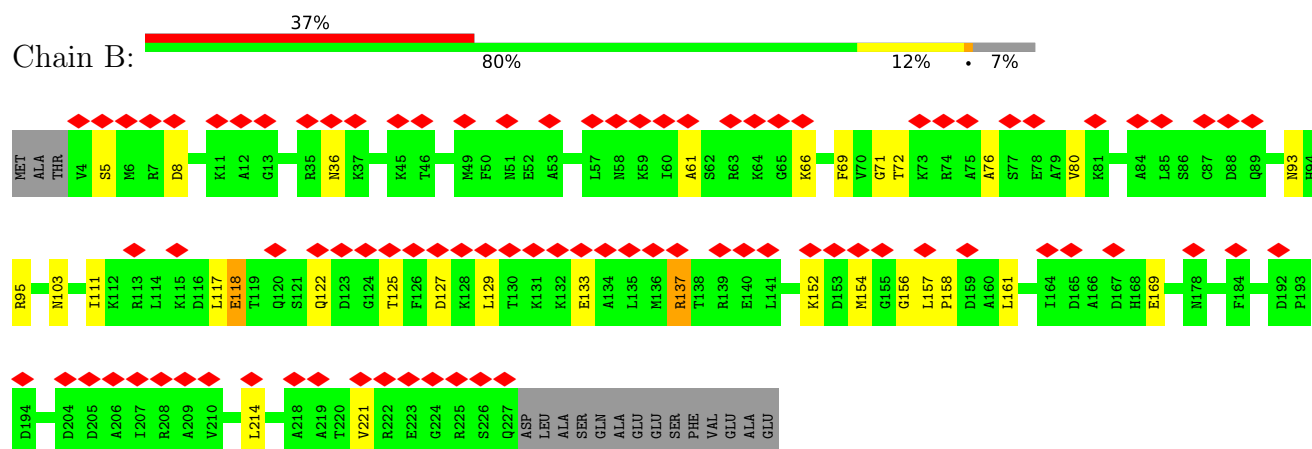
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 16S rRNA

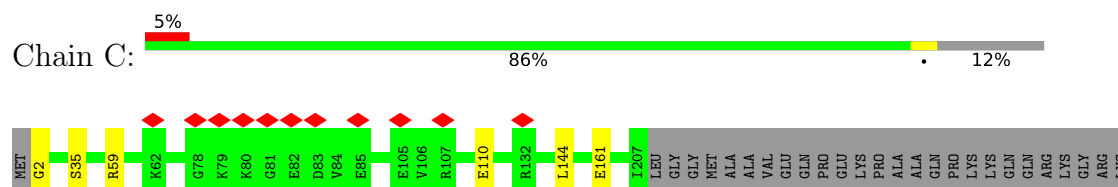




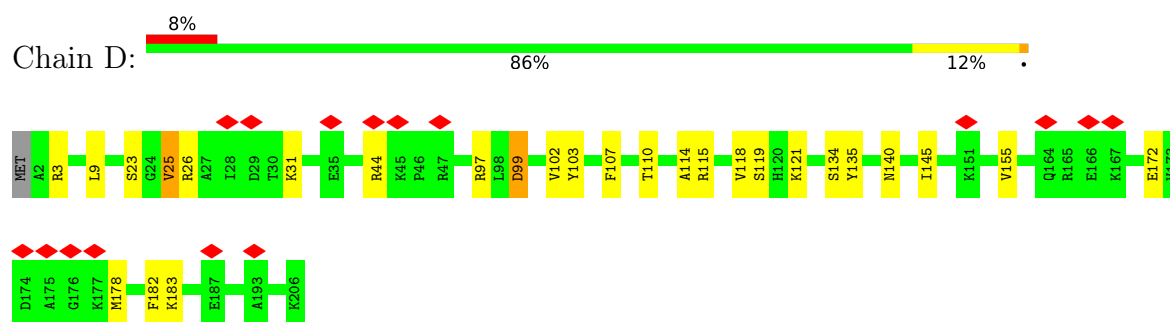
• Molecule 2: Small ribosomal subunit protein uS2



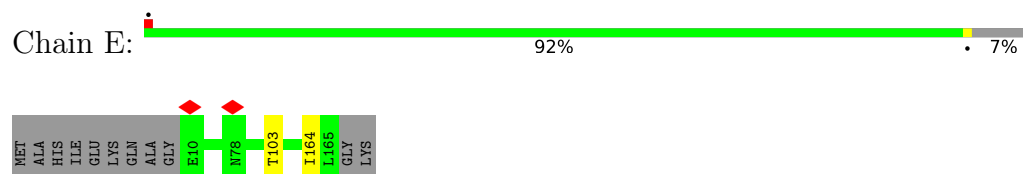
• Molecule 3: Small ribosomal subunit protein uS3



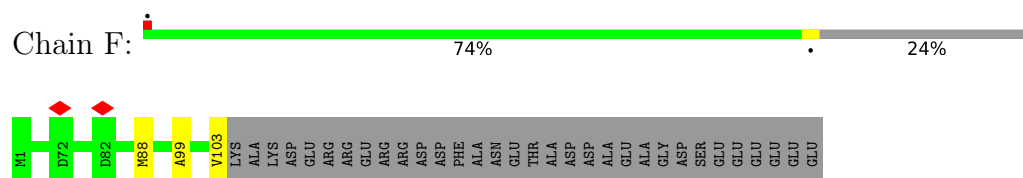
• Molecule 4: Small ribosomal subunit protein uS4



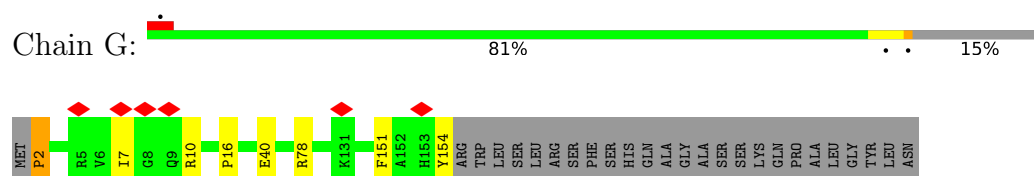
• Molecule 5: Small ribosomal subunit protein uS5



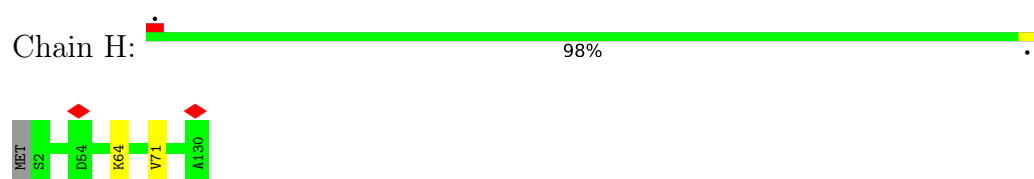
- Molecule 6: Small ribosomal subunit protein bS6, fully modified isoform



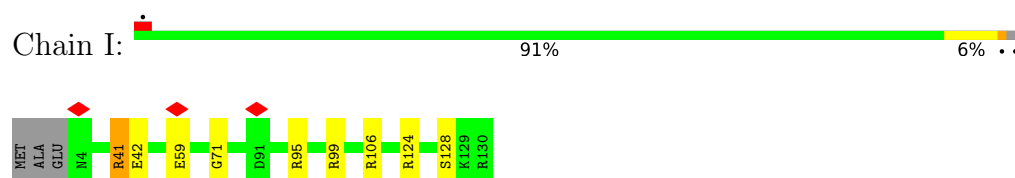
- Molecule 7: Small ribosomal subunit protein uS7



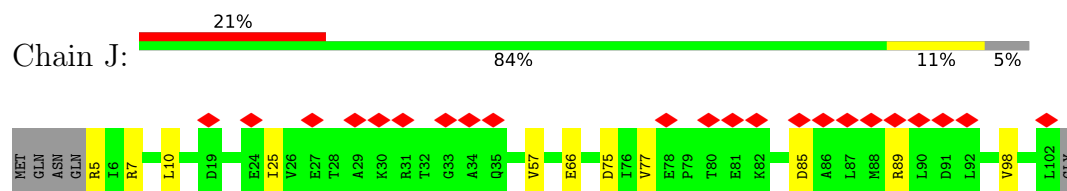
- Molecule 8: Small ribosomal subunit protein uS8



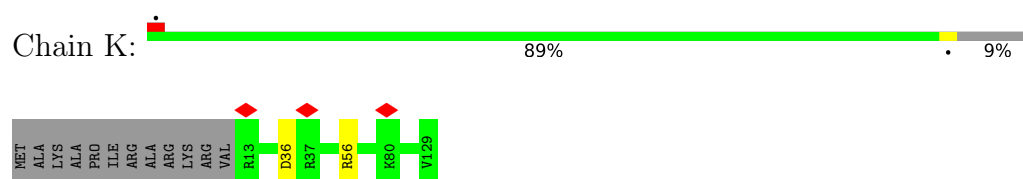
- Molecule 9: Small ribosomal subunit protein uS9



- Molecule 10: Small ribosomal subunit protein uS10

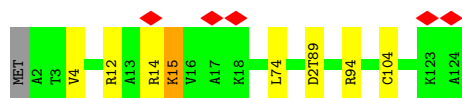


- Molecule 11: Small ribosomal subunit protein uS11

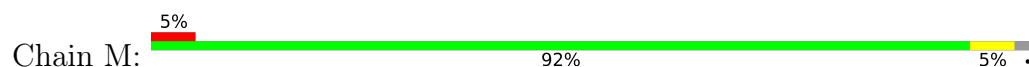


- Molecule 12: Small ribosomal subunit protein uS12

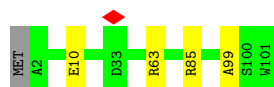




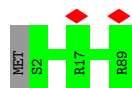
- Molecule 13: Small ribosomal subunit protein uS13



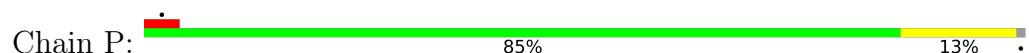
- Molecule 14: Small ribosomal subunit protein uS14



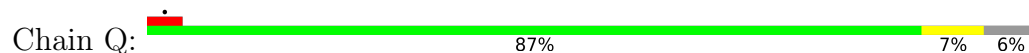
- Molecule 15: Small ribosomal subunit protein uS15



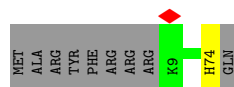
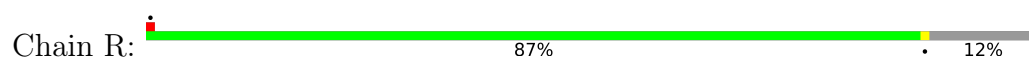
- Molecule 16: Small ribosomal subunit protein bS16



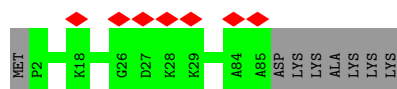
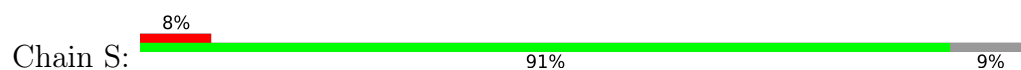
- Molecule 17: Small ribosomal subunit protein uS17



- Molecule 18: Small ribosomal subunit protein bS18



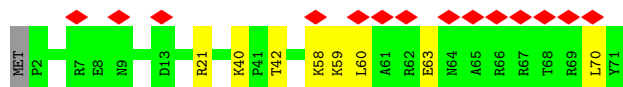
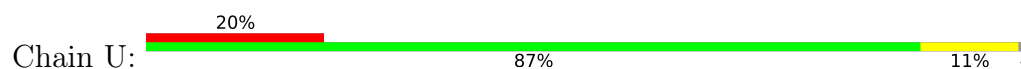
- Molecule 19: Small ribosomal subunit protein uS19



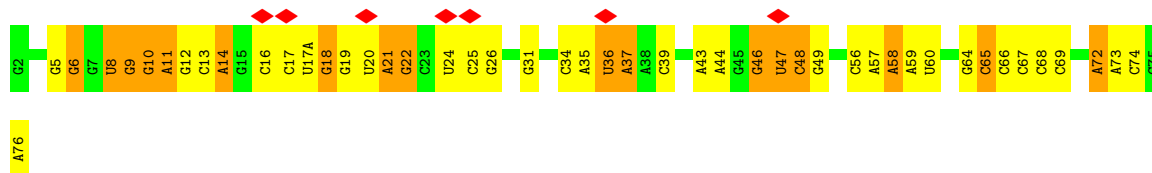
- Molecule 20: Small ribosomal subunit protein bS20



- Molecule 21: Small ribosomal subunit protein bS21



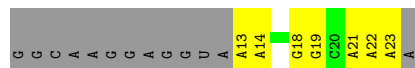
- Molecule 22: tRNA(fMet)



- Molecule 22: tRNA(fMet)

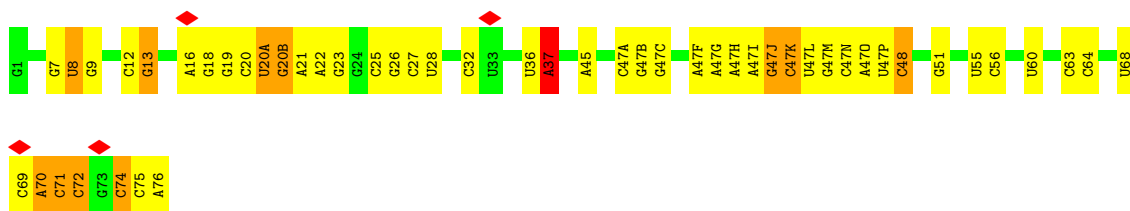


- Molecule 23: mRNA



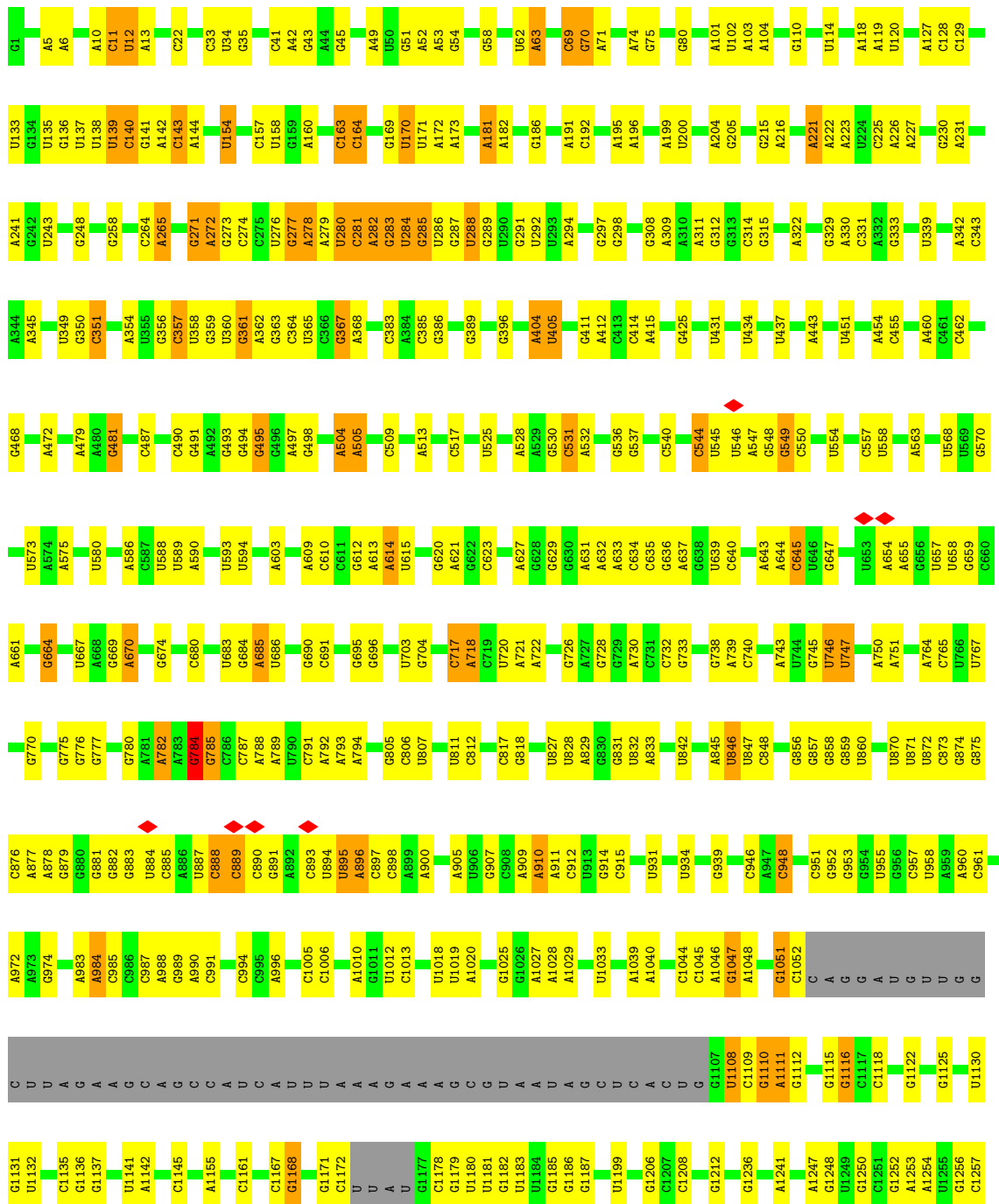
- Molecule 24: tRNA(Ser3)





● Molecule 25: 23S rRNA

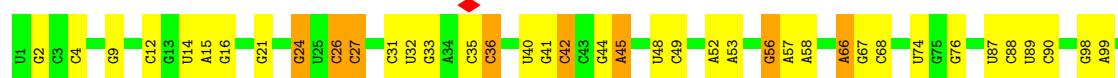
Chain a: 62% 29% 5% 5%



A2657	U2548	U2441	A2322	G2204	G	G2067	U1963	A1847	C1732	A1593	A1495	A1383	A1268
A2660	U2552	G2445	G2323	G2209	U	U2068	G1964	A1848	U1736	A1594	A1496	C1386	A1271
G2663	C2556	G2445	U2324	U2210	G	G1849	G1965	G1850	G	A1597	C1497	A1387	A1273
C2666	A2448	A2448	G2326	A2211	A	C2072	A1966	U1856	G1738	U1602	A1505	U1391	A1274
A2670	U2449	U2449	A2327	U2213	C	A2077	G1968	G1857	A1739	U1506	U1405	U1391	A1275
A2670	A2451	A2451	A2328	U2220	C	C2078	A1970	A1858	G1740	C1607	U1406	U1391	A1275
C2678	C2456	C2456	A2333	C2221	C	U2079	U1971	U1865	A1746	A1608	A1509	U1406	A1286
C2678	U2457	U2457	A2335	C2222	A	A2080	G1972	A1866	U1747	C1611	G1510	G1407	A1287
A2682	C2467	C2467	A2336	A2225	U	U2085	G1973	G1867	G1750	C1612	U1513	U1411	G1288
C2683	C2470	C2470	C2339	G2230	C	C2091	G1980	G1868	G1756	G1613	U1514	U1411	C1289
U2684	G2470	G2470	A2340	G2230	U	U2092	C1985	G1869	A1757	A1618	C1414	C1414	C1300
U2686	U2474	U2474	G2341	G2239	G	G2093	U1991	A1871	U1758	G1619	U1415	U1415	A1301
U2687	C2475	C2475	G2342	G2239	A	A2094	G1992	A1872	A1759	C1417	C1417	C1417	A1301
U2689	A2476	A2476	G2345	U2243	U	U2095	G1993	G1873	C1760	A1626	A1528	A1418	A1304
U2690	G2481	G2481	C2347	U2244	G	A2097	U1994	A1874	C1764	A1634	G1529	A1419	C1305
C2714	C2488	C2488	C2350	G2251	A	U2098	U1995	G1875	U1765	A1637	U1534	A1420	C1306
C2715	G2488	G2488	G2361	G2255	G	U	C1996	A1877	U1769	A1637	A1535	A1427	U1312
C2716	U2491	U2491	A2369	G2258	C	G	G2002	C1878	G1770	A1637	C1536	C1428	C1315
C2717	U2492	U2492	C2369	C2258	C	A	C2006	U1880	A1773	U1647	A1434	A1434	C1320
U2724	U2493	U2493	U2325	U2259	C	C	A2014	C1879	G1776	U1648	C1435	C1435	A1321
A2725	G2494	G2494	A2381	A2268	U	U	A2015	U1881	C1776	G1649	G1436	G1436	A1322
A2726	G2495	G2495	G2382	A2268	U	U	G1906	G1884	U1782	A1651	U1542	A1438	C1323
U2609	C2496	C2496	G2383	A2268	G	U	G1906	G1884	U1782	A1651	G1543	A1439	G1324
C2610	A2497	A2497	U2384	A2273	A	A	A2020	U1911	A1786	G1667	A1548	G1449	A1327
C2611	G2502	G2502	C2385	A2274	A	U	C2021	A1912	A1787	U1667	A1549	G1450	A1328
C2612	U2503	U2503	G2389	A2278	G	G	U2022	A1913	C1788	U1667	G1451	U1329	U1329
U2613	U2504	U2504	U2390	G2279	A	U	C2023	C1914	U1796	G1674	G1554	G1452	C1330
U2615	G2505	G2505	G2391	G2280	U	U	A2030	3TD1915	U1796	U1693	C1555	A1453	G1331
G2618	U2511	U2511	C2394	A2281	C	G	A2031	A1916	G1799	U1694	C1557	U1458	G1332
C2618	A2513	A2513	C2395	G2282	C	U	G2032	U1917	C1800	C1694	C1558	G1459	G1333
C2618	G2514	G2514	G2396	C2283	A	G	U2034	C1920	A1801	A1700	U1559	U1460	G1334
C2621	C2515	C2515	A2287	A2287	C	U	C2035	U1923	A1802	A1701	G1560	G1341	G1341
G2625	C2515	C2515	A2288	A2288	U	A	G2037	U1923	A1803	U1709	A1566	G1473	A1342
C2626	U2401	U2401	G2289	G2289	U	G	A2037	A1927	G1807	U1709	G1567	U1474	G1343
U2629	C2403	C2403	G2290	G2290	U	U	U2039	A1928	A1808	G1715	G1568	G1475	G1343
U2629	A2406	A2406	U2291	U2292	A	G	U2039	G1929	A1809	U1715	A1570	U1476	C1345
U2629	G2409	G2409	U2292	U2292	G	U	C2043	G1930	A1809	G1718	A1571	A1477	U1352
A2632	G2409	G2409	U2296	U2296	U	G	U2043	U1931	C1816	G1718	G1479	G1479	U1352
A2639	U2423	U2423	A2297	A2297	C	A	A2052	A1932	U1720	U1720	G1479	G1479	C1357
G2640	C2424	C2424	A2298	A2298	U	G	C2055	G1933	G1721	G1721	A1579	U1481	G1358
G2641	A2425	A2425	U2305	U2305	U	C	G2056	A1937	A1722	G1722	G1580	G1483	A1365
C2646	A2426	A2426	G2308	G2308	U	U	G2057	A1938	G1724	G1724	G1581	U1484	U1370
C2649	G2429	G2429	A2309	A2309	U	U	A2058	U1939	A1829	G1725	A1583	U1485	C1370
U2700	A2430	A2430	G2312	G2312	A	G	A2059	U1955	G1835	C1726	U1584	U1486	G1371
C2651	U2431	U2431	U2202	U2202	A	A	A2060	U1955	U1841	C1728	C1585	U1372	U1372
A2547	A2435	A2435	U2203	G2319	U	U	G2061	C1958	G1846	U1729	A1586	G1489	A1373
			U2203	G2319	U	U	A2062	C1958	G1846	G1730	G1587	C1493	U1379
							C2066	C1962		G1731	A1591	A1494	



• Molecule 26: 5S rRNA



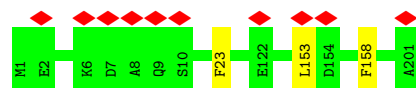
• Molecule 27: Large ribosomal subunit protein uL2



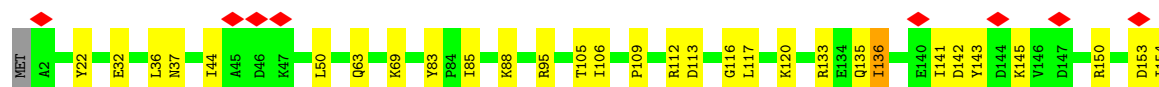
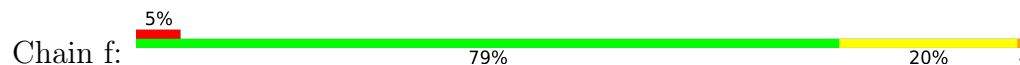
• Molecule 28: Large ribosomal subunit protein uL3



• Molecule 29: Large ribosomal subunit protein uL4



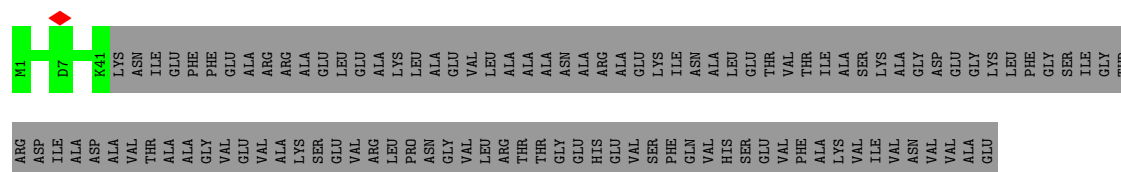
• Molecule 30: Large ribosomal subunit protein uL5



• Molecule 31: Large ribosomal subunit protein uL6



- Chain h:  28% 72%



- Chain i:  98%



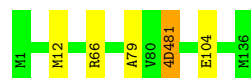
- Chain j:  96%



- Chain k:  96%



- Chain 1: 96%



- Chain m:  91% 7%



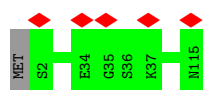
- Molecule 38: Large ribosomal subunit protein uL18

Chain n: 85% 14% ..



- Molecule 39: Large ribosomal subunit protein bL19

Chain o: 99% .



- Molecule 40: Large ribosomal subunit protein bL20

Chain p: 93% 5% ..



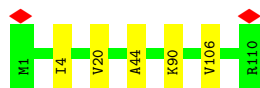
- Molecule 41: Large ribosomal subunit protein bL21

Chain q: 5% 94% 6%



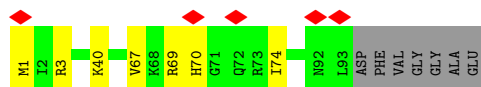
- Molecule 42: Large ribosomal subunit protein uL22

Chain r: 95% 5%

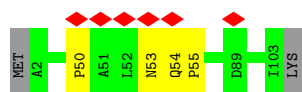
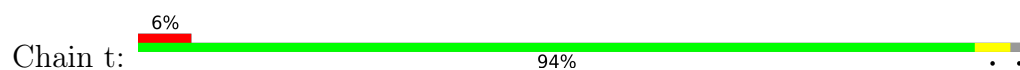


- Molecule 43: Large ribosomal subunit protein uL23

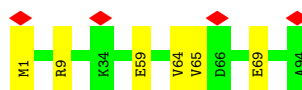
Chain s: 5% 86% 7% 7%



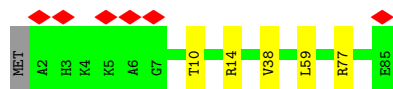
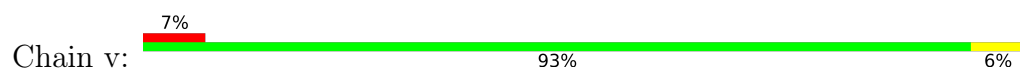
- Molecule 44: Large ribosomal subunit protein uL24



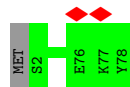
- Molecule 45: Large ribosomal subunit protein bL25



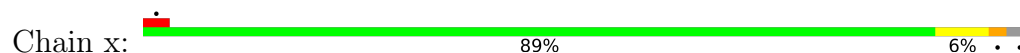
- Molecule 46: Large ribosomal subunit protein bL27



- Molecule 47: Large ribosomal subunit protein bL28



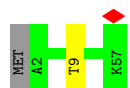
- Molecule 48: Large ribosomal subunit protein uL29




- Molecule 49: Large ribosomal subunit protein uL30

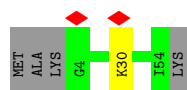


- Molecule 50: Large ribosomal subunit protein bL32



- Molecule 51: Large ribosomal subunit protein bL33

Chain 0:  91% 7%



- Molecule 52: Large ribosomal subunit protein bL34

Chain 1:  96%



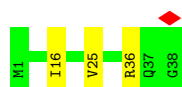
- Molecule 53: Large ribosomal subunit protein bL35

Chain 2:  94% 5%



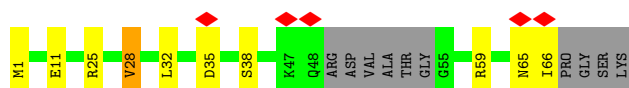
- Molecule 54: Large ribosomal subunit protein bL36A

Chain 3:  92% 8%



- Molecule 55: Large ribosomal subunit protein bL31A

Chain 4:  7% 71% 13% 14%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	196921	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	28.29	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	190000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.586	Depositor
Minimum map value	-0.231	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.085	Depositor
Map size (Å)	447.78, 447.78, 447.78	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8745703, 0.8745703, 0.8745703	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: G7M, MA6, RSP, MG, MS6, IAS, 2MG, UR3, 3TD, T6A, OMC, D2T, SPM, 5MU, OMU, 2MA, SPD, MEQ, 4SU, PSU, ZN, H2U, PUT, 4D4, 1MG, 6MZ, OMG, 4OC, 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	A	0.55	1/36261 (0.0%)	0.85	7/56559 (0.0%)
2	B	0.54	0/1784	1.03	2/2403 (0.1%)
3	C	0.52	0/1651	0.92	0/2225
4	D	0.51	0/1665	1.00	0/2227
5	E	0.58	0/1165	1.00	2/1568 (0.1%)
6	F	0.52	0/858	0.91	0/1160
7	G	0.52	0/1219	0.96	0/1635
8	H	0.54	0/989	0.97	0/1326
9	I	0.54	0/1034	0.96	1/1375 (0.1%)
10	J	0.53	0/796	0.96	0/1077
11	K	0.60	0/884	0.97	1/1191 (0.1%)
12	L	0.56	0/960	0.97	0/1286
13	M	0.53	0/900	0.98	0/1204
14	N	0.52	0/817	0.97	0/1088
15	O	0.52	0/722	0.94	0/964
16	P	0.55	0/653	0.90	1/877 (0.1%)
17	Q	0.54	0/650	0.95	0/871
18	R	0.54	0/553	0.93	0/742
19	S	0.55	0/685	0.93	0/922
20	T	0.53	0/676	1.02	0/895
21	U	0.62	1/597 (0.2%)	1.03	1/792 (0.1%)
22	V	0.58	0/1813	0.85	0/2825
22	Z	0.59	0/1813	0.83	0/2825
23	X	0.62	0/270	0.81	0/419
24	Y	0.58	2/2088 (0.1%)	0.79	0/3255
25	a	0.60	2/65697 (0.0%)	0.94	41/102482 (0.0%)
26	b	0.56	0/2850	0.92	1/4444 (0.0%)
27	c	0.64	1/2121 (0.0%)	1.02	0/2852
28	d	0.58	0/1576	0.95	0/2119
29	e	0.57	0/1571	0.97	0/2113
30	f	0.46	0/1434	0.80	0/1926

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	g	0.52	0/1315	0.92	0/1783
32	h	0.56	0/306	0.98	0/413
33	i	0.57	0/1152	0.97	0/1551
34	j	0.59	0/955	1.01	0/1279
35	k	0.61	0/1062	0.98	0/1413
36	l	0.58	0/1073	0.96	0/1433
37	m	0.62	1/958 (0.1%)	0.97	0/1281
38	n	0.52	0/902	0.83	0/1209
39	o	0.59	0/929	0.94	0/1242
40	p	0.59	0/960	1.05	3/1278 (0.2%)
41	q	0.56	0/829	0.93	0/1107
42	r	0.59	0/864	0.97	0/1156
43	s	0.52	0/744	0.95	0/994
44	t	0.52	0/787	0.91	0/1051
45	u	0.53	0/766	0.92	0/1025
46	v	0.63	0/636	0.96	0/841
47	w	0.62	0/635	1.01	0/848
48	x	0.44	0/496	0.97	0/660
49	y	0.55	0/453	0.93	0/605
50	z	0.64	0/450	1.05	0/599
51	0	0.56	0/424	0.93	0/565
52	1	0.65	0/380	1.16	2/498 (0.4%)
53	2	0.67	0/513	1.05	0/676
54	3	0.59	0/303	0.94	0/397
55	4	0.53	0/488	0.92	0/649
All	All	0.58	8/155132 (0.0%)	0.92	62/232200 (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
2	B	0	1
4	D	0	2
7	G	0	1
9	I	0	4
10	J	0	1
12	L	0	1
14	N	0	1
27	c	0	1
40	p	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
46	v	0	1
48	x	0	3
52	1	0	1
53	2	0	1
54	3	0	1
55	4	0	1
All	All	0	22

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	U	21	ARG	NE-CZ	6.77	1.40	1.33
27	c	53	HIS	CG-CD2	-6.12	1.29	1.35
37	m	3	HIS	CG-CD2	-5.89	1.29	1.35
25	a	2069	G7M	O3'-P	5.54	1.61	1.56
25	a	2552	OMU	O3'-P	5.53	1.61	1.56
24	Y	37	T6A	O3'-P	5.40	1.61	1.56
24	Y	8	4SU	O3'-P	5.16	1.61	1.56
1	A	1498	UR3	O3'-P	5.08	1.61	1.56

All (62) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	a	531	C	O3'-P-O5'	11.59	121.38	104.00
21	U	21	ARG	CD-NE-CZ	8.30	136.02	124.40
25	a	504	A	O3'-P-O5'	-7.60	92.60	104.00
25	a	271	G	C2'-C3'-O3'	7.49	120.74	109.50
25	a	557	C	O3'-P-O5'	-6.96	93.55	104.00
25	a	2683	C	O3'-P-O5'	-6.90	93.65	104.00
25	a	1971	U	C4'-C3'-O3'	-6.85	102.72	113.00
25	a	1136	G	C4'-C3'-C2'	-6.81	95.79	102.60
52	1	14	ARG	NE-CZ-NH1	-6.79	114.71	121.50
25	a	2324	U	C2'-C3'-O3'	-6.56	103.86	113.70
16	P	23	ASP	CA-CB-CG	6.53	119.13	112.60
2	B	69	PHE	CA-C-N	-6.47	114.30	123.11
2	B	69	PHE	C-N-CA	-6.47	114.30	123.11
9	I	128	SER	O-C-N	-6.47	115.63	123.27
25	a	544	C	O3'-P-O5'	-6.21	94.69	104.00
25	a	1969	A	O3'-P-O5'	-6.20	94.70	104.00
26	b	12	C	O3'-P-O5'	-6.20	94.70	104.00
1	A	429	U	C2'-C3'-O3'	6.17	118.75	109.50
52	1	14	ARG	NE-CZ-NH2	6.12	124.71	119.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	a	2346	A	O3'-P-O5'	-6.08	94.89	104.00
25	a	1992	G	O3'-P-O5'	-6.02	94.97	104.00
25	a	631	A	C2'-C3'-O3'	-5.91	104.83	113.70
25	a	1025	G	O3'-P-O5'	5.74	112.60	104.00
1	A	1447	A	O3'-P-O5'	-5.68	95.47	104.00
25	a	2523	G	C4'-C3'-C2'	-5.66	96.94	102.60
1	A	574	A	O3'-P-O5'	-5.64	95.55	104.00
25	a	972	A	O3'-P-O5'	-5.63	95.55	104.00
25	a	2714	G	O3'-P-O5'	5.54	112.31	104.00
25	a	2641	G	C4'-C3'-C2'	-5.53	97.07	102.60
1	A	575	G	O5'-C5'-C4'	-5.48	103.48	111.70
25	a	2544	G	C4'-C3'-C2'	-5.47	97.13	102.60
25	a	1252	G	O3'-P-O5'	-5.43	95.86	104.00
25	a	2687	U	C2'-C3'-O3'	-5.40	105.61	113.70
1	A	1398	A	C4'-C3'-C2'	-5.39	97.21	102.60
25	a	1930	G	C3'-C2'-C1'	-5.37	96.13	101.50
25	a	1131	G	O3'-P-O5'	-5.29	96.06	104.00
25	a	1728	C	C4'-C3'-C2'	-5.29	97.31	102.60
5	E	164	ILE	CA-C-N	-5.26	112.24	121.70
5	E	164	ILE	C-N-CA	-5.26	112.24	121.70
1	A	682	G	C4'-C3'-C2'	-5.25	97.35	102.60
25	a	661	A	C4'-C3'-C2'	-5.24	97.36	102.60
25	a	2882	A	O3'-P-O5'	-5.23	96.16	104.00
25	a	784	G	O3'-P-O5'	-5.22	96.17	104.00
25	a	205	G	C3'-C2'-C1'	-5.15	96.35	101.50
25	a	2601	C	O3'-P-O5'	-5.14	96.30	104.00
40	p	33	ARG	NE-CZ-NH1	-5.14	116.36	121.50
25	a	1787	A	C2'-C3'-O3'	-5.12	106.02	113.70
11	K	36	ASP	CA-CB-CG	5.09	117.69	112.60
25	a	204	A	O3'-P-O5'	-5.09	96.36	104.00
25	a	664	G	C4'-C3'-C2'	-5.08	97.52	102.60
25	a	1566	A	O3'-P-O5'	-5.07	96.39	104.00
40	p	91	ASP	CA-CB-CG	5.07	117.67	112.60
40	p	31	VAL	N-CA-CB	-5.06	104.36	111.25
25	a	505	A	O3'-P-O5'	-5.06	96.41	104.00
1	A	182	A	O3'-P-O5'	-5.05	96.42	104.00
25	a	953	G	C4'-C3'-C2'	-5.05	97.55	102.60
25	a	2072	C	C4'-C3'-C2'	-5.05	97.55	102.60
25	a	104	A	O3'-P-O5'	5.05	111.58	104.00
25	a	951	C	O3'-P-O5'	5.04	111.57	104.00
25	a	2085	U	C4'-C3'-C2'	-5.04	97.56	102.60
25	a	1185	G	O3'-P-O5'	-5.04	96.45	104.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	a	807	U	C4'-C3'-C2'	-5.00	97.60	102.60

There are no chirality outliers.

All (22) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
52	1	41	ARG	Sidechain
53	2	13	ARG	Sidechain
54	3	36	ARG	Sidechain
55	4	59	ARG	Sidechain
2	B	137	ARG	Sidechain
4	D	44	ARG	Sidechain
4	D	97	ARG	Sidechain
7	G	10	ARG	Sidechain
9	I	106	ARG	Sidechain
9	I	124	ARG	Sidechain
9	I	41	ARG	Sidechain
9	I	95	ARG	Sidechain
10	J	7	ARG	Sidechain
12	L	94	ARG	Sidechain
14	N	85	ARG	Sidechain
27	c	156	ARG	Sidechain
40	p	13	ARG	Sidechain
40	p	51	ARG	Sidechain
46	v	14	ARG	Sidechain
48	x	29	ARG	Sidechain
48	x	47	ARG	Sidechain
48	x	52	ARG	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32634	0	16443	233	0
2	B	1753	0	1780	20	0
3	C	1624	0	1696	4	0
4	D	1643	0	1707	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	E	1152	0	1196	1	0
6	F	839	0	833	2	0
7	G	1203	0	1254	6	0
8	H	979	0	1031	1	0
9	I	1022	0	1070	4	0
10	J	786	0	828	6	0
11	K	877	0	884	1	0
12	L	957	0	1017	4	0
13	M	891	0	952	8	0
14	N	805	0	844	2	0
15	O	714	0	734	0	0
16	P	643	0	661	6	0
17	Q	641	0	682	5	0
18	R	544	0	565	0	0
19	S	668	0	693	0	0
20	T	670	0	719	0	0
21	U	589	0	629	3	0
22	V	1623	0	825	21	0
22	Z	1623	0	825	9	0
23	X	240	0	121	4	0
24	Y	2000	0	1020	39	0
25	a	59172	0	29791	237	0
26	b	2549	0	1291	16	0
27	c	2082	0	2154	6	0
28	d	1566	0	1618	5	0
29	e	1552	0	1619	2	0
30	f	1410	0	1444	22	0
31	g	1295	0	1332	0	0
32	h	303	0	327	0	0
33	i	1129	0	1162	2	0
34	j	946	0	1023	3	0
35	k	1053	0	1129	6	0
36	l	1075	0	1145	4	0
37	m	945	0	989	4	0
38	n	892	0	923	12	0
39	o	917	0	962	0	0
40	p	947	0	1019	4	0
41	q	816	0	839	4	0
42	r	857	0	922	4	0
43	s	738	0	807	6	0
44	t	779	0	831	5	0
45	u	753	0	780	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
46	v	628	0	642	2	0
47	w	625	0	652	0	0
48	x	495	0	526	1	0
49	y	449	0	488	0	0
50	z	444	0	458	1	0
51	0	417	0	451	1	0
52	1	377	0	418	1	0
53	2	504	0	572	2	0
54	3	302	0	340	1	0
55	4	480	0	478	10	0
56	A	87	0	0	0	0
56	Y	4	0	0	0	0
56	a	187	0	0	0	0
56	b	5	0	0	0	0
56	c	1	0	0	0	0
56	d	2	0	0	0	0
56	m	1	0	0	0	0
56	z	1	0	0	0	0
57	A	10	0	19	0	0
57	a	60	0	114	3	0
58	A	6	0	12	0	0
58	a	36	0	72	0	0
59	a	14	0	26	2	0
60	3	1	0	0	0	0
60	4	1	0	0	0	0
All	All	144033	0	96384	680	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 3.

All (680) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:84:U:H3'	1:A:86:G:H21	1.34	0.90
25:a:276:U:H2'	25:a:277:G:C8	2.19	0.77
25:a:284:U:H2'	25:a:285:G:H5''	1.67	0.76
30:f:158:THR:HG22	30:f:160:ALA:H	1.49	0.76
25:a:280:U:H2'	25:a:281:C:C6	2.20	0.76
1:A:1492:A:O2'	25:a:1913[A]:A:C2	2.40	0.75
13:M:57:ARG:NH2	55:4:35:ASP:HB3	2.01	0.75
25:a:1730:C:H5''	25:a:1730:C:H6	1.52	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:C:HO2'	1:A:86:G:H1	1.36	0.73
25:a:460:A:OP1	52:1:41:ARG:NH1	2.20	0.73
26:b:48:U:O2'	38:n:100:HIS:HE1	1.72	0.73
25:a:284:U:C3'	25:a:285:G:H5''	2.18	0.73
25:a:1051:G:H3'	25:a:1052:C:C6	2.24	0.73
25:a:284:U:C2'	25:a:285:G:H5''	2.18	0.72
25:a:1179:G:H2'	25:a:1180:U:O4'	1.89	0.72
22:Z:21:A:H61	22:Z:46:G:H2'	1.54	0.72
25:a:1478:G:H1	25:a:1513:U:H3	1.37	0.72
4:D:172:GLU:HG3	4:D:183:LYS:HD2	1.73	0.71
25:a:272:A:H2'	25:a:273:G:O4'	1.91	0.71
1:A:1005:A:O5'	1:A:1005:A:H8	1.73	0.70
1:A:1133:G:O2'	1:A:1134:G:H5'	1.92	0.69
1:A:1356:G:H2'	1:A:1357:A:C8	2.26	0.69
1:A:227:G:O2'	1:A:228:A:H5'	1.92	0.69
22:V:18:G:H21	22:V:58:A:H5'	1.57	0.69
1:A:477:C:H2'	1:A:478:A:C8	2.27	0.69
1:A:664:G:H22	1:A:741:G:H1	1.38	0.69
25:a:568:U:H1'	25:a:2030:6MZ:H9C1	1.74	0.69
1:A:299:G:H2'	1:A:300:A:C8	2.29	0.68
1:A:429:U:H1'	1:A:430:A:H5''	1.74	0.67
1:A:85:U:H1'	1:A:86:G:C2	2.29	0.67
1:A:382:A:H2'	1:A:383:A:C8	2.30	0.67
1:A:946:A:H2'	1:A:947:G:C8	2.29	0.67
24:Y:56:C:O2	25:a:896:A:H2'	1.94	0.67
25:a:1482:G:H1'	25:a:1509:A:H61	1.58	0.67
1:A:461:A:O2'	1:A:462:G:H5'	1.95	0.66
13:M:8:ASN:ND2	30:f:143:TYR:CE1	2.63	0.66
24:Y:75:C:H2'	24:Y:76:A:C8	2.31	0.66
12:L:15:LYS:HD3	12:L:15:LYS:H	1.60	0.66
4:D:114:ALA:O	4:D:118:VAL:HG23	1.96	0.66
1:A:1169:A:H2'	1:A:1170:A:C8	2.30	0.65
1:A:1053:G:N7	1:A:1200:C:H5''	2.12	0.65
25:a:364:C:H2'	25:a:365:U:C6	2.33	0.64
25:a:877:A:H2	25:a:900:A:N7	1.95	0.64
1:A:140:U:H2'	1:A:141:G:H5''	1.80	0.64
25:a:154:U:OP2	25:a:154:U:H6	1.81	0.64
1:A:1135:U:H3'	1:A:1137:C:H41	1.63	0.63
1:A:195:A:H2'	1:A:196:A:C8	2.33	0.63
1:A:455:G:H3'	1:A:456:A:H8	1.63	0.63
1:A:188:C:H2'	1:A:189:A:O4'	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:a:1721:G:C2'	25:a:1739:A:H61	2.12	0.63
1:A:177:G:C2'	1:A:178:C:H5'	2.29	0.62
1:A:1029:U:HO2'	1:A:1032:G:H1	1.45	0.62
25:a:1051:G:H3'	25:a:1052:C:H6	1.65	0.62
25:a:1746:A:H2'	25:a:1747:U:C6	2.35	0.62
38:n:90:VAL:O	38:n:117:PHE:HB3	1.99	0.61
26:b:48:U:O2'	38:n:100:HIS:CE1	2.53	0.61
1:A:1086:U:H3	1:A:1099:G:H22	1.46	0.61
25:a:1579:A:H2'	25:a:1580:A:C8	2.35	0.61
1:A:1009:U:H2'	1:A:1010:U:C6	2.36	0.61
25:a:2333:A:OP1	46:v:77:ARG:NH2	2.31	0.61
22:Z:76:A:H2'	25:a:2451:A:H1'	1.83	0.61
26:b:66:A:H61	26:b:107:G:H2'	1.65	0.61
25:a:695:G:O6	59:a:6193:SPM:H122	2.01	0.60
1:A:524:G:H2'	1:A:525:C:C6	2.36	0.60
24:Y:12:C:H2'	24:Y:13:G:C8	2.36	0.60
25:a:2204:G:OP2	27:c:147:LYS:HE3	2.01	0.60
25:a:1494:A:H2'	25:a:1495:A:C8	2.36	0.60
1:A:661:G:O2'	1:A:662:U:H5'	2.01	0.60
25:a:139:U:H3'	25:a:140:C:H6	1.67	0.60
1:A:177:G:H2'	1:A:178:C:H5'	1.84	0.60
25:a:1535:A:H3'	25:a:1536:C:H5''	1.82	0.60
2:B:76:ALA:O	2:B:80:VAL:HG23	2.02	0.59
25:a:2209:G:H3'	25:a:2210:U:H2'	1.84	0.59
30:f:37:ASN:HB3	30:f:153:ASP:OD1	2.02	0.59
1:A:677:U:H3	1:A:713:G:H22	1.49	0.59
25:a:1434:A:H2'	25:a:1435:G:C8	2.38	0.59
1:A:632:U:H3'	1:A:633:G:H5'	1.85	0.59
24:Y:47(L):U:H2'	24:Y:47(M):G:H8	1.67	0.59
22:V:9:G:O4'	22:V:46:G:H1'	2.03	0.59
1:A:1011:C:H2'	1:A:1012:A:C8	2.37	0.59
1:A:262:A:H2'	1:A:263:A:C8	2.37	0.59
1:A:429:U:H3'	4:D:9:LEU:HD12	1.85	0.59
1:A:1224:U:H3'	1:A:1225:A:H5''	1.85	0.59
4:D:155:VAL:HG11	4:D:178:MET:HE1	1.83	0.59
22:V:11:A:H2'	22:V:12:G:O4'	2.03	0.59
48:x:6:LEU:HB3	48:x:56:LEU:HD12	1.85	0.58
22:V:48:C:C2	22:V:59:A:H1'	2.38	0.58
24:Y:47(N):C:H2'	24:Y:47(O):A:C8	2.39	0.58
1:A:1005:A:O5'	1:A:1005:A:C8	2.56	0.58
24:Y:47(L):U:H2'	24:Y:47(M):G:C8	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:171:A:H2'	1:A:172:A:C8	2.39	0.58
24:Y:76:A:N1	25:a:2583:G:O2'	2.35	0.58
4:D:99:ASP:OD2	4:D:115:ARG:HA	2.03	0.58
25:a:1548:A:H2'	25:a:1549:A:C8	2.38	0.58
22:V:34:C:H2'	22:V:35:A:C8	2.38	0.58
25:a:1534:U:H2'	25:a:1536:C:C6	2.39	0.58
25:a:1045:C:H42	25:a:1111:A:H2'	1.69	0.57
16:P:6:LEU:CD2	16:P:19:VAL:HG22	2.35	0.57
25:a:811:U:H2'	35:k:21:ARG:HA	1.85	0.57
1:A:1014:A:C2	1:A:1219:A:H1'	2.40	0.57
25:a:2798:U:H6	25:a:2798:U:H5'	1.70	0.57
1:A:1027:C:H2'	1:A:1028:C:C6	2.39	0.57
13:M:57:ARG:CZ	55:4:35:ASP:HB2	2.34	0.56
22:V:36:U:H1'	22:V:39:C:N4	2.20	0.56
25:a:2291:U:H2'	25:a:2292:U:C6	2.40	0.56
1:A:80:A:H2'	1:A:81:A:C8	2.40	0.56
25:a:495:G:H5''	42:r:4:ILE:HG13	1.86	0.56
25:a:1567:G:H5'	27:c:58:HIS:ND1	2.20	0.56
2:B:66:LYS:NZ	2:B:157:LEU:O	2.38	0.56
1:A:465:A:H2'	1:A:466:A:C8	2.41	0.56
1:A:190:A:O5'	1:A:190:A:H8	1.89	0.56
6:F:99:ALA:HB1	6:F:103:VAL:HG23	1.88	0.56
24:Y:47(K):C:H2'	24:Y:47(L):U:C6	2.40	0.56
2:B:129:LEU:HB3	2:B:133:GLU:HB2	1.89	0.55
1:A:585:G:OP1	17:Q:39:LYS:HE2	2.06	0.55
2:B:117:LEU:HD11	2:B:137:ARG:HB3	1.86	0.55
25:a:948:C:H1'	25:a:984:A:C8	2.42	0.55
25:a:1802:A:H2'	25:a:1803:A:C8	2.42	0.55
25:a:1721:G:C2'	25:a:1739:A:N6	2.70	0.55
1:A:189:A:H2'	1:A:190:A:C8	2.42	0.55
25:a:1968:G:H4'	25:a:1973:G:H5'	1.87	0.55
30:f:112:ARG:HH12	30:f:133:ARG:HH22	1.53	0.55
1:A:269:C:H2'	1:A:270:A:C8	2.41	0.55
12:L:4:VAL:HG23	17:Q:34:TYR:HB3	1.87	0.55
25:a:277:G:H4'	25:a:278:A:O5'	2.07	0.55
25:a:669:G:O2'	25:a:670:A:H5'	2.06	0.55
1:A:1453:G:H2'	1:A:1454:G:O4'	2.07	0.55
25:a:1873:G:H2'	25:a:1874:C:C6	2.41	0.55
1:A:1176:A:H2'	1:A:1177:G:C8	2.42	0.55
1:A:1135:U:C2	1:A:1137:C:C4	2.95	0.54
25:a:1047:G:H1'	25:a:1110:G:N1	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:a:2333:A:H5'	25:a:2335:A:H1'	1.89	0.54
42:r:4:ILE:HG22	42:r:106:VAL:HG22	1.89	0.54
1:A:147:G:H2'	1:A:148:G:C8	2.42	0.54
1:A:673:A:H2'	1:A:674:G:C8	2.41	0.54
1:A:1027:C:H2'	1:A:1028:C:H6	1.72	0.54
1:A:1492:A:O2'	25:a:1913[A]:A:H2	1.89	0.54
1:A:84:U:H3'	1:A:86:G:N2	2.15	0.54
1:A:1323:G:H2'	1:A:1324:A:C8	2.42	0.54
1:A:1125:U:O2'	1:A:1126:U:H5''	2.07	0.54
25:a:1428:C:C5	25:a:1569:A:H5''	2.42	0.54
25:a:1651:G:H5'	37:m:39:PRO:CG	2.37	0.54
25:a:2287:A:OP1	51:0:30:LYS:NZ	2.40	0.54
1:A:408:A:O2'	1:A:409:U:H5'	2.08	0.54
25:a:2547:A:H2'	25:a:2548:U:C6	2.43	0.53
1:A:538:G:O2'	1:A:539:A:H5'	2.09	0.53
1:A:1236:A:H2'	1:A:1237:C:C6	2.43	0.53
25:a:2038:G:H2'	25:a:2039:U:O4'	2.09	0.53
25:a:139:U:H3'	25:a:140:C:C6	2.43	0.53
25:a:888:C:H2'	25:a:889:C:O4'	2.09	0.53
26:b:66:A:N6	26:b:107:G:H2'	2.24	0.53
1:A:838:G:H2'	1:A:839:C:O4'	2.08	0.53
2:B:80:VAL:HG22	2:B:214:LEU:HD11	1.90	0.53
25:a:549:G:H2'	25:a:550:C:C6	2.43	0.53
25:a:639:U:H2'	25:a:640:C:C6	2.44	0.53
25:a:751:A:H5'	42:r:90:LYS:HA	1.91	0.53
25:a:877:A:C2	25:a:900:A:N7	2.77	0.53
44:t:50:PRO:HA	44:t:54:GLN:HB3	1.90	0.53
1:A:1530:G:H2'	1:A:1531:A:C8	2.44	0.53
27:c:29:PRO:HG2	27:c:34:LEU:HD11	1.90	0.53
1:A:458:U:H2'	1:A:459:A:C8	2.44	0.53
24:Y:47(H):A:H2'	24:Y:47(I):A:C8	2.44	0.53
1:A:481:G:O2'	1:A:483:C:N4	2.42	0.52
24:Y:36:U:H3'	24:Y:37:T6A:H8	1.74	0.52
1:A:109:A:H2'	1:A:326:G:N2	2.25	0.52
25:a:2494:G:O2'	36:l:79:ALA:HA	2.10	0.52
1:A:1164:G:O2'	1:A:1165:U:H5'	2.09	0.52
1:A:1268:G:H2'	1:A:1269:A:C8	2.44	0.52
2:B:154:MET:HG3	2:B:156:GLY:O	2.09	0.52
25:a:1914[A]:C:H2'	25:a:1915:3TD:H6	1.91	0.52
2:B:111:ILE:HD12	2:B:152:LYS:HA	1.91	0.52
21:U:40:LYS:HE3	21:U:42:THR:CG2	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:b:40:U:H1'	26:b:45:A:H61	1.74	0.52
24:Y:63:C:H2'	24:Y:64:C:C6	2.45	0.52
25:a:1418:G:H2'	25:a:1579:A:N6	2.25	0.52
29:e:153:LEU:HD21	29:e:158:PHE:HB2	1.92	0.52
25:a:612:G:C2	25:a:614:A:H5''	2.45	0.52
25:a:1651:G:H5'	37:m:39:PRO:HG2	1.91	0.52
36:l:66:ARG:NH1	36:l:104:GLU:OE2	2.41	0.52
1:A:410:G:OP2	4:D:31:LYS:HE2	2.10	0.52
1:A:993:G:H2'	1:A:993:G:N3	2.25	0.52
1:A:1255:G:O2'	1:A:1258:G:N3	2.35	0.52
25:a:143:C:H1'	43:s:1:MET:HE2	1.91	0.52
25:a:717:C:H3'	25:a:718:A:H8	1.75	0.52
25:a:191:A:H2'	25:a:192:C:C6	2.45	0.52
25:a:690:G:H2'	25:a:691:C:O4'	2.10	0.52
25:a:2210:U:H4'	25:a:2211:A:H5'	1.92	0.52
30:f:142:ASP:HB3	30:f:145:LYS:HB2	1.91	0.52
1:A:1285:A:H4'	1:A:1286:U:OP1	2.09	0.51
1:A:87:C:H3'	1:A:88:U:C6	2.45	0.51
26:b:42:C:O2'	30:f:63:GLN:HG2	2.10	0.51
2:B:125:THR:C	2:B:127:ASP:H	2.18	0.51
24:Y:47(I):A:C5	24:Y:47(J):G:H1'	2.45	0.51
22:Z:11:A:H2'	22:Z:12:G:C8	2.46	0.51
55:4:28:VAL:HG21	55:4:32:LEU:HD21	1.92	0.51
1:A:1218:C:H2'	1:A:1219:A:C8	2.44	0.51
45:u:64:VAL:HG22	45:u:69:GLU:HG2	1.92	0.51
22:Z:46:G:H5''	22:Z:46:G:H8	1.75	0.51
25:a:284:U:H2'	25:a:285:G:H8	1.74	0.51
25:a:910:A:H2'	25:a:911:A:C8	2.45	0.51
16:P:61:VAL:HG21	16:P:67:ILE:HD11	1.93	0.51
1:A:131:A:H2'	1:A:132:C:C6	2.46	0.51
1:A:1162:C:H2'	1:A:1163:A:C8	2.45	0.51
1:A:1338:G:H2'	1:A:1339:A:C8	2.46	0.51
25:a:1484:U:H2'	25:a:1485:U:C6	2.46	0.51
1:A:1144:G:N2	1:A:1146:A:H62	2.09	0.51
24:Y:68:U:H2'	24:Y:69:C:H6	1.76	0.51
1:A:945:G:H2'	1:A:945:G:N3	2.25	0.50
1:A:1302:C:C5	13:M:17:ILE:HG13	2.46	0.50
25:a:1721:G:O2'	25:a:1739:A:N6	2.38	0.50
25:a:2788:C:H2'	25:a:2789:C:C6	2.46	0.50
38:n:39:VAL:HB	38:n:49:VAL:HG22	1.93	0.50
22:V:36:U:H1'	22:V:39:C:H42	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:376:G:H5''	16:P:5:ARG:HB2	1.93	0.50
1:A:1413:A:H2	1:A:1487:G:H22	1.59	0.50
25:a:170:U:H2'	25:a:171:U:C6	2.46	0.50
25:a:1586:A:H3'	25:a:1587:G:H8	1.75	0.50
25:a:2804:U:H2'	25:a:2805:C:C6	2.46	0.50
1:A:493:A:H2'	1:A:494:G:C8	2.47	0.50
1:A:859:G:H2'	1:A:860:A:C8	2.45	0.50
1:A:1287:A:H2'	1:A:1288:A:C8	2.47	0.50
30:f:105:THR:HA	55:4:38:SER:HB2	1.93	0.50
3:C:35:SER:OG	3:C:59:ARG:NH2	2.45	0.50
13:M:57:ARG:NH2	55:4:35:ASP:CB	2.72	0.50
13:M:57:ARG:CZ	55:4:35:ASP:CB	2.88	0.50
24:Y:47(G):A:H2'	24:Y:47(H):A:C8	2.46	0.50
38:n:2:ASP:N	38:n:2:ASP:OD1	2.44	0.50
1:A:458:U:H2'	1:A:459:A:H8	1.75	0.50
1:A:579:A:H2'	1:A:580:C:C6	2.47	0.50
1:A:1055:A:O2'	3:C:161:GLU:O	2.27	0.50
30:f:95:ARG:CZ	55:4:1:MET:HE2	2.41	0.50
1:A:471:U:H2'	1:A:472:U:C6	2.47	0.50
1:A:1000:A:H2'	1:A:1001:C:C6	2.46	0.50
2:B:118:GLU:O	2:B:122:GLN:HG2	2.12	0.50
25:a:2798:U:H5'	25:a:2798:U:C6	2.47	0.50
10:J:10:LEU:HD11	10:J:25:ILE:HD12	1.94	0.50
22:V:46:G:H3'	22:V:47:U:H5''	1.93	0.50
25:a:2849:U:H4'	25:a:2868:A:C2	2.46	0.50
1:A:1042:A:H2'	1:A:1043:G:C8	2.46	0.50
4:D:102:VAL:HG21	4:D:118:VAL:HG22	1.92	0.50
1:A:421:U:H3'	1:A:422:C:O2	2.12	0.49
25:a:2014:A:H2'	25:a:2015:A:C8	2.47	0.49
1:A:451:A:H61	1:A:481:G:H5'	1.76	0.49
25:a:308:G:H2'	25:a:309:A:C8	2.47	0.49
25:a:1528:A:H2'	25:a:1529:G:O4'	2.12	0.49
24:Y:27:C:H2'	24:Y:28:U:C6	2.47	0.49
25:a:154:U:OP2	25:a:154:U:C6	2.63	0.49
26:b:26:C:O5'	26:b:26:C:H6	1.96	0.49
1:A:1516:2MG:N2	1:A:1519:MA6:OP2	2.43	0.49
25:a:1722:A:H61	25:a:1738:G:H1'	1.77	0.49
35:k:57:LEU:HD22	53:2:54:ASP:HB3	1.93	0.49
1:A:714:G:H2'	1:A:715:A:C8	2.48	0.49
1:A:1088:G:H4'	21:U:70:LEU:HD13	1.94	0.49
7:G:16:PRO:HB2	9:I:42:GLU:HB3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:f:44:ILE:HA	30:f:83:TYR:CE2	2.48	0.49
1:A:666:G:H5'	1:A:726:C:H1'	1.94	0.49
1:A:1062:U:H2'	1:A:1063:C:C6	2.47	0.49
7:G:2:PRO:HD3	7:G:7:ILE:HD11	1.95	0.49
30:f:135:GLN:HG2	30:f:141:ILE:HG21	1.94	0.49
1:A:409:U:OP1	4:D:23:SER:HB2	2.13	0.49
1:A:1356:G:H2'	1:A:1357:A:H8	1.75	0.49
25:a:636:G:OP1	35:k:129:LYS:HG2	2.13	0.49
25:a:657:U:H2'	25:a:658:U:C6	2.48	0.49
25:a:1438:U:H2'	25:a:1439:A:H8	1.77	0.49
23:X:21:A:H2'	23:X:22:A:C8	2.48	0.49
24:Y:47(P):U:H4'	24:Y:51:G:OP2	2.13	0.49
25:a:414:C:H2'	25:a:415:A:C8	2.48	0.49
2:B:66:LYS:HE3	2:B:157:LEU:O	2.13	0.48
25:a:52:A:H2'	25:a:53:A:C8	2.48	0.48
1:A:6:G:N2	5:E:103:THR:OG1	2.46	0.48
1:A:839:C:H2'	1:A:839:C:O2	2.14	0.48
1:A:864:A:H2'	1:A:865:A:C8	2.48	0.48
1:A:1180:A:P	9:I:99:ARG:HH12	2.35	0.48
25:a:221:A:N1	25:a:265:A:O2'	2.46	0.48
1:A:991:U:H2'	1:A:1212:U:O2	2.13	0.48
25:a:644:A:H2'	25:a:645:C:O4'	2.13	0.48
1:A:266:G:H2'	1:A:266:G:N3	2.28	0.48
25:a:143:C:H2'	25:a:144:A:C8	2.49	0.48
22:V:72:A:H3'	22:V:73:A:H8	1.77	0.48
25:a:1799:G:O2'	27:c:180:GLU:OE2	2.32	0.48
26:b:52:A:N7	38:n:64:TYR:OH	2.43	0.48
30:f:116:GLY:HA3	30:f:178:ARG:HB3	1.96	0.48
54:3:16:ILE:HD13	54:3:25:VAL:HG22	1.94	0.48
25:a:243:U:OP2	53:2:8:ARG:NH1	2.47	0.48
25:a:1722:A:N6	25:a:1738:G:H1'	2.29	0.48
25:a:2312:U:H5'	30:f:85:ILE:HD11	1.96	0.48
25:a:2803:G:H2'	25:a:2804:U:C6	2.48	0.48
1:A:16:A:N1	1:A:919:A:H2	2.11	0.48
24:Y:47(B):G:H1	24:Y:47(L):U:H3	1.60	0.48
25:a:12:U:O2	25:a:12:U:H2'	2.13	0.48
1:A:1371:G:O3'	9:I:71:GLY:HA3	2.14	0.48
7:G:151:PHE:CZ	11:K:56:ARG:HG2	2.49	0.48
25:a:281:C:H42	25:a:359:G:H1	1.60	0.48
25:a:2898:U:H2'	25:a:2899:A:C8	2.49	0.48
26:b:36:C:N4	26:b:49:C:O2	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:713:G:H2'	1:A:714:G:C8	2.49	0.48
4:D:103:TYR:CD1	4:D:110:THR:C	2.92	0.48
22:V:9:G:H4'	22:V:10:G:OP2	2.13	0.48
25:a:1651:G:OP1	37:m:39:PRO:HG2	2.14	0.48
1:A:662:U:H2'	1:A:663:A:C8	2.49	0.47
1:A:1073:U:O2'	2:B:103:ASN:ND2	2.46	0.47
25:a:1874:C:H2'	25:a:1875:G:O4'	2.13	0.47
1:A:483:C:O2	16:P:13:LYS:NZ	2.48	0.47
1:A:486:U:H2'	1:A:487:A:H8	1.78	0.47
1:A:458:U:O2'	1:A:459:A:H5'	2.14	0.47
1:A:1100:C:H3'	2:B:95:ARG:HH12	1.79	0.47
1:A:1238:A:C2	1:A:1241:G:N3	2.82	0.47
22:V:8:U:H1'	22:V:21:A:H2	1.79	0.47
35:k:23:ILE:HG12	41:q:82:HIS:CD2	2.49	0.47
55:4:11:GLU:HA	55:4:25:ARG:HA	1.96	0.47
24:Y:71:C:H2'	24:Y:72:C:C6	2.50	0.47
22:Z:21:A:N6	22:Z:46:G:H2'	2.27	0.47
25:a:1736:U:H2'	25:a:1737:G:O4'	2.14	0.47
1:A:1363:A:N3	1:A:1363:A:H2'	2.29	0.47
24:Y:76:A:OP2	25:a:2602:A:N6	2.38	0.47
25:a:1585:C:H2'	25:a:1586:A:O4'	2.15	0.47
44:t:53:ASN:ND2	44:t:55:PRO:O	2.48	0.47
1:A:95:C:H2'	1:A:96:U:C6	2.49	0.47
1:A:1369:C:H2'	1:A:1370:G:C8	2.49	0.47
4:D:119:SER:C	4:D:121:LYS:H	2.22	0.47
22:V:48:C:H6	22:V:48:C:H5''	1.79	0.47
25:a:846:U:H6	25:a:848:C:H41	1.62	0.47
25:a:1482:G:H1'	25:a:1509:A:N6	2.29	0.47
1:A:475:C:H2'	1:A:476:U:C6	2.50	0.47
25:a:2273:A:H2'	25:a:2274:A:C8	2.50	0.47
33:i:4:PHE:O	40:p:64:ARG:NH2	2.47	0.47
1:A:113:G:N3	1:A:353:A:O2'	2.47	0.47
1:A:1005:A:H4'	1:A:1037:C:H1'	1.97	0.47
14:N:10:GLU:HG3	14:N:63:ARG:HD2	1.97	0.47
24:Y:68:U:H2'	24:Y:69:C:C6	2.50	0.47
25:a:493:G:H2'	25:a:494:G:O4'	2.15	0.47
25:a:750:A:OP2	57:a:6191:SPD:N10	2.48	0.47
25:a:1542:U:H2'	25:a:1543:G:O4'	2.14	0.47
1:A:946:A:H2'	1:A:947:G:H8	1.79	0.47
24:Y:20(B):G:H4'	24:Y:21:A:O5'	2.15	0.47
24:Y:47(F):A:H3'	24:Y:47(G):A:C8	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:a:225:C:H2'	25:a:226:A:O4'	2.14	0.47
25:a:1720:U:H2'	25:a:1721:G:O4'	2.14	0.47
25:a:2756:U:H1'	25:a:2757:A:H5''	1.97	0.47
28:d:1:MET:HE2	28:d:205:PRO:HG2	1.96	0.47
1:A:486:U:H2'	1:A:487:A:C8	2.50	0.46
10:J:66:GLU:HB2	14:N:99:ALA:HB2	1.98	0.46
25:a:284:U:H3'	25:a:285:G:H5''	1.94	0.46
25:a:2625:G:H2'	25:a:2626:C:O4'	2.16	0.46
1:A:67:C:H2'	1:A:68:G:C8	2.51	0.46
1:A:161:A:H2'	1:A:162:A:C8	2.50	0.46
1:A:663:A:H5'	1:A:836:G:OP1	2.15	0.46
1:A:1032:G:H3'	1:A:1032:G:N3	2.30	0.46
10:J:85:ASP:HB3	10:J:89:ARG:HH21	1.80	0.46
25:a:181:A:H2'	25:a:182:A:C8	2.50	0.46
25:a:1028:A:H2'	25:a:1029:A:C8	2.49	0.46
25:a:1187:G:H5''	41:q:83:TYR:CE1	2.50	0.46
1:A:216:U:H2'	1:A:217:C:C6	2.50	0.46
1:A:769:G:H4'	1:A:1513:A:H4'	1.97	0.46
38:n:56:LYS:HD2	38:n:56:LYS:N	2.30	0.46
1:A:320:A:H2'	1:A:321:A:O4'	2.16	0.46
1:A:1014:A:H2	1:A:1219:A:H1'	1.78	0.46
25:a:613:A:H3'	25:a:614:A:H8	1.81	0.46
1:A:73:C:H2'	1:A:74:A:O4'	2.16	0.46
25:a:685:A:H5''	25:a:788:A:H62	1.80	0.46
25:a:1167:C:O2'	25:a:1168:G:H5'	2.16	0.46
1:A:1130:A:H61	1:A:1144:G:H1'	1.81	0.46
1:A:1306:A:H1'	1:A:1332:A:C2	2.50	0.46
25:a:2020:A:H5'	50:z:9:THR:CG2	2.45	0.46
1:A:745:G:O2'	1:A:746:A:H5'	2.15	0.46
1:A:1009:U:H2'	1:A:1010:U:H6	1.78	0.46
22:Z:46:G:H3'	22:Z:47:U:H5''	1.97	0.46
25:a:282:A:H3'	25:a:283:G:H8	1.79	0.46
25:a:593:U:H2'	25:a:594:U:C6	2.51	0.46
24:Y:47(F):A:H3'	24:Y:47(G):A:H8	1.80	0.46
25:a:1357:C:H2'	25:a:1358:G:O4'	2.15	0.46
1:A:519:C:H2'	1:A:520:A:C8	2.51	0.46
1:A:1128:C:O2'	1:A:1129:C:H5'	2.15	0.46
25:a:987:C:H2'	25:a:988:A:O4'	2.16	0.46
1:A:71:A:H5'	1:A:71:A:H8	1.80	0.46
1:A:337:G:H2'	1:A:338:A:C8	2.50	0.46
1:A:1028:C:H3'	1:A:1029:U:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:5:ARG:HG3	10:J:77:VAL:HG22	1.97	0.46
17:Q:64:CYS:SG	17:Q:74:THR:HG23	2.56	0.46
24:Y:22:A:H2'	24:Y:23:G:O4'	2.16	0.46
28:d:121:THR:HB	28:d:127:PHE:CD2	2.51	0.46
1:A:69:G:H2'	1:A:69:G:N3	2.31	0.45
2:B:5:SER:HB2	2:B:8:ASP:HB2	1.98	0.45
25:a:314:C:H2'	25:a:315:G:O4'	2.15	0.45
25:a:720:U:H2'	25:a:721:A:C8	2.50	0.45
25:a:1723:G:H2'	25:a:1724:G:O4'	2.16	0.45
25:a:2532:G:O2'	25:a:2657:A:N1	2.49	0.45
2:B:61:ALA:CB	2:B:221:VAL:HG13	2.45	0.45
25:a:1438:U:H2'	25:a:1439:A:C8	2.50	0.45
25:a:2514:U:H2'	25:a:2515:C:C6	2.51	0.45
25:a:2649:C:H2'	25:a:2650:U:C6	2.52	0.45
26:b:40:U:H1'	26:b:45:A:N6	2.31	0.45
1:A:384:G:H2'	1:A:385:C:C6	2.51	0.45
1:A:751:U:H2'	1:A:752:G:O4'	2.16	0.45
25:a:871:U:H2'	25:a:872:U:C6	2.51	0.45
25:a:1730:C:H5''	25:a:1730:C:C6	2.42	0.45
38:n:4:LYS:O	38:n:8:ILE:HG12	2.16	0.45
22:V:8:U:H1'	22:V:21:A:C2	2.51	0.45
25:a:277:G:H1'	25:a:278:A:C6	2.52	0.45
1:A:258:G:O2'	1:A:259:G:H5'	2.17	0.45
1:A:509:A:H2'	1:A:510:A:C8	2.52	0.45
1:A:999:C:O2	1:A:999:C:H2'	2.15	0.45
1:A:1412:C:H2'	1:A:1413:A:C8	2.51	0.45
4:D:103:TYR:HE1	4:D:110:THR:HA	1.80	0.45
25:a:139:U:H5''	25:a:140:C:H5	1.81	0.45
25:a:739:A:H1'	25:a:740:C:H5	1.82	0.45
1:A:691:G:H1'	1:A:696:A:N6	2.32	0.45
25:a:1869:G:N2	25:a:1871:A:H3'	2.32	0.45
1:A:697:U:H2'	1:A:698:G:H5'	1.99	0.45
1:A:1100:C:H3'	2:B:95:ARG:NH1	2.32	0.45
24:Y:47(F):A:N3	24:Y:47(F):A:H2'	2.31	0.45
25:a:2545:G:H2'	25:a:2546:U:O4'	2.16	0.45
26:b:117:G:OP1	38:n:56:LYS:HD3	2.17	0.45
25:a:1051:G:H3'	25:a:1052:C:C5	2.51	0.45
1:A:562:U:H1'	12:L:12:ARG:HB3	1.99	0.45
25:a:1323:C:C2'	25:a:1324:G:H5'	2.47	0.45
34:j:58:LEU:HD11	34:j:86:LEU:HD13	1.99	0.45
36:l:12:MET:HE3	36:l:12:MET:HB2	1.87	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:4:65:ASN:O	55:4:66:ILE:C	2.60	0.45
1:A:1435:G:H2'	1:A:1436:U:C6	2.52	0.45
2:B:66:LYS:CE	2:B:157:LEU:O	2.65	0.45
2:B:72:THR:OG1	2:B:169:GLU:OE2	2.33	0.45
25:a:1971:U:H5'	25:a:1972:G:H5''	1.98	0.45
25:a:2251:OMG:HM23	25:a:2251:OMG:H1'	1.59	0.45
1:A:31:G:O2'	1:A:48:C:N4	2.50	0.44
1:A:455:G:H3'	1:A:456:A:C8	2.49	0.44
1:A:591:U:O2'	1:A:592:G:H5'	2.17	0.44
1:A:909:A:H2'	1:A:910:C:O4'	2.16	0.44
1:A:945:G:C2	1:A:946:A:C8	3.05	0.44
22:Z:46:G:H5'	22:Z:47:U:OP2	2.17	0.44
25:a:2491:U:O2'	25:a:2492:U:H5'	2.17	0.44
41:q:6:GLN:HG3	41:q:39:LEU:HD11	1.98	0.44
1:A:235:C:H2'	1:A:236:A:C8	2.52	0.44
1:A:1305:G:N2	1:A:1331:G:H1'	2.31	0.44
2:B:71:GLY:O	2:B:93:ASN:HA	2.17	0.44
25:a:1199:U:H1'	40:p:4:VAL:HG22	1.98	0.44
1:A:123:U:OP1	1:A:312:C:H5'	2.18	0.44
3:C:110:GLU:HB2	3:C:144:LEU:HD12	1.99	0.44
4:D:178:MET:HE2	4:D:178:MET:HB3	1.73	0.44
25:a:11:C:H6	25:a:11:C:O5'	2.00	0.44
25:a:1637:A:H5'	25:a:1760:C:O2'	2.17	0.44
30:f:36:LEU:HD22	30:f:154:ILE:HG12	1.98	0.44
1:A:50:A:O2'	1:A:360:G:N2	2.50	0.44
1:A:476:U:H2'	1:A:477:C:C6	2.53	0.44
25:a:479:A:N3	25:a:481:G:H5''	2.32	0.44
25:a:643:A:N1	25:a:2369:A:O2'	2.42	0.44
1:A:59:A:H1'	1:A:354:G:N2	2.31	0.44
1:A:142:G:H3'	1:A:143:A:H8	1.82	0.44
1:A:1135:U:N3	1:A:1137:C:N3	2.66	0.44
13:M:67:GLY:HA3	30:f:113:ASP:OD2	2.17	0.44
24:Y:9:G:H1	24:Y:21:A:H2'	1.82	0.44
25:a:832:U:H2'	25:a:833:A:C8	2.52	0.44
25:a:2646:C:H6	25:a:2646:C:O5'	2.01	0.44
25:a:472:A:OP1	57:a:6190:SPD:H72	2.17	0.44
25:a:2895:G:H2'	25:a:2896:C:C6	2.52	0.44
30:f:95:ARG:NH2	55:4:1:MET:HE2	2.32	0.44
1:A:389:A:N3	1:A:389:A:H2'	2.32	0.44
1:A:746:A:H2'	1:A:747:A:C8	2.52	0.44
38:n:53:THR:HG21	38:n:70:ALA:HB1	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1469:C:H2'	1:A:1470:U:O4'	2.18	0.44
25:a:1019:U:H2'	25:a:1020:A:C8	2.53	0.44
1:A:455:G:H5'	1:A:456:A:OP2	2.17	0.44
1:A:651:C:N4	1:A:753:A:OP2	2.45	0.44
25:a:1342:A:OP1	43:s:40:LYS:NZ	2.40	0.44
25:a:1878:G:H2'	25:a:1879:C:O4'	2.17	0.44
25:a:2788:C:O2'	25:a:2809:A:N3	2.51	0.44
34:j:41:ILE:CD1	34:j:86:LEU:HD22	2.48	0.44
1:A:860:A:H2'	1:A:861:G:O4'	2.18	0.43
1:A:1001:C:H2'	1:A:1002:G:C8	2.52	0.43
25:a:1323:C:H2'	25:a:1324:G:H5'	2.00	0.43
28:d:1:MET:HG2	28:d:2:ILE:H	1.82	0.43
44:t:54:GLN:HG2	44:t:55:PRO:HD3	2.00	0.43
1:A:820:U:H4'	1:A:821:G:OP2	2.18	0.43
22:Z:17:C:H3'	22:Z:17(A):U:H6	1.83	0.43
25:a:609:A:H2'	25:a:610:C:O4'	2.17	0.43
26:b:76:G:OP1	45:u:9:ARG:NH1	2.49	0.43
1:A:1238:A:H2	1:A:1241:G:N3	2.17	0.43
1:A:1477:U:H2'	1:A:1478:U:C6	2.53	0.43
24:Y:47(B):G:H2'	24:Y:47(C):G:C8	2.53	0.43
24:Y:74:C:O2	24:Y:74:C:H2'	2.18	0.43
25:a:297:G:H2'	25:a:298:G:O4'	2.18	0.43
25:a:588:U:H2'	25:a:589:U:C6	2.53	0.43
25:a:817:C:H2'	25:a:818:G:O4'	2.17	0.43
45:u:1:MET:HG3	45:u:59:GLU:CD	2.43	0.43
1:A:82:G:N3	1:A:82:G:H2'	2.34	0.43
1:A:1377:A:H2'	7:G:7:ILE:CD1	2.49	0.43
22:V:59:A:H3'	22:V:60:U:H6	1.84	0.43
26:b:24:G:N7	26:b:56:G:H2'	2.33	0.43
33:i:4:PHE:O	40:p:64:ARG:NH1	2.48	0.43
1:A:1002:G:H1	1:A:1038:C:H42	1.64	0.43
24:Y:47(O):A:H2'	24:Y:47(P):U:C6	2.53	0.43
25:a:1028:A:N6	25:a:1125:G:H2'	2.33	0.43
1:A:86:G:H1'	1:A:87:C:C1'	2.49	0.43
2:B:125:THR:C	2:B:127:ASP:N	2.77	0.43
22:Z:23:C:H2'	22:Z:24:U:C6	2.54	0.43
25:a:881:G:H1	25:a:895:U:H3	1.66	0.43
34:j:63:VAL:HG12	34:j:107:LEU:HD11	2.00	0.43
1:A:215:C:H2'	1:A:216:U:C6	2.54	0.43
1:A:381:C:H2'	1:A:382:A:O4'	2.19	0.43
17:Q:47:HIS:HB3	17:Q:74:THR:HG22	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Y:76:A:H2	25:a:2583:G:N3	2.17	0.43
25:a:284:U:H2'	25:a:285:G:C8	2.54	0.43
46:v:38:VAL:HG12	46:v:59:LEU:HB2	1.99	0.43
25:a:357:C:H2'	25:a:358:U:C6	2.52	0.43
25:a:1816:C:N4	27:c:35:GLU:OE1	2.47	0.43
30:f:117:LEU:HD12	30:f:176:PRO:HD2	2.01	0.43
1:A:461:A:HO2'	1:A:462:G:H5'	1.82	0.43
1:A:839:C:H42	1:A:847:G:H1	1.67	0.43
25:a:909:A:H2'	25:a:912:C:C5	2.54	0.43
25:a:2511:U:H2'	25:a:2512:C:O4'	2.19	0.43
25:a:2812:G:H2'	25:a:2813:A:O4'	2.19	0.43
41:q:14:VAL:HG11	41:q:20:VAL:HG21	2.01	0.43
1:A:1397:C:N4	23:X:22:A:H2'	2.34	0.43
25:a:5:A:H2'	25:a:6:A:C8	2.53	0.43
25:a:367:G:H3'	25:a:368:A:H8	1.83	0.43
25:a:857:G:H2'	25:a:858:G:O4'	2.19	0.43
12:L:74:LEU:HD21	12:L:104:CYS:HA	2.00	0.42
25:a:139:U:H5''	25:a:140:C:C5	2.54	0.42
25:a:738:G:H2'	25:a:739:A:C8	2.54	0.42
25:a:784:G:H5'	25:a:785:G:OP1	2.19	0.42
30:f:69:LYS:HE3	30:f:69:LYS:HB3	1.84	0.42
44:t:54:GLN:N	44:t:55:PRO:HD2	2.34	0.42
1:A:1043:G:H2'	1:A:1044:A:O4'	2.18	0.42
1:A:1534:A:O5'	1:A:1534:A:H8	2.02	0.42
25:a:636:G:N7	35:k:109:LYS:NZ	2.58	0.42
43:s:69:ARG:NH1	43:s:74:ILE:HD13	2.34	0.42
44:t:54:GLN:H	44:t:54:GLN:CD	2.24	0.42
1:A:405:U:OP2	4:D:3:ARG:NH1	2.43	0.42
1:A:746:A:H8	1:A:746:A:OP2	2.01	0.42
1:A:996:A:O2'	1:A:997:U:H5'	2.19	0.42
1:A:1062:U:O4	3:C:2:GLY:HA2	2.19	0.42
16:P:12:LYS:HG2	16:P:13:LYS:HG2	2.00	0.42
26:b:26:C:H2'	26:b:27:C:O4'	2.19	0.42
1:A:555:U:H2'	1:A:556:C:C6	2.55	0.42
22:V:65:C:H2'	22:V:66:C:C6	2.55	0.42
25:a:350:G:H2'	25:a:351:C:O4'	2.19	0.42
25:a:634:C:H2'	25:a:635:C:C6	2.54	0.42
25:a:1108:U:O2	25:a:1108:U:H2'	2.18	0.42
25:a:2618:G:H21	28:d:155:VAL:HG21	1.85	0.42
26:b:15:A:H3'	26:b:16:G:H8	1.85	0.42
1:A:184:G:H2'	1:A:185:U:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:908:A:H2'	1:A:909:A:C8	2.55	0.42
24:Y:20(A):H2U:H62	24:Y:20(A):H2U:H2'	1.86	0.42
25:a:404:A:H4'	25:a:405:U:O5'	2.19	0.42
25:a:1180:U:H2'	25:a:1181:U:O4'	2.19	0.42
25:a:2395:C:H2'	25:a:2396:G:O4'	2.19	0.42
28:d:62:LYS:N	28:d:63:PRO:HD2	2.34	0.42
38:n:39:VAL:HG11	38:n:87:ILE:HD13	2.01	0.42
1:A:125:U:O2'	1:A:126:G:H5'	2.20	0.42
1:A:1497:G:H1'	1:A:1518:MA6:H2	2.00	0.42
7:G:78:ARG:HH21	7:G:154:TYR:HB3	1.84	0.42
21:U:58:LYS:O	21:U:59:LYS:C	2.63	0.42
30:f:106:ILE:C	30:f:109:PRO:HD2	2.44	0.42
30:f:162:SER:OG	30:f:165:GLU:OE2	2.34	0.42
10:J:5:ARG:HD3	10:J:75:ASP:HB3	2.02	0.42
10:J:10:LEU:HD22	10:J:98:VAL:HG22	2.02	0.42
24:Y:76:A:C2	25:a:2583:G:N3	2.88	0.42
25:a:363:G:H2'	25:a:364:C:C6	2.54	0.42
25:a:2339:C:H2'	25:a:2340:A:C8	2.54	0.42
43:s:67:VAL:HG12	43:s:74:ILE:HD11	2.02	0.42
7:G:40:GLU:CD	9:I:41:ARG:HH22	2.28	0.42
25:a:172:A:H2'	25:a:173:A:C8	2.55	0.42
25:a:1880:U:H2'	25:a:1881:C:C6	2.54	0.42
25:a:2799:A:O2'	25:a:2800:A:H5''	2.19	0.42
1:A:399:G:H2'	1:A:400:C:C6	2.54	0.42
1:A:502:A:H2'	1:A:503:C:O4'	2.20	0.42
1:A:953:G:H2'	1:A:954:G:O4'	2.20	0.42
4:D:25:VAL:HG23	4:D:26:ARG:H	1.85	0.42
25:a:1386:C:H2'	25:a:1387:A:C8	2.55	0.42
1:A:188:C:H2'	1:A:189:A:C8	2.55	0.41
1:A:462:G:H2'	1:A:463:U:O5'	2.20	0.41
1:A:494:G:O2'	1:A:496:A:H1'	2.20	0.41
1:A:868:C:H2'	1:A:869:G:O4'	2.20	0.41
1:A:891:U:H2'	1:A:892:A:H8	1.85	0.41
1:A:1142:G:H2'	1:A:1143:G:O4'	2.20	0.41
4:D:140:ASN:N	4:D:182:PHE:O	2.46	0.41
25:a:570:G:H2'	25:a:2030:6MZ:N7	2.35	0.41
25:a:1846:G:H2'	25:a:1847:A:O4'	2.20	0.41
29:e:23:PHE:CE1	35:k:1:MET:SD	3.13	0.41
1:A:86:G:H1'	1:A:87:C:O4'	2.19	0.41
1:A:1141:C:H2'	1:A:1142:G:C8	2.55	0.41
25:a:1370:C:H2'	25:a:1371:G:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:a:2243:U:H2'	25:a:2244:U:C6	2.55	0.41
26:b:31:C:O2'	26:b:53:A:N1	2.46	0.41
30:f:22:TYR:OH	30:f:165:GLU:HG2	2.19	0.41
1:A:17:U:H2'	1:A:18:C:C6	2.55	0.41
1:A:371:A:H2'	1:A:372:C:O4'	2.20	0.41
1:A:470:C:H2'	1:A:471:U:C6	2.54	0.41
1:A:1391:U:H2'	1:A:1392:G:C8	2.55	0.41
1:A:1450:U:H3'	1:A:1452:C:N4	2.36	0.41
22:V:35:A:H2'	22:V:37:A:C8	2.55	0.41
23:X:13:A:O5'	23:X:13:A:H8	2.03	0.41
25:a:360:U:C4	25:a:361:G:C6	3.07	0.41
25:a:767:U:O4	59:a:6193:SPM:H131	2.20	0.41
25:a:2869:G:H2'	25:a:2870:C:O4'	2.20	0.41
1:A:1314:C:H2'	1:A:1315:U:C6	2.54	0.41
22:V:24:U:H2'	22:V:25:C:C6	2.55	0.41
24:Y:47(A):C:H2'	24:Y:47(B):G:C8	2.55	0.41
25:a:580:U:O3'	40:p:31:VAL:HG13	2.20	0.41
1:A:250:A:H4'	1:A:251:G:O5'	2.21	0.41
1:A:1001:C:H2'	1:A:1002:G:H8	1.85	0.41
1:A:1029:U:O3'	1:A:1032:G:O6	2.38	0.41
24:Y:19:G:OP2	24:Y:20:C:N4	2.53	0.41
25:a:1044:C:O2'	25:a:1111:A:N1	2.47	0.41
22:V:6:G:C2	22:V:68:C:C2	3.09	0.41
25:a:63:A:H2	43:s:70:HIS:CE1	2.39	0.41
43:s:3:ARG:H	43:s:3:ARG:HG3	1.64	0.41
1:A:1273:C:H2'	1:A:1274:A:O4'	2.21	0.41
4:D:102:VAL:HG13	4:D:107:PHE:HB2	2.02	0.41
4:D:134:SER:O	4:D:135:TYR:C	2.62	0.41
24:Y:47(N):C:H2'	24:Y:47(O):A:H8	1.84	0.41
24:Y:69:C:H3'	24:Y:70:A:H8	1.86	0.41
25:a:127:A:H5''	25:a:128:C:C6	2.56	0.41
25:a:2496:C:OP1	36:l:81:4D4:H5	2.20	0.41
1:A:179:A:H2'	1:A:180:U:O4'	2.21	0.41
1:A:190:A:H2'	1:A:191:G:O4'	2.21	0.41
1:A:691:G:H1'	1:A:696:A:H61	1.86	0.41
2:B:66:LYS:HE3	2:B:158:PRO:HA	2.02	0.41
22:V:72:A:H3'	22:V:73:A:C8	2.55	0.41
24:Y:25:C:H2'	24:Y:26:G:O4'	2.21	0.41
24:Y:47(I):A:C8	24:Y:47(J):G:H1'	2.56	0.41
25:a:158:U:H1'	25:a:169:G:N2	2.36	0.41
1:A:82:G:N2	1:A:84:U:OP1	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:604:G:H2'	1:A:605:U:O4'	2.21	0.41
1:A:1144:G:O2'	1:A:1145:A:H5'	2.21	0.41
1:A:1451:U:H5''	1:A:1452:C:C5	2.56	0.41
4:D:103:TYR:CE1	4:D:110:THR:HA	2.55	0.41
16:P:45:GLU:O	16:P:46:LYS:HB3	2.21	0.41
23:X:14:A:O5'	23:X:14:A:H8	2.04	0.41
24:Y:20(B):G:O6	24:Y:48:C:H5''	2.21	0.41
25:a:1039:A:H2	25:a:1116:G:H22	1.68	0.41
25:a:1181:U:H2'	25:a:1182:G:C8	2.56	0.41
25:a:1570:A:H2'	25:a:1571:A:C8	2.56	0.41
30:f:36:LEU:O	30:f:88:LYS:HA	2.21	0.41
1:A:1296:C:H4'	1:A:1302:C:N4	2.36	0.41
25:a:163:C:H2'	25:a:164:C:C6	2.55	0.41
25:a:984:A:N3	25:a:984:A:H2'	2.37	0.41
27:c:232:HIS:HA	27:c:242:LYS:HD2	2.03	0.41
30:f:136:ILE:HD13	30:f:136:ILE:HA	1.87	0.41
1:A:442:G:H1	1:A:492:C:H42	1.69	0.40
1:A:487:A:H2'	1:A:488:C:O4'	2.20	0.40
1:A:977:A:O2'	1:A:979:C:OP2	2.39	0.40
4:D:145:ILE:HG21	4:D:178:MET:SD	2.60	0.40
25:a:287:G:H2'	25:a:288:U:C6	2.56	0.40
25:a:1649:G:O2'	37:m:106:ASP:OD2	2.29	0.40
25:a:1858:A:N6	25:a:1884:G:H1'	2.36	0.40
25:a:2496:C:O2'	25:a:2497:A:H5'	2.21	0.40
42:r:20:VAL:HG11	42:r:44:ALA:HA	2.03	0.40
1:A:68:G:C5	1:A:69:G:H1'	2.56	0.40
1:A:736:C:H5'	6:F:88:MET:HE2	2.02	0.40
8:H:64:LYS:HG3	8:H:71:VAL:HG21	2.02	0.40
13:M:11:ASP:HA	13:M:45:ILE:HB	2.04	0.40
22:V:14:A:C2	22:V:22:G:H1'	2.56	0.40
22:V:66:C:H2'	22:V:67:C:C6	2.57	0.40
25:a:528:A:N7	25:a:2043:C:H5'	2.36	0.40
25:a:546:U:O2	25:a:546:U:O4'	2.39	0.40
25:a:747:5MU:C5M	25:a:2612:C:H4'	2.51	0.40
25:a:876:C:H2'	25:a:877:A:O4'	2.22	0.40
25:a:1808:A:H3'	25:a:1809:A:C8	2.56	0.40
38:n:110:ALA:HB3	38:n:117:PHE:HZ	1.86	0.40
1:A:594:U:H2'	1:A:595:A:O4'	2.21	0.40
25:a:286:U:H2'	25:a:287:G:C8	2.57	0.40
25:a:780:G:H2'	25:a:782:A:N7	2.37	0.40
1:A:203:G:N2	1:A:215:C:C2	2.89	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:941:G:C2'	1:A:942:G:O5'	2.70	0.40
1:A:1518:MA6:H103	1:A:1519:MA6:H102	2.04	0.40
25:a:1027:A:C2	25:a:2488:G:H5'	2.56	0.40
25:a:1333:G:C2'	25:a:1334:G:H5'	2.52	0.40
25:a:1995:U:H3'	25:a:1996:C:H2'	2.03	0.40
25:a:2079:U:H2'	25:a:2080:A:O4'	2.22	0.40
25:a:2389:G:H5''	25:a:2390:U:O4'	2.21	0.40
1:A:127:G:O2'	17:Q:6:ARG:NH1	2.54	0.40
4:D:103:TYR:HD1	4:D:110:THR:C	2.29	0.40
25:a:69:C:C2'	25:a:70:G:H5'	2.51	0.40
25:a:632:A:H2'	25:a:633:A:C8	2.56	0.40
25:a:703:U:H2'	25:a:704:G:O4'	2.22	0.40
25:a:911:A:OP1	57:a:6192:SPD:H51	2.21	0.40
25:a:1496:A:H2'	25:a:1498:C:C5	2.55	0.40
25:a:2066:C:O2'	25:a:2067:G:H5'	2.21	0.40
25:a:2345:G:N3	25:a:2381:A:H2'	2.36	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	222/241 (92%)	208 (94%)	14 (6%)	0	100	100
3	C	204/233 (88%)	199 (98%)	5 (2%)	0	100	100
4	D	203/206 (98%)	194 (96%)	9 (4%)	0	100	100
5	E	154/167 (92%)	149 (97%)	5 (3%)	0	100	100
6	F	101/135 (75%)	97 (96%)	4 (4%)	0	100	100
7	G	151/179 (84%)	147 (97%)	4 (3%)	0	100	100
8	H	127/130 (98%)	119 (94%)	8 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	I	125/130 (96%)	119 (95%)	6 (5%)	0	100	100
10	J	96/103 (93%)	94 (98%)	1 (1%)	1 (1%)	13	26
11	K	113/129 (88%)	110 (97%)	3 (3%)	0	100	100
12	L	120/124 (97%)	118 (98%)	2 (2%)	0	100	100
13	M	113/118 (96%)	111 (98%)	2 (2%)	0	100	100
14	N	98/101 (97%)	98 (100%)	0	0	100	100
15	O	86/89 (97%)	85 (99%)	1 (1%)	0	100	100
16	P	79/82 (96%)	78 (99%)	1 (1%)	0	100	100
17	Q	77/84 (92%)	76 (99%)	1 (1%)	0	100	100
18	R	64/75 (85%)	63 (98%)	1 (2%)	0	100	100
19	S	82/92 (89%)	81 (99%)	1 (1%)	0	100	100
20	T	84/87 (97%)	84 (100%)	0	0	100	100
21	U	68/71 (96%)	66 (97%)	2 (3%)	0	100	100
27	c	269/273 (98%)	262 (97%)	7 (3%)	0	100	100
28	d	206/209 (99%)	200 (97%)	6 (3%)	0	100	100
29	e	199/201 (99%)	194 (98%)	5 (2%)	0	100	100
30	f	175/179 (98%)	171 (98%)	4 (2%)	0	100	100
31	g	171/177 (97%)	165 (96%)	6 (4%)	0	100	100
32	h	39/149 (26%)	36 (92%)	3 (8%)	0	100	100
33	i	140/142 (99%)	140 (100%)	0	0	100	100
34	j	121/123 (98%)	118 (98%)	3 (2%)	0	100	100
35	k	142/144 (99%)	139 (98%)	3 (2%)	0	100	100
36	l	132/136 (97%)	128 (97%)	4 (3%)	0	100	100
37	m	116/127 (91%)	113 (97%)	3 (3%)	0	100	100
38	n	114/117 (97%)	112 (98%)	2 (2%)	0	100	100
39	o	112/115 (97%)	108 (96%)	4 (4%)	0	100	100
40	p	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
41	q	101/103 (98%)	99 (98%)	2 (2%)	0	100	100
42	r	108/110 (98%)	107 (99%)	1 (1%)	0	100	100
43	s	91/100 (91%)	88 (97%)	3 (3%)	0	100	100
44	t	100/104 (96%)	96 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	u	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
46	v	82/85 (96%)	78 (95%)	4 (5%)	0	100	100
47	w	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
48	x	59/63 (94%)	59 (100%)	0	0	100	100
49	y	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
50	z	54/57 (95%)	53 (98%)	1 (2%)	0	100	100
51	0	49/55 (89%)	49 (100%)	0	0	100	100
52	1	44/46 (96%)	44 (100%)	0	0	100	100
53	2	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
54	3	36/38 (95%)	36 (100%)	0	0	100	100
55	4	56/70 (80%)	51 (91%)	5 (9%)	0	100	100
All	All	5483/5913 (93%)	5335 (97%)	147 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	J	57	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	
2	B	186/199 (94%)	183 (98%)	3 (2%)	58	78
3	C	170/190 (90%)	170 (100%)	0	100	100
4	D	172/173 (99%)	170 (99%)	2 (1%)	67	84
5	E	119/126 (94%)	119 (100%)	0	100	100
6	F	90/116 (78%)	90 (100%)	0	100	100
7	G	126/147 (86%)	125 (99%)	1 (1%)	79	91
8	H	104/105 (99%)	104 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	I	105/107 (98%)	104 (99%)	1 (1%)	73	87
10	J	86/90 (96%)	86 (100%)	0	100	100
11	K	89/98 (91%)	89 (100%)	0	100	100
12	L	102/103 (99%)	100 (98%)	2 (2%)	50	73
13	M	93/96 (97%)	93 (100%)	0	100	100
14	N	83/84 (99%)	83 (100%)	0	100	100
15	O	76/77 (99%)	76 (100%)	0	100	100
16	P	65/65 (100%)	64 (98%)	1 (2%)	60	80
17	Q	73/78 (94%)	73 (100%)	0	100	100
18	R	57/65 (88%)	56 (98%)	1 (2%)	54	76
19	S	72/79 (91%)	72 (100%)	0	100	100
20	T	65/66 (98%)	65 (100%)	0	100	100
21	U	60/61 (98%)	58 (97%)	2 (3%)	33	57
27	c	216/218 (99%)	215 (100%)	1 (0%)	86	95
28	d	163/163 (100%)	161 (99%)	2 (1%)	67	84
29	e	165/165 (100%)	165 (100%)	0	100	100
30	f	148/150 (99%)	143 (97%)	5 (3%)	32	56
31	g	134/138 (97%)	132 (98%)	2 (2%)	60	80
32	h	32/114 (28%)	32 (100%)	0	100	100
33	i	116/116 (100%)	114 (98%)	2 (2%)	56	77
34	j	104/104 (100%)	104 (100%)	0	100	100
35	k	103/103 (100%)	103 (100%)	0	100	100
36	l	107/107 (100%)	107 (100%)	0	100	100
37	m	98/103 (95%)	98 (100%)	0	100	100
38	n	86/87 (99%)	82 (95%)	4 (5%)	22	43
39	o	99/100 (99%)	99 (100%)	0	100	100
40	p	89/90 (99%)	89 (100%)	0	100	100
41	q	84/84 (100%)	84 (100%)	0	100	100
42	r	93/93 (100%)	93 (100%)	0	100	100
43	s	80/84 (95%)	80 (100%)	0	100	100
44	t	83/85 (98%)	83 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	u	78/78 (100%)	77 (99%)	1 (1%)	65	83
46	v	61/63 (97%)	60 (98%)	1 (2%)	58	78
47	w	67/68 (98%)	67 (100%)	0	100	100
48	x	54/55 (98%)	53 (98%)	1 (2%)	52	75
49	y	48/49 (98%)	48 (100%)	0	100	100
50	z	47/48 (98%)	47 (100%)	0	100	100
51	0	46/49 (94%)	46 (100%)	0	100	100
52	1	38/38 (100%)	38 (100%)	0	100	100
53	2	51/52 (98%)	51 (100%)	0	100	100
54	3	34/34 (100%)	34 (100%)	0	100	100
55	4	55/62 (89%)	54 (98%)	1 (2%)	54	76
All	All	4572/4825 (95%)	4539 (99%)	33 (1%)	80	92

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	36	ASN
2	B	118	GLU
2	B	161	LEU
4	D	25	VAL
4	D	99	ASP
7	G	2	PRO
9	I	59	GLU
12	L	14	ARG
12	L	15	LYS
16	P	55	ASP
18	R	74	HIS
21	U	60	LEU
21	U	63	GLU
27	c	37	ASN
28	d	32	ASN
28	d	208	LYS
30	f	32	GLU
30	f	50	LEU
30	f	120	LYS
30	f	136	ILE
30	f	150	ARG
31	g	43	VAL

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Mol	Chain	Res	Type
31	g	48	ASN
33	i	1	MET
33	i	9	GLU
38	n	13	ARG
38	n	16	ARG
38	n	45	SER
38	n	87	ILE
45	u	65	VAL
46	v	10	THR
48	x	6	LEU
55	4	28	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (61) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	58	ASN
2	B	103	ASN
2	B	146	ASN
2	B	170	HIS
2	B	177	ASN
2	B	178	ASN
3	C	102	ASN
3	C	139	GLN
3	C	140	ASN
4	D	136	GLN
4	D	152	GLN
5	E	82	GLN
5	E	132	ASN
5	E	148	ASN
6	F	46	GLN
6	F	68	GLN
7	G	68	ASN
7	G	86	GLN
8	H	21	ASN
9	I	4	ASN
9	I	31	ASN
9	I	32	GLN
10	J	56	HIS
10	J	58	ASN
11	K	118	HIS
12	L	112	GLN
13	M	8	ASN

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Mol	Chain	Res	Type
14	N	4	GLN
15	O	35	GLN
15	O	80	GLN
16	P	79	ASN
17	Q	9	GLN
18	R	52	GLN
20	T	3	ASN
20	T	13	GLN
20	T	61	GLN
27	c	25	HIS
28	d	164	GLN
29	e	92	HIS
31	g	30	ASN
31	g	73	ASN
32	h	20	ASN
33	i	58	ASN
33	i	80	HIS
33	i	86	GLN
34	j	5	GLN
35	k	104	GLN
36	l	97	GLN
37	m	73	ASN
38	n	100	HIS
41	q	6	GLN
41	q	12	HIS
42	r	9	HIS
43	s	70	HIS
44	t	53	ASN
48	x	15	ASN
48	x	27	ASN
48	x	39	GLN
48	x	45	GLN
55	4	20	ASN
55	4	61	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1517/1542 (98%)	203 (13%)	27 (1%)
22	V	75/76 (98%)	35 (46%)	3 (4%)
22	Z	75/76 (98%)	27 (36%)	4 (5%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
23	X	10/24 (41%)	3 (30%)	1 (10%)
24	Y	92/93 (98%)	16 (17%)	1 (1%)
25	a	2747/2904 (94%)	689 (25%)	0
26	b	118/120 (98%)	32 (27%)	0
All	All	4634/4835 (95%)	1005 (21%)	36 (0%)

All (1005) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	3	A
1	A	4	U
1	A	5	U
1	A	6	G
1	A	7	A
1	A	8	A
1	A	9	G
1	A	31	G
1	A	32	A
1	A	39	G
1	A	47	C
1	A	48	C
1	A	50	A
1	A	51	A
1	A	60	A
1	A	70	U
1	A	71	A
1	A	72	A
1	A	74	A
1	A	75	G
1	A	81	A
1	A	82	G
1	A	83	C
1	A	84	U
1	A	85	U
1	A	86	G
1	A	87	C
1	A	88	U
1	A	94	G
1	A	95	C
1	A	96	U
1	A	120	A
1	A	121	U

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Mol	Chain	Res	Type
1	A	128	G
1	A	131	A
1	A	141	G
1	A	144	G
1	A	164	G
1	A	166	U
1	A	183	C
1	A	197	A
1	A	240	G
1	A	245	U
1	A	247	G
1	A	250	A
1	A	251	G
1	A	266	G
1	A	267	C
1	A	280	C
1	A	289	G
1	A	321	A
1	A	328	C
1	A	330	C
1	A	339	C
1	A	346	G
1	A	352	C
1	A	354	G
1	A	367	U
1	A	368	U
1	A	372	C
1	A	406	G
1	A	412	A
1	A	413	G
1	A	421	U
1	A	424	G
1	A	428	G
1	A	429	U
1	A	430	A
1	A	436	C
1	A	439	U
1	A	455	G
1	A	456	A
1	A	457	G
1	A	458	U
1	A	459	A

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Mol	Chain	Res	Type
1	A	463	U
1	A	468	A
1	A	469	C
1	A	479	U
1	A	481	G
1	A	486	U
1	A	498	A
1	A	511	C
1	A	517	G
1	A	518	C
1	A	519	C
1	A	547	A
1	A	572	A
1	A	573	A
1	A	575	G
1	A	576	C
1	A	596	A
1	A	653	U
1	A	665	A
1	A	687	A
1	A	688	G
1	A	703	G
1	A	723	U
1	A	724	G
1	A	734	G
1	A	746	A
1	A	748	G
1	A	755	G
1	A	759	A
1	A	777	A
1	A	793	U
1	A	794	A
1	A	815	A
1	A	817	C
1	A	832	G
1	A	839	C
1	A	871	U
1	A	890	G
1	A	902	G
1	A	914	A
1	A	926	G
1	A	934	C

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Mol	Chain	Res	Type
1	A	960	U
1	A	966	2MG
1	A	969	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	984	C
1	A	991	U
1	A	992	U
1	A	993	G
1	A	994	A
1	A	997	U
1	A	1000	A
1	A	1003	G
1	A	1004	A
1	A	1008	U
1	A	1009	U
1	A	1010	U
1	A	1026	G
1	A	1027	C
1	A	1029	U
1	A	1031	C
1	A	1033	G
1	A	1034	G
1	A	1035	A
1	A	1036	A
1	A	1039	G
1	A	1042	A
1	A	1044	A
1	A	1055	A
1	A	1065	U
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1124	G
1	A	1126	U
1	A	1129	C
1	A	1132	C
1	A	1137	C
1	A	1139	G
1	A	1145	A
1	A	1146	A

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Mol	Chain	Res	Type
1	A	1157	A
1	A	1159	U
1	A	1196	A
1	A	1197	A
1	A	1200	C
1	A	1213	A
1	A	1225	A
1	A	1227	A
1	A	1236	A
1	A	1238	A
1	A	1256	A
1	A	1257	A
1	A	1260	G
1	A	1279	G
1	A	1280	A
1	A	1286	U
1	A	1287	A
1	A	1300	G
1	A	1302	C
1	A	1317	C
1	A	1319	A
1	A	1320	C
1	A	1338	G
1	A	1346	A
1	A	1353	G
1	A	1363	A
1	A	1378	C
1	A	1379	G
1	A	1397	C
1	A	1419	G
1	A	1441	A
1	A	1445	U
1	A	1448	C
1	A	1451	U
1	A	1493	A
1	A	1494	G
1	A	1497	G
1	A	1503	A
1	A	1505	G
1	A	1506	U
1	A	1517	G
1	A	1529	G

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Mol	Chain	Res	Type
1	A	1530	G
1	A	1534	A
22	V	5	G
22	V	6	G
22	V	8	U
22	V	9	G
22	V	10	G
22	V	11	A
22	V	13	C
22	V	14	A
22	V	16	C
22	V	17	C
22	V	17(A)	U
22	V	18	G
22	V	19	G
22	V	20	U
22	V	21	A
22	V	22	G
22	V	26	G
22	V	31	G
22	V	36	U
22	V	37	A
22	V	43	A
22	V	44	A
22	V	46	G
22	V	47	U
22	V	48	C
22	V	49	G
22	V	56	C
22	V	57	A
22	V	58	A
22	V	64	G
22	V	65	C
22	V	69	C
22	V	72	A
22	V	74	C
22	V	76	A
23	X	18	G
23	X	19	G
23	X	23	A
24	Y	7	G
24	Y	8	4SU

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Mol	Chain	Res	Type
24	Y	13	G
24	Y	16	A
24	Y	18	G
24	Y	20(B)	G
24	Y	32	RSP
24	Y	37	T6A
24	Y	45	A
24	Y	47(J)	G
24	Y	47(K)	C
24	Y	48	C
24	Y	70	A
24	Y	71	C
24	Y	72	C
24	Y	74	C
22	Z	7	G
22	Z	8	U
22	Z	9	G
22	Z	13	C
22	Z	14	A
22	Z	17	C
22	Z	17(A)	U
22	Z	18	G
22	Z	19	G
22	Z	20	U
22	Z	21	A
22	Z	31	G
22	Z	32	C
22	Z	34	C
22	Z	39	C
22	Z	43	A
22	Z	46	G
22	Z	47	U
22	Z	48	C
22	Z	49	G
22	Z	52	G
22	Z	56	C
22	Z	58	A
22	Z	61	C
22	Z	70	G
22	Z	71	C
22	Z	76	A
25	a	10	A

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Mol	Chain	Res	Type
25	a	11	C
25	a	12	U
25	a	13	A
25	a	22	C
25	a	33	C
25	a	34	U
25	a	35	G
25	a	41	C
25	a	42	A
25	a	43	G
25	a	45	G
25	a	49	A
25	a	51	G
25	a	54	G
25	a	58	G
25	a	62	U
25	a	63	A
25	a	69	C
25	a	70	G
25	a	71	A
25	a	74	A
25	a	75	G
25	a	80	G
25	a	101	A
25	a	102	U
25	a	103	A
25	a	110	G
25	a	114	U
25	a	118	A
25	a	119	A
25	a	120	U
25	a	129	C
25	a	133	U
25	a	135	U
25	a	136	G
25	a	137	U
25	a	138	U
25	a	139	U
25	a	140	C
25	a	141	G
25	a	142	A
25	a	143	C

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Mol	Chain	Res	Type
25	a	154	U
25	a	157	C
25	a	160	A
25	a	163	C
25	a	164	C
25	a	170	U
25	a	181	A
25	a	186	G
25	a	195	A
25	a	196	A
25	a	199	A
25	a	200	U
25	a	215	G
25	a	216	A
25	a	221	A
25	a	222	A
25	a	223	A
25	a	227	A
25	a	230	G
25	a	231	A
25	a	241	A
25	a	248	G
25	a	258	G
25	a	264	C
25	a	265	A
25	a	271	G
25	a	272	A
25	a	274	C
25	a	277	G
25	a	278	A
25	a	279	A
25	a	280	U
25	a	281	C
25	a	282	A
25	a	283	G
25	a	284	U
25	a	285	G
25	a	288	U
25	a	289	G
25	a	291	G
25	a	292	U
25	a	294	A

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Mol	Chain	Res	Type
25	a	311	A
25	a	312	G
25	a	322	A
25	a	329	G
25	a	330	A
25	a	331	C
25	a	333	G
25	a	339	U
25	a	342	A
25	a	343	C
25	a	345	A
25	a	349	U
25	a	351	C
25	a	354	A
25	a	356	G
25	a	357	C
25	a	361	G
25	a	362	A
25	a	367	G
25	a	383	C
25	a	385	C
25	a	386	G
25	a	389	G
25	a	396	G
25	a	404	A
25	a	405	U
25	a	411	G
25	a	412	A
25	a	425	G
25	a	431	U
25	a	434	U
25	a	437	U
25	a	443	A
25	a	451	U
25	a	454	A
25	a	455	C
25	a	462	C
25	a	468	G
25	a	481	G
25	a	487	C
25	a	490	C
25	a	491	G

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Mol	Chain	Res	Type
25	a	495	G
25	a	497	A
25	a	498	G
25	a	504	A
25	a	505	A
25	a	509	C
25	a	513	A
25	a	517	C
25	a	525	U
25	a	530	G
25	a	531	C
25	a	532	A
25	a	536	G
25	a	537	G
25	a	540	C
25	a	544	C
25	a	545	U
25	a	547	A
25	a	548	G
25	a	549	G
25	a	554	U
25	a	558	U
25	a	563	A
25	a	573	U
25	a	575	A
25	a	586	A
25	a	590	A
25	a	603	A
25	a	614	A
25	a	615	U
25	a	620	G
25	a	621	A
25	a	623	C
25	a	627	A
25	a	629	G
25	a	637	A
25	a	645	C
25	a	647	G
25	a	654	A
25	a	655	A
25	a	659	G
25	a	664	G

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Mol	Chain	Res	Type
25	a	667	U
25	a	670	A
25	a	674	G
25	a	680	C
25	a	683	U
25	a	684	G
25	a	685	A
25	a	686	U
25	a	696	G
25	a	717	C
25	a	718	A
25	a	722	A
25	a	726	G
25	a	728	G
25	a	730	A
25	a	732	C
25	a	733	G
25	a	743	A
25	a	746	PSU
25	a	747	5MU
25	a	764	A
25	a	765	C
25	a	770	G
25	a	775	G
25	a	776	G
25	a	777	G
25	a	782	A
25	a	784	G
25	a	785	G
25	a	787	C
25	a	789	A
25	a	791	C
25	a	792	A
25	a	793	A
25	a	794	A
25	a	805	G
25	a	806	C
25	a	812	C
25	a	827	U
25	a	828	U
25	a	829	A
25	a	831	G

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Mol	Chain	Res	Type
25	a	842	U
25	a	845	A
25	a	846	U
25	a	847	U
25	a	856	G
25	a	859	G
25	a	860	U
25	a	870	U
25	a	873	C
25	a	874	G
25	a	875	G
25	a	878	A
25	a	879	G
25	a	882	G
25	a	883	G
25	a	884	U
25	a	885	C
25	a	887	U
25	a	888	C
25	a	889	C
25	a	890	C
25	a	891	G
25	a	893	C
25	a	894	U
25	a	895	U
25	a	896	A
25	a	897	C
25	a	898	C
25	a	905	A
25	a	907	G
25	a	910	A
25	a	914	G
25	a	915	C
25	a	931	U
25	a	934	U
25	a	939	G
25	a	946	C
25	a	948	C
25	a	952	G
25	a	957	C
25	a	958	U
25	a	960	A

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Mol	Chain	Res	Type
25	a	961	C
25	a	974	G
25	a	983	A
25	a	984	A
25	a	985	C
25	a	989	G
25	a	990	A
25	a	991	C
25	a	994	C
25	a	996	A
25	a	1005	C
25	a	1006	C
25	a	1010	A
25	a	1012	U
25	a	1013	C
25	a	1018	U
25	a	1033	U
25	a	1040	A
25	a	1046	A
25	a	1047	G
25	a	1048	A
25	a	1051	G
25	a	1108	U
25	a	1109	C
25	a	1110	G
25	a	1111	A
25	a	1112	G
25	a	1115	G
25	a	1116	G
25	a	1118	C
25	a	1122	G
25	a	1130	U
25	a	1132	U
25	a	1135	C
25	a	1137	G
25	a	1141	U
25	a	1142	A
25	a	1145	C
25	a	1155	A
25	a	1161	C
25	a	1168	G
25	a	1171	G

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Mol	Chain	Res	Type
25	a	1172	C
25	a	1178	C
25	a	1183	U
25	a	1186	G
25	a	1206	G
25	a	1208	C
25	a	1212	G
25	a	1236	G
25	a	1241	A
25	a	1247	A
25	a	1248	G
25	a	1250	G
25	a	1253	A
25	a	1254	A
25	a	1256	G
25	a	1257	C
25	a	1268	A
25	a	1271	G
25	a	1272	A
25	a	1273	U
25	a	1274	A
25	a	1275	A
25	a	1286	A
25	a	1287	A
25	a	1289	C
25	a	1300	G
25	a	1301	A
25	a	1304	A
25	a	1306	C
25	a	1312	U
25	a	1315	C
25	a	1320	C
25	a	1321	A
25	a	1324	G
25	a	1327	A
25	a	1329	U
25	a	1330	C
25	a	1331	G
25	a	1334	G
25	a	1341	G
25	a	1344	U
25	a	1345	C

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Mol	Chain	Res	Type
25	a	1352	U
25	a	1365	A
25	a	1373	A
25	a	1379	U
25	a	1383	A
25	a	1386	C
25	a	1387	A
25	a	1391	U
25	a	1405	U
25	a	1407	G
25	a	1411	U
25	a	1414	C
25	a	1415	U
25	a	1416	G
25	a	1419	A
25	a	1420	A
25	a	1427	A
25	a	1428	C
25	a	1434	A
25	a	1435	G
25	a	1436	G
25	a	1449	G
25	a	1451	C
25	a	1452	G
25	a	1453	A
25	a	1458	U
25	a	1460	U
25	a	1473	G
25	a	1475	G
25	a	1476	U
25	a	1478	G
25	a	1480	C
25	a	1482	G
25	a	1484	U
25	a	1486	U
25	a	1489	C
25	a	1493	C
25	a	1494	A
25	a	1498	C
25	a	1505	A
25	a	1506	U
25	a	1509	A

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Mol	Chain	Res	Type
25	a	1510	G
25	a	1514	G
25	a	1515	A
25	a	1524	G
25	a	1534	U
25	a	1535	A
25	a	1536	C
25	a	1537	G
25	a	1554	U
25	a	1556	C
25	a	1558	C
25	a	1560	G
25	a	1566	A
25	a	1567	G
25	a	1569	A
25	a	1578	U
25	a	1581	G
25	a	1582	C
25	a	1585	C
25	a	1591	A
25	a	1592	C
25	a	1593	A
25	a	1594	U
25	a	1597	A
25	a	1602	U
25	a	1607	C
25	a	1608	A
25	a	1611	C
25	a	1613	G
25	a	1618	6MZ
25	a	1619	G
25	a	1620	G
25	a	1626	A
25	a	1634	A
25	a	1647	U
25	a	1648	U
25	a	1649	G
25	a	1651	G
25	a	1653	G
25	a	1667	G
25	a	1674	G
25	a	1693	U

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Mol	Chain	Res	Type
25	a	1694	C
25	a	1700	A
25	a	1701	A
25	a	1709	U
25	a	1715	G
25	a	1718	G
25	a	1721	G
25	a	1723	G
25	a	1726	C
25	a	1729	U
25	a	1730	C
25	a	1731	G
25	a	1732	C
25	a	1738	G
25	a	1739	A
25	a	1740	G
25	a	1750	G
25	a	1756	G
25	a	1757	A
25	a	1758	U
25	a	1759	A
25	a	1764	C
25	a	1765	U
25	a	1769	U
25	a	1770	G
25	a	1773	A
25	a	1776	G
25	a	1782	U
25	a	1786	A
25	a	1788	C
25	a	1796	U
25	a	1800	C
25	a	1801	A
25	a	1802	A
25	a	1807	G
25	a	1808	A
25	a	1816	C
25	a	1819	A
25	a	1823	G
25	a	1829	A
25	a	1841	U
25	a	1847	A

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Mol	Chain	Res	Type
25	a	1848	A
25	a	1850	G
25	a	1856	U
25	a	1858	A
25	a	1865	U
25	a	1866	A
25	a	1868	C
25	a	1869	G
25	a	1870	C
25	a	1872	A
25	a	1876	A
25	a	1906	G
25	a	1912	A
25	a	1920	C
25	a	1923	U
25	a	1927	A
25	a	1929	G
25	a	1930	G
25	a	1932	A
25	a	1933	G
25	a	1937	A
25	a	1938	A
25	a	1939	5MU
25	a	1955	U
25	a	1958	C
25	a	1962	5MC
25	a	1964	G
25	a	1965	C
25	a	1966	A
25	a	1967	C
25	a	1970	A
25	a	1971	U
25	a	1972	G
25	a	1973	G
25	a	1980	G
25	a	1985	C
25	a	1991	U
25	a	1992	G
25	a	1993	U
25	a	1996	C
25	a	2002	G
25	a	2006	C

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Mol	Chain	Res	Type
25	a	2020	A
25	a	2021	C
25	a	2023	C
25	a	2030	6MZ
25	a	2031	A
25	a	2033	A
25	a	2035	G
25	a	2036	C
25	a	2037	A
25	a	2043	C
25	a	2052	A
25	a	2055	C
25	a	2056	G
25	a	2057	G
25	a	2058	A
25	a	2060	A
25	a	2061	G
25	a	2062	A
25	a	2069	G7M
25	a	2077	A
25	a	2091	C
25	a	2093	G
25	a	2095	A
25	a	2096	C
25	a	2097	A
25	a	2192	U
25	a	2198	A
25	a	2202	U
25	a	2203	U
25	a	2204	G
25	a	2210	U
25	a	2211	A
25	a	2212	A
25	a	2213	U
25	a	2220	U
25	a	2221	G
25	a	2222	C
25	a	2225	A
25	a	2230	G
25	a	2238	G
25	a	2239	G
25	a	2243	U

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Mol	Chain	Res	Type
25	a	2255	G
25	a	2258	C
25	a	2259	U
25	a	2268	A
25	a	2278	A
25	a	2279	G
25	a	2281	A
25	a	2282	G
25	a	2283	C
25	a	2287	A
25	a	2289	G
25	a	2296	U
25	a	2298	A
25	a	2305	U
25	a	2308	G
25	a	2309	A
25	a	2312	U
25	a	2319	G
25	a	2322	A
25	a	2325	G
25	a	2327	A
25	a	2328	A
25	a	2333	A
25	a	2334	U
25	a	2335	A
25	a	2336	A
25	a	2344	U
25	a	2345	G
25	a	2347	C
25	a	2350	C
25	a	2361	G
25	a	2383	G
25	a	2384	U
25	a	2385	C
25	a	2391	G
25	a	2394	C
25	a	2396	G
25	a	2401	U
25	a	2402	U
25	a	2403	C
25	a	2406	A
25	a	2409	G

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Mol	Chain	Res	Type
25	a	2423	U
25	a	2425	A
25	a	2426	A
25	a	2429	G
25	a	2430	A
25	a	2431	U
25	a	2435	A
25	a	2441	U
25	a	2448	A
25	a	2449	H2U
25	a	2456	C
25	a	2467	C
25	a	2470	G
25	a	2474	U
25	a	2476	A
25	a	2481	G
25	a	2491	U
25	a	2492	U
25	a	2502	G
25	a	2504	PSU
25	a	2505	G
25	a	2515	C
25	a	2518	A
25	a	2525	G
25	a	2529	G
25	a	2535	G
25	a	2546	U
25	a	2547	A
25	a	2552	OMU
25	a	2556	C
25	a	2560	A
25	a	2564	A
25	a	2566	A
25	a	2567	G
25	a	2568	U
25	a	2573	C
25	a	2574	G
25	a	2581	G
25	a	2582	G
25	a	2585	U
25	a	2602	A
25	a	2609	U

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Mol	Chain	Res	Type
25	a	2610	C
25	a	2613	U
25	a	2615	U
25	a	2621	G
25	a	2626	C
25	a	2629	U
25	a	2632	A
25	a	2639	A
25	a	2640	G
25	a	2652	C
25	a	2660	A
25	a	2663	G
25	a	2666	C
25	a	2670	A
25	a	2678	C
25	a	2682	A
25	a	2684	U
25	a	2685	G
25	a	2689	U
25	a	2690	U
25	a	2714	G
25	a	2715	C
25	a	2716	C
25	a	2717	C
25	a	2724	U
25	a	2725	A
25	a	2726	A
25	a	2732	G
25	a	2733	A
25	a	2742	G
25	a	2744	G
25	a	2746	U
25	a	2748	A
25	a	2765	A
25	a	2769	U
25	a	2778	A
25	a	2779	U
25	a	2781	A
25	a	2790	U
25	a	2791	G
25	a	2792	A
25	a	2795	C

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Mol	Chain	Res	Type
25	a	2798	U
25	a	2799	A
25	a	2808	G
25	a	2811	G
25	a	2820	A
25	a	2821	A
25	a	2835	A
25	a	2836	U
25	a	2855	C
25	a	2873	A
25	a	2874	C
25	a	2875	C
25	a	2879	A
25	a	2884	U
25	a	2891	U
25	a	2901	C
26	b	2	G
26	b	4	C
26	b	9	G
26	b	14	U
26	b	21	G
26	b	24	G
26	b	26	C
26	b	27	C
26	b	32	U
26	b	33	G
26	b	35	C
26	b	36	C
26	b	41	G
26	b	42	C
26	b	44	G
26	b	45	A
26	b	56	G
26	b	57	A
26	b	58	A
26	b	66	A
26	b	67	G
26	b	68	C
26	b	74	U
26	b	87	U
26	b	88	C
26	b	89	U

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Mol	Chain	Res	Type
26	b	90	C
26	b	98	G
26	b	99	A
26	b	103	U
26	b	109	A
26	b	116	G

All (36) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	7	A
1	A	30	U
1	A	49	U
1	A	84	U
1	A	120	A
1	A	199	A
1	A	315	A
1	A	428	G
1	A	429	U
1	A	446	G
1	A	516	PSU
1	A	559	A
1	A	776	G
1	A	827	U
1	A	858	G
1	A	991	U
1	A	993	G
1	A	1034	G
1	A	1046	A
1	A	1047	G
1	A	1111	A
1	A	1145	A
1	A	1319	A
1	A	1320	C
1	A	1447	A
1	A	1493	A
1	A	1505	G
22	V	16	C
22	V	17(A)	U
22	V	18	G
23	X	18	G
24	Y	60	U

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Mol	Chain	Res	Type
22	Z	7	G
22	Z	16	C
22	Z	18	G
22	Z	48	C

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

45 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	$\# Z > 2$
24	PSU	Y	55	24	18,21,22	0.88	1 (5%)	22,30,33	0.70	0
28	MEQ	d	150	28	8,9,10	0.50	0	5,10,12	0.60	0
25	2MA	a	2503	56,25	19,25,26	1.01	2 (10%)	21,37,40	1.82	4 (19%)
25	5MU	a	1939	25	19,22,23	0.48	0	28,32,35	0.63	0
25	PSU	a	2604	25	18,21,22	1.00	1 (5%)	22,30,33	1.45	4 (18%)
36	4D4	l	81	36	9,11,12	0.49	0	8,13,15	0.79	1 (12%)
1	PSU	A	516	1,56	18,21,22	0.86	1 (5%)	22,30,33	0.95	1 (4%)
25	OMG	a	2251	22,25	18,26,27	0.96	2 (11%)	19,38,41	0.77	1 (5%)
25	H2U	a	2449	25	18,21,22	0.79	1 (5%)	21,30,33	0.87	1 (4%)
25	PSU	a	746	56,25	18,21,22	1.13	2 (11%)	22,30,33	0.89	0
25	PSU	a	2580	25	18,21,22	0.95	1 (5%)	22,30,33	0.83	1 (4%)
1	2MG	A	966	1	18,26,27	1.07	2 (11%)	16,38,41	0.78	0
1	UR3	A	1498	1	19,22,23	0.40	0	26,32,35	0.68	0
11	IAS	K	119	11	6,7,8	0.95	0	6,8,10	0.95	0
1	MA6	A	1519	1	18,26,27	0.78	1 (5%)	19,38,41	0.79	1 (5%)
25	PSU	a	955	25	18,21,22	0.84	1 (5%)	22,30,33	0.85	0
25	G7M	a	2069	25	20,26,27	1.44	3 (15%)	17,39,42	0.76	0
1	MA6	A	1518	1	18,26,27	0.83	1 (5%)	19,38,41	0.47	0
12	D2T	L	89	12	7,9,10	1.01	0	6,11,13	1.92	4 (66%)
1	5MC	A	1407	1	18,22,23	0.42	0	26,32,35	0.76	1 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	T6A	Y	37	24	27,34,35	0.80	0	29,49,52	0.79	1 (3%)
1	2MG	A	1207	1	18,26,27	1.01	1 (5%)	16,38,41	0.76	0
24	5MU	Y	54	24	19,22,23	0.37	0	28,32,35	0.33	0
25	2MG	a	2445	25	18,26,27	1.24	3 (16%)	16,38,41	0.68	0
1	4OC	A	1402	1,56	20,23,24	0.37	0	26,32,35	0.57	0
1	5MC	A	967	1	18,22,23	0.29	0	26,32,35	0.51	0
25	1MG	a	745	25	18,26,27	1.07	2 (11%)	19,39,42	0.95	1 (5%)
1	2MG	A	1516	1	18,26,27	1.08	3 (16%)	16,38,41	0.79	0
24	4SU	Y	8	24	18,21,22	0.23	0	26,30,33	0.29	0
25	PSU	a	2457	25	18,21,22	1.01	1 (5%)	22,30,33	0.69	0
25	6MZ	a	1618	25	18,25,26	0.95	0	16,36,39	0.69	0
24	H2U	Y	20(A)	24	18,21,22	0.62	0	21,30,33	0.82	1 (4%)
25	5MU	a	747	25	19,22,23	0.39	0	28,32,35	0.47	0
25	3TD	a	1915	25	18,22,23	0.92	1 (5%)	22,32,35	0.65	0
25	PSU	a	1917	25	18,21,22	0.86	1 (5%)	22,30,33	0.85	0
24	RSP	Y	32	24	17,21,22	0.26	0	22,30,33	0.33	0
1	G7M	A	527	1	20,26,27	1.12	2 (10%)	17,39,42	0.50	0
25	PSU	a	1911	25	18,21,22	0.86	1 (5%)	22,30,33	0.71	0
25	5MC	a	1962	25	18,22,23	0.41	0	26,32,35	0.45	0
25	2MG	a	1835	25	18,26,27	1.00	1 (5%)	16,38,41	0.87	0
25	6MZ	a	2030	25	18,25,26	0.72	0	16,36,39	0.77	0
25	PSU	a	2504	25	18,21,22	0.98	1 (5%)	22,30,33	0.87	1 (4%)
25	OMU	a	2552	25	19,22,23	0.49	0	26,31,34	0.68	1 (3%)
25	PSU	a	2605	25	18,21,22	1.03	1 (5%)	22,30,33	0.80	0
25	OMC	a	2498	56,25	19,22,23	0.62	0	26,31,34	0.52	0

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
24	PSU	Y	55	24	-	0/7/25/26	0/2/2/2
28	MEQ	d	150	28	-	2/8/9/11	-
25	2MA	a	2503	56,25	-	2/3/25/26	0/3/3/3
25	5MU	a	1939	25	-	0/7/25/26	0/2/2/2
25	PSU	a	2604	25	-	0/7/25/26	0/2/2/2
36	4D4	l	81	36	-	0/11/12/14	-
1	PSU	A	516	1,56	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
25	OMG	a	2251	22,25	-	1/5/27/28	0/3/3/3
25	H2U	a	2449	25	-	3/7/38/39	0/2/2/2
25	PSU	a	746	56,25	-	1/7/25/26	0/2/2/2
25	PSU	a	2580	25	-	0/7/25/26	0/2/2/2
1	2MG	A	966	1	-	0/5/27/28	0/3/3/3
1	UR3	A	1498	1	-	0/7/25/26	0/2/2/2
11	IAS	K	119	11	-	1/7/7/8	-
1	MA6	A	1519	1	-	0/7/29/30	0/3/3/3
25	PSU	a	955	25	-	0/7/25/26	0/2/2/2
25	G7M	a	2069	25	-	1/3/25/26	0/3/3/3
1	MA6	A	1518	1	-	0/7/29/30	0/3/3/3
12	D2T	L	89	12	-	4/7/12/14	-
1	5MC	A	1407	1	-	0/7/25/26	0/2/2/2
24	T6A	Y	37	24	-	6/19/41/42	0/3/3/3
1	2MG	A	1207	1	-	0/5/27/28	0/3/3/3
24	5MU	Y	54	24	-	0/7/25/26	0/2/2/2
25	2MG	a	2445	25	-	1/5/27/28	0/3/3/3
1	4OC	A	1402	1,56	-	1/9/29/30	0/2/2/2
1	5MC	A	967	1	-	0/7/25/26	0/2/2/2
25	1MG	a	745	25	-	0/3/25/26	0/3/3/3
1	2MG	A	1516	1	-	0/5/27/28	0/3/3/3
24	4SU	Y	8	24	-	0/7/25/26	0/2/2/2
25	PSU	a	2457	25	-	0/7/25/26	0/2/2/2
25	6MZ	a	1618	25	-	2/5/27/28	0/3/3/3
24	H2U	Y	20(A)	24	-	3/7/38/39	0/2/2/2
25	5MU	a	747	25	-	1/7/25/26	0/2/2/2
25	3TD	a	1915	25	-	2/7/25/26	0/2/2/2
25	PSU	a	1917	25	-	0/7/25/26	0/2/2/2
24	RSP	Y	32	24	-	2/7/25/26	0/2/2/2
1	G7M	A	527	1	-	1/3/25/26	0/3/3/3
25	PSU	a	1911	25	-	0/7/25/26	0/2/2/2
25	5MC	a	1962	25	-	0/7/25/26	0/2/2/2
25	2MG	a	1835	25	-	0/5/27/28	0/3/3/3
25	6MZ	a	2030	25	-	2/5/27/28	0/3/3/3
25	PSU	a	2504	25	-	2/7/25/26	0/2/2/2
25	OMU	a	2552	25	-	0/9/27/28	0/2/2/2
25	PSU	a	2605	25	-	0/7/25/26	0/2/2/2
25	OMC	a	2498	56,25	-	0/9/27/28	0/2/2/2

All (37) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	a	1915	3TD	C6-C5	3.62	1.39	1.35
25	a	2069	G7M	C8-N9	3.52	1.39	1.33
1	A	527	G7M	C8-N9	3.50	1.39	1.33
25	a	2605	PSU	C6-C5	3.42	1.39	1.35
25	a	2504	PSU	C6-C5	3.38	1.39	1.35
24	Y	55	PSU	C6-C5	3.36	1.39	1.35
25	a	2069	G7M	C5-C6	-3.30	1.37	1.45
25	a	2069	G7M	C8-N7	3.27	1.39	1.33
25	a	1911	PSU	C6-C5	3.24	1.39	1.35
25	a	1917	PSU	C6-C5	3.19	1.39	1.35
1	A	516	PSU	C6-C5	3.14	1.39	1.35
25	a	2580	PSU	C6-C5	3.06	1.38	1.35
25	a	2445	2MG	C5-C6	-2.84	1.41	1.47
25	a	2604	PSU	C6-C5	2.82	1.38	1.35
25	a	746	PSU	C6-C5	2.81	1.38	1.35
25	a	745	1MG	C5-C4	-2.76	1.36	1.43
1	A	1516	2MG	C5-C6	-2.76	1.41	1.47
25	a	2251	OMG	C5-C6	-2.70	1.41	1.47
25	a	2457	PSU	C6-C5	2.65	1.38	1.35
1	A	966	2MG	C5-C6	-2.64	1.42	1.47
25	a	955	PSU	C6-C5	2.54	1.38	1.35
25	a	2445	2MG	C8-N7	-2.52	1.30	1.35
25	a	1835	2MG	C5-C6	-2.46	1.42	1.47
1	A	1207	2MG	C5-C6	-2.42	1.42	1.47
1	A	527	G7M	C5-C6	-2.41	1.39	1.45
25	a	2449	H2U	C2-N1	-2.40	1.32	1.35
25	a	2503	2MA	C2-N3	2.27	1.38	1.34
25	a	2445	2MG	C5-C4	-2.26	1.37	1.43
1	A	966	2MG	C8-N7	-2.23	1.31	1.35
1	A	1516	2MG	C8-N7	-2.23	1.31	1.35
25	a	745	1MG	C5-C6	-2.13	1.41	1.47
1	A	1519	MA6	C8-N7	-2.05	1.31	1.34
1	A	1518	MA6	C8-N7	-2.04	1.31	1.34
1	A	1516	2MG	C5-C4	-2.03	1.37	1.43
25	a	2251	OMG	C5-C4	-2.03	1.37	1.43
25	a	2503	2MA	C6-N1	2.02	1.37	1.33
25	a	746	PSU	C4-C5	-2.00	1.38	1.44

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	a	2503	2MA	C5-C6-N1	-5.47	117.42	121.01
25	a	2503	2MA	C5-C6-N6	4.55	127.26	120.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	a	2604	PSU	C6-C5-C4	3.62	120.73	118.20
25	a	2604	PSU	C5-C6-N1	-3.23	117.27	122.11
25	a	2503	2MA	CM2-C2-N1	2.70	121.36	117.15
25	a	2503	2MA	N3-C2-N1	-2.65	120.89	125.73
1	A	1407	5MC	C5-C6-N1	-2.55	120.71	123.34
12	L	89	D2T	OD1-CG-CB	-2.46	117.30	122.44
24	Y	20(A)	H2U	C4-N3-C2	-2.43	123.78	125.79
12	L	89	D2T	O-C-CA	-2.41	118.47	124.78
25	a	2504	PSU	C2'-C3'-C4'	-2.40	97.98	102.64
1	A	516	PSU	C2'-C3'-C4'	-2.39	97.99	102.64
25	a	2580	PSU	C3'-C2'-C1'	2.38	104.41	101.64
12	L	89	D2T	OD2-CG-CB	2.36	118.24	113.15
1	A	1519	MA6	C2'-C3'-C4'	-2.34	98.09	102.64
25	a	2604	PSU	C2'-C3'-C4'	-2.33	98.11	102.64
25	a	2552	OMU	C2'-C1'-N1	-2.19	109.97	114.22
12	L	89	D2T	CB-CA-N	2.15	113.68	109.10
25	a	2251	OMG	O6-C6-C5	2.12	128.51	124.37
25	a	2604	PSU	C3'-C2'-C1'	-2.11	99.17	101.64
25	a	745	1MG	O4'-C4'-C3'	-2.11	100.94	105.11
24	Y	37	T6A	N6-C6-N1	2.11	121.55	118.72
25	a	2449	H2U	O4'-C1'-C2'	-2.07	102.12	106.64
36	l	81	4D4	O-C-CA	-2.06	119.38	124.78

There are no chirality outliers.

All (38) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1402	4OC	C1'-C2'-O2'-CM2
12	L	89	D2T	CA-CB-CG-OD1
12	L	89	D2T	CA-CB-CG-OD2
24	Y	32	RSP	C3'-C4'-C5'-O5'
24	Y	32	RSP	O4'-C4'-C5'-O5'
24	Y	37	T6A	O4'-C4'-C5'-O5'
24	Y	37	T6A	C3'-C4'-C5'-O5'
25	a	1618	6MZ	O4'-C4'-C5'-O5'
25	a	2030	6MZ	O4'-C4'-C5'-O5'
25	a	2251	OMG	C1'-C2'-O2'-CM2
25	a	2504	PSU	O4'-C4'-C5'-O5'
25	a	1618	6MZ	C3'-C4'-C5'-O5'
25	a	2030	6MZ	C3'-C4'-C5'-O5'
25	a	2504	PSU	C3'-C4'-C5'-O5'
28	d	150	MEQ	OE1-CD-CG-CB

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Mol	Chain	Res	Type	Atoms
28	d	150	MEQ	NE2-CD-CG-CB
25	a	1915	3TD	O4'-C4'-C5'-O5'
25	a	1915	3TD	C3'-C4'-C5'-O5'
24	Y	20(A)	H2U	C2'-C1'-N1-C6
24	Y	37	T6A	C4'-C5'-O5'-P
25	a	2449	H2U	O4'-C4'-C5'-O5'
1	A	527	G7M	C3'-C4'-C5'-O5'
25	a	2445	2MG	C3'-C4'-C5'-O5'
25	a	2503	2MA	C4'-C5'-O5'-P
24	Y	37	T6A	C5-C6-N6-C10
24	Y	20(A)	H2U	C2'-C1'-N1-C2
24	Y	37	T6A	N11-C12-C13-ODA
24	Y	37	T6A	N11-C12-C13-ODB
24	Y	20(A)	H2U	O4'-C1'-N1-C2
11	K	119	IAS	O-C-CA-N
12	L	89	D2T	SB-CB-CG-OD2
25	a	2449	H2U	C3'-C4'-C5'-O5'
12	L	89	D2T	CG-CB-SB-CB1
25	a	746	PSU	O4'-C1'-C5-C6
25	a	2069	G7M	O4'-C4'-C5'-O5'
25	a	2503	2MA	O4'-C4'-C5'-O5'
25	a	747	5MU	C3'-C4'-C5'-O5'
25	a	2449	H2U	C4'-C5'-O5'-P

There are no ring outliers.

10 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
36	l	81	4D4	1	0
25	a	2251	OMG	1	0
1	A	1519	MA6	2	0
1	A	1518	MA6	2	0
24	Y	37	T6A	1	0
1	A	1516	2MG	1	0
24	Y	20(A)	H2U	1	0
25	a	747	5MU	1	0
25	a	1915	3TD	1	0
25	a	2030	6MZ	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 305 ligands modelled in this entry, 290 are monoatomic - leaving 15 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	$\# Z > 2$
58	PUT	A	1686	-	5,5,5	0.15	0	4,4,4	0.12	0
57	SPD	a	6192	-	9,9,9	0.17	0	8,8,8	0.32	0
59	SPM	a	6193	-	13,13,13	0.17	0	12,12,12	0.31	0
57	SPD	A	1685	-	9,9,9	0.20	0	8,8,8	0.21	0
58	PUT	a	6194	-	5,5,5	0.19	0	4,4,4	0.32	0
57	SPD	a	6189	-	9,9,9	0.20	0	8,8,8	0.35	0
58	PUT	a	6197	-	5,5,5	0.18	0	4,4,4	0.30	0
58	PUT	a	6196	-	5,5,5	0.16	0	4,4,4	0.41	0
57	SPD	a	6188	-	9,9,9	0.17	0	8,8,8	0.40	0
57	SPD	a	6187	-	9,9,9	0.25	0	8,8,8	0.27	0
57	SPD	a	6191	-	9,9,9	0.20	0	8,8,8	0.22	0
58	PUT	a	6198	-	5,5,5	0.20	0	4,4,4	0.35	0
58	PUT	a	6200	-	5,5,5	0.13	0	4,4,4	0.23	0
57	SPD	a	6190	-	9,9,9	0.19	0	8,8,8	0.20	0
58	PUT	a	6199	-	5,5,5	0.19	0	4,4,4	0.25	0

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
58	PUT	A	1686	-	-	0/3/3/3	-
57	SPD	a	6192	-	-	0/7/7/7	-
59	SPM	a	6193	-	-	3/11/11/11	-
57	SPD	A	1685	-	-	0/7/7/7	-
58	PUT	a	6194	-	-	0/3/3/3	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
57	SPD	a	6189	-	-	1/7/7/7	-
58	PUT	a	6197	-	-	0/3/3/3	-
58	PUT	a	6196	-	-	0/3/3/3	-
57	SPD	a	6188	-	-	0/7/7/7	-
57	SPD	a	6187	-	-	1/7/7/7	-
57	SPD	a	6191	-	-	0/7/7/7	-
58	PUT	a	6198	-	-	1/3/3/3	-
58	PUT	a	6200	-	-	1/3/3/3	-
57	SPD	a	6190	-	-	0/7/7/7	-
58	PUT	a	6199	-	-	0/3/3/3	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	a	6193	SPM	C7-C6-N5-C4
59	a	6193	SPM	N10-C11-C12-C13
58	a	6198	PUT	C1-C2-C3-C4
58	a	6200	PUT	C1-C2-C3-C4
57	a	6187	SPD	C2-C3-C4-C5
59	a	6193	SPM	C11-C12-C13-N14
57	a	6189	SPD	C3-C4-C5-N6

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	a	6192	SPD	1	0
59	a	6193	SPM	2	0
57	a	6191	SPD	1	0
57	a	6190	SPD	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

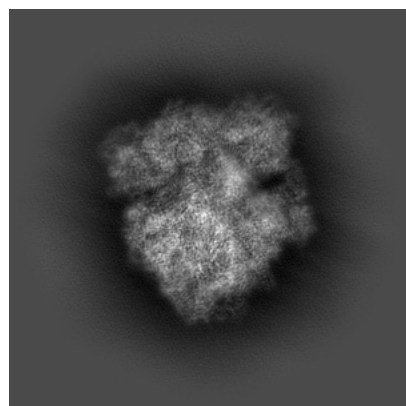
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51679. These allow visual inspection of the internal detail of the map and identification of artifacts.

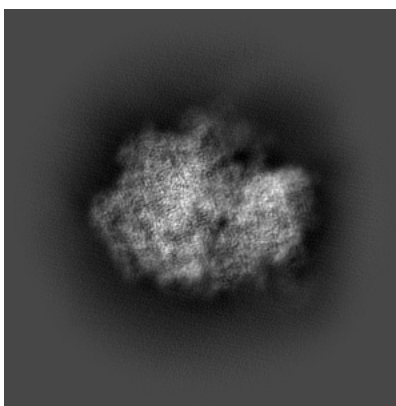
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

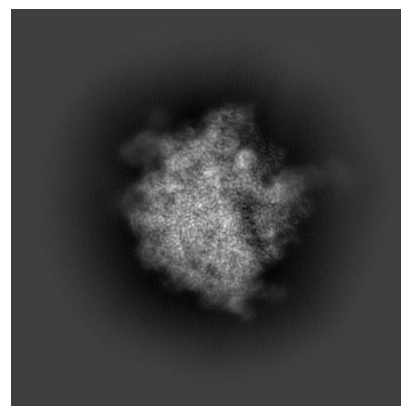
6.1.1 Primary map



X

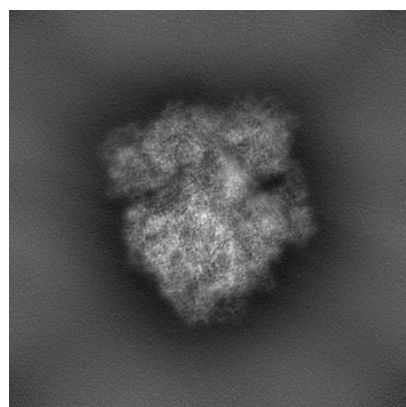


Y

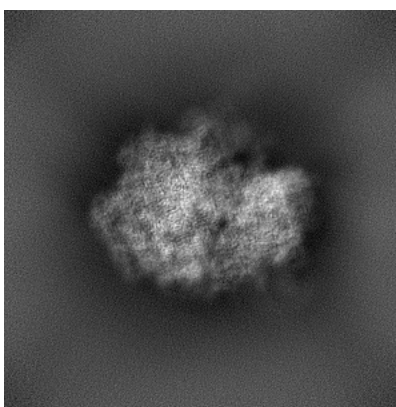


Z

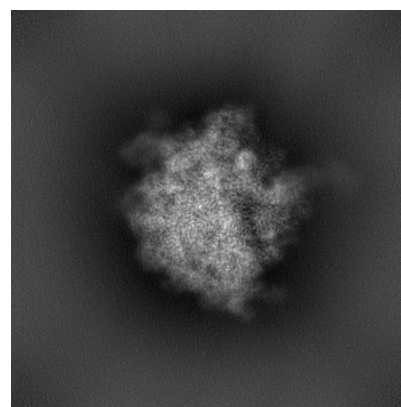
6.1.2 Raw map



X



Y

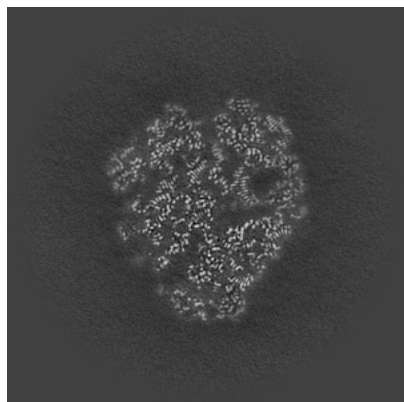


Z

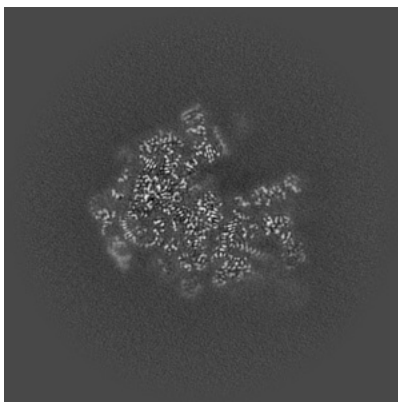
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

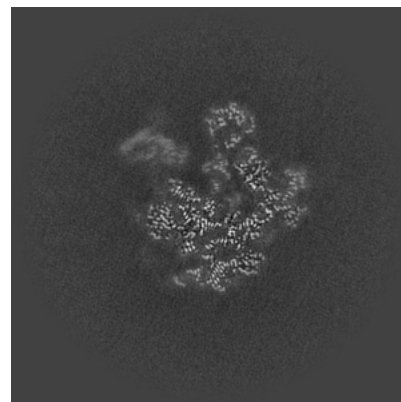
6.2.1 Primary map



X Index: 256

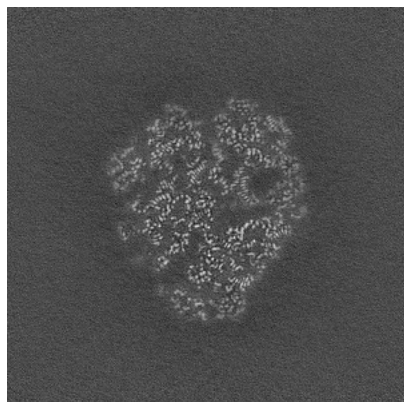


Y Index: 256

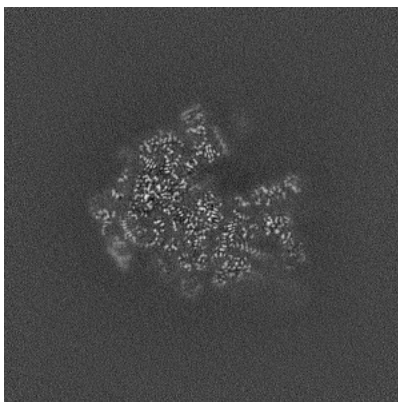


Z Index: 256

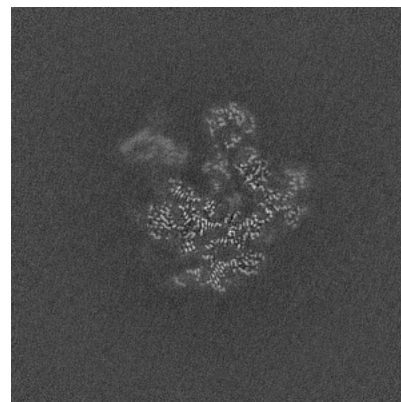
6.2.2 Raw map



X Index: 256



Y Index: 256

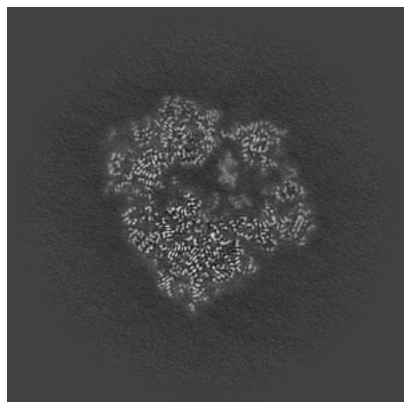


Z Index: 256

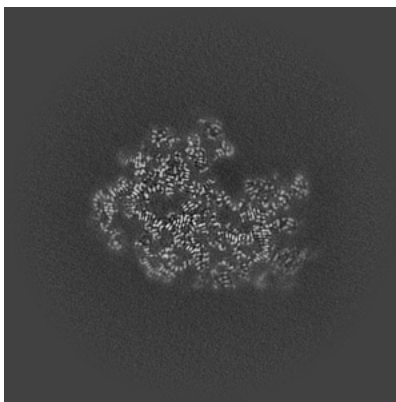
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

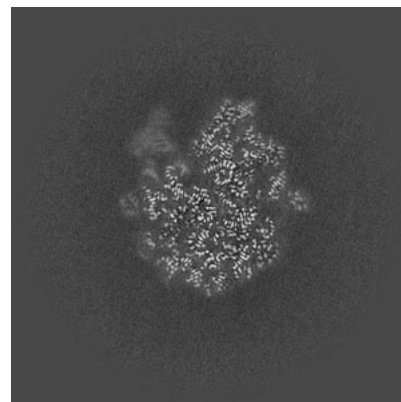
6.3.1 Primary map



X Index: 278

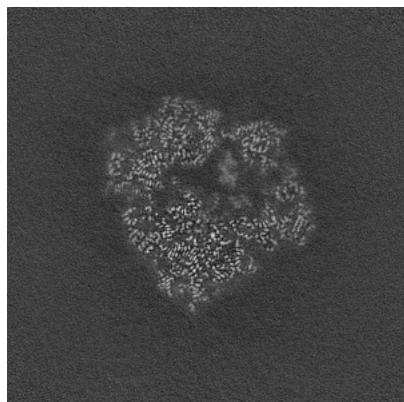


Y Index: 241

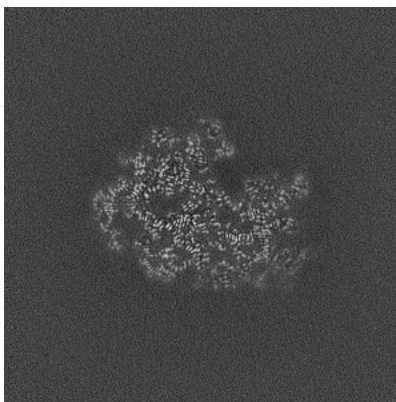


Z Index: 232

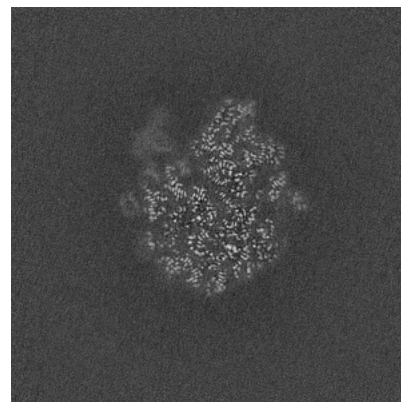
6.3.2 Raw map



X Index: 278



Y Index: 241

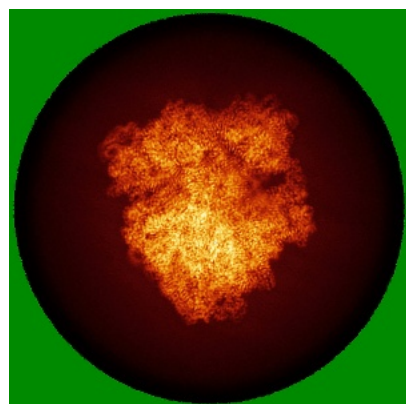


Z Index: 231

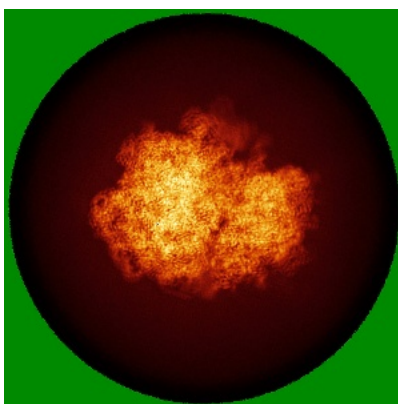
The images above show the largest variance slices of the map in three orthogonal directions.

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

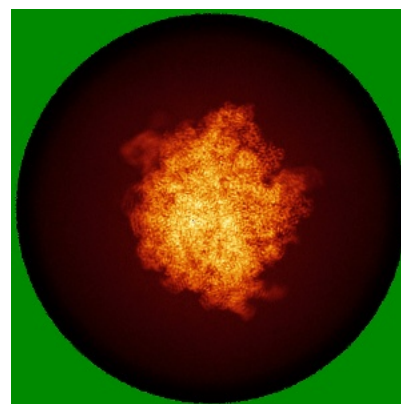
6.4.1 Primary map



X



Y

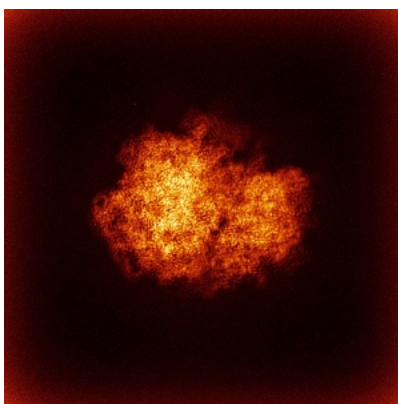


Z

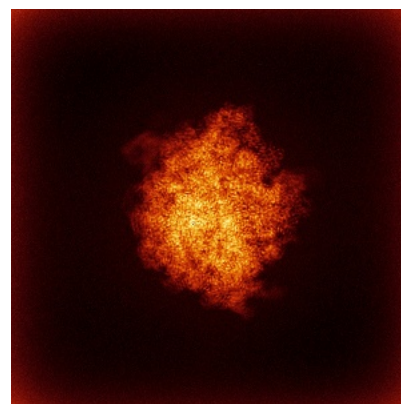
6.4.2 Raw map



X



Y

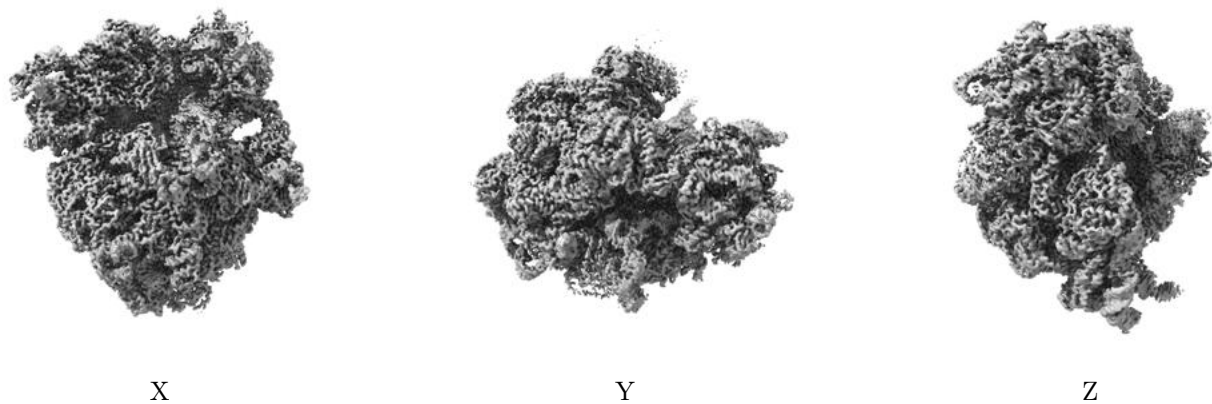


Z

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.

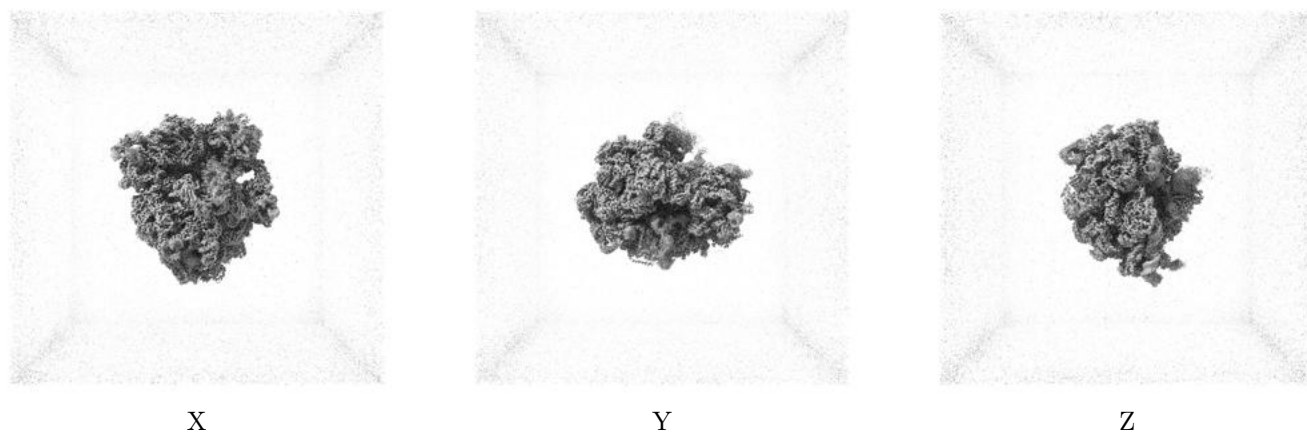
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.085. 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.

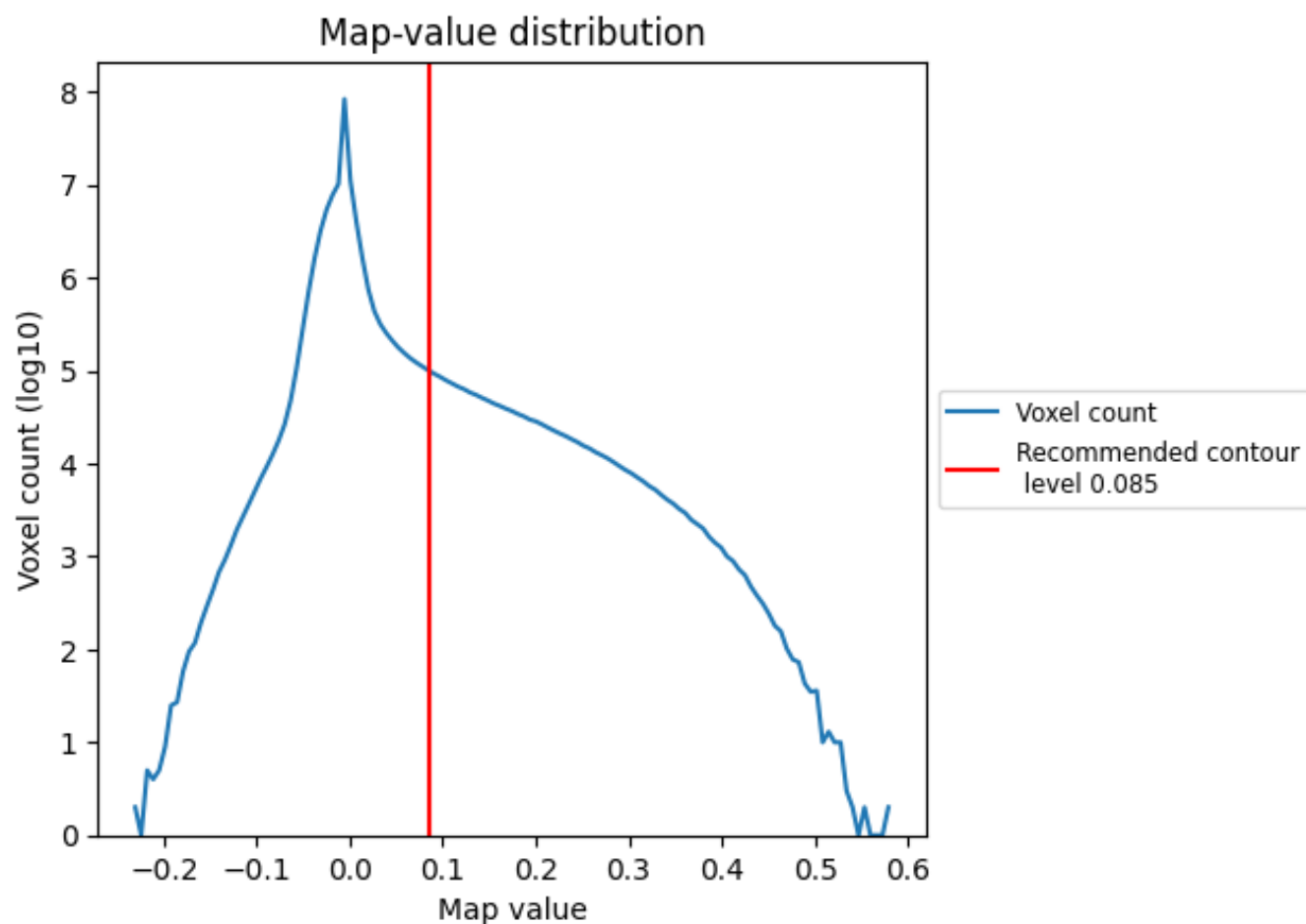
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

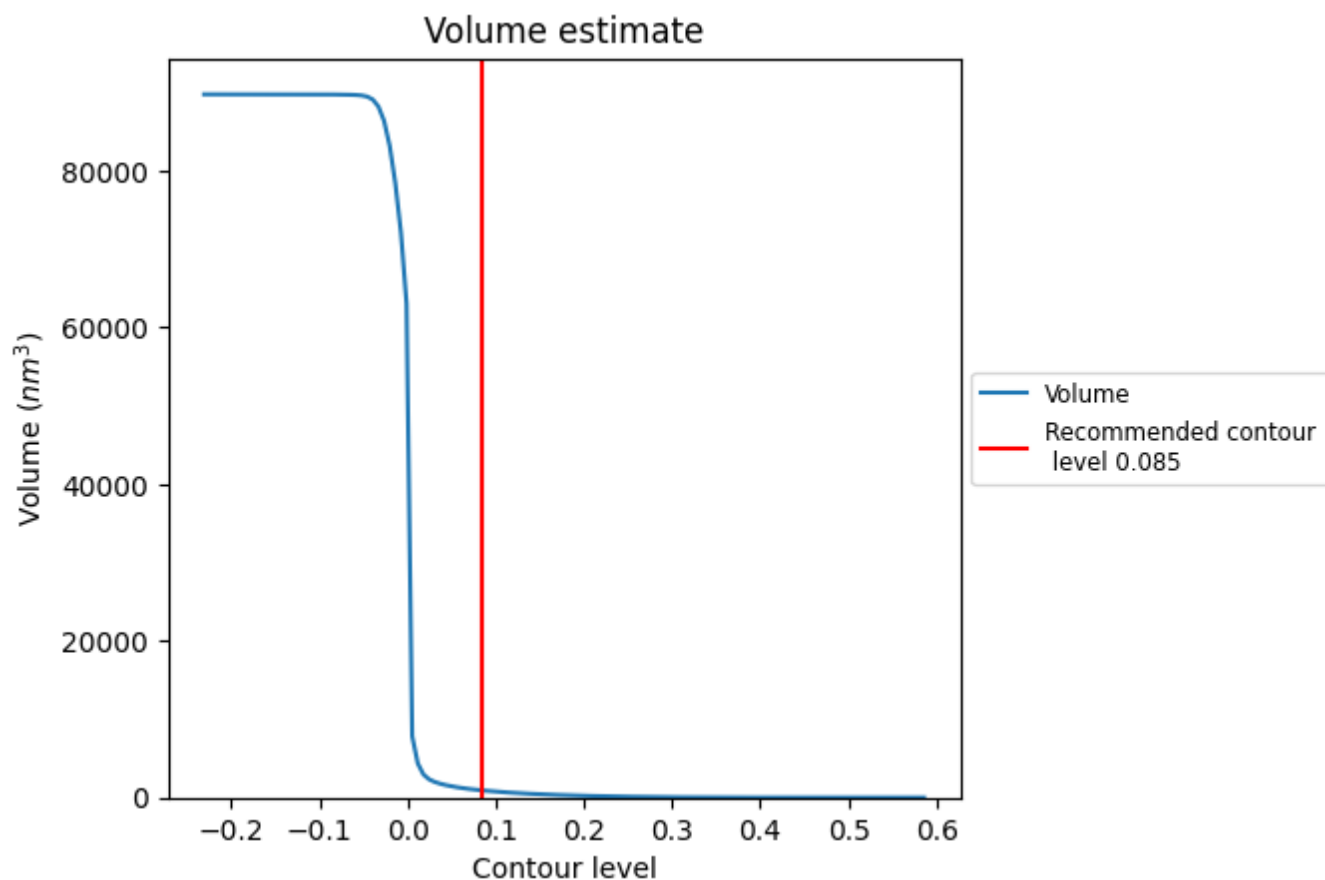
This section contains the results of statistical analysis of the map.

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.

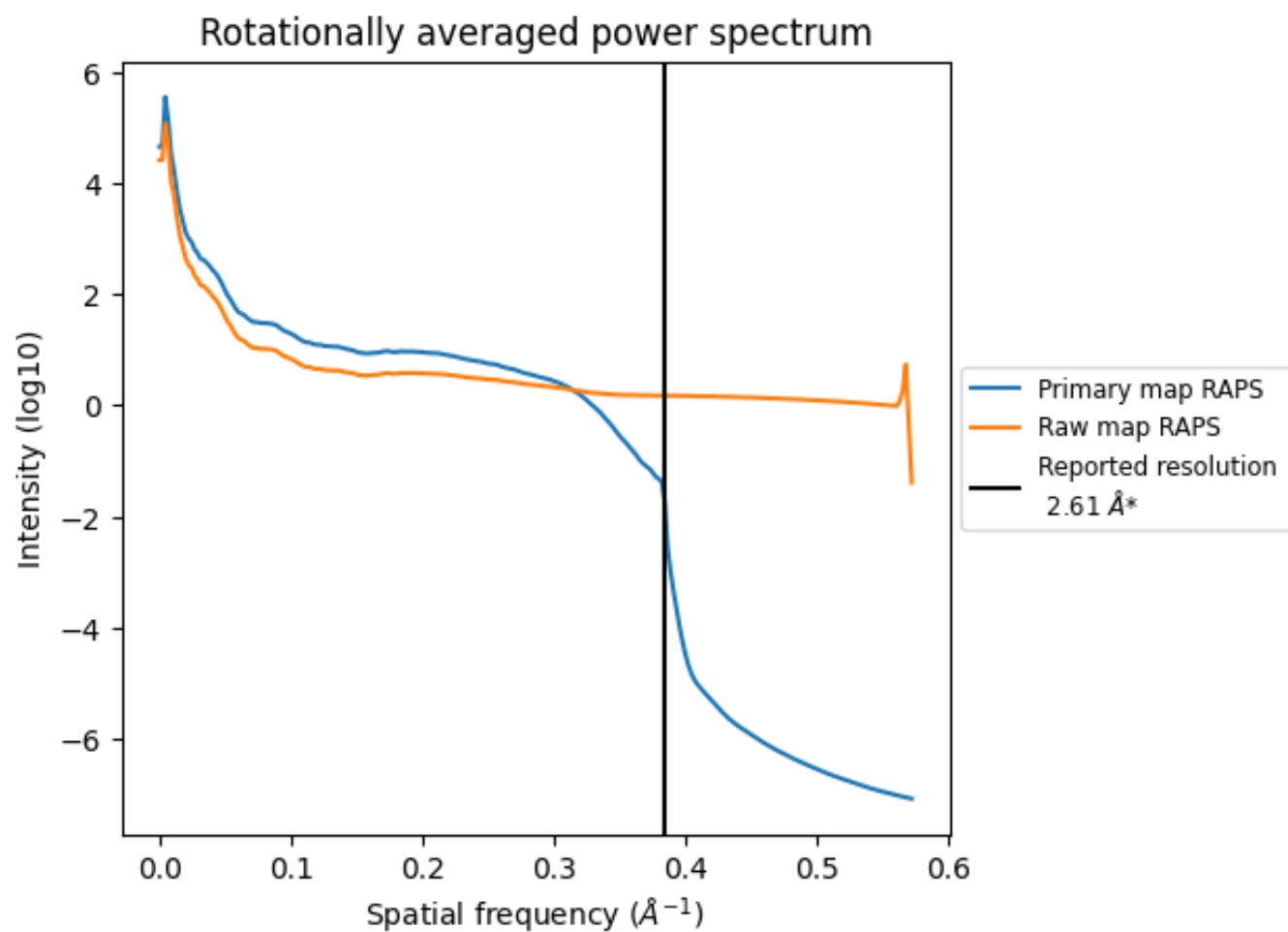
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 912 nm³; this corresponds to an approximate mass of 824 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 ⓘ

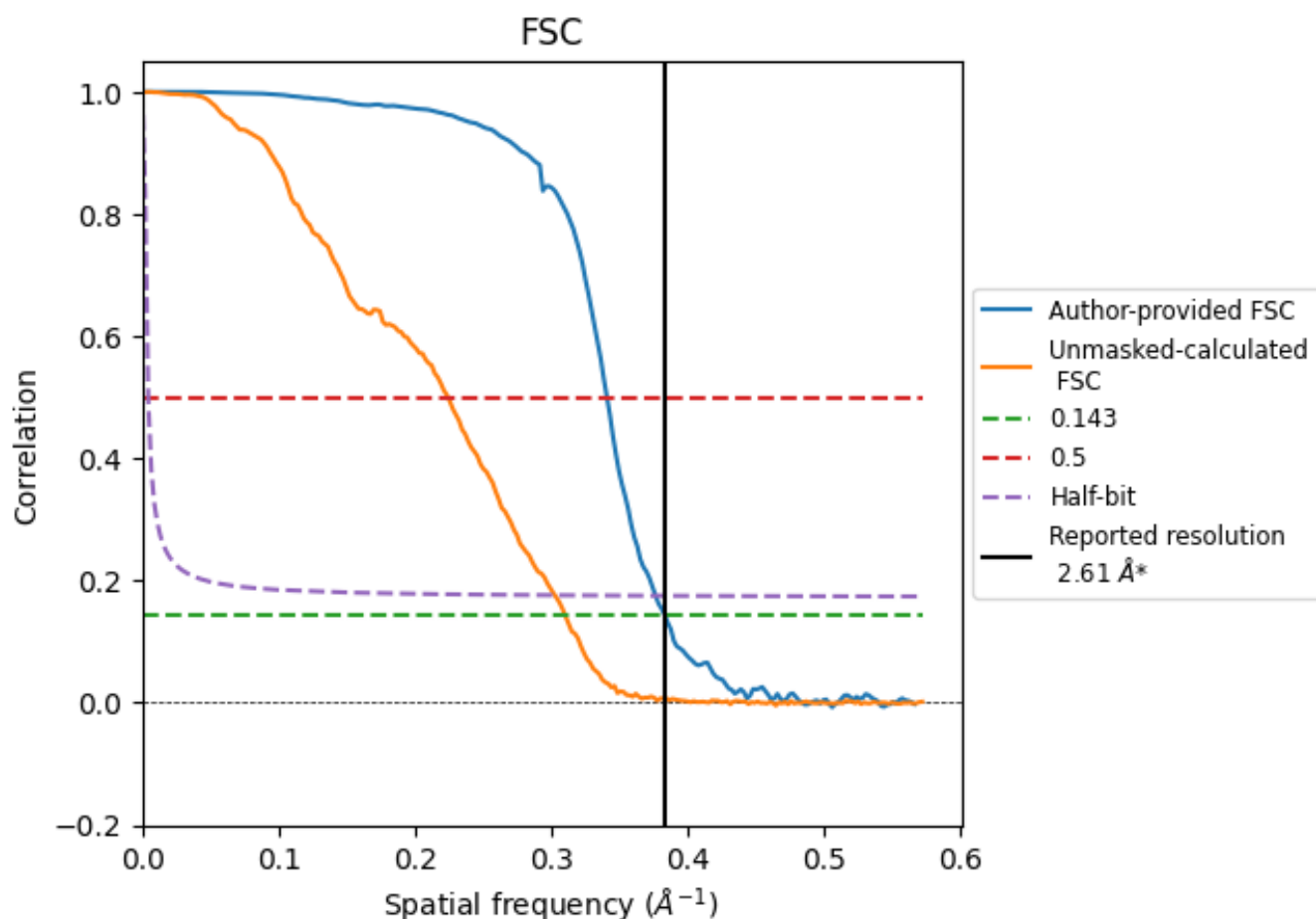


*Reported resolution corresponds to spatial frequency of 0.383 Å⁻¹

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 0.383 \AA^{-1}

8.2 Resolution estimates [i](#)

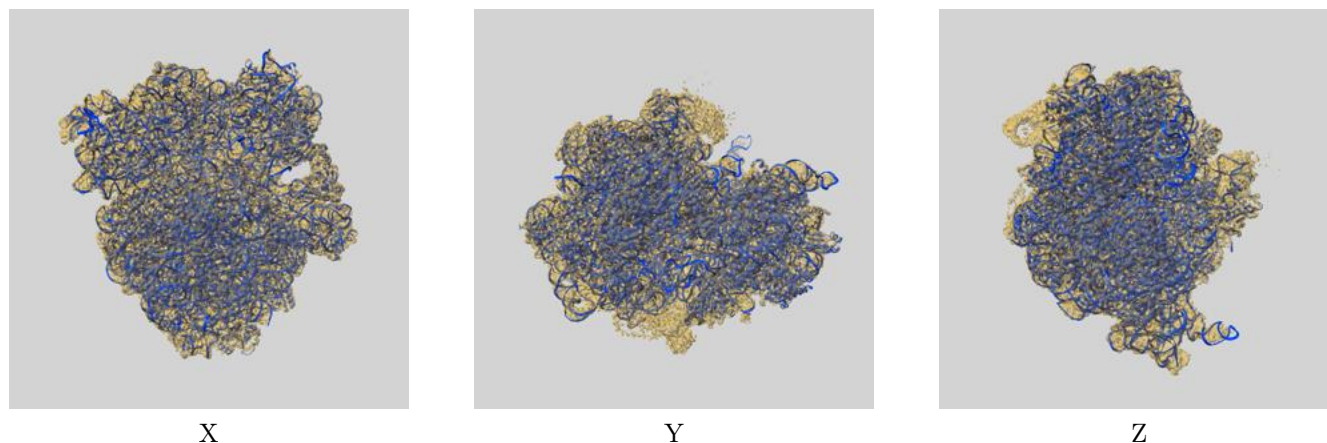
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.61	-	-
Author-provided FSC curve	2.61	2.94	2.66
Unmasked-calculated*	3.23	4.46	3.31

*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 3.23 differs from the reported value 2.61 by more than 10 %

9 Map-model fit [i](#)

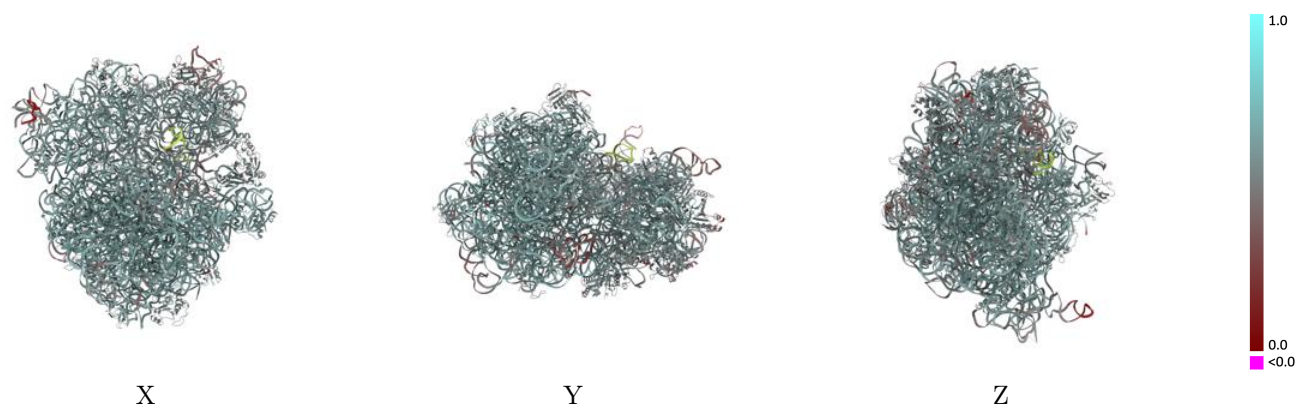
This section contains information regarding the fit between EMDB map EMD-51679 and PDB model 9GXX. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



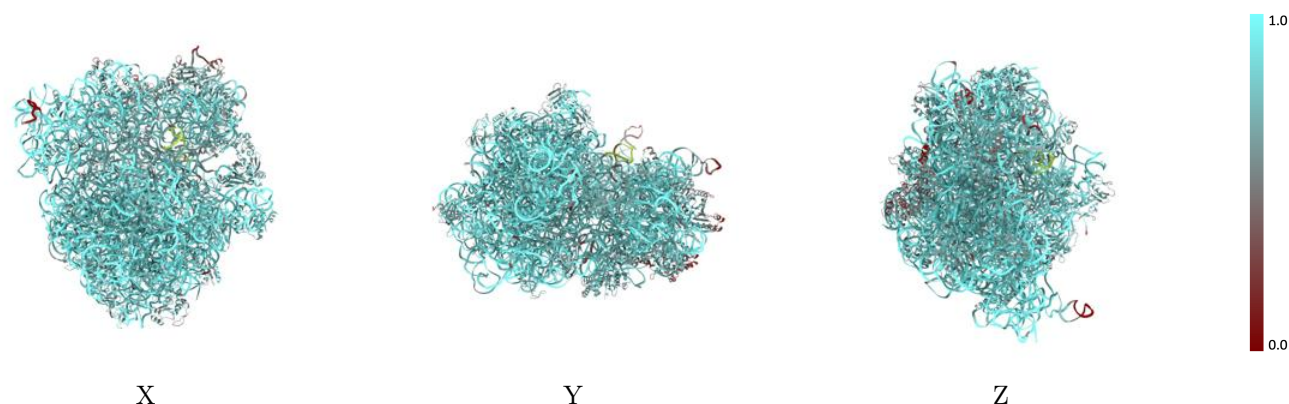
The images above show the 3D surface view of the map at the recommended contour level 0.085 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



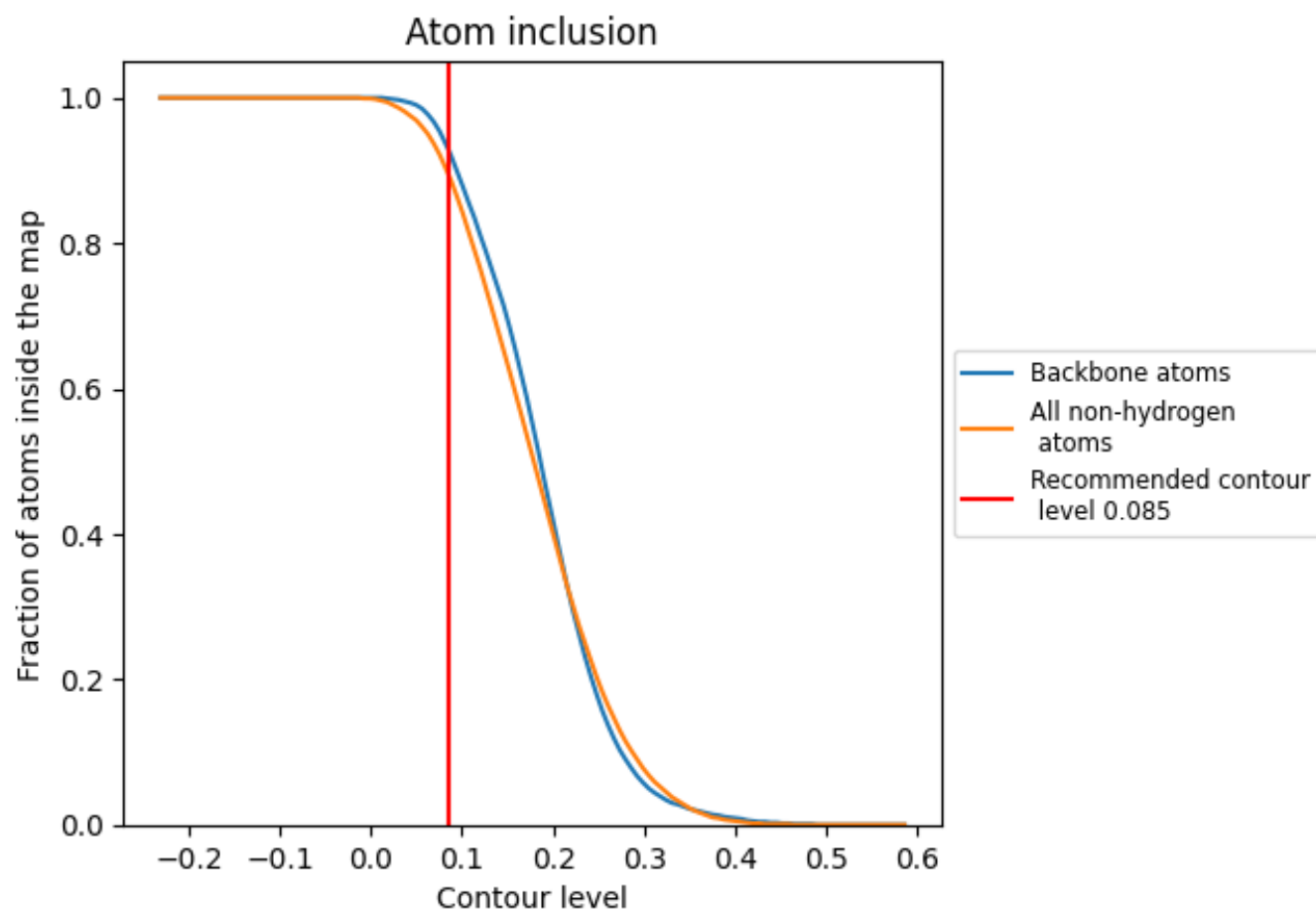
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.085).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 90% 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 (0.085) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8950	 0.5780
0	 0.8120	 0.5740
1	 0.9150	 0.6230
2	 0.9210	 0.6220
3	 0.8460	 0.5910
4	 0.6460	 0.5090
A	 0.9450	 0.5780
B	 0.4610	 0.4770
C	 0.7140	 0.5390
D	 0.7210	 0.5410
E	 0.7820	 0.5670
F	 0.7410	 0.5230
G	 0.7060	 0.5220
H	 0.7940	 0.5690
I	 0.7390	 0.5320
J	 0.6050	 0.4810
K	 0.7800	 0.5590
L	 0.7630	 0.5750
M	 0.7290	 0.5410
N	 0.7870	 0.5460
O	 0.7800	 0.5580
P	 0.8500	 0.5690
Q	 0.7580	 0.5390
R	 0.7920	 0.5450
S	 0.7300	 0.5340
T	 0.8260	 0.5600
U	 0.6050	 0.4680
V	 0.6830	 0.3790
X	 0.8960	 0.5800
Y	 0.7150	 0.4650
Z	 0.8290	 0.5610
a	 0.9670	 0.6020
b	 0.9560	 0.5840
c	 0.8950	 0.6090
d	 0.8600	 0.5990



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Chain	Atom inclusion	Q-score
e	 0.7660	 0.5630
f	 0.7280	 0.5210
g	 0.7120	 0.5090
h	 0.7000	 0.5180
i	 0.8670	 0.5850
j	 0.7740	 0.5930
k	 0.8530	 0.5870
l	 0.8420	 0.5990
m	 0.9040	 0.6080
n	 0.8130	 0.5590
o	 0.7970	 0.5880
p	 0.8950	 0.6020
q	 0.8040	 0.5770
r	 0.8390	 0.5910
s	 0.7730	 0.5500
t	 0.7240	 0.5260
u	 0.7850	 0.5630
v	 0.8320	 0.6000
w	 0.8570	 0.5880
x	 0.7180	 0.5270
y	 0.8050	 0.5820
z	 0.8350	 0.5870