



Full wwPDB EM Validation Report ⓘ

Dec 26, 2024 – 01:22 PM EST

PDB ID : 6OLE
EMDB ID : EMD-0600
Title : Human ribosome nascent chain complex (CDH1-RNC) stalled by a drug-like molecule with AP and PE tRNAs
Authors : Li, W.; Cate, J.H.D.
Deposited on : 2019-04-16
Resolution : 3.10 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

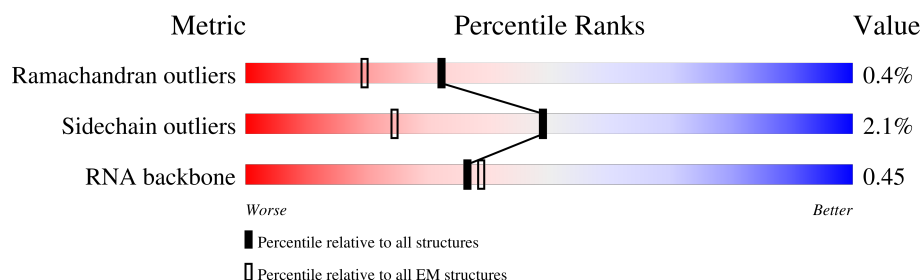
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	S2	1714	
2	SA	221	
3	SB	214	
4	SD	226	
5	SE	259	
6	SF	189	
7	SH	189	
8	SI	204	

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Mol	Chain	Length	Quality of chain
9	SK	98	<div> <div>24%</div> <div>97%</div> <div>.</div> </div>
10	SL	153	<div> <div>19%</div> <div>97%</div> <div>.</div> </div>
11	SP	127	<div> <div>17%</div> <div>98%</div> <div>.</div> </div>
12	SQ	146	<div> <div>16%</div> <div>97%</div> <div>.</div> </div>
13	SR	134	<div> <div>28%</div> <div>96%</div> <div>.</div> </div>
14	SS	145	<div> <div>15%</div> <div>99%</div> <div>.</div> </div>
15	ST	143	<div> <div>10%</div> <div>98%</div> <div>..</div> </div>
16	SU	104	<div> <div>36%</div> <div>95%</div> <div>5%</div> </div>
17	SV	82	<div> <div>7%</div> <div>98%</div> <div>.</div> </div>
18	SX	141	<div> <div>6%</div> <div>98%</div> <div>.</div> </div>
19	Sa	102	<div> <div>11%</div> <div>97%</div> <div>.</div> </div>
20	Sc	64	<div> <div>30%</div> <div>100%</div> </div>
21	Sd	55	<div> <div>11%</div> <div>85%</div> <div>15%</div> </div>
22	Sg	312	<div> <div>43%</div> <div>98%</div> <div>.</div> </div>
23	SC	220	<div> <div>9%</div> <div>98%</div> <div>.</div> </div>
24	SG	237	<div> <div>32%</div> <div>97%</div> <div>.</div> </div>
25	SJ	185	<div> <div>15%</div> <div>95%</div> <div>5%</div> </div>
26	SM	118	<div> <div>83%</div> <div>97%</div> <div>.</div> </div>
27	SN	150	<div> <div>6%</div> <div>100%</div> </div>
28	SO	137	<div> <div>12%</div> <div>100%</div> </div>
29	SW	129	<div> <div>.</div> <div>98%</div> <div>.</div> </div>
30	SY	131	<div> <div>18%</div> <div>97%</div> <div>.</div> </div>
31	SZ	73	<div> <div>22%</div> <div>95%</div> <div>..</div> </div>
32	Sb	82	<div> <div>20%</div> <div>100%</div> </div>
33	Se	57	<div> <div>25%</div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain
34	Sf	67	
35	A	252	
36	B	397	
37	C	363	
38	D	157	
39	E	121	
40	F	294	
41	G	247	
42	H	225	
43	I	234	
44	J	191	
45	K	211	
46	L	169	
47	M	205	
48	N	139	
49	O	203	
50	P	195	
51	Q	153	
52	R	187	
53	S	181	
54	T	175	
55	U	157	
56	V	99	
57	W	129	
58	X	61	

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Mol	Chain	Length	Quality of chain
59	Y	117	
60	Z	134	
61	a	134	
62	b	147	
63	c	121	
64	d	103	
65	e	106	
66	f	129	
67	g	109	
68	h	114	
69	i	122	
70	j	97	
71	k	84	
72	l	69	
73	m	50	
74	n	50	
75	o	25	
76	p	105	
77	q	91	
78	r	122	
79	t	3607	
80	u	76	
81	v	76	
82	w	10	
83	y	39	

2 Entry composition

There are 87 unique types of molecules in this entry. The entry contains 214951 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 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	S2	1714	Total	C	N	O	P	0	0
			36501	16306	6533	11949	1713		

- Molecule 2 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	SA	221	Total	C	N	O	S	0	0
			1741	1106	305	322	8		

- Molecule 3 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SB	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

- Molecule 4 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SD	226	Total	C	N	O	S	0	0
			1757	1120	316	314	7		

- Molecule 5 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	SE	259	Total	C	N	O	S	0	0
			2059	1316	383	352	8		

- Molecule 6 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SF	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		

- Molecule 7 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SH	186	Total	C	N	O	S	0	0
			1497	956	274	266	1		

- Molecule 8 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SI	204	Total	C	N	O	S	0	0
			1673	1050	329	289	5		

- Molecule 9 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 10 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SL	153	Total	C	N	O	S	0	0
			1247	793	234	214	6		

- Molecule 11 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SP	127	Total	C	N	O	S	0	0
			1045	663	198	177	7		

- Molecule 12 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SQ	146	Total	C	N	O	S	0	0
			1158	736	218	200	4		

- Molecule 13 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SR	134	Total	C	N	O	S	0	0
			1082	680	201	197	4		

- Molecule 14 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SS	145	Total	C	N	O	S	0	0
			1198	751	242	203	2		

- Molecule 15 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	ST	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

- Molecule 16 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SU	104	Total	C	N	O	S	0	0
			821	514	155	148	4		

- Molecule 17 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SV	82	Total	C	N	O	S	0	0
			625	384	116	120	5		

- Molecule 18 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 19 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Sa	102	Total	C	N	O	S	0	0
			821	512	171	133	5		

- Molecule 20 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Sc	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 21 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Sd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 22 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Sg	312	Total	C	N	O	S	0	0
			2429	1531	423	463	12		

- Molecule 23 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	SC	220	Total	C	N	O	S	1	0
			1715	1109	296	300	10		

- Molecule 24 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	SG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 25 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	SJ	185	Total	C	N	O	S	1	0
			1533	974	309	248	2		

- Molecule 26 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	SM	118	Total	C	N	O	S	0	0
			912	571	161	173	7		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SM	52	GLN	LEU	conflict	UNP P25398
SM	69	LEU	CYS	conflict	UNP P25398
SM	99	ASN	LYS	conflict	UNP P25398

- Molecule 27 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	SN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 28 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	SO	137	Total	C	N	O	S	0	0
			1024	627	200	191	6		

- Molecule 29 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	SW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 30 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	SY	131	Total	C	N	O	S	1	0
			1073	678	212	178	5		

- Molecule 31 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	SZ	73	Total	C	N	O	S	0	0
			579	372	106	100	1		

- Molecule 32 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Sb	82	Total	C	N	O	S	0	0
			640	402	118	113	7		

- Molecule 33 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Se	57	Total	C	N	O	S	0	0
			452	281	99	71	1		

- Molecule 34 is a protein called 40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Sf	67	Total	C	N	O	S	0	0
			548	346	102	93	7		

- Molecule 35 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	A	252	Total	C	N	O	S	0	0
			1930	1209	395	320	6		

- Molecule 36 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	B	397	Total	C	N	O	S	0	0
			3202	2039	602	547	14		

- Molecule 37 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	C	363	Total	C	N	O	S	0	0
			2888	1817	577	480	14		

- Molecule 38 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	D	157	Total	C	N	O	P	0	0
			3337	1489	587	1104	157		

- Molecule 39 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	E	119	Total	C	N	O	P	0	0
			2541	1132	454	836	119		

- Molecule 40 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	F	294	Total	C	N	O	S	0	0
			2392	1510	436	432	14		

- Molecule 41 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	G	236	Total	C	N	O	S	0	0
			1904	1222	361	317	4		

- Molecule 42 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	H	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 43 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	I	234	Total	C	N	O	S	0	0
			1880	1197	362	317	4		

- Molecule 44 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	J	191	Total	C	N	O	S	0	0
			1526	960	285	275	6		

- Molecule 45 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	K	208	Total	C	N	O	S	0	0
			1692	1074	327	278	13		

- Molecule 46 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	L	169	Total	C	N	O	S	0	0
			1353	855	252	240	6		

- Molecule 47 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	M	205	Total	C	N	O	S	0	0
			1657	1036	344	273	4		

- Molecule 48 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	N	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 49 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	O	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 50 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	P	195	Total	C	N	O	S	0	0
			1606	1034	315	252	5		

- Molecule 51 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Q	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 52 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	R	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 53 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	S	181	Total	C	N	O	S	0	0
			1517	938	329	241	9		

- Molecule 54 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	T	175	Total	C	N	O	S	0	0
			1449	921	283	234	11		

- Molecule 55 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	U	157	Total	C	N	O	S	0	0
			1284	815	250	214	5		

- Molecule 56 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	V	99	Total	C	N	O	S	0	0
			808	518	141	147	2		

- Molecule 57 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	W	129	Total	C	N	O	S	0	0
			969	613	182	169	5		

- Molecule 58 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	X	61	Total	C	N	O	S	0	0
			511	327	100	82	2		

- Molecule 59 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Y	117	Total	C	N	O	S	0	0
			958	612	180	165	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Z	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 61 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	a	134	Total	C	N	O	S	0	0
			1103	712	207	181	3		

- Molecule 62 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	b	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 63 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	c	100	Total	C	N	O	S	0	0
			814	506	179	125	4		

- Molecule 64 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	d	103	Total	C	N	O	S	0	0
			801	508	141	145	7		

- Molecule 65 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	e	106	Total	C	N	O	S	0	0
			879	555	170	152	2		

- Molecule 66 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	f	129	Total	C	N	O	S	0	0
			1064	673	220	166	5		

- Molecule 67 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	g	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 68 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	h	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 69 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	i	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 70 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	j	97	Total	C	N	O	S	0	0
			794	497	168	124	5		

- Molecule 71 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	k	84	Total	C	N	O	S	0	0
			689	423	152	109	5		

- Molecule 72 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	l	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 73 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	m	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 74 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	n	50	Total	C	N	O	S	0	0
			411	254	87	64	6		

- Molecule 75 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	o	25	Total	C	N	O	S	0	0
			240	145	64	28	3		

- Molecule 76 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	p	105	Total	C	N	O	S	0	0
			863	542	175	140	6		

- Molecule 77 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	q	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 78 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	r	122	Total	C	N	O	S	0	0
			980	607	204	165	4		

- Molecule 79 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	t	3607	Total	C	N	O	P	0	0
			77332	34436	14150	25139	3607		

- Molecule 80 is a RNA chain called AP RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	u	76	Total	C	N	O	P	0	0
			1613	720	283	535	75		

- Molecule 81 is a RNA chain called PE RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	v	76	Total	C	N	O	P	0	0
			1618	721	287	534	76		

- Molecule 82 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	w	10	Total	C	N	O	P	0	0
			213	95	37	72	9		

- Molecule 83 is a protein called Cadherin-1.

Mol	Chain	Residues	Atoms				AltConf	Trace
83	y	39	Total	C	N	O	0	0
			262	180	40	42		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
y	6	ALA	-	insertion	UNP P12830

- Molecule 84 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
84	S2	3	Total	Mg	0
			3	3	
84	A	1	Total	Mg	0
			1	1	
84	B	1	Total	Mg	0
			1	1	
84	D	8	Total	Mg	0
			8	8	
84	E	9	Total	Mg	0
			9	9	
84	O	1	Total	Mg	0
			1	1	
84	Z	1	Total	Mg	0
			1	1	
84	b	1	Total	Mg	0
			1	1	
84	t	6	Total	Mg	0
			6	6	

- Molecule 85 is ZINC ION (three-letter code: ZN) (formula: Zn).

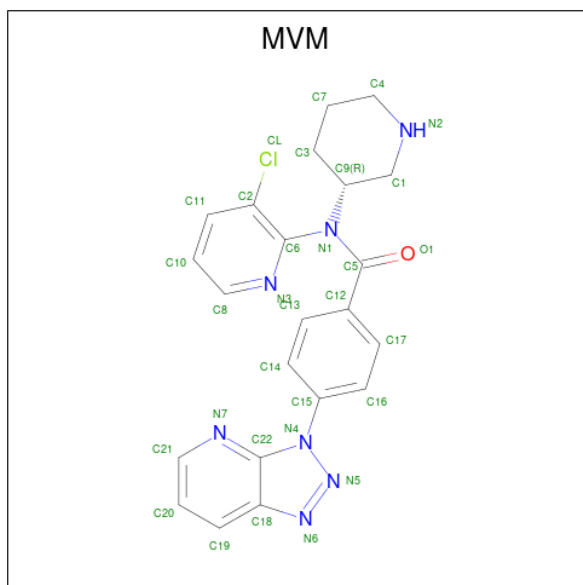
Mol	Chain	Residues	Atoms		AltConf
85	S2	1	Total	Zn	0
			1	1	
85	Sa	1	Total	Zn	0
			1	1	
85	Sf	1	Total	Zn	0
			1	1	
85	k	1	Total	Zn	0
			1	1	
85	p	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
85	q	1	Total	Zn	0
			1	1	

- Molecule 86 is N-(3-chloropyridin-2-yl)-N-[(3R)-piperidin-3-yl]-4-(3H-[1,2,3]triazolo[4,5-b]pyridin-3-yl)benzamide (three-letter code: MVM) (formula: C₂₂H₂₀ClN₇O).



Mol	Chain	Residues	Atoms					AltConf
86	y	1	Total	C	Cl	N	O	0
			31	22	1	7	1	

- Molecule 87 is water.

Mol	Chain	Residues	Atoms		AltConf
87	S2	4	Total	O	0
			4	4	
87	SP	1	Total	O	0
			1	1	
87	SQ	1	Total	O	0
			1	1	
87	SR	1	Total	O	0
			1	1	
87	SS	2	Total	O	0
			2	2	
87	SC	1	Total	O	0
			1	1	
87	SN	1	Total	O	0
			1	1	

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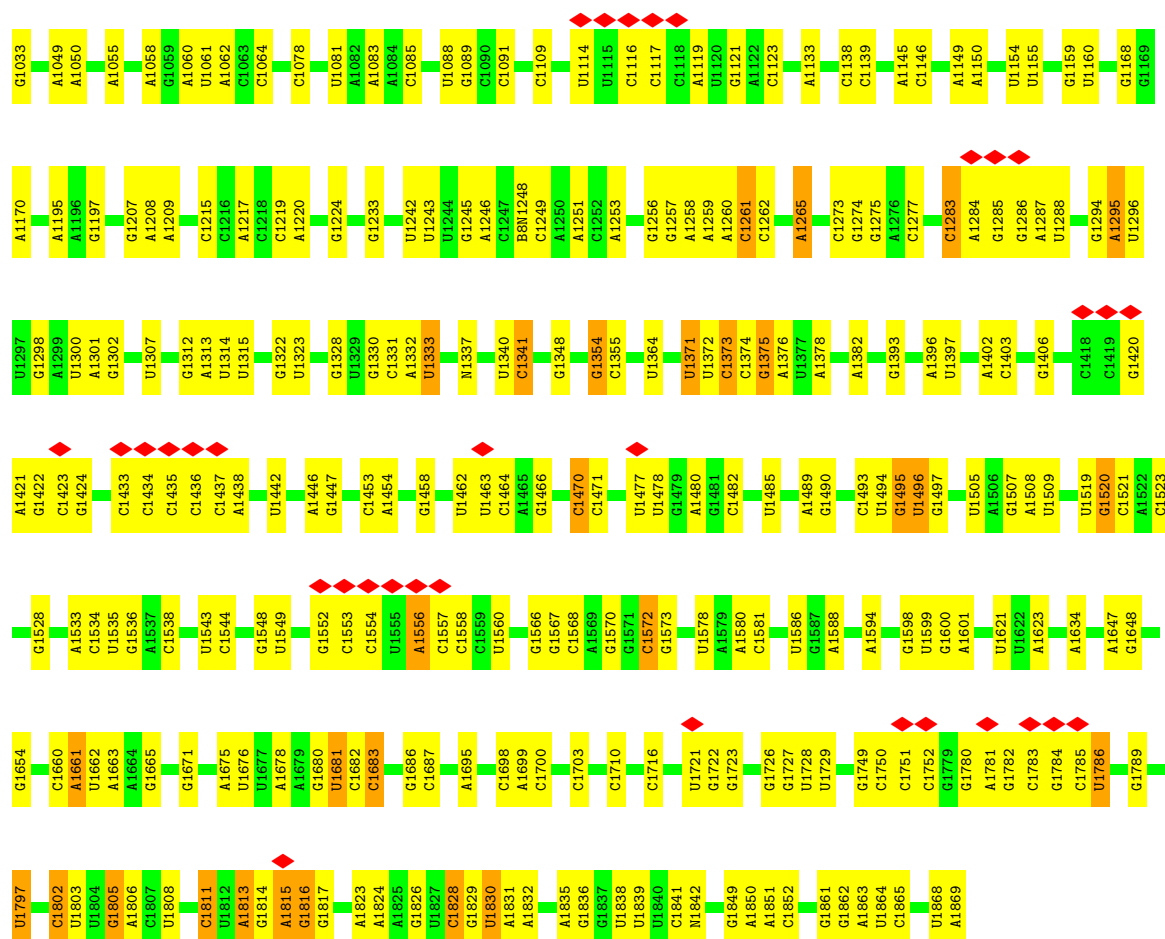
Mol	Chain	Residues	Atoms		AltConf
87	Sf	1	Total 1	O 1	0
87	u	1	Total 1	O 1	0
87	v	1	Total 1	O 1	0

3 Residue-property plots

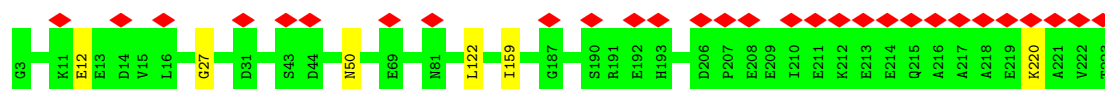
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 18S ribosomal RNA

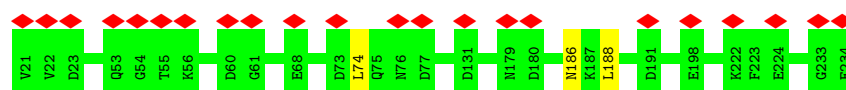




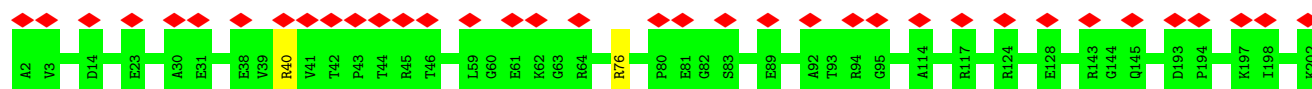
• Molecule 2: 40S ribosomal protein SA

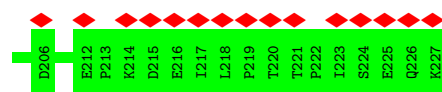


• Molecule 3: 40S ribosomal protein S3a

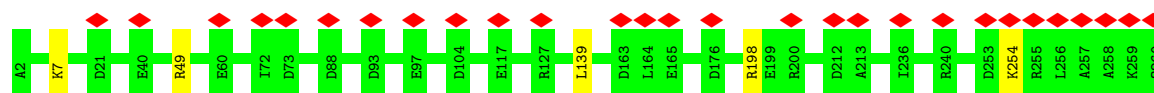


• Molecule 4: 40S ribosomal protein S3

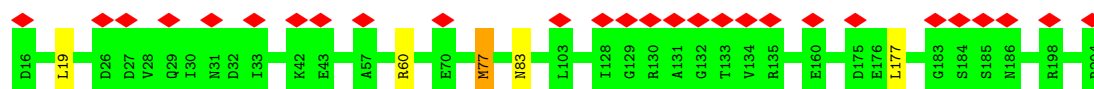




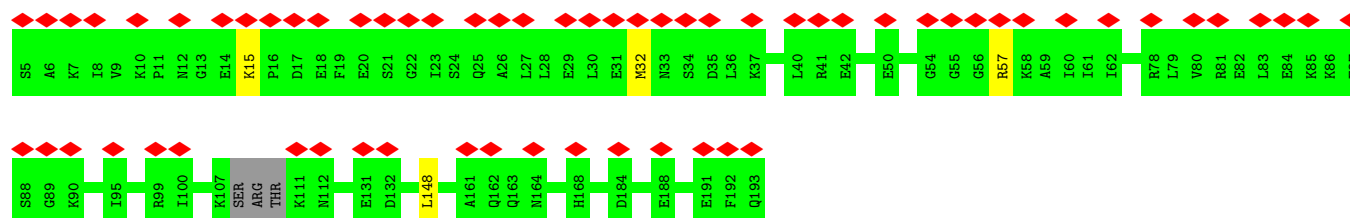
- Molecule 5: 40S ribosomal protein S4, X isoform



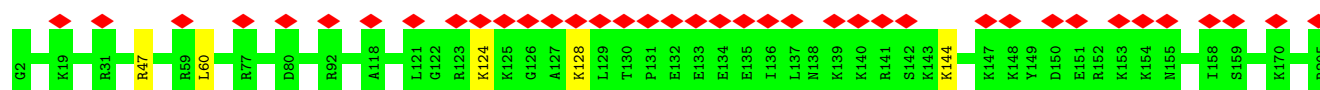
- Molecule 6: 40S ribosomal protein S5



- Molecule 7: 40S ribosomal protein S7



- Molecule 8: 40S ribosomal protein S8

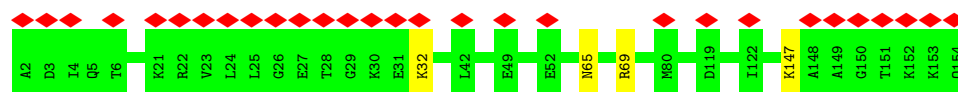


- Molecule 9: 40S ribosomal protein S10

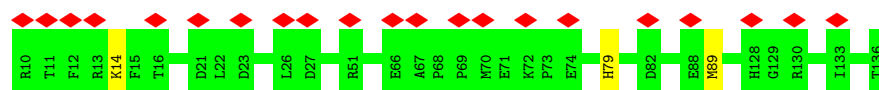


- Molecule 10: 40S ribosomal protein S11

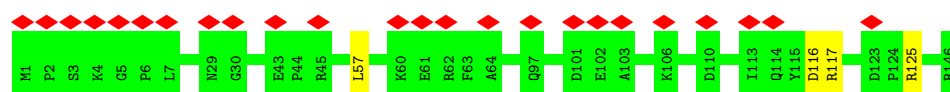




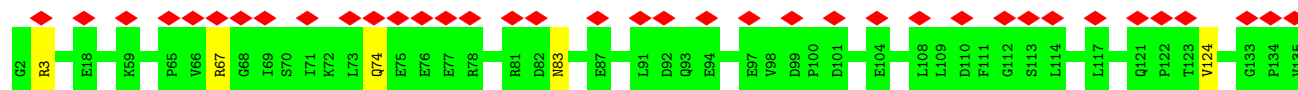
- Molecule 11: 40S ribosomal protein S15



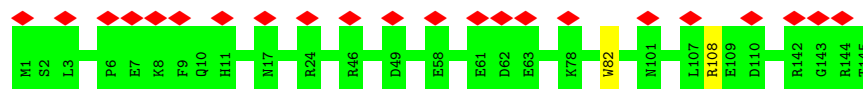
- Molecule 12: 40S ribosomal protein S16



- Molecule 13: 40S ribosomal protein S17



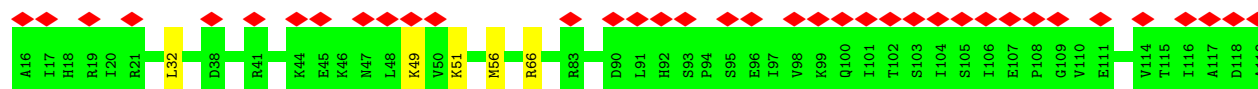
- Molecule 14: 40S ribosomal protein S18



- Molecule 15: 40S ribosomal protein S19



- Molecule 16: 40S ribosomal protein S20



- Molecule 17: 40S ribosomal protein S21



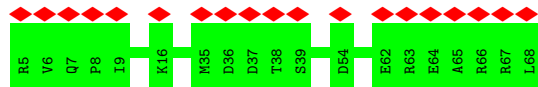
- Molecule 18: 40S ribosomal protein S23



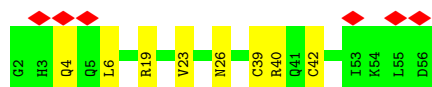
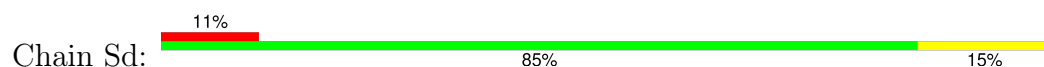
- Molecule 19: 40S ribosomal protein S26



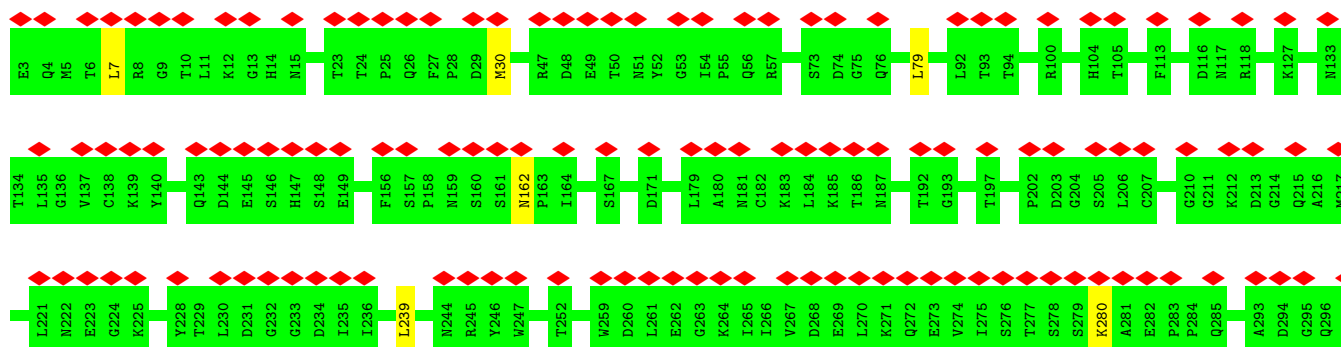
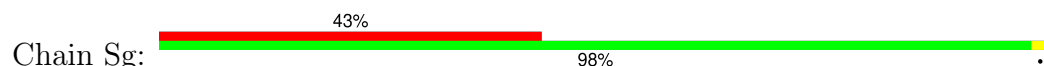
- Molecule 20: 40S ribosomal protein S28

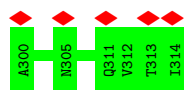


- Molecule 21: 40S ribosomal protein S29

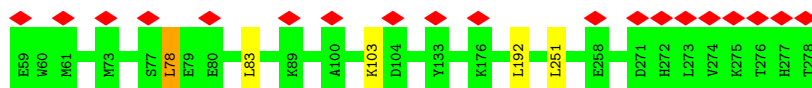


- Molecule 22: Receptor of activated protein C kinase 1

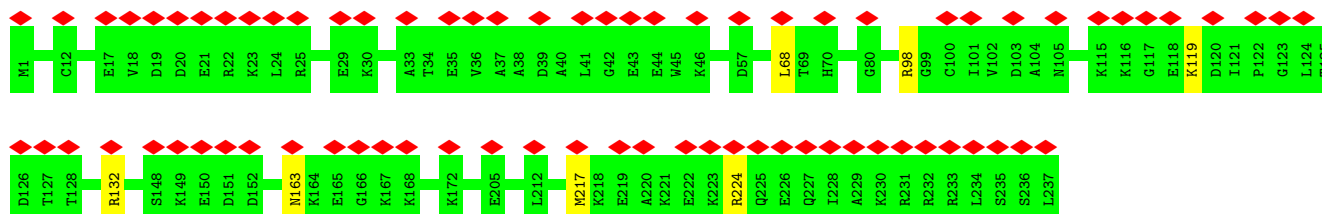




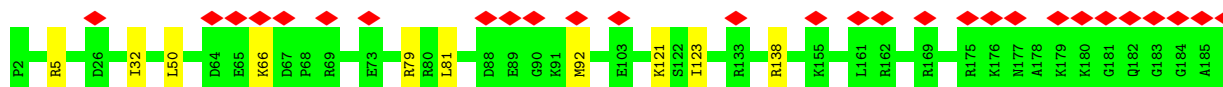
- Molecule 23: 40S ribosomal protein S2



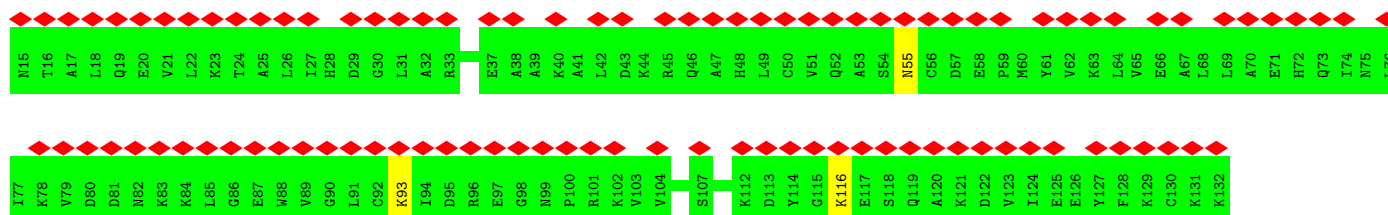
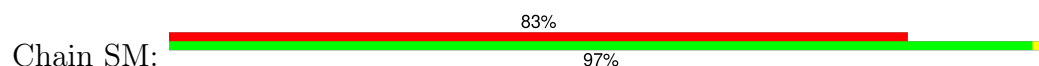
- Molecule 24: 40S ribosomal protein S6



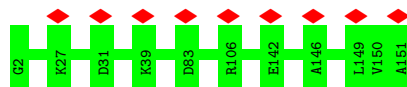
- Molecule 25: 40S ribosomal protein S9



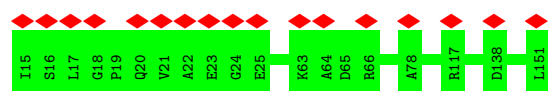
- Molecule 26: 40S ribosomal protein S12



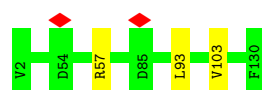
- Molecule 27: 40S ribosomal protein S13



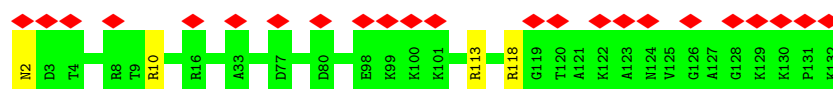
- Molecule 28: 40S ribosomal protein S14



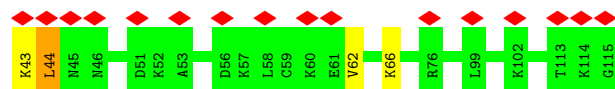
- Molecule 29: 40S ribosomal protein S15a



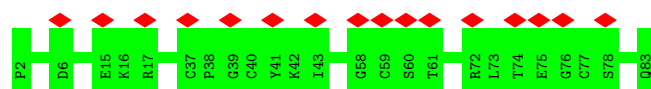
- Molecule 30: 40S ribosomal protein S24



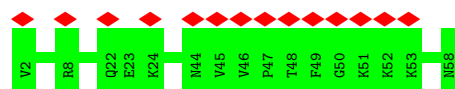
- Molecule 31: 40S ribosomal protein S25



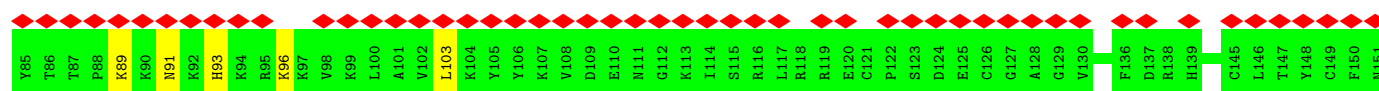
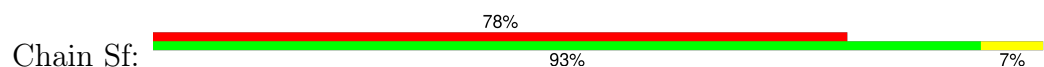
- Molecule 32: 40S ribosomal protein S27



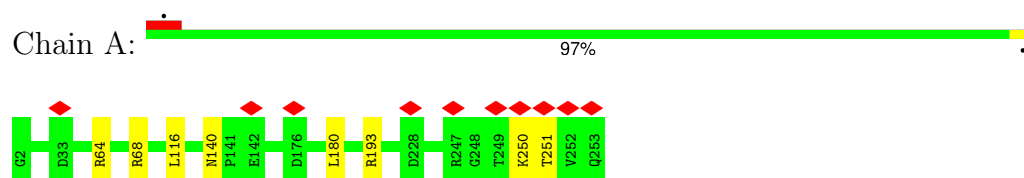
- Molecule 33: 40S ribosomal protein S30



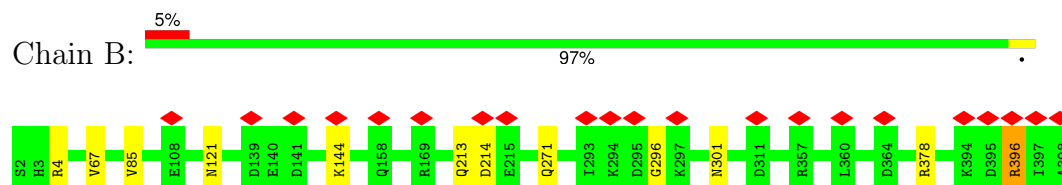
- Molecule 34: 40S ribosomal protein S27a



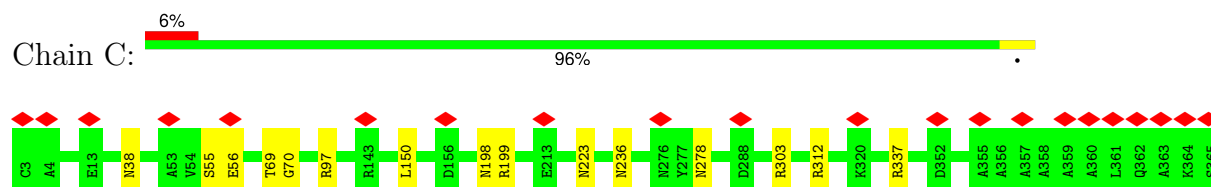
- Molecule 35: 60S ribosomal protein L8



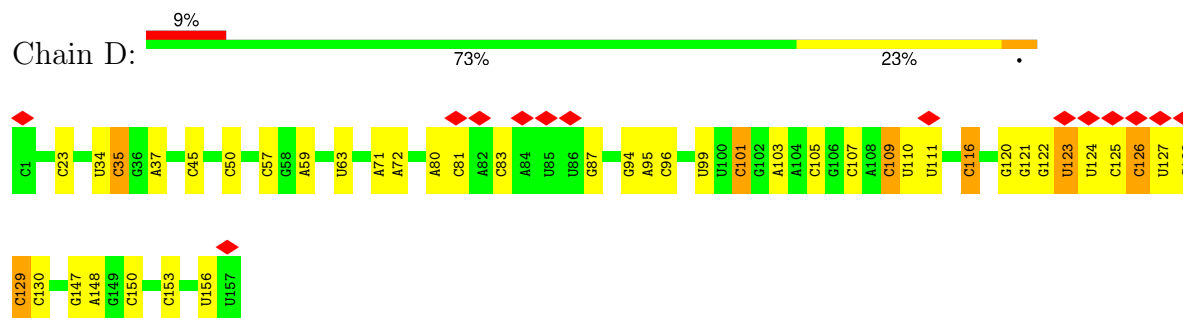
- Molecule 36: 60S ribosomal protein L3



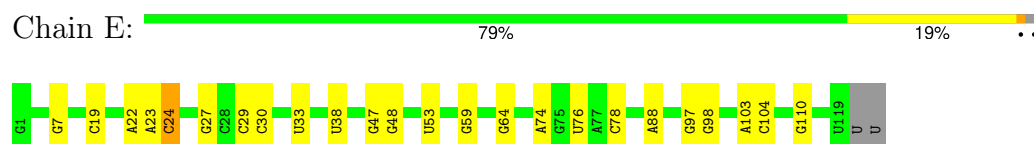
- Molecule 37: 60S ribosomal protein L4



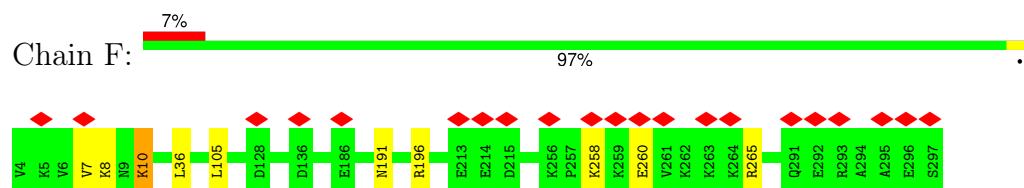
- Molecule 38: 5.8S ribosomal RNA



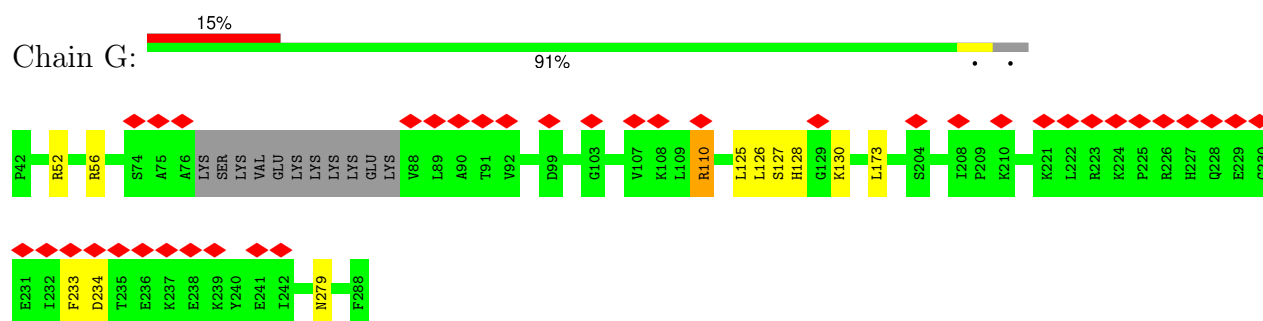
- Molecule 39: 5S ribosomal RNA



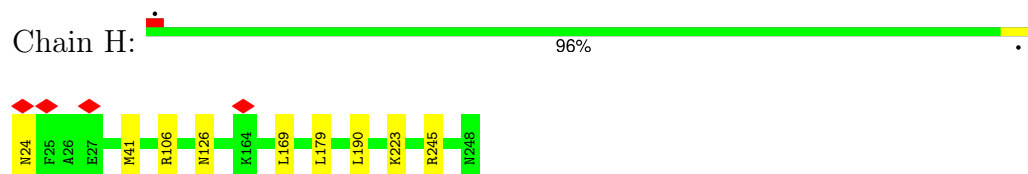
- Molecule 40: 60S ribosomal protein L5



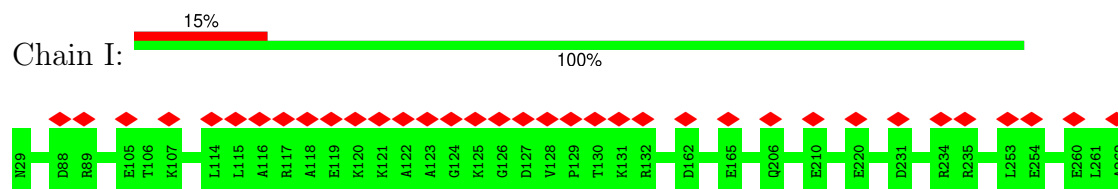
- Molecule 41: 60S ribosomal protein L6



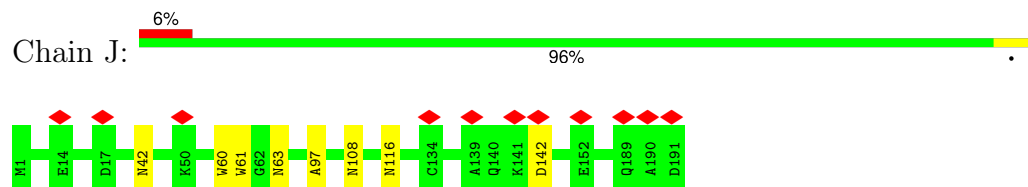
- Molecule 42: 60S ribosomal protein L7



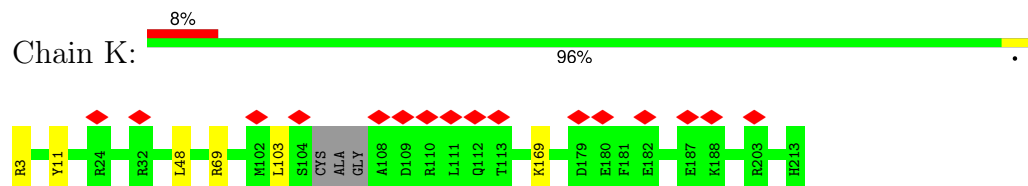
- Molecule 43: 60S ribosomal protein L7a



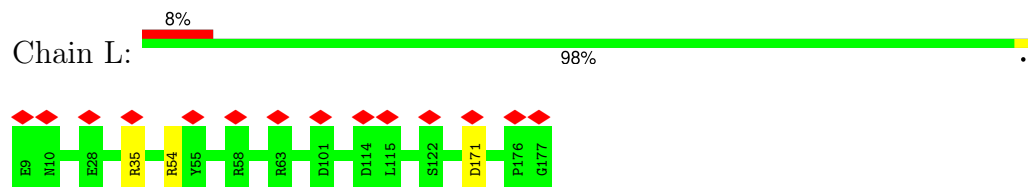
- Molecule 44: 60S ribosomal protein L9



- Molecule 45: 60S ribosomal protein L10

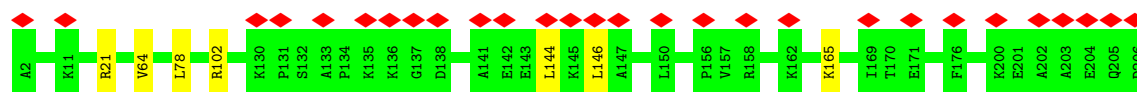


- Molecule 46: 60S ribosomal protein L11

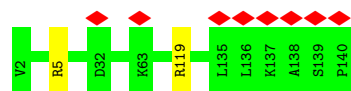


- Molecule 47: 60S ribosomal protein L13





- Molecule 48: 60S ribosomal protein L14



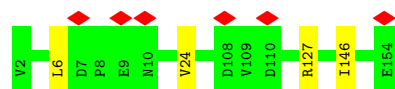
- Molecule 49: 60S ribosomal protein L15



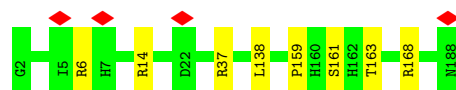
- Molecule 50: 60S ribosomal protein L13a



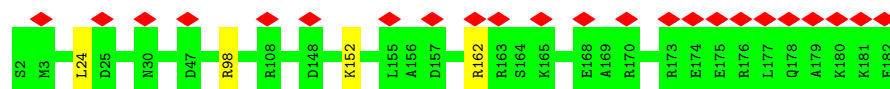
- Molecule 51: 60S ribosomal protein L17



- Molecule 52: 60S ribosomal protein L18

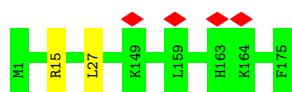


- Molecule 53: 60S ribosomal protein L19



- Molecule 54: 60S ribosomal protein L18a

Chain T:  99%



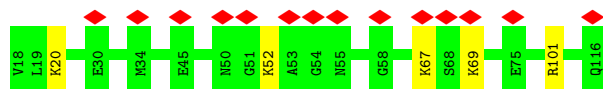
- Molecule 55: 60S ribosomal protein L21

Chain U:  96%



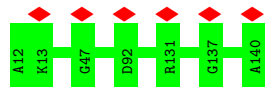
- Molecule 56: 60S ribosomal protein L22

Chain V:  14% 95% 5%



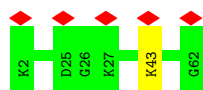
- Molecule 57: 60S ribosomal protein L23

Chain W:  5% 100%



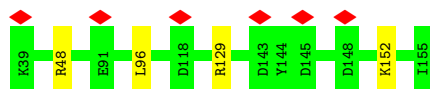
- Molecule 58: 60S ribosomal protein L24

Chain X:  8% 98%



- Molecule 59: 60S ribosomal protein L23a

Chain Y:  5% 97%



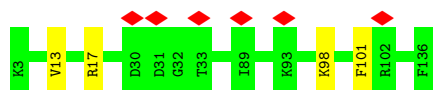
- Molecule 60: 60S ribosomal protein L26

Chain Z:  1% 99%



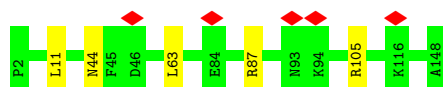
- Molecule 61: 60S ribosomal protein L27

Chain a:  97%




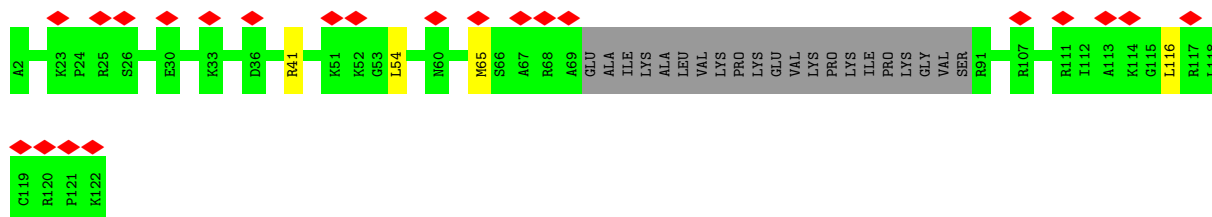
- Molecule 62: 60S ribosomal protein L27a

Chain b:  97%



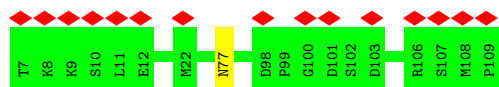
- Molecule 63: 60S ribosomal protein L29

Chain c:  18% 79% 17%



- Molecule 64: 60S ribosomal protein L30

Chain d:  15% 99%



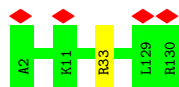
- Molecule 65: 60S ribosomal protein L31

Chain e:  11% 98%



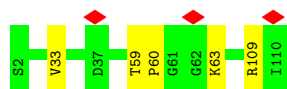
- Molecule 66: 60S ribosomal protein L32

Chain f:  99%



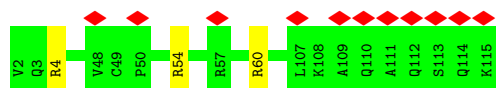
- Molecule 67: 60S ribosomal protein L35a

Chain g:  95% 5%



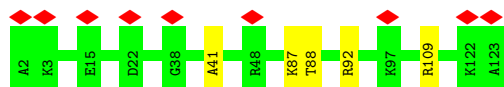
- Molecule 68: 60S ribosomal protein L34

Chain h:  10% 97%



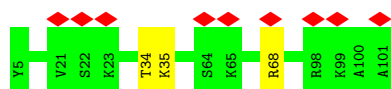
- Molecule 69: 60S ribosomal protein L35

Chain i:  7% 96%



- Molecule 70: 60S ribosomal protein L36

Chain j:  9% 97%



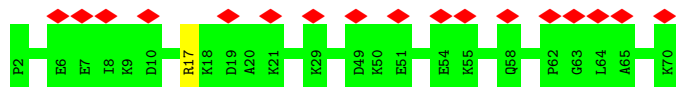
- Molecule 71: 60S ribosomal protein L37

Chain k:  99%



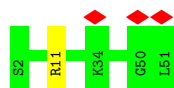
- Molecule 72: 60S ribosomal protein L38

Chain l:  25% 99%

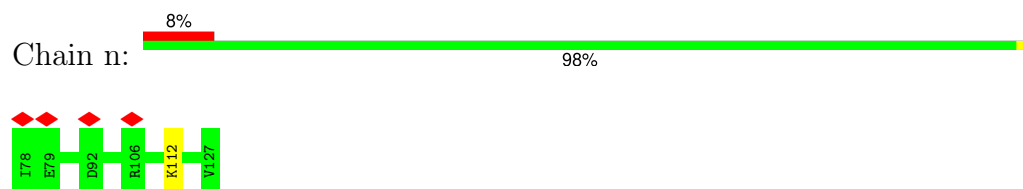


- Molecule 73: 60S ribosomal protein L39

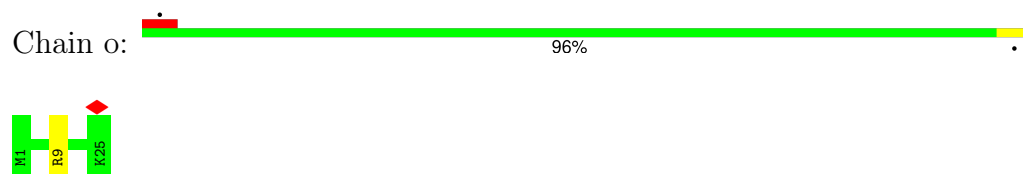
Chain m:  6% 98%



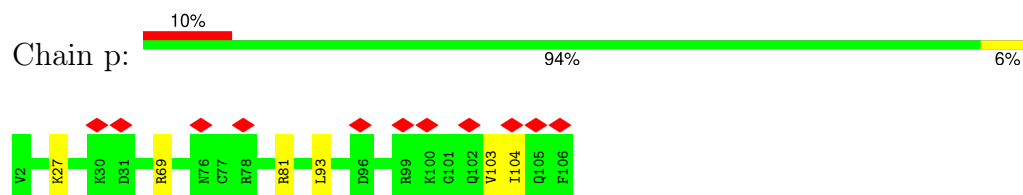
- Molecule 74: 60S ribosomal protein L40



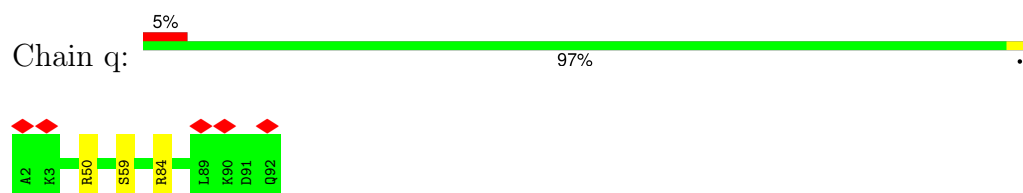
- Molecule 75: 60S ribosomal protein L41



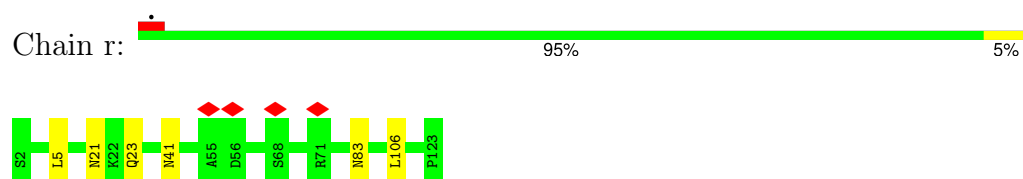
- Molecule 76: 60S ribosomal protein L36a



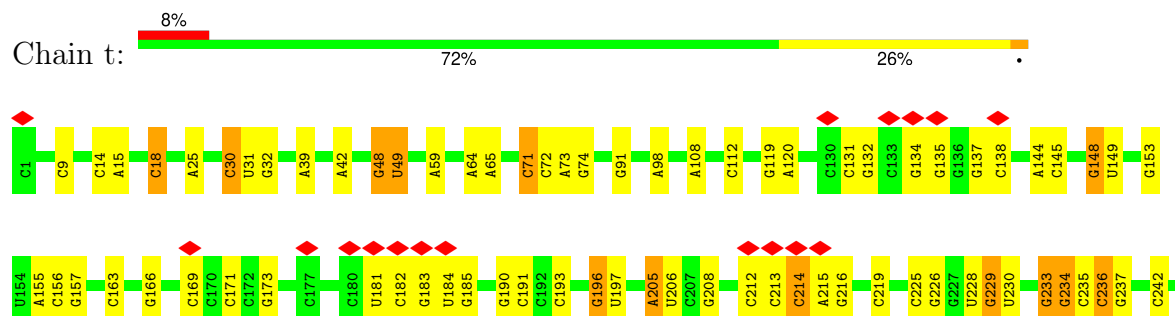
- Molecule 77: 60S ribosomal protein L37a



- Molecule 78: 60S ribosomal protein L28

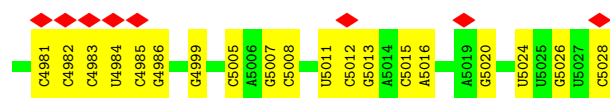


- Molecule 79: 28S ribosomal RNA





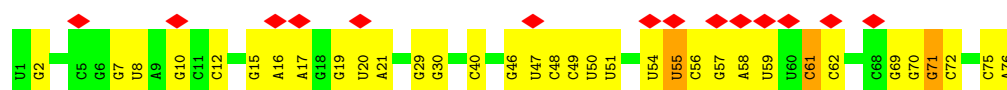




• Molecule 80: AP RNA



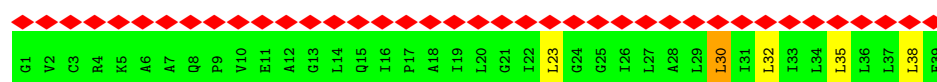
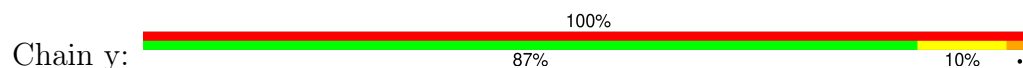
• Molecule 81: PE RNA



• Molecule 82: mRNA



• Molecule 83: Cadherin-1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	73110	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.149	Depositor
Minimum map value	-0.067	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.02	Depositor
Map size (\AA)	460.0, 460.0, 460.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.15, 1.15, 1.15	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: B8Q, M7A, MG, MA6, A2M, ZN, E3C, 5MC, OMC, OMG, UR3, PSU, B8N, 6MZ, 5MU, MVM, OMU, 4AC

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	S2	0.62	1/39959 (0.0%)	1.07	182/62253 (0.3%)
2	SA	0.38	0/1778	0.65	1/2416 (0.0%)
3	SB	0.36	0/1765	0.64	3/2362 (0.1%)
4	SD	0.35	0/1785	0.65	0/2404
5	SE	0.36	0/2101	0.63	1/2828 (0.0%)
6	SF	0.37	0/1516	0.65	3/2037 (0.1%)
7	SH	0.32	0/1519	0.65	1/2033 (0.0%)
8	SI	0.35	0/1702	0.62	0/2271
9	SK	0.37	0/851	0.65	1/1147 (0.1%)
10	SL	0.39	0/1268	0.66	0/1696
11	SP	0.38	0/1065	0.64	0/1423
12	SQ	0.39	0/1177	0.71	1/1575 (0.1%)
13	SR	0.33	0/1097	0.70	0/1474
14	SS	0.34	0/1216	0.65	1/1628 (0.1%)
15	ST	0.36	0/1131	0.67	1/1515 (0.1%)
16	SU	0.32	0/831	0.65	1/1115 (0.1%)
17	SV	0.37	0/631	0.64	0/844
18	SX	0.38	0/1116	0.65	0/1490
19	Sa	0.45	0/836	0.61	0/1121
20	Sc	0.35	0/508	0.71	0/680
21	Sd	0.50	0/470	0.80	1/623 (0.2%)
22	Sg	0.33	0/2486	0.70	3/3384 (0.1%)
23	SC	0.41	0/1755	0.75	4/2371 (0.2%)
24	SG	0.31	0/1946	0.64	1/2590 (0.0%)
25	SJ	0.36	0/1561	0.76	3/2083 (0.1%)
26	SM	0.30	0/922	0.65	0/1238
27	SN	0.34	0/1232	0.60	0/1656
28	SO	0.34	0/1037	0.66	0/1391
29	SW	0.39	0/1051	0.64	0/1406
30	SY	0.32	0/1094	0.62	0/1452
31	SZ	0.35	0/585	0.79	1/785 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Sb	0.35	0/653	0.56	0/876
33	Se	0.30	0/458	0.61	0/604
34	Sf	0.32	0/560	0.75	1/745 (0.1%)
35	A	0.45	0/1968	0.67	2/2639 (0.1%)
36	B	0.43	0/3270	0.70	1/4377 (0.0%)
37	C	0.43	0/2942	0.67	0/3951
38	D	0.72	1/3726 (0.0%)	1.10	24/5804 (0.4%)
39	E	0.71	0/2839	1.05	4/4425 (0.1%)
40	F	0.40	0/2437	0.66	2/3262 (0.1%)
41	G	0.36	0/1942	0.81	7/2606 (0.3%)
42	H	0.45	0/1905	0.72	3/2539 (0.1%)
43	I	0.39	0/1913	0.65	0/2576
44	J	0.38	0/1545	0.64	1/2077 (0.0%)
45	K	0.41	0/1730	0.67	2/2311 (0.1%)
46	L	0.36	0/1376	0.68	1/1841 (0.1%)
47	M	0.39	0/1688	0.69	2/2260 (0.1%)
48	N	0.39	0/1161	0.60	0/1554
49	O	0.46	0/1746	0.70	1/2338 (0.0%)
50	P	0.42	0/1638	0.63	1/2191 (0.0%)
51	Q	0.43	0/1268	0.66	1/1701 (0.1%)
52	R	0.42	0/1537	0.73	2/2052 (0.1%)
53	S	0.38	0/1533	0.64	1/2025 (0.0%)
54	T	0.46	0/1488	0.65	1/1997 (0.1%)
55	U	0.42	0/1312	0.66	0/1753
56	V	0.36	0/822	0.63	0/1103
57	W	0.41	0/983	0.62	0/1319
58	X	0.43	0/524	0.61	0/698
59	Y	0.38	0/975	0.62	0/1312
60	Z	0.42	0/1132	0.60	0/1504
61	a	0.40	0/1126	0.66	1/1502 (0.1%)
62	b	0.43	0/1191	0.73	1/1591 (0.1%)
63	c	0.34	0/826	0.65	2/1088 (0.2%)
64	d	0.40	0/812	0.71	0/1089
65	e	0.41	0/894	0.64	1/1204 (0.1%)
66	f	0.42	0/1082	0.67	0/1443
67	g	0.48	0/895	0.70	0/1198
68	h	0.43	0/916	0.74	1/1220 (0.1%)
69	i	0.37	0/1023	0.68	1/1351 (0.1%)
70	j	0.36	0/805	0.65	0/1065
71	k	0.44	0/703	0.62	0/929
72	l	0.37	0/575	0.66	0/761
73	m	0.42	0/454	0.69	0/599
74	n	0.38	0/417	0.65	0/553

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	o	0.34	0/241	0.73	0/305
76	p	0.43	0/877	0.70	0/1156
77	q	0.43	0/718	0.65	1/953 (0.1%)
78	r	0.43	0/995	0.74	2/1334 (0.1%)
79	t	0.74	3/86502 (0.0%)	1.10	460/134927 (0.3%)
80	u	0.47	0/1799	1.31	26/2800 (0.9%)
81	v	0.50	0/1802	1.20	16/2797 (0.6%)
82	w	0.63	0/235	1.32	1/365 (0.3%)
83	y	0.39	0/263	1.18	4/359 (1.1%)
All	All	0.59	5/230213 (0.0%)	0.96	783/338320 (0.2%)

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	SA	0	1
7	SH	0	2
11	SP	0	1
13	SR	0	2
18	SX	0	1
21	Sd	0	2
31	SZ	0	1
36	B	0	1
37	C	0	1
40	F	0	1
44	J	0	1
67	g	0	1
76	p	0	1
All	All	0	16

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	S2	1495	G	C2-N3	-6.58	1.27	1.32
38	D	37	A	N9-C4	-6.46	1.33	1.37
79	t	148	G	N9-C4	-6.29	1.32	1.38
79	t	155	A	N9-C4	-5.47	1.34	1.37
79	t	4234	G	N9-C4	-5.12	1.33	1.38

All (783) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	S2	115	U	C2-N3-C4	20.37	139.22	127.00
1	S2	65	C	N1-C2-O2	13.85	127.21	118.90
1	S2	65	C	C2-N1-C1'	13.16	133.27	118.80
81	v	61	C	C2-N1-C1'	12.46	132.51	118.80
81	v	61	C	N1-C2-O2	12.27	126.26	118.90
80	u	55	U	N1-C2-O2	12.02	131.21	122.80
80	u	55	U	N3-C2-O2	-11.95	113.84	122.20
1	S2	501	C	N1-C2-O2	11.89	126.03	118.90
79	t	3616	U	N3-C2-O2	-11.76	113.97	122.20
1	S2	115	U	N3-C4-C5	11.56	121.53	114.60
79	t	3616	U	N1-C2-O2	11.46	130.82	122.80
80	u	55	U	C2-N1-C1'	11.40	131.38	117.70
1	S2	1283	C	N1-C2-O2	10.92	125.45	118.90
1	S2	1453	C	N1-C2-O2	10.72	125.33	118.90
1	S2	1453	C	C2-N1-C1'	10.63	130.49	118.80
1	S2	53	C	C6-N1-C2	-10.44	116.12	120.30
1	S2	501	C	C2-N1-C1'	10.38	130.22	118.80
1	S2	65	C	C6-N1-C1'	-10.23	108.53	120.80
79	t	2447	U	N3-C2-O2	-10.12	115.11	122.20
79	t	918	C	C2-N1-C1'	10.10	129.91	118.80
1	S2	501	C	N3-C2-O2	-9.97	114.92	121.90
79	t	4234	G	N3-C4-N9	-9.93	120.04	126.00
1	S2	65	C	N3-C2-O2	-9.82	115.03	121.90
42	H	169	LEU	CA-CB-CG	9.81	137.87	115.30
1	S2	501	C	C6-N1-C2	-9.68	116.43	120.30
1	S2	118	C	N1-C2-O2	9.67	124.70	118.90
80	u	48	C	N1-C2-O2	9.65	124.69	118.90
1	S2	1341	C	N1-C2-O2	9.60	124.66	118.90
79	t	148	G	N3-C4-N9	-9.55	120.27	126.00
79	t	649	C	N1-C2-O2	9.54	124.62	118.90
79	t	148	G	N3-C4-C5	9.53	133.37	128.60
1	S2	115	U	N1-C2-N3	9.49	120.60	114.90
38	D	129	C	N1-C2-O2	9.35	124.51	118.90
79	t	219	C	C2-N1-C1'	9.25	128.97	118.80
81	v	61	C	N3-C2-O2	-9.23	115.44	121.90
79	t	4736	C	C2-N1-C1'	9.20	128.92	118.80
1	S2	1139	C	C2-N1-C1'	9.18	128.90	118.80
80	u	48	C	N3-C2-O2	-9.18	115.48	121.90
79	t	958	U	C2-N1-C1'	9.15	128.69	117.70
38	D	126	C	N1-C2-O2	9.15	124.39	118.90
41	G	234	ASP	CB-CG-OD1	9.10	126.49	118.30
1	S2	1283	C	N3-C2-O2	-9.08	115.54	121.90
1	S2	1341	C	N3-C2-O2	-9.06	115.56	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
79	t	956	C	C2-N1-C1'	9.05	128.76	118.80
54	T	27	LEU	CA-CB-CG	9.05	136.12	115.30
79	t	225	C	C6-N1-C2	-8.98	116.71	120.30
79	t	1930	U	N3-C2-O2	-8.92	115.96	122.20
80	u	43	C	N1-C2-O2	8.88	124.23	118.90
1	S2	1139	C	N1-C2-O2	8.87	124.22	118.90
38	D	126	C	C2-N1-C1'	8.86	128.54	118.80
79	t	2323	U	N1-C2-O2	8.85	128.99	122.80
79	t	2398	C	C2-N1-C1'	8.82	128.50	118.80
81	v	61	C	C6-N1-C1'	-8.82	110.22	120.80
1	S2	1139	C	N3-C2-O2	-8.75	115.77	121.90
1	S2	1495	G	N1-C2-N2	8.70	124.03	116.20
23	SC	78	LEU	CA-CB-CG	8.68	135.27	115.30
79	t	956	C	N1-C2-O2	8.66	124.10	118.90
80	u	43	C	C2-N1-C1'	8.65	128.31	118.80
79	t	214	C	N1-C2-O2	8.61	124.06	118.90
1	S2	118	C	C2-N1-C1'	8.58	128.24	118.80
1	S2	1283	C	C2-N1-C1'	8.52	128.17	118.80
79	t	2727	C	C2-N1-C1'	8.50	128.16	118.80
79	t	958	U	N1-C2-O2	8.50	128.75	122.80
79	t	905	G	C4-N9-C1'	8.47	137.52	126.50
79	t	1989	U	C2-N1-C1'	8.46	127.86	117.70
1	S2	578	C	N1-C2-O2	8.43	123.96	118.90
38	D	129	C	N3-C2-O2	-8.41	116.01	121.90
51	Q	6	LEU	CA-CB-CG	8.40	134.62	115.30
79	t	3849	C	C2-N1-C1'	8.38	128.01	118.80
79	t	2323	U	N3-C2-O2	-8.35	116.36	122.20
78	r	106	LEU	CA-CB-CG	8.29	134.37	115.30
79	t	1959	C	N1-C2-O2	8.28	123.87	118.90
1	S2	839	C	C2-N1-C1'	8.26	127.88	118.80
1	S2	1578	U	N1-C2-O2	8.19	128.53	122.80
79	t	225	C	C5-C6-N1	8.18	125.09	121.00
79	t	918	C	N1-C2-O2	8.17	123.80	118.90
79	t	4234	G	N3-C2-N2	-8.17	114.18	119.90
79	t	1989	U	N1-C2-O2	8.13	128.49	122.80
79	t	4736	C	N1-C2-O2	8.11	123.77	118.90
79	t	1261	C	N1-C2-O2	8.11	123.77	118.90
79	t	1466	G	N3-C4-N9	8.09	130.85	126.00
79	t	2499	C	C2-N1-C1'	8.04	127.65	118.80
79	t	216	G	N3-C2-N2	-8.01	114.29	119.90
81	v	71	G	C4-N9-C1'	8.01	136.91	126.50
79	t	233	G	N3-C2-N2	-8.01	114.30	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
79	t	4234	G	C8-N9-C1'	8.00	137.39	127.00
1	S2	53	C	C5-C6-N1	7.98	124.99	121.00
79	t	3616	U	C2-N1-C1'	7.97	127.27	117.70
79	t	4880	C	N1-C2-O2	7.97	123.68	118.90
79	t	2228	C	N1-C2-O2	7.95	123.67	118.90
1	S2	1495	G	N3-C2-N2	-7.95	114.34	119.90
38	D	126	C	N3-C2-O2	-7.93	116.35	121.90
79	t	1989	U	N3-C2-O2	-7.92	116.65	122.20
79	t	2388	U	N1-C2-O2	7.90	128.33	122.80
79	t	727	C	C6-N1-C2	-7.90	117.14	120.30
1	S2	839	C	N1-C2-O2	7.89	123.64	118.90
79	t	504	U	O5'-P-OP2	-7.88	98.60	105.70
24	SG	68	LEU	CA-CB-CG	7.88	133.41	115.30
79	t	2388	U	C2-N1-C1'	7.86	127.13	117.70
80	u	48	C	C2-N1-C1'	7.86	127.44	118.80
79	t	214	C	C2-N1-C1'	7.84	127.42	118.80
79	t	3849	C	N1-C2-O2	7.83	123.60	118.90
79	t	649	C	C2-N1-C1'	7.83	127.42	118.80
81	v	71	G	C8-N9-C1'	-7.81	116.85	127.00
1	S2	118	C	N3-C2-O2	-7.80	116.44	121.90
79	t	2447	U	N1-C2-O2	7.79	128.25	122.80
79	t	256	C	N1-C2-O2	7.79	123.57	118.90
1	S2	356	C	C2-N1-C1'	7.76	127.34	118.80
42	H	179	LEU	CA-CB-CG	7.76	133.15	115.30
1	S2	1520	G	C4-N9-C1'	7.75	136.58	126.50
81	v	71	G	N3-C4-N9	7.75	130.65	126.00
79	t	1466	G	C4-N9-C1'	7.71	136.52	126.50
79	t	2499	C	N1-C2-O2	7.70	123.52	118.90
1	S2	1453	C	C6-N1-C1'	-7.69	111.57	120.80
79	t	958	U	N3-C2-O2	-7.65	116.85	122.20
1	S2	578	C	N3-C2-O2	-7.63	116.56	121.90
79	t	4717	G	N3-C2-N2	-7.63	114.56	119.90
1	S2	1578	U	N3-C2-O2	-7.62	116.86	122.20
79	t	1564	U	N3-C2-O2	-7.61	116.88	122.20
79	t	197	U	C2-N1-C1'	7.61	126.83	117.70
79	t	2282	C	C6-N1-C2	-7.59	117.26	120.30
79	t	905	G	N3-C4-N9	7.58	130.54	126.00
79	t	1564	U	C2-N1-C1'	7.57	126.79	117.70
79	t	4717	G	N3-C4-N9	-7.57	121.46	126.00
81	v	61	C	C6-N1-C2	-7.57	117.27	120.30
79	t	1261	C	N3-C2-O2	-7.55	116.61	121.90
79	t	918	C	C6-N1-C1'	-7.55	111.74	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
79	t	2236	C	N1-C2-O2	7.54	123.42	118.90
79	t	444	G	O4'-C1'-N9	7.53	114.23	108.20
1	S2	356	C	N1-C2-O2	7.52	123.41	118.90
79	t	1930	U	C2-N1-C1'	7.51	126.71	117.70
79	t	339	C	N1-C2-O2	7.50	123.40	118.90
52	R	138	LEU	CA-CB-CG	7.50	132.54	115.30
1	S2	1453	C	N3-C2-O2	-7.49	116.66	121.90
79	t	2239	C	N1-C2-O2	7.46	123.38	118.90
79	t	2398	C	N1-C2-O2	7.45	123.37	118.90
79	t	4267	G	N3-C2-N2	-7.43	114.70	119.90
79	t	3595	A	P-O3'-C3'	7.43	128.62	119.70
1	S2	1022	U	C2-N1-C1'	7.39	126.57	117.70
79	t	225	C	C2-N3-C4	7.38	123.59	119.90
79	t	918	C	N3-C2-O2	-7.38	116.74	121.90
79	t	4267	G	C8-N9-C4	-7.37	103.45	106.40
79	t	905	G	C8-N9-C1'	-7.37	117.42	127.00
79	t	1746	G	C4-N9-C1'	7.37	136.08	126.50
1	S2	1005	G	N3-C4-C5	-7.36	124.92	128.60
79	t	4633	C	N1-C2-O2	7.36	123.31	118.90
79	t	4391	C	C6-N1-C2	-7.35	117.36	120.30
79	t	197	U	N3-C2-O2	-7.34	117.06	122.20
79	t	443	C	N1-C2-O2	7.33	123.30	118.90
79	t	4234	G	C4-N9-C1'	-7.33	116.97	126.50
1	S2	1828	C	C6-N1-C2	-7.33	117.37	120.30
79	t	659	G	C4-N9-C1'	7.33	136.02	126.50
79	t	2388	U	N3-C2-O2	-7.33	117.07	122.20
45	K	103	LEU	CA-CB-CG	7.31	132.12	115.30
79	t	197	U	N1-C2-O2	7.29	127.90	122.80
38	D	109	C	N1-C2-O2	7.21	123.23	118.90
79	t	18	C	N1-C2-O2	7.21	123.23	118.90
81	v	61	C	C5-C6-N1	7.21	124.61	121.00
79	t	2617	G	N3-C4-N9	-7.21	121.67	126.00
79	t	1466	G	N3-C4-C5	-7.21	125.00	128.60
79	t	471	C	C5-C6-N1	7.20	124.60	121.00
80	u	37	U	N3-C2-O2	-7.20	117.16	122.20
79	t	219	C	C6-N1-C2	-7.18	117.43	120.30
80	u	59	U	N1-C2-O2	7.18	127.83	122.80
79	t	4838	C	N1-C2-O2	7.18	123.21	118.90
80	u	43	C	N3-C2-O2	-7.18	116.88	121.90
79	t	2373	G	N7-C8-N9	7.17	116.69	113.10
1	S2	548	C	N1-C2-O2	7.16	123.20	118.90
79	t	1930	U	N1-C2-O2	7.14	127.80	122.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
79	t	4234	G	N1-C2-N2	7.14	122.62	116.20
1	S2	1307	U	N3-C2-O2	-7.13	117.21	122.20
79	t	1321	G	N3-C4-C5	7.11	132.15	128.60
1	S2	1139	C	C6-N1-C2	-7.10	117.46	120.30
7	SH	148	LEU	CA-CB-CG	7.09	131.60	115.30
79	t	2373	G	C4-N9-C1'	7.09	135.71	126.50
79	t	1321	G	N3-C4-N9	-7.08	121.75	126.00
80	u	55	U	C6-N1-C1'	-7.06	111.31	121.20
79	t	901	U	P-O3'-C3'	7.06	128.17	119.70
38	D	129	C	C2-N1-C1'	7.05	126.56	118.80
79	t	905	G	N3-C4-C5	-7.04	125.08	128.60
79	t	649	C	N3-C2-O2	-7.03	116.98	121.90
1	S2	1578	U	C2-N1-C1'	7.01	126.11	117.70
79	t	2373	G	O4'-C1'-N9	7.00	113.80	108.20
79	t	4234	G	N3-C4-C5	7.00	132.10	128.60
79	t	214	C	N3-C2-O2	-6.99	117.01	121.90
79	t	2556	C	N1-C2-O2	6.99	123.09	118.90
53	S	24	LEU	CA-CB-CG	6.98	131.36	115.30
79	t	2499	C	N3-C2-O2	-6.98	117.02	121.90
79	t	3897	C	N1-C2-O2	6.97	123.08	118.90
79	t	1564	U	N1-C2-O2	6.97	127.68	122.80
1	S2	501	C	C5-C6-N1	6.96	124.48	121.00
79	t	4633	C	C2-N1-C1'	6.95	126.44	118.80
1	S2	751	G	C4-N9-C1'	6.92	135.50	126.50
79	t	4946	U	P-O3'-C3'	6.92	128.01	119.70
3	SB	74	LEU	CA-CB-CG	6.91	131.19	115.30
79	t	1060	C	C5-C6-N1	6.88	124.44	121.00
1	S2	578	C	C6-N1-C2	-6.87	117.55	120.30
62	b	11	LEU	CA-CB-CG	6.85	131.06	115.30
79	t	1060	C	C6-N1-C2	-6.85	117.56	120.30
79	t	3849	C	N3-C2-O2	-6.84	117.11	121.90
79	t	153	G	N3-C4-N9	-6.84	121.89	126.00
79	t	657	C	C6-N1-C2	-6.84	117.57	120.30
79	t	2727	C	N3-C2-O2	-6.83	117.12	121.90
79	t	1466	G	C8-N9-C1'	-6.82	118.14	127.00
1	S2	578	C	C2-N1-C1'	6.81	126.29	118.80
1	S2	751	G	N3-C4-C5	-6.81	125.20	128.60
80	u	48	C	C6-N1-C2	-6.81	117.58	120.30
1	S2	356	C	N3-C2-O2	-6.80	117.14	121.90
80	u	61	C	N1-C2-O2	6.79	122.98	118.90
1	S2	1005	G	N3-C4-N9	6.79	130.08	126.00
1	S2	1815	A	P-O3'-C3'	6.79	127.85	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
79	t	4717	G	N9-C4-C5	6.79	108.12	105.40
79	t	289	A	O4'-C1'-N9	6.79	113.63	108.20
79	t	2065	C	N3-C2-O2	-6.79	117.15	121.90
79	t	670	C	N1-C2-O2	6.76	122.96	118.90
79	t	4545	C	N1-C2-O2	6.76	122.96	118.90
1	S2	1453	C	C5-C6-N1	6.74	124.37	121.00
79	t	2532	A	O4'-C1'-N9	6.72	113.58	108.20
80	u	37	U	N1-C2-O2	6.72	127.51	122.80
79	t	2236	C	C2-N1-C1'	6.71	126.19	118.80
79	t	2447	U	C6-N1-C2	-6.71	116.97	121.00
1	S2	427	U	C2-N1-C1'	6.70	125.74	117.70
79	t	2398	C	N3-C2-O2	-6.70	117.21	121.90
79	t	219	C	O4'-C1'-N1	6.69	113.55	108.20
79	t	956	C	N3-C2-O2	-6.69	117.22	121.90
80	u	59	U	C2-N1-C1'	6.69	125.73	117.70
79	t	411	G	O4'-C1'-N9	6.68	113.55	108.20
1	S2	1520	G	C8-N9-C1'	-6.68	118.32	127.00
79	t	4267	G	C4-N9-C1'	6.68	135.18	126.50
79	t	4832	A	O4'-C1'-N9	6.68	113.54	108.20
79	t	700	C	N3-C2-O2	-6.67	117.23	121.90
79	t	2474	U	N1-C2-O2	6.67	127.47	122.80
79	t	670	C	N3-C2-O2	-6.66	117.24	121.90
79	t	4629	C	C6-N1-C2	-6.65	117.64	120.30
79	t	2373	G	C8-N9-C4	-6.65	103.74	106.40
79	t	2239	C	C2-N1-C1'	6.64	126.10	118.80
79	t	3890	C	C6-N1-C2	-6.64	117.64	120.30
1	S2	559	G	P-O3'-C3'	6.63	127.66	119.70
79	t	698	C	N1-C2-O2	6.63	122.88	118.90
81	v	59	U	N1-C2-O2	6.63	127.44	122.80
15	ST	131	LEU	CA-CB-CG	6.62	130.53	115.30
79	t	18	C	N3-C2-O2	-6.62	117.27	121.90
79	t	2325	C	N3-C2-O2	-6.61	117.28	121.90
79	t	4717	G	C8-N9-C1'	6.60	135.58	127.00
1	S2	1716	C	N1-C2-O2	6.59	122.86	118.90
79	t	2236	C	N3-C2-O2	-6.59	117.29	121.90
79	t	2065	C	N1-C2-O2	6.58	122.85	118.90
79	t	4632	C	N1-C2-O2	6.58	122.85	118.90
79	t	4736	C	C6-N1-C2	-6.55	117.68	120.30
79	t	4880	C	C2-N1-C1'	6.55	126.01	118.80
1	S2	1495	G	C8-N9-C1'	6.54	135.51	127.00
79	t	493	G	C4-N9-C1'	6.54	135.00	126.50
81	v	55	U	C5-C6-N1	6.53	125.97	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	SB	188	LEU	CA-CB-CG	6.53	130.32	115.30
79	t	219	C	C5-C6-N1	6.52	124.26	121.00
79	t	2330	C	N1-C2-O2	6.51	122.80	118.90
79	t	4951	G	N3-C4-N9	-6.50	122.10	126.00
79	t	2474	U	N3-C2-O2	-6.50	117.65	122.20
1	S2	548	C	C2-N1-C1'	6.49	125.94	118.80
79	t	2398	C	C6-N1-C1'	-6.48	113.02	120.80
1	S2	1277	C	N1-C2-O2	6.46	122.78	118.90
31	SZ	44	LEU	CA-CB-CG	6.46	130.16	115.30
1	S2	1841	C	N1-C2-O2	6.45	122.77	118.90
79	t	2228	C	C6-N1-C2	-6.45	117.72	120.30
38	D	126	C	C6-N1-C2	-6.45	117.72	120.30
79	t	4736	C	N3-C2-O2	-6.44	117.39	121.90
1	S2	1307	U	C2-N1-C1'	6.44	125.43	117.70
79	t	509	C	C6-N1-C2	-6.44	117.72	120.30
79	t	2228	C	C2-N1-C1'	6.44	125.88	118.80
80	u	59	U	N3-C2-O2	-6.44	117.69	122.20
81	v	71	G	N3-C4-C5	-6.44	125.38	128.60
38	D	129	C	C6-N1-C2	-6.43	117.73	120.30
80	u	43	C	C6-N1-C2	-6.43	117.73	120.30
79	t	49	U	N3-C2-O2	-6.43	117.70	122.20
79	t	2228	C	N3-C2-O2	-6.43	117.40	121.90
1	S2	1314	U	C2-N1-C1'	6.43	125.41	117.70
79	t	669	G	N3-C2-N2	-6.43	115.40	119.90
1	S2	1813	A	P-O3'-C3'	6.42	127.41	119.70
41	G	125	LEU	CA-CB-CG	6.42	130.06	115.30
79	t	1429	C	C6-N1-C2	-6.41	117.73	120.30
79	t	959	C	C6-N1-C2	-6.41	117.73	120.30
1	S2	1261	C	C6-N1-C2	-6.41	117.74	120.30
79	t	233	G	N1-C2-N2	6.40	121.96	116.20
79	t	659	G	C8-N9-C1'	-6.40	118.68	127.00
79	t	2483	C	C6-N1-C2	-6.39	117.74	120.30
79	t	471	C	C6-N1-C2	-6.38	117.75	120.30
79	t	509	C	C5-C6-N1	6.38	124.19	121.00
79	t	2727	C	N1-C2-O2	6.38	122.72	118.90
1	S2	1307	U	N1-C2-O2	6.37	127.26	122.80
1	S2	1022	U	N1-C2-O2	6.37	127.26	122.80
38	D	45	C	C6-N1-C2	-6.37	117.75	120.30
79	t	2241	G	C4-N9-C1'	6.37	134.77	126.50
36	B	214	ASP	CB-CG-OD1	6.36	124.03	118.30
79	t	4217	A	O4'-C1'-N9	6.36	113.29	108.20
1	S2	913	A	C2-N3-C4	6.36	113.78	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
79	t	407	G	C4-N9-C1'	6.36	134.77	126.50
79	t	698	C	N3-C2-O2	-6.36	117.45	121.90
79	t	4671	U	N1-C2-O2	6.36	127.25	122.80
79	t	1746	G	N3-C4-C5	-6.34	125.43	128.60
83	y	30	LEU	CA-CB-CG	6.34	129.88	115.30
1	S2	632	C	N1-C2-O2	6.31	122.69	118.90
1	S2	1341	C	C2-N1-C1'	6.31	125.75	118.80
79	t	2234	C	C2-N1-C1'	6.31	125.74	118.80
79	t	4633	C	N3-C2-O2	-6.31	117.48	121.90
79	t	3638	C	C6-N1-C2	-6.30	117.78	120.30
79	t	1350	C	N1-C2-O2	6.30	122.68	118.90
79	t	1767	C	N1-C2-O2	6.29	122.68	118.90
1	S2	751	G	N3-C4-N9	6.29	129.78	126.00
1	S2	125	C	N1-C2-O2	6.29	122.67	118.90
79	t	4946	U	OP1-P-O3'	6.28	119.02	105.20
79	t	4713	G	C4-N9-C1'	-6.28	118.33	126.50
1	S2	1786	U	C5-C6-N1	6.28	125.84	122.70
79	t	1959	C	N3-C2-O2	-6.28	117.50	121.90
1	S2	1811	C	N1-C2-O2	6.27	122.66	118.90
79	t	956	C	C6-N1-C1'	-6.26	113.28	120.80
69	i	87	LYS	C-N-CA	6.26	137.35	121.70
38	D	109	C	C2-N1-C1'	6.26	125.68	118.80
1	S2	303	C	N1-C2-O2	6.25	122.65	118.90
81	v	50	U	P-O3'-C3'	6.25	127.19	119.70
1	S2	501	C	C6-N1-C1'	-6.24	113.31	120.80
1	S2	659	G	C4-N9-C1'	6.24	134.61	126.50
38	D	147	G	O4'-C1'-N9	6.24	113.19	108.20
79	t	4880	C	N3-C2-O2	-6.23	117.54	121.90
1	S2	118	C	C6-N1-C1'	-6.21	113.35	120.80
79	t	242	C	N3-C2-O2	-6.21	117.55	121.90
1	S2	681	U	C6-N1-C2	-6.21	117.28	121.00
1	S2	1520	G	N3-C4-N9	6.20	129.72	126.00
79	t	4880	C	C6-N1-C2	-6.20	117.82	120.30
79	t	649	C	C5-C6-N1	6.19	124.09	121.00
79	t	2793	C	N1-C2-O2	6.18	122.61	118.90
79	t	4736	C	C6-N1-C1'	-6.17	113.39	120.80
80	u	55	U	C6-N1-C2	-6.16	117.30	121.00
79	t	148	G	C4-N9-C1'	-6.16	118.49	126.50
79	t	659	G	N3-C4-N9	6.16	129.69	126.00
1	S2	1265	A	C2-N3-C4	6.15	113.67	110.60
50	P	141	LEU	CA-CB-CG	6.14	129.42	115.30
79	t	3849	C	C6-N1-C1'	-6.14	113.44	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
79	t	4234	G	N9-C4-C5	6.14	107.86	105.40
1	S2	867	G	N3-C4-N9	6.13	129.68	126.00
1	S2	1283	C	C6-N1-C2	-6.13	117.85	120.30
1	S2	1495	G	O5'-P-OP1	-6.13	100.18	105.70
1	S2	579	C	N1-C2-O2	6.12	122.57	118.90
79	t	18	C	C6-N1-C2	-6.12	117.85	120.30
47	M	144	LEU	CA-CB-CG	6.12	129.37	115.30
79	t	2568	C	N1-C2-O2	6.11	122.57	118.90
38	D	45	C	C5-C6-N1	6.11	124.06	121.00
79	t	1594	G	C4-N9-C1'	6.10	134.44	126.50
1	S2	1495	G	C2-N3-C4	6.10	114.95	111.90
79	t	964	C	N1-C2-O2	6.09	122.56	118.90
79	t	1193	C	N1-C2-O2	6.09	122.56	118.90
79	t	1910	A	C2-N3-C4	6.08	113.64	110.60
1	S2	1520	G	N3-C4-C5	-6.08	125.56	128.60
38	D	57	C	N1-C2-O2	6.07	122.54	118.90
79	t	4713	G	N3-C4-N9	-6.07	122.36	126.00
79	t	49	U	N1-C2-O2	6.06	127.04	122.80
1	S2	79	A	P-O3'-C3'	6.06	126.97	119.70
80	u	55	U	C5-C6-N1	6.04	125.72	122.70
79	t	669	G	N3-C4-N9	-6.02	122.39	126.00
1	S2	356	C	C6-N1-C2	-6.02	117.89	120.30
79	t	2323	U	C2-N1-C1'	6.02	124.93	117.70
1	S2	839	C	N3-C2-O2	-6.02	117.69	121.90
79	t	4601	G	N3-C2-N2	-6.02	115.69	119.90
1	S2	1660	C	C2-N1-C1'	6.01	125.42	118.80
79	t	1614	A	C2-N3-C4	6.01	113.61	110.60
79	t	3742	C	N1-C2-O2	6.01	122.51	118.90
79	t	219	C	C6-N1-C1'	-6.01	113.59	120.80
1	S2	1716	C	N3-C2-O2	-6.00	117.70	121.90
79	t	2478	C	N1-C2-O2	6.00	122.50	118.90
41	G	173	LEU	CA-CB-CG	6.00	129.09	115.30
79	t	219	C	N1-C2-O2	6.00	122.50	118.90
79	t	4267	G	N7-C8-N9	5.99	116.09	113.10
1	S2	1139	C	C6-N1-C1'	-5.99	113.61	120.80
79	t	1298	C	C6-N1-C2	-5.99	117.91	120.30
1	S2	839	C	C6-N1-C1'	-5.98	113.62	120.80
1	S2	1816	G	O4'-C1'-N9	5.98	112.98	108.20
79	t	5026	G	C4-N9-C1'	5.98	134.28	126.50
79	t	4042	C	N1-C2-O2	5.98	122.49	118.90
1	S2	1716	C	C6-N1-C2	-5.95	117.92	120.30
1	S2	53	C	N1-C2-O2	5.94	122.46	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	S2	872	A	P-O3'-C3'	5.94	126.82	119.70
1	S2	65	C	C5-C6-N1	5.93	123.97	121.00
45	K	48	LEU	CA-CB-CG	5.93	128.95	115.30
79	t	958	U	C6-N1-C1'	-5.93	112.89	121.20
79	t	2323	U	C5-C6-N1	5.93	125.67	122.70
79	t	2016	C	C6-N1-C2	-5.92	117.93	120.30
79	t	2239	C	N3-C2-O2	-5.92	117.75	121.90
79	t	4713	G	C8-N9-C1'	5.92	134.70	127.00
79	t	2067	G	N3-C4-N9	-5.91	122.46	126.00
1	S2	1453	C	C6-N1-C2	-5.90	117.94	120.30
79	t	4936	G	O4'-C1'-N9	5.90	112.92	108.20
79	t	443	C	C6-N1-C2	-5.90	117.94	120.30
79	t	1746	G	C8-N9-C1'	-5.90	119.34	127.00
38	D	126	C	C6-N1-C1'	-5.89	113.73	120.80
3	SB	74	LEU	CB-CG-CD2	-5.89	100.99	111.00
21	Sd	6	LEU	CA-CB-CG	5.88	128.82	115.30
38	D	116	C	C6-N1-C2	-5.88	117.95	120.30
1	S2	1661	A	P-O3'-C3'	5.88	126.75	119.70
41	G	126	LEU	N-CA-C	5.88	126.87	111.00
79	t	276	C	N1-C2-O2	5.88	122.43	118.90
83	y	38	LEU	CA-CB-CG	5.87	128.79	115.30
79	t	956	C	C6-N1-C2	-5.86	117.96	120.30
79	t	1155	C	C6-N1-C2	-5.85	117.96	120.30
38	D	101	C	N1-C2-O2	5.85	122.41	118.90
79	t	1746	G	N3-C4-N9	5.85	129.51	126.00
79	t	2673	G	N3-C4-C5	5.85	131.53	128.60
49	O	134	LEU	CA-CB-CG	5.85	128.75	115.30
79	t	2389	C	N1-C2-O2	5.84	122.40	118.90
79	t	4826	G	N3-C2-N2	-5.83	115.82	119.90
79	t	1261	C	C6-N1-C2	-5.83	117.97	120.30
79	t	2727	C	C6-N1-C1'	-5.83	113.81	120.80
79	t	1614	A	C4-N9-C1'	5.83	136.79	126.30
39	E	47	G	O4'-C1'-N9	5.82	112.86	108.20
79	t	727	C	C5-C6-N1	5.82	123.91	121.00
79	t	225	C	C6-N1-C1'	5.82	127.78	120.80
79	t	2325	C	N1-C2-O2	5.82	122.39	118.90
79	t	2447	U	C2-N1-C1'	5.82	124.68	117.70
79	t	2727	C	C6-N1-C2	-5.81	117.97	120.30
79	t	4736	C	C5-C6-N1	5.81	123.91	121.00
25	SJ	32	ILE	CG1-CB-CG2	-5.81	98.62	111.40
79	t	2256	C	N1-C2-O2	5.81	122.38	118.90
79	t	148	G	N3-C2-N2	-5.80	115.84	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
79	t	289	A	N3-C4-N9	5.80	132.04	127.40
1	S2	548	C	N3-C2-O2	-5.79	117.84	121.90
79	t	649	C	C6-N1-C2	-5.79	117.98	120.30
38	D	57	C	N3-C2-O2	-5.79	117.85	121.90
79	t	2323	U	C6-N1-C2	-5.78	117.53	121.00
35	A	116	LEU	CA-CB-CG	5.76	128.55	115.30
79	t	3742	C	C6-N1-C2	-5.76	118.00	120.30
79	t	339	C	N3-C2-O2	-5.76	117.87	121.90
79	t	4671	U	N3-C2-O2	-5.75	118.17	122.20
1	S2	445	A	P-O3'-C3'	5.75	126.60	119.70
79	t	710	C	N3-C2-O2	-5.74	117.88	121.90
79	t	2067	G	N3-C2-N2	-5.74	115.88	119.90
79	t	3890	C	N1-C2-O2	5.74	122.34	118.90
38	D	101	C	N3-C2-O2	-5.73	117.89	121.90
79	t	1335	C	N1-C2-O2	5.72	122.33	118.90
79	t	4632	C	C2-N1-C1'	5.72	125.09	118.80
1	S2	867	G	N3-C4-C5	-5.72	125.74	128.60
46	L	171	ASP	CB-CG-OD1	5.72	123.44	118.30
79	t	3742	C	C2-N1-C1'	5.71	125.09	118.80
79	t	4333	G	P-O3'-C3'	5.71	126.56	119.70
79	t	234	G	C6-N1-C2	5.71	128.53	125.10
1	S2	386	C	P-O3'-C3'	5.71	126.55	119.70
25	SJ	81	LEU	CA-CB-CG	5.71	128.43	115.30
79	t	2373	G	C6-C5-N7	-5.70	126.98	130.40
80	u	43	C	C6-N1-C1'	-5.70	113.96	120.80
1	S2	53	C	N3-C2-O2	-5.69	117.92	121.90
79	t	226	G	C4-N9-C1'	-5.69	119.10	126.50
1	S2	115	U	N3-C4-O4	-5.69	115.42	119.40
1	S2	1283	C	C6-N1-C1'	-5.68	113.98	120.80
41	G	233	PHE	C-N-CA	5.68	135.91	121.70
79	t	18	C	C2-N1-C1'	5.68	125.04	118.80
82	w	20	G	P-O3'-C3'	5.68	126.51	119.70
79	t	407	G	C8-N9-C1'	-5.67	119.63	127.00
79	t	493	G	N3-C4-N9	5.67	129.40	126.00
1	S2	1683	C	N3-C2-O2	-5.66	117.94	121.90
79	t	407	G	N3-C4-N9	5.66	129.40	126.00
79	t	695	C	N1-C2-O2	5.66	122.30	118.90
79	t	1069	C	N1-C2-O2	5.66	122.30	118.90
44	J	142	ASP	CB-CG-OD1	5.66	123.39	118.30
79	t	112	C	N3-C2-O2	-5.65	117.94	121.90
1	S2	1556	A	C2-N3-C4	5.64	113.42	110.60
79	t	4545	C	C2-N1-C1'	5.64	125.00	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
79	t	5015	C	N1-C2-O2	5.64	122.28	118.90
79	t	2499	C	C6-N1-C1'	-5.62	114.05	120.80
79	t	2241	G	N3-C4-N9	5.61	129.37	126.00
79	t	2691	G	N3-C4-N9	5.61	129.37	126.00
79	t	4717	G	C4-N9-C1'	-5.61	119.20	126.50
79	t	214	C	C6-N1-C1'	-5.59	114.09	120.80
79	t	2751	C	N1-C2-O2	5.59	122.26	118.90
79	t	1335	C	N3-C2-O2	-5.59	117.98	121.90
79	t	2003	C	N1-C2-O2	5.59	122.25	118.90
22	Sg	79	LEU	CA-CB-CG	5.59	128.15	115.30
79	t	2241	G	N3-C4-C5	-5.59	125.81	128.60
40	F	36	LEU	CA-CB-CG	5.59	128.15	115.30
79	t	2282	C	C5-C6-N1	5.58	123.79	121.00
79	t	2871	C	N1-C2-O2	5.58	122.25	118.90
1	S2	585	C	N1-C2-O2	5.58	122.25	118.90
1	S2	1802	C	C6-N1-C2	-5.57	118.07	120.30
1	S2	659	G	N3-C4-N9	5.57	129.34	126.00
79	t	256	C	C5-C6-N1	5.57	123.78	121.00
79	t	2256	C	C6-N1-C2	-5.57	118.07	120.30
79	t	5026	G	N3-C4-N9	5.56	129.34	126.00
1	S2	751	G	C8-N9-C1'	-5.56	119.77	127.00
1	S2	1261	C	P-O3'-C3'	5.56	126.37	119.70
79	t	493	G	C8-N9-C1'	-5.56	119.78	127.00
80	u	61	C	N3-C2-O2	-5.56	118.01	121.90
35	A	180	LEU	CA-CB-CG	5.55	128.07	115.30
79	t	890	C	N1-C2-O2	5.55	122.23	118.90
79	t	1163	C	N1-C2-O2	5.55	122.23	118.90
79	t	256	C	N3-C2-O2	-5.55	118.01	121.90
79	t	2344	C	C6-N1-C2	-5.55	118.08	120.30
79	t	4824	C	N1-C2-O2	5.55	122.23	118.90
79	t	1794	C	O4'-C1'-N1	5.55	112.64	108.20
1	S2	1375	G	P-O3'-C3'	5.54	126.34	119.70
5	SE	139	LEU	CA-CB-CG	5.54	128.04	115.30
79	t	3732	C	P-O3'-C3'	5.54	126.34	119.70
39	E	78	C	C6-N1-C2	-5.53	118.09	120.30
79	t	659	G	N3-C4-C5	-5.53	125.83	128.60
79	t	4837	C	N1-C2-O2	5.53	122.22	118.90
79	t	4870	G	P-O3'-C3'	5.53	126.33	119.70
79	t	1959	C	C2-N1-C1'	5.52	124.87	118.80
1	S2	681	U	N3-C2-O2	-5.52	118.34	122.20
1	S2	682	U	N3-C2-O2	-5.52	118.34	122.20
1	S2	1470	C	N1-C2-O2	5.52	122.21	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	SF	19	LEU	CA-CB-CG	5.52	128.00	115.30
79	t	1592	C	C6-N1-C2	-5.52	118.09	120.30
79	t	443	C	N3-C2-O2	-5.51	118.04	121.90
83	y	23	LEU	CA-CB-CG	5.51	127.98	115.30
63	c	54	LEU	CA-CB-CG	5.51	127.98	115.30
79	t	671	C	C6-N1-C2	-5.50	118.10	120.30
79	t	153	G	N3-C4-C5	5.50	131.35	128.60
42	H	190	LEU	CA-CB-CG	5.49	127.93	115.30
38	D	35	C	C6-N1-C2	-5.49	118.10	120.30
79	t	660	C	N1-C2-O2	5.49	122.19	118.90
79	t	71	C	C6-N1-C2	-5.49	118.10	120.30
79	t	3897	C	N3-C2-O2	-5.49	118.06	121.90
79	t	1268	U	O4'-C1'-N1	5.49	112.59	108.20
79	t	2249	G	N3-C4-N9	-5.48	122.71	126.00
79	t	4349	C	N1-C2-O2	5.48	122.19	118.90
79	t	339	C	C2-N1-C1'	5.48	124.83	118.80
79	t	2234	C	N1-C2-O2	5.48	122.19	118.90
79	t	4928	C	N1-C2-O2	5.48	122.19	118.90
1	S2	867	G	C4-N9-C1'	5.47	133.62	126.50
79	t	1193	C	N3-C2-O2	-5.46	118.08	121.90
79	t	2341	U	N1-C2-O2	5.46	126.62	122.80
79	t	2617	G	N3-C4-C5	5.46	131.33	128.60
79	t	229	G	N3-C2-N2	-5.46	116.08	119.90
79	t	256	C	C6-N1-C2	-5.46	118.12	120.30
79	t	242	C	N1-C2-O2	5.46	122.17	118.90
79	t	4665	U	N3-C2-O2	-5.46	118.38	122.20
38	D	99	U	N1-C2-O2	5.45	126.62	122.80
1	S2	1538	C	N1-C2-O2	5.45	122.17	118.90
79	t	2691	G	C4-N9-C1'	5.45	133.58	126.50
79	t	4713	G	C6-C5-N7	5.45	133.67	130.40
79	t	704	C	N3-C2-O2	-5.44	118.09	121.90
79	t	359	U	N3-C2-O2	-5.44	118.39	122.20
79	t	3890	C	N3-C2-O2	-5.44	118.09	121.90
79	t	4250	C	C6-N1-C2	-5.44	118.12	120.30
1	S2	1005	G	C4-N9-C1'	5.43	133.57	126.50
1	S2	1032	C	C6-N1-C2	-5.43	118.13	120.30
79	t	229	G	N3-C4-N9	-5.43	122.74	126.00
79	t	1261	C	C2-N1-C1'	5.43	124.78	118.80
79	t	2076	G	C4-N9-C1'	5.43	133.56	126.50
79	t	958	U	C5-C6-N1	5.43	125.42	122.70
1	S2	115	U	N3-C2-O2	-5.43	118.40	122.20
22	Sg	7	LEU	CA-CB-CG	5.43	127.79	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
79	t	2344	C	C5-C6-N1	5.43	123.72	121.00
79	t	930	A	C6-N1-C2	5.42	121.86	118.60
1	S2	1277	C	N3-C2-O2	-5.42	118.10	121.90
79	t	493	G	N3-C4-C5	-5.42	125.89	128.60
1	S2	1354	G	OP2-P-O3'	5.41	117.10	105.20
61	a	101	PHE	C-N-CA	5.41	135.22	121.70
79	t	3621	C	C6-N1-C2	-5.41	118.14	120.30
1	S2	42	A	P-O3'-C3'	5.40	126.19	119.70
79	t	4875	C	C6-N1-C2	-5.40	118.14	120.30
1	S2	1091	C	C6-N1-C2	-5.40	118.14	120.30
1	S2	1716	C	C2-N1-C1'	5.40	124.74	118.80
79	t	918	C	C6-N1-C2	-5.40	118.14	120.30
1	S2	418	A	O5'-P-OP1	-5.40	100.84	105.70
1	S2	1371	U	C2-N1-C1'	5.40	124.18	117.70
79	t	71	C	P-O3'-C3'	5.40	126.18	119.70
79	t	2325	C	C2-N1-C1'	5.40	124.74	118.80
14	SS	82	TRP	CA-CB-CG	5.40	123.95	113.70
23	SC	192	LEU	CA-CB-CG	5.40	127.72	115.30
79	t	153	G	N3-C2-N2	-5.40	116.12	119.90
47	M	146	LEU	CA-CB-CG	5.39	127.70	115.30
79	t	905	G	C6-C5-N7	-5.39	127.17	130.40
79	t	3667	C	N1-C2-O2	5.39	122.14	118.90
79	t	1272	C	N3-C2-O2	-5.39	118.13	121.90
23	SC	83	LEU	CA-CB-CG	5.39	127.69	115.30
79	t	657	C	C5-C6-N1	5.38	123.69	121.00
79	t	1433	C	N1-C2-O2	5.38	122.13	118.90
79	t	4601	G	N1-C2-N2	5.37	121.03	116.20
39	E	24	C	C6-N1-C2	-5.37	118.15	120.30
79	t	4601	G	N3-C4-N9	-5.37	122.78	126.00
79	t	4545	C	N3-C2-O2	-5.37	118.14	121.90
1	S2	1333	U	N3-C2-O2	-5.36	118.45	122.20
1	S2	1495	G	C4-N9-C1'	-5.36	119.53	126.50
79	t	1767	C	N3-C2-O2	-5.36	118.15	121.90
79	t	4205	C	N1-C2-O2	5.36	122.11	118.90
39	E	29	C	N1-C2-O2	5.36	122.11	118.90
79	t	4624	C	C6-N1-C2	-5.36	118.16	120.30
79	t	4880	C	C5-C6-N1	5.36	123.68	121.00
79	t	148	G	C8-N9-C1'	5.35	133.96	127.00
1	S2	563	G	P-O3'-C3'	5.35	126.12	119.70
79	t	3826	C	C6-N1-C2	-5.35	118.16	120.30
1	S2	632	C	N3-C2-O2	-5.35	118.16	121.90
79	t	964	C	N3-C2-O2	-5.35	118.16	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
79	t	1466	G	C6-C5-N7	-5.35	127.19	130.40
1	S2	659	G	C8-N9-C1'	-5.34	120.05	127.00
25	SJ	50	LEU	CA-CB-CG	5.34	127.59	115.30
63	c	116	LEU	CA-CB-CG	5.34	127.58	115.30
9	SK	43	LEU	CA-CB-CG	5.33	127.57	115.30
79	t	703	C	N1-C2-O2	5.33	122.10	118.90
79	t	703	C	N3-C2-O2	-5.33	118.17	121.90
79	t	4268	U	N1-C2-O2	5.33	126.53	122.80
79	t	4671	U	C2-N1-C1'	5.33	124.09	117.70
1	S2	1797	U	N1-C2-O2	5.32	126.53	122.80
79	t	2388	U	C6-N1-C1'	-5.32	113.75	121.20
6	SF	77	MET	CA-CB-CG	5.32	122.34	113.30
79	t	2846	C	N1-C2-O2	5.32	122.09	118.90
79	t	1910	A	C4-N9-C1'	5.32	135.87	126.30
1	S2	1006	C	C6-N1-C2	-5.32	118.17	120.30
79	t	2228	C	C5-C6-N1	5.31	123.66	121.00
1	S2	1022	U	N3-C2-O2	-5.31	118.48	122.20
79	t	4105	C	C6-N1-C2	-5.31	118.18	120.30
1	S2	192	C	C6-N1-C2	-5.31	118.18	120.30
1	S2	632	C	C2-N1-C1'	5.31	124.64	118.80
79	t	236	C	N3-C2-O2	-5.30	118.19	121.90
79	t	695	C	N3-C2-O2	-5.30	118.19	121.90
79	t	2556	C	N3-C2-O2	-5.30	118.19	121.90
79	t	2256	C	N3-C2-O2	-5.30	118.19	121.90
79	t	191	C	C6-N1-C2	-5.29	118.18	120.30
2	SA	159	ILE	CG1-CB-CG2	-5.29	99.77	111.40
79	t	2389	C	C2-N1-C1'	5.29	124.61	118.80
79	t	4629	C	N1-C2-O2	5.29	122.07	118.90
79	t	2562	C	N1-C2-O2	5.28	122.07	118.90
79	t	2617	G	N3-C2-N2	-5.28	116.20	119.90
79	t	359	U	N1-C2-O2	5.28	126.50	122.80
1	S2	427	U	O4'-C1'-N1	5.28	112.42	108.20
65	e	95	ASP	CB-CG-OD1	5.28	123.05	118.30
1	S2	1496	U	C2-N1-C1'	5.28	124.03	117.70
1	S2	1022	U	C6-N1-C1'	-5.27	113.82	121.20
79	t	2064	C	C6-N1-C2	-5.27	118.19	120.30
79	t	2777	A	O4'-C1'-N9	5.27	112.42	108.20
79	t	4838	C	C2-N1-C1'	5.27	124.60	118.80
34	Sf	103	LEU	CA-CB-CG	5.27	127.41	115.30
79	t	1862	C	OP2-P-O3'	5.27	116.78	105.20
1	S2	554	A	P-O3'-C3'	5.26	126.02	119.70
79	t	2330	C	N3-C2-O2	-5.26	118.21	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	y	32	LEU	CA-CB-CG	5.26	127.41	115.30
1	S2	65	C	C6-N1-C2	-5.26	118.20	120.30
1	S2	1805	G	N3-C4-N9	5.26	129.16	126.00
79	t	1989	U	C6-N1-C1'	-5.26	113.84	121.20
79	t	4299	C	N1-C2-O2	5.26	122.06	118.90
1	S2	879	C	N1-C2-O2	5.25	122.05	118.90
1	S2	1828	C	P-O3'-C3'	5.25	126.00	119.70
79	t	4865	G	P-O3'-C3'	5.25	126.00	119.70
80	u	45	U	C2-N1-C1'	5.25	124.00	117.70
1	S2	1314	U	N1-C2-O2	5.25	126.47	122.80
38	D	123	U	OP1-P-O3'	5.25	116.75	105.20
79	t	2341	U	C2-N1-C1'	5.25	124.00	117.70
1	S2	1660	C	N1-C2-O2	5.25	122.05	118.90
79	t	649	C	C6-N1-C1'	-5.24	114.51	120.80
1	S2	1661	A	C8-N9-C4	-5.24	103.70	105.80
79	t	2313	C	N1-C2-O2	5.24	122.04	118.90
79	t	3651	U	N1-C2-O2	5.24	126.47	122.80
79	t	4133	C	N1-C2-O2	5.24	122.04	118.90
79	t	700	C	N1-C2-O2	5.24	122.04	118.90
1	S2	1538	C	N3-C2-O2	-5.23	118.24	121.90
79	t	166	G	N3-C2-N2	-5.23	116.24	119.90
81	v	40	C	N1-C2-O2	5.23	122.04	118.90
79	t	196	G	C4-N9-C1'	-5.23	119.71	126.50
52	R	159	PRO	C-N-CA	5.22	134.76	121.70
81	v	59	U	N3-C2-O2	-5.22	118.54	122.20
79	t	4415	C	C6-N1-C2	-5.22	118.21	120.30
79	t	190	G	N3-C2-N2	-5.22	116.25	119.90
16	SU	32	LEU	CA-CB-CG	5.21	127.29	115.30
68	h	60	ARG	CA-CB-CG	5.21	124.86	113.40
79	t	425	G	C8-N9-C4	-5.20	104.32	106.40
79	t	1579	G	C8-N9-C1'	5.20	133.76	127.00
1	S2	682	U	N1-C2-O2	5.20	126.44	122.80
1	S2	1841	C	C5-C6-N1	5.20	123.60	121.00
79	t	1959	C	C6-N1-C2	-5.20	118.22	120.30
79	t	2241	G	C8-N9-C1'	-5.20	120.24	127.00
1	S2	1660	C	N3-C2-O2	-5.19	118.26	121.90
1	S2	1572	C	C6-N1-C2	-5.19	118.22	120.30
41	G	128	HIS	CB-CA-C	-5.19	100.02	110.40
1	S2	1496	U	N3-C2-O2	-5.18	118.57	122.20
79	t	956	C	C5-C6-N1	5.18	123.59	121.00
79	t	1966	G	C4-N9-C1'	5.18	133.24	126.50
79	t	1260	G	N3-C4-N9	-5.18	122.89	126.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
80	u	43	C	C5-C6-N1	5.17	123.59	121.00
1	S2	36	U	N1-C2-O2	5.17	126.42	122.80
1	S2	1373	C	N3-C2-O2	-5.17	118.28	121.90
79	t	1298	C	C5-C6-N1	5.16	123.58	121.00
79	t	4103	C	N1-C2-O2	5.16	122.00	118.90
79	t	1433	C	N3-C2-O2	-5.16	118.29	121.90
79	t	4820	G	C5-C6-O6	-5.16	125.50	128.60
79	t	4713	G	N3-C4-C5	5.16	131.18	128.60
79	t	3742	C	C5-C6-N1	5.15	123.58	121.00
1	S2	681	U	C5-C6-N1	5.15	125.28	122.70
79	t	704	C	N1-C2-O2	5.15	121.99	118.90
79	t	1645	C	C6-N1-C2	-5.15	118.24	120.30
79	t	1910	A	N3-C4-N9	5.15	131.52	127.40
79	t	4042	C	N3-C2-O2	-5.15	118.29	121.90
1	S2	1805	G	C4-N9-C1'	5.14	133.19	126.50
79	t	288	G	C4-N9-C1'	5.14	133.19	126.50
79	t	2078	G	N3-C2-N2	-5.14	116.30	119.90
79	t	4253	G	N3-C4-C5	5.14	131.17	128.60
79	t	650	C	N1-C2-O2	5.14	121.98	118.90
79	t	4069	G	P-O3'-C3'	5.14	125.87	119.70
1	S2	659	G	N3-C4-C5	-5.13	126.03	128.60
79	t	48	G	O4'-C1'-N9	5.13	112.31	108.20
79	t	2829	A	C4-N9-C1'	5.13	135.54	126.30
38	D	96	C	N1-C2-O2	5.13	121.98	118.90
79	t	1669	U	N1-C2-O2	5.13	126.39	122.80
1	S2	60	A	P-O3'-C3'	5.13	125.85	119.70
1	S2	1333	U	N1-C2-O2	5.13	126.39	122.80
79	t	4870	G	C8-N9-C4	-5.13	104.35	106.40
79	t	276	C	N3-C2-O2	-5.13	118.31	121.90
79	t	2499	C	C6-N1-C2	-5.13	118.25	120.30
79	t	225	C	N3-C4-C5	-5.12	119.85	121.90
79	t	4736	C	O4'-C1'-N1	5.12	112.30	108.20
79	t	670	C	C6-N1-C2	-5.12	118.25	120.30
79	t	1163	C	C2-N1-C1'	5.12	124.44	118.80
79	t	2059	C	C6-N1-C2	-5.12	118.25	120.30
79	t	4632	C	N3-C2-O2	-5.12	118.31	121.90
79	t	1087	C	C6-N1-C2	-5.12	118.25	120.30
79	t	2256	C	C2-N1-C1'	5.12	124.43	118.80
38	D	109	C	N3-C2-O2	-5.12	118.32	121.90
79	t	4133	C	N3-C2-O2	-5.12	118.32	121.90
79	t	4708	C	N1-C2-O2	5.11	121.97	118.90
79	t	2330	C	C6-N1-C2	-5.11	118.26	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
79	t	3616	U	C6-N1-C1'	-5.11	114.05	121.20
1	S2	14	C	C6-N1-C2	-5.11	118.26	120.30
1	S2	409	C	N1-C2-O2	5.10	121.96	118.90
79	t	3864	C	N1-C2-O2	5.10	121.96	118.90
79	t	30	C	N1-C2-O2	5.10	121.96	118.90
79	t	4311	C	N1-C2-O2	5.10	121.96	118.90
1	S2	1681	U	P-O3'-C3'	5.10	125.81	119.70
79	t	443	C	C5-C6-N1	5.10	123.55	121.00
79	t	930	A	N1-C2-N3	-5.09	126.75	129.30
79	t	4939	G	C4-N9-C1'	5.09	133.12	126.50
1	S2	337	C	C6-N1-C2	-5.09	118.26	120.30
40	F	105	LEU	CA-CB-CG	5.09	127.01	115.30
79	t	473	G	N3-C2-N2	-5.08	116.34	119.90
1	S2	1797	U	N3-C2-O2	-5.08	118.64	122.20
79	t	2373	G	C8-N9-C1'	-5.08	120.39	127.00
1	S2	632	C	C6-N1-C2	-5.08	118.27	120.30
81	v	40	C	N3-C2-O2	-5.08	118.34	121.90
79	t	4633	C	C6-N1-C1'	-5.08	114.71	120.80
1	S2	1295	A	C2-N3-C4	5.07	113.14	110.60
23	SC	251	LEU	C-N-CA	5.07	134.38	121.70
79	t	1350	C	N3-C2-O2	-5.07	118.35	121.90
79	t	205	A	C2-N3-C4	5.07	113.13	110.60
1	S2	579	C	N3-C2-O2	-5.07	118.35	121.90
1	S2	1578	U	C6-N1-C1'	-5.07	114.11	121.20
79	t	1260	G	N3-C2-N2	-5.07	116.35	119.90
79	t	229	G	C8-N9-C1'	5.07	133.59	127.00
79	t	2313	C	N3-C2-O2	-5.06	118.36	121.90
1	S2	1808	U	N3-C2-O2	-5.06	118.66	122.20
78	r	5	LEU	CA-CB-CG	5.06	126.94	115.30
79	t	710	C	N1-C2-O2	5.06	121.94	118.90
1	S2	79	A	OP1-P-O3'	5.06	116.33	105.20
79	t	1837	C	C6-N1-C2	-5.06	118.28	120.30
79	t	1871	G	N3-C4-C5	5.06	131.13	128.60
79	t	49	U	C2-N1-C1'	5.06	123.77	117.70
1	S2	579	C	C2-N1-C1'	5.06	124.36	118.80
79	t	2691	G	C8-N9-C1'	-5.06	120.43	127.00
79	t	2341	U	N3-C2-O2	-5.05	118.66	122.20
22	Sg	239	LEU	CA-CB-CG	5.05	126.92	115.30
79	t	1579	G	O4'-C1'-N9	5.05	112.24	108.20
79	t	2727	C	O4'-C1'-N1	5.05	112.24	108.20
79	t	4268	U	N3-C2-O2	-5.05	118.67	122.20
79	t	4936	G	C4-N9-C1'	5.05	133.06	126.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
79	t	4629	C	N3-C2-O2	-5.04	118.37	121.90
79	t	145	C	N3-C2-O2	-5.04	118.37	121.90
79	t	289	A	C4-C5-N7	5.04	113.22	110.70
1	S2	356	C	C6-N1-C1'	-5.04	114.75	120.80
1	S2	501	C	C2-N3-C4	5.04	122.42	119.90
77	q	59	SER	C-N-CA	5.04	134.29	121.70
79	t	31	U	P-O3'-C3'	5.04	125.75	119.70
79	t	715	C	N3-C2-O2	-5.03	118.38	121.90
80	u	61	C	C2-N1-C1'	5.03	124.33	118.80
1	S2	1265	A	N3-C4-N9	5.03	131.42	127.40
6	SF	177	LEU	CA-CB-CG	5.03	126.86	115.30
41	G	110	ARG	CA-CB-CG	5.03	124.46	113.40
79	t	4267	G	N3-C4-C5	-5.02	126.09	128.60
79	t	214	C	C6-N1-C2	-5.02	118.29	120.30
79	t	226	G	C8-N9-C1'	5.02	133.52	127.00
79	t	425	G	N7-C8-N9	5.01	115.61	113.10
79	t	1592	C	C2-N1-C1'	5.01	124.31	118.80
79	t	236	C	C6-N1-C2	-5.01	118.30	120.30
79	t	236	C	N1-C2-O2	5.01	121.91	118.90
79	t	2398	C	O4'-C1'-N1	5.01	112.21	108.20
79	t	4878	C	N1-C2-O2	5.01	121.91	118.90
12	SQ	57	LEU	CA-CB-CG	5.01	126.81	115.30
80	u	43	C	O4'-C1'-N1	5.01	112.21	108.20
79	t	2568	C	N3-C2-O2	-5.00	118.40	121.90
79	t	14	C	N1-C2-O2	5.00	121.90	118.90
79	t	1442	C	C6-N1-C2	-5.00	118.30	120.30

There are no chirality outliers.

All (16) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
36	B	296	GLY	Peptide
37	C	55	SER	Peptide
40	F	7	VAL	Peptide
44	J	60	TRP	Peptide
2	SA	27	GLY	Peptide
7	SH	15	LYS	Peptide
7	SH	32	MET	Peptide
11	SP	14	LYS	Peptide
13	SR	124	VAL	Peptide
13	SR	67	ARG	Peptide
18	SX	60	LYS	Peptide

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Mol	Chain	Res	Type	Group
31	SZ	44	LEU	Peptide
21	Sd	23	VAL	Peptide
21	Sd	42	CYS	Peptide
67	g	60	PRO	Peptide
76	p	103	VAL	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	SA	219/221 (99%)	194 (89%)	24 (11%)	1 (0%)	25	58
3	SB	212/214 (99%)	197 (93%)	15 (7%)	0	100	100
4	SD	224/226 (99%)	200 (89%)	24 (11%)	0	100	100
5	SE	257/259 (99%)	237 (92%)	20 (8%)	0	100	100
6	SF	187/189 (99%)	170 (91%)	17 (9%)	0	100	100
7	SH	182/189 (96%)	160 (88%)	22 (12%)	0	100	100
8	SI	202/204 (99%)	180 (89%)	22 (11%)	0	100	100
9	SK	96/98 (98%)	85 (88%)	11 (12%)	0	100	100
10	SL	151/153 (99%)	134 (89%)	17 (11%)	0	100	100
11	SP	125/127 (98%)	116 (93%)	9 (7%)	0	100	100
12	SQ	144/146 (99%)	121 (84%)	21 (15%)	2 (1%)	9	34
13	SR	132/134 (98%)	115 (87%)	17 (13%)	0	100	100
14	SS	143/145 (99%)	127 (89%)	16 (11%)	0	100	100
15	ST	141/143 (99%)	134 (95%)	6 (4%)	1 (1%)	19	51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	SU	102/104 (98%)	95 (93%)	7 (7%)	0	100	100
17	SV	80/82 (98%)	72 (90%)	8 (10%)	0	100	100
18	SX	139/141 (99%)	126 (91%)	13 (9%)	0	100	100
19	Sa	100/102 (98%)	88 (88%)	11 (11%)	1 (1%)	13	42
20	Sc	62/64 (97%)	50 (81%)	12 (19%)	0	100	100
21	Sd	53/55 (96%)	47 (89%)	5 (9%)	1 (2%)	6	27
22	Sg	310/312 (99%)	254 (82%)	56 (18%)	0	100	100
23	SC	219/220 (100%)	201 (92%)	17 (8%)	1 (0%)	25	58
24	SG	235/237 (99%)	210 (89%)	25 (11%)	0	100	100
25	SJ	184/185 (100%)	168 (91%)	15 (8%)	1 (0%)	25	58
26	SM	116/118 (98%)	98 (84%)	18 (16%)	0	100	100
27	SN	148/150 (99%)	142 (96%)	6 (4%)	0	100	100
28	SO	135/137 (98%)	118 (87%)	17 (13%)	0	100	100
29	SW	127/129 (98%)	115 (91%)	12 (9%)	0	100	100
30	SY	130/131 (99%)	119 (92%)	11 (8%)	0	100	100
31	SZ	71/73 (97%)	54 (76%)	17 (24%)	0	100	100
32	Sb	80/82 (98%)	67 (84%)	13 (16%)	0	100	100
33	Se	55/57 (96%)	46 (84%)	9 (16%)	0	100	100
34	Sf	65/67 (97%)	49 (75%)	15 (23%)	1 (2%)	8	33
35	A	250/252 (99%)	226 (90%)	23 (9%)	1 (0%)	30	63
36	B	395/397 (100%)	359 (91%)	34 (9%)	2 (0%)	25	58
37	C	361/363 (99%)	329 (91%)	27 (8%)	5 (1%)	9	34
40	F	292/294 (99%)	263 (90%)	26 (9%)	3 (1%)	13	42
41	G	232/247 (94%)	193 (83%)	38 (16%)	1 (0%)	30	63
42	H	223/225 (99%)	206 (92%)	16 (7%)	1 (0%)	30	63
43	I	232/234 (99%)	213 (92%)	19 (8%)	0	100	100
44	J	189/191 (99%)	170 (90%)	17 (9%)	2 (1%)	12	39
45	K	204/211 (97%)	185 (91%)	18 (9%)	1 (0%)	25	58
46	L	167/169 (99%)	149 (89%)	18 (11%)	0	100	100
47	M	203/205 (99%)	173 (85%)	28 (14%)	2 (1%)	13	42
48	N	137/139 (99%)	127 (93%)	10 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	O	201/203 (99%)	184 (92%)	16 (8%)	1 (0%)	25	58
50	P	193/195 (99%)	187 (97%)	6 (3%)	0	100	100
51	Q	151/153 (99%)	145 (96%)	6 (4%)	0	100	100
52	R	185/187 (99%)	170 (92%)	14 (8%)	1 (0%)	25	58
53	S	179/181 (99%)	168 (94%)	11 (6%)	0	100	100
54	T	173/175 (99%)	163 (94%)	10 (6%)	0	100	100
55	U	155/157 (99%)	133 (86%)	20 (13%)	2 (1%)	10	36
56	V	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
57	W	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
58	X	59/61 (97%)	56 (95%)	3 (5%)	0	100	100
59	Y	115/117 (98%)	107 (93%)	8 (7%)	0	100	100
60	Z	132/134 (98%)	122 (92%)	10 (8%)	0	100	100
61	a	132/134 (98%)	118 (89%)	14 (11%)	0	100	100
62	b	145/147 (99%)	127 (88%)	18 (12%)	0	100	100
63	c	94/121 (78%)	79 (84%)	15 (16%)	0	100	100
64	d	101/103 (98%)	87 (86%)	14 (14%)	0	100	100
65	e	104/106 (98%)	98 (94%)	6 (6%)	0	100	100
66	f	127/129 (98%)	116 (91%)	11 (9%)	0	100	100
67	g	107/109 (98%)	97 (91%)	10 (9%)	0	100	100
68	h	112/114 (98%)	103 (92%)	9 (8%)	0	100	100
69	i	120/122 (98%)	109 (91%)	9 (8%)	2 (2%)	7	30
70	j	95/97 (98%)	85 (90%)	8 (8%)	2 (2%)	5	25
71	k	82/84 (98%)	80 (98%)	2 (2%)	0	100	100
72	l	67/69 (97%)	61 (91%)	6 (9%)	0	100	100
73	m	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
74	n	48/50 (96%)	43 (90%)	5 (10%)	0	100	100
75	o	23/25 (92%)	21 (91%)	2 (9%)	0	100	100
76	p	103/105 (98%)	95 (92%)	7 (7%)	1 (1%)	13	42
77	q	89/91 (98%)	82 (92%)	6 (7%)	1 (1%)	12	39
78	r	120/122 (98%)	102 (85%)	16 (13%)	2 (2%)	7	30
83	y	37/39 (95%)	18 (49%)	18 (49%)	1 (3%)	4	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	11232/11429 (98%)	10097 (90%)	1095 (10%)	40 (0%)	32	63

All (40) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	ST	41	LYS
23	SC	78	LEU
34	Sf	93	HIS
41	G	127	SER
47	M	64	VAL
52	R	161	SER
69	i	88	THR
2	SA	12	GLU
12	SQ	117	ARG
19	Sa	47	ALA
21	Sd	4	GLN
36	B	4	ARG
37	C	69	THR
40	F	260	GLU
47	M	78	LEU
70	j	35	LYS
12	SQ	116	ASP
35	A	251	THR
36	B	396	ARG
37	C	56	GLU
40	F	10	LYS
42	H	223	LYS
55	U	53	PRO
83	y	30	LEU
25	SJ	123	ILE
49	O	95	ALA
69	i	41	ALA
78	r	21	ASN
37	C	303	ARG
40	F	8	LYS
44	J	61	TRP
44	J	97	ALA
45	K	11	TYR
55	U	18	PRO
77	q	50	ARG
78	r	23	GLN
37	C	198	ASN

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Mol	Chain	Res	Type
70	j	34	THR
76	p	104	ILE
37	C	70	GLY

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	SA	183/183 (100%)	180 (98%)	3 (2%)	58	79
3	SB	195/195 (100%)	194 (100%)	1 (0%)	86	92
4	SD	189/189 (100%)	187 (99%)	2 (1%)	70	84
5	SE	222/222 (100%)	218 (98%)	4 (2%)	54	76
6	SF	159/159 (100%)	156 (98%)	3 (2%)	52	75
7	SH	166/169 (98%)	165 (99%)	1 (1%)	84	91
8	SI	177/177 (100%)	172 (97%)	5 (3%)	38	66
9	SK	89/89 (100%)	87 (98%)	2 (2%)	47	71
10	SL	137/137 (100%)	133 (97%)	4 (3%)	37	65
11	SP	113/113 (100%)	111 (98%)	2 (2%)	54	76
12	SQ	121/121 (100%)	120 (99%)	1 (1%)	79	89
13	SR	121/121 (100%)	118 (98%)	3 (2%)	42	69
14	SS	126/126 (100%)	125 (99%)	1 (1%)	79	89
15	ST	113/113 (100%)	110 (97%)	3 (3%)	40	67
16	SU	94/94 (100%)	90 (96%)	4 (4%)	25	55
17	SV	66/66 (100%)	64 (97%)	2 (3%)	36	64
18	SX	113/113 (100%)	111 (98%)	2 (2%)	54	76
19	Sa	89/89 (100%)	87 (98%)	2 (2%)	47	71
20	Sc	57/57 (100%)	57 (100%)	0	100	100
21	Sd	48/48 (100%)	44 (92%)	4 (8%)	9	33
22	Sg	271/271 (100%)	268 (99%)	3 (1%)	70	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	SC	187/186 (100%)	186 (100%)	1 (0%)	86	92
24	SG	207/207 (100%)	201 (97%)	6 (3%)	37	65
25	SJ	162/161 (101%)	155 (96%)	7 (4%)	25	55
26	SM	98/100 (98%)	95 (97%)	3 (3%)	35	63
27	SN	130/130 (100%)	130 (100%)	0	100	100
28	SO	107/107 (100%)	107 (100%)	0	100	100
29	SW	112/112 (100%)	109 (97%)	3 (3%)	40	67
30	SY	114/113 (101%)	109 (96%)	5 (4%)	24	54
31	SZ	64/64 (100%)	61 (95%)	3 (5%)	22	52
32	Sb	74/74 (100%)	74 (100%)	0	100	100
33	Se	46/46 (100%)	46 (100%)	0	100	100
34	Sf	60/60 (100%)	57 (95%)	3 (5%)	20	50
35	A	194/194 (100%)	189 (97%)	5 (3%)	41	68
36	B	345/345 (100%)	336 (97%)	9 (3%)	41	68
37	C	302/302 (100%)	293 (97%)	9 (3%)	36	64
40	F	248/248 (100%)	243 (98%)	5 (2%)	50	74
41	G	209/220 (95%)	204 (98%)	5 (2%)	44	70
42	H	194/194 (100%)	189 (97%)	5 (3%)	41	68
43	I	199/199 (100%)	199 (100%)	0	100	100
44	J	170/170 (100%)	166 (98%)	4 (2%)	44	70
45	K	178/179 (99%)	175 (98%)	3 (2%)	56	78
46	L	142/142 (100%)	140 (99%)	2 (1%)	62	81
47	M	171/171 (100%)	168 (98%)	3 (2%)	54	76
48	N	118/118 (100%)	116 (98%)	2 (2%)	56	78
49	O	171/171 (100%)	167 (98%)	4 (2%)	45	70
50	P	168/168 (100%)	160 (95%)	8 (5%)	21	51
51	Q	134/134 (100%)	131 (98%)	3 (2%)	47	71
52	R	164/164 (100%)	159 (97%)	5 (3%)	36	64
53	S	160/160 (100%)	157 (98%)	3 (2%)	52	75
54	T	156/156 (100%)	155 (99%)	1 (1%)	84	91
55	U	138/138 (100%)	134 (97%)	4 (3%)	37	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
56	V	89/89 (100%)	84 (94%)	5 (6%)	17	46
57	W	100/100 (100%)	100 (100%)	0	100	100
58	X	53/53 (100%)	52 (98%)	1 (2%)	52	75
59	Y	105/105 (100%)	101 (96%)	4 (4%)	28	59
60	Z	124/124 (100%)	123 (99%)	1 (1%)	79	89
61	a	117/117 (100%)	114 (97%)	3 (3%)	41	68
62	b	120/120 (100%)	116 (97%)	4 (3%)	33	62
63	c	82/101 (81%)	80 (98%)	2 (2%)	44	70
64	d	88/88 (100%)	87 (99%)	1 (1%)	70	84
65	e	97/97 (100%)	96 (99%)	1 (1%)	73	86
66	f	115/115 (100%)	114 (99%)	1 (1%)	75	88
67	g	88/88 (100%)	84 (96%)	4 (4%)	23	53
68	h	98/98 (100%)	96 (98%)	2 (2%)	50	74
69	i	109/109 (100%)	107 (98%)	2 (2%)	54	76
70	j	83/83 (100%)	82 (99%)	1 (1%)	67	83
71	k	71/71 (100%)	70 (99%)	1 (1%)	62	81
72	l	64/64 (100%)	63 (98%)	1 (2%)	58	79
73	m	47/47 (100%)	46 (98%)	1 (2%)	48	72
74	n	46/46 (100%)	45 (98%)	1 (2%)	47	71
75	o	24/24 (100%)	23 (96%)	1 (4%)	25	56
76	p	93/93 (100%)	89 (96%)	4 (4%)	25	55
77	q	74/74 (100%)	73 (99%)	1 (1%)	62	81
78	r	106/106 (100%)	104 (98%)	2 (2%)	52	75
83	y	23/29 (79%)	22 (96%)	1 (4%)	25	55
All	All	9787/9826 (100%)	9579 (98%)	208 (2%)	49	72

All (208) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	SA	50	ASN
2	SA	122	LEU
2	SA	220	LYS
3	SB	186	ASN
4	SD	40	ARG

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Mol	Chain	Res	Type
4	SD	76	ARG
5	SE	7	LYS
5	SE	49	ARG
5	SE	198	ARG
5	SE	254	LYS
6	SF	60	ARG
6	SF	77	MET
6	SF	83	ASN
7	SH	57	ARG
8	SI	47	ARG
8	SI	60	LEU
8	SI	124	LYS
8	SI	128	LYS
8	SI	144	LYS
9	SK	46	MET
9	SK	55	ARG
10	SL	32	LYS
10	SL	65	ASN
10	SL	69	ARG
10	SL	147	LYS
11	SP	79	HIS
11	SP	89	MET
12	SQ	125	ARG
13	SR	3	ARG
13	SR	74	GLN
13	SR	83	ASN
14	SS	108	ARG
15	ST	41	LYS
15	ST	82	ARG
15	ST	131	LEU
16	SU	49	LYS
16	SU	51	LYS
16	SU	56	MET
16	SU	66	ARG
17	SV	21	ASN
17	SV	27	LYS
18	SX	8	ARG
18	SX	18	ARG
19	Sa	28	ARG
19	Sa	51	ARG
21	Sd	19	ARG
21	Sd	26	ASN

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Mol	Chain	Res	Type
21	Sd	39	CYS
21	Sd	40	ARG
22	Sg	30	MET
22	Sg	162	ASN
22	Sg	280	LYS
23	SC	103	LYS
24	SG	98	ARG
24	SG	119	LYS
24	SG	132	ARG
24	SG	163	ASN
24	SG	217	MET
24	SG	224	ARG
25	SJ	5	ARG
25	SJ	66	LYS
25	SJ	79	ARG
25	SJ	92	MET
25	SJ	121	LYS
25	SJ	138[A]	ARG
25	SJ	138[B]	ARG
26	SM	55	ASN
26	SM	93	LYS
26	SM	116	LYS
29	SW	57	ARG
29	SW	93	LEU
29	SW	103	VAL
30	SY	2	ASN
30	SY	10	ARG
30	SY	113[A]	ARG
30	SY	113[B]	ARG
30	SY	118	ARG
31	SZ	43	LYS
31	SZ	62	VAL
31	SZ	66	LYS
34	Sf	89	LYS
34	Sf	91	ASN
34	Sf	96	LYS
35	A	64	ARG
35	A	68	ARG
35	A	140	ASN
35	A	193	ARG
35	A	250	LYS
36	B	67	VAL

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Mol	Chain	Res	Type
36	B	85	VAL
36	B	121	ASN
36	B	144	LYS
36	B	213	GLN
36	B	271	GLN
36	B	301	ASN
36	B	378	ARG
36	B	396	ARG
37	C	38	ASN
37	C	97	ARG
37	C	150	LEU
37	C	199	ARG
37	C	223	ASN
37	C	236	ASN
37	C	278	ASN
37	C	312	ARG
37	C	337	ARG
40	F	10	LYS
40	F	191	ASN
40	F	196	ARG
40	F	258	LYS
40	F	265	ARG
41	G	52	ARG
41	G	56	ARG
41	G	110	ARG
41	G	130	LYS
41	G	279	ASN
42	H	24	ASN
42	H	41	MET
42	H	106	ARG
42	H	126	ASN
42	H	245	ARG
44	J	42	ASN
44	J	63	ASN
44	J	108	ASN
44	J	116	ASN
45	K	3	ARG
45	K	69	ARG
45	K	169	LYS
46	L	35	ARG
46	L	54	ARG
47	M	21	ARG

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Mol	Chain	Res	Type
47	M	102	ARG
47	M	165	LYS
48	N	5	ARG
48	N	119	ARG
49	O	63	ARG
49	O	64	ILE
49	O	133	ILE
49	O	183	THR
50	P	63	ASN
50	P	94	ARG
50	P	101	ARG
50	P	140	ARG
50	P	169	ARG
50	P	178	ARG
50	P	185	VAL
50	P	188	LYS
51	Q	24	VAL
51	Q	127	ARG
51	Q	146	ILE
52	R	6	ARG
52	R	14	ARG
52	R	37	ARG
52	R	163	THR
52	R	168	ARG
53	S	98	ARG
53	S	152	LYS
53	S	162	ARG
54	T	15	ARG
55	U	9	ARG
55	U	12	ARG
55	U	107	LYS
55	U	117	LYS
56	V	20	LYS
56	V	52	LYS
56	V	67	LYS
56	V	69	LYS
56	V	101	ARG
58	X	43	LYS
59	Y	48	ARG
59	Y	96	LEU
59	Y	129	ARG
59	Y	152	LYS

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Mol	Chain	Res	Type
60	Z	104	VAL
61	a	13	VAL
61	a	17	ARG
61	a	98	LYS
62	b	44	ASN
62	b	63	LEU
62	b	87	ARG
62	b	105	ARG
63	c	41	ARG
63	c	65	MET
64	d	77	ASN
65	e	93	ASN
66	f	33	ARG
67	g	33	VAL
67	g	59	THR
67	g	63	LYS
67	g	109	ARG
68	h	4	ARG
68	h	54	ARG
69	i	92	ARG
69	i	109	ARG
70	j	68	ARG
71	k	79	ARG
72	l	17	ARG
73	m	11	ARG
74	n	112	LYS
75	o	9	ARG
76	p	27	LYS
76	p	69	ARG
76	p	81	ARG
76	p	93	LEU
77	q	84	ARG
78	r	41	ASN
78	r	83	ASN
83	y	35	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (118) such sidechains are listed below:

Mol	Chain	Res	Type
2	SA	50	ASN
3	SB	40	ASN
3	SB	186	ASN

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Mol	Chain	Res	Type
3	SB	202	GLN
4	SD	159	HIS
5	SE	138	HIS
7	SH	39	GLN
7	SH	162	GLN
7	SH	165	ASN
8	SI	155	ASN
10	SL	19	ASN
10	SL	65	ASN
10	SL	83	GLN
11	SP	24	GLN
11	SP	32	GLN
11	SP	103	ASN
12	SQ	24	HIS
13	SR	83	ASN
15	ST	128	GLN
16	SU	92	HIS
17	SV	21	ASN
21	Sd	5	GLN
21	Sd	45	GLN
22	Sg	14	HIS
22	Sg	162	ASN
24	SG	59	GLN
24	SG	81	HIS
24	SG	163	ASN
24	SG	197	GLN
25	SJ	111	GLN
25	SJ	125	HIS
27	SN	5	HIS
29	SW	16	ASN
29	SW	98	GLN
30	SY	2	ASN
32	Sb	19	HIS
32	Sb	83	GLN
34	Sf	91	ASN
35	A	50	HIS
35	A	83	HIS
35	A	132	ASN
35	A	140	ASN
35	A	209	HIS
36	B	55	HIS
36	B	121	ASN

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Mol	Chain	Res	Type
36	B	184	GLN
36	B	186	ASN
36	B	301	ASN
37	C	94	ASN
37	C	198	ASN
37	C	223	ASN
37	C	236	ASN
37	C	278	ASN
37	C	347	HIS
40	F	111	ASN
40	F	191	ASN
40	F	198	HIS
41	G	128	HIS
41	G	190	HIS
41	G	191	GLN
41	G	279	ASN
42	H	24	ASN
42	H	80	ASN
42	H	126	ASN
42	H	131	ASN
42	H	226	HIS
43	I	64	GLN
44	J	42	ASN
44	J	63	ASN
44	J	108	ASN
44	J	116	ASN
45	K	14	ASN
45	K	86	HIS
45	K	163	GLN
45	K	213	HIS
46	L	112	HIS
47	M	19	GLN
47	M	87	HIS
47	M	104	ASN
48	N	44	GLN
48	N	56	GLN
48	N	70	GLN
49	O	87	HIS
49	O	182	HIS
49	O	199	GLN
50	P	14	HIS
50	P	63	ASN

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Mol	Chain	Res	Type
51	Q	80	GLN
52	R	8	ASN
53	S	39	GLN
53	S	58	HIS
53	S	130	ASN
54	T	163	HIS
55	U	49	GLN
55	U	98	HIS
57	W	77	HIS
57	W	101	ASN
57	W	135	ASN
58	X	50	ASN
59	Y	111	GLN
59	Y	151	ASN
62	b	25	HIS
62	b	44	ASN
63	c	6	ASN
63	c	19	ASN
64	d	77	ASN
65	e	93	ASN
66	f	43	ASN
66	f	57	ASN
66	f	102	ASN
70	j	26	HIS
71	k	66	HIS
73	m	43	HIS
76	p	19	GLN
77	q	56	HIS
78	r	41	ASN
78	r	45	HIS
78	r	100	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	S2	1690/1714 (98%)	570 (33%)	31 (1%)
38	D	156/157 (99%)	37 (23%)	0
39	E	118/121 (97%)	21 (17%)	0
79	t	3590/3607 (99%)	888 (24%)	0
80	u	74/76 (97%)	30 (40%)	0
81	v	71/76 (93%)	31 (43%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
82	w	9/10 (90%)	4 (44%)	0
All	All	5708/5761 (99%)	1581 (27%)	31 (0%)

All (1581) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	S2	2	A
1	S2	4	C
1	S2	9	U
1	S2	10	G
1	S2	11	A
1	S2	23	G
1	S2	24	C
1	S2	25	A
1	S2	33	G
1	S2	37	C
1	S2	38	A
1	S2	39	A
1	S2	41	G
1	S2	42	A
1	S2	43	U
1	S2	44	U
1	S2	46	A
1	S2	54	A
1	S2	55	U
1	S2	56	G
1	S2	59	U
1	S2	60	A
1	S2	61	A
1	S2	64	A
1	S2	65	C
1	S2	66	G
1	S2	67	C
1	S2	68	A
1	S2	69	C
1	S2	70	G
1	S2	72	C
1	S2	73	C
1	S2	74	G
1	S2	76	U
1	S2	78	C
1	S2	79	A

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Mol	Chain	Res	Type
1	S2	80	G
1	S2	82	G
1	S2	100	U
1	S2	103	A
1	S2	104	A
1	S2	111	A
1	S2	112	U
1	S2	113	G
1	S2	115	U
1	S2	116	OMU
1	S2	119	PSU
1	S2	121	OMU
1	S2	122	G
1	S2	125	C
1	S2	126	G
1	S2	129	C
1	S2	130	G
1	S2	139	C
1	S2	142	C
1	S2	143	U
1	S2	147	A
1	S2	155	G
1	S2	159	A2M
1	S2	160	U
1	S2	161	U
1	S2	163	U
1	S2	168	C
1	S2	170	A
1	S2	173	A
1	S2	175	A
1	S2	176	U
1	S2	182	C
1	S2	183	G
1	S2	189	U
1	S2	191	A
1	S2	192	C
1	S2	193	C
1	S2	194	C
1	S2	195	C
1	S2	196	C
1	S2	197	U
1	S2	198	U

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Mol	Chain	Res	Type
1	S2	199	C
1	S2	200	G
1	S2	203	G
1	S2	204	G
1	S2	206	G
1	S2	208	G
1	S2	209	A
1	S2	215	G
1	S2	293	C
1	S2	294	U
1	S2	295	C
1	S2	305	U
1	S2	308	G
1	S2	311	C
1	S2	312	G
1	S2	316	G
1	S2	318	A
1	S2	323	C
1	S2	324	C
1	S2	325	C
1	S2	326	C
1	S2	327	G
1	S2	328	U
1	S2	329	G
1	S2	333	G
1	S2	338	G
1	S2	340	C
1	S2	347	G
1	S2	352	U
1	S2	360	A
1	S2	362	C
1	S2	364	A
1	S2	367	U
1	S2	368	U
1	S2	369	C
1	S2	370	G
1	S2	371	A
1	S2	376	A
1	S2	377	G
1	S2	379	C
1	S2	380	G
1	S2	382	C

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Mol	Chain	Res	Type
1	S2	385	G
1	S2	386	C
1	S2	387	C
1	S2	400	C
1	S2	408	A
1	S2	409	C
1	S2	413	G
1	S2	417	C
1	S2	418	A
1	S2	419	G
1	S2	429	C
1	S2	436	G
1	S2	446	G
1	S2	447	A
1	S2	448	A
1	S2	449	A
1	S2	450	C
1	S2	452	G
1	S2	464	A
1	S2	466	G
1	S2	467	G
1	S2	470	G
1	S2	471	G
1	S2	472	C
1	S2	473	A
1	S2	474	G
1	S2	481	C
1	S2	482	G
1	S2	485	A
1	S2	487	U
1	S2	488	U
1	S2	492	C
1	S2	493	A
1	S2	496	C
1	S2	502	C
1	S2	516	A
1	S2	528	A
1	S2	531	A
1	S2	532	C
1	S2	534	G
1	S2	535	G
1	S2	537	C

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Mol	Chain	Res	Type
1	S2	538	U
1	S2	540	U
1	S2	541	U
1	S2	542	U
1	S2	543	C
1	S2	544	G
1	S2	545	A
1	S2	546	G
1	S2	547	G
1	S2	548	C
1	S2	549	C
1	S2	553	U
1	S2	554	A
1	S2	555	A
1	S2	556	U
1	S2	557	U
1	S2	558	G
1	S2	559	G
1	S2	560	A
1	S2	561	A
1	S2	564	A
1	S2	578	C
1	S2	579	C
1	S2	583	C
1	S2	585	C
1	S2	587	A
1	S2	588	G
1	S2	589	G
1	S2	590	A
1	S2	591	U
1	S2	594	A
1	S2	603	C
1	S2	604	A
1	S2	607	U
1	S2	608	C
1	S2	614	C
1	S2	617	G
1	S2	620	G
1	S2	621	C
1	S2	625	G
1	S2	626	G
1	S2	627	U

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Mol	Chain	Res	Type
1	S2	628	A
1	S2	629	A
1	S2	631	U
1	S2	643	A
1	S2	655	A
1	S2	659	G
1	S2	660	C
1	S2	662	G
1	S2	668	A2M
1	S2	669	A
1	S2	670	A
1	S2	671	A
1	S2	672	A
1	S2	673	G
1	S2	675	U
1	S2	683	OMG
1	S2	690	G
1	S2	691	G
1	S2	692	G
1	S2	693	A
1	S2	695	C
1	S2	696	G
1	S2	697	G
1	S2	698	G
1	S2	731	G
1	S2	732	U
1	S2	733	C
1	S2	734	C
1	S2	735	C
1	S2	736	C
1	S2	737	G
1	S2	738	C
1	S2	739	C
1	S2	748	C
1	S2	749	U
1	S2	750	C
1	S2	751	G
1	S2	752	G
1	S2	753	C
1	S2	788	G
1	S2	789	G
1	S2	790	C

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Mol	Chain	Res	Type
1	S2	791	C
1	S2	792	C
1	S2	794	A
1	S2	797	C
1	S2	798	A
1	S2	799	U
1	S2	804	U
1	S2	810	A
1	S2	811	A
1	S2	815	U
1	S2	816	A
1	S2	821	G
1	S2	822	PSU
1	S2	823	PSU
1	S2	830	A
1	S2	831	G
1	S2	834	C
1	S2	835	C
1	S2	836	G
1	S2	837	A
1	S2	838	G
1	S2	839	C
1	S2	841	G
1	S2	842	C
1	S2	847	A
1	S2	857	U
1	S2	858	A
1	S2	859	G
1	S2	865	A
1	S2	867	G
1	S2	868	G
1	S2	870	A
1	S2	871	U
1	S2	873	G
1	S2	878	G
1	S2	880	G
1	S2	881	G
1	S2	883	U
1	S2	886	A
1	S2	887	U
1	S2	889	U
1	S2	890	U

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Mol	Chain	Res	Type
1	S2	891	G
1	S2	892	U
1	S2	893	U
1	S2	894	G
1	S2	895	G
1	S2	896	U
1	S2	897	U
1	S2	898	U
1	S2	899	U
1	S2	900	C
1	S2	903	A
1	S2	907	G
1	S2	908	A
1	S2	910	G
1	S2	913	A
1	S2	914	U
1	S2	917	U
1	S2	920	A
1	S2	922	A
1	S2	933	G
1	S2	936	G
1	S2	938	A
1	S2	943	U
1	S2	969	U
1	S2	970	G
1	S2	971	G
1	S2	978	G
1	S2	990	A
1	S2	992	A
1	S2	996	A
1	S2	999	G
1	S2	1001	A
1	S2	1002	U
1	S2	1003	U
1	S2	1005	G
1	S2	1007	C
1	S2	1016	U
1	S2	1017	U
1	S2	1021	U
1	S2	1023	A
1	S2	1026	C
1	S2	1027	A

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Mol	Chain	Res	Type
1	S2	1028	A
1	S2	1033	G
1	S2	1049	A
1	S2	1050	A
1	S2	1055	A
1	S2	1058	A
1	S2	1060	A
1	S2	1061	U
1	S2	1062	A
1	S2	1064	C
1	S2	1078	C
1	S2	1083	A
1	S2	1085	C
1	S2	1088	U
1	S2	1089	G
1	S2	1109	C
1	S2	1114	U
1	S2	1116	C
1	S2	1117	C
1	S2	1119	A
1	S2	1121	G
1	S2	1123	C
1	S2	1133	A
1	S2	1138	C
1	S2	1145	A
1	S2	1146	C
1	S2	1149	A
1	S2	1150	A
1	S2	1154	U
1	S2	1155	U
1	S2	1159	G
1	S2	1160	U
1	S2	1168	G
1	S2	1170	A
1	S2	1195	A
1	S2	1197	G
1	S2	1207	G
1	S2	1208	A
1	S2	1209	A
1	S2	1215	C
1	S2	1217	A
1	S2	1220	A

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Mol	Chain	Res	Type
1	S2	1224	G
1	S2	1233	G
1	S2	1242	U
1	S2	1245	G
1	S2	1246	A
1	S2	1249	C
1	S2	1251	A
1	S2	1253	A
1	S2	1256	G
1	S2	1257	G
1	S2	1258	A
1	S2	1259	A
1	S2	1260	A
1	S2	1262	C
1	S2	1265	A
1	S2	1273	C
1	S2	1274	G
1	S2	1275	G
1	S2	1283	C
1	S2	1284	A
1	S2	1285	G
1	S2	1286	G
1	S2	1287	A
1	S2	1288	U
1	S2	1294	G
1	S2	1295	A
1	S2	1296	U
1	S2	1298	G
1	S2	1300	U
1	S2	1301	A
1	S2	1302	G
1	S2	1312	G
1	S2	1313	A
1	S2	1315	U
1	S2	1322	G
1	S2	1323	U
1	S2	1328	G
1	S2	1330	G
1	S2	1331	C
1	S2	1332	A
1	S2	1333	U
1	S2	1340	U

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Mol	Chain	Res	Type
1	S2	1341	C
1	S2	1348	G
1	S2	1354	G
1	S2	1355	C
1	S2	1364	U
1	S2	1371	U
1	S2	1372	U
1	S2	1373	C
1	S2	1376	A
1	S2	1378	A
1	S2	1382	A
1	S2	1393	G
1	S2	1396	A
1	S2	1397	U
1	S2	1402	A
1	S2	1403	C
1	S2	1406	G
1	S2	1420	G
1	S2	1421	A
1	S2	1422	G
1	S2	1423	C
1	S2	1424	G
1	S2	1433	C
1	S2	1434	C
1	S2	1435	C
1	S2	1436	C
1	S2	1437	C
1	S2	1438	A
1	S2	1442	U
1	S2	1446	A
1	S2	1447	G
1	S2	1454	A
1	S2	1458	G
1	S2	1462	U
1	S2	1463	U
1	S2	1464	C
1	S2	1466	G
1	S2	1470	C
1	S2	1471	C
1	S2	1477	U
1	S2	1478	U
1	S2	1480	A

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Mol	Chain	Res	Type
1	S2	1482	C
1	S2	1485	U
1	S2	1489	A
1	S2	1490	G
1	S2	1493	C
1	S2	1494	U
1	S2	1495	G
1	S2	1496	U
1	S2	1497	G
1	S2	1505	U
1	S2	1507	G
1	S2	1508	A
1	S2	1509	U
1	S2	1519	U
1	S2	1520	G
1	S2	1521	C
1	S2	1523	C
1	S2	1528	G
1	S2	1533	A
1	S2	1534	C
1	S2	1535	U
1	S2	1536	G
1	S2	1543	U
1	S2	1544	C
1	S2	1548	G
1	S2	1549	U
1	S2	1552	G
1	S2	1553	C
1	S2	1554	C
1	S2	1556	A
1	S2	1557	C
1	S2	1558	C
1	S2	1560	U
1	S2	1566	G
1	S2	1568	C
1	S2	1570	G
1	S2	1573	G
1	S2	1580	A
1	S2	1581	C
1	S2	1586	U
1	S2	1588	A
1	S2	1594	A

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Mol	Chain	Res	Type
1	S2	1598	G
1	S2	1599	U
1	S2	1601	A
1	S2	1621	U
1	S2	1623	A
1	S2	1634	A
1	S2	1647	A
1	S2	1648	G
1	S2	1654	G
1	S2	1661	A
1	S2	1662	U
1	S2	1663	A
1	S2	1665	G
1	S2	1671	G
1	S2	1675	A
1	S2	1676	U
1	S2	1680	G
1	S2	1682	C
1	S2	1683	C
1	S2	1686	G
1	S2	1687	C
1	S2	1695	A
1	S2	1698	C
1	S2	1699	A
1	S2	1700	C
1	S2	1721	U
1	S2	1722	G
1	S2	1723	G
1	S2	1726	G
1	S2	1727	G
1	S2	1728	U
1	S2	1729	U
1	S2	1749	G
1	S2	1750	C
1	S2	1751	C
1	S2	1752	C
1	S2	1780	G
1	S2	1781	A
1	S2	1782	G
1	S2	1783	C
1	S2	1784	G
1	S2	1785	C

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Mol	Chain	Res	Type
1	S2	1786	U
1	S2	1789	G
1	S2	1797	U
1	S2	1803	U
1	S2	1805	G
1	S2	1811	C
1	S2	1813	A
1	S2	1814	G
1	S2	1815	A
1	S2	1816	G
1	S2	1817	G
1	S2	1823	A
1	S2	1824	A
1	S2	1826	G
1	S2	1829	G
1	S2	1830	UR3
1	S2	1831	A
1	S2	1835	A
1	S2	1836	G
1	S2	1838	U
1	S2	1839	U
1	S2	1849	G
1	S2	1852	C
1	S2	1861	G
1	S2	1862	G
1	S2	1863	A
1	S2	1864	U
1	S2	1865	C
1	S2	1868	U
1	S2	1869	A
38	D	23	C
38	D	34	U
38	D	35	C
38	D	50	C
38	D	59	A
38	D	63	U
38	D	71	A
38	D	72	A
38	D	80	A
38	D	81	C
38	D	83	C
38	D	87	G

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Mol	Chain	Res	Type
38	D	94	G
38	D	95	A
38	D	101	C
38	D	103	A
38	D	105	C
38	D	107	C
38	D	109	C
38	D	110	U
38	D	111	U
38	D	116	C
38	D	120	G
38	D	121	G
38	D	122	G
38	D	123	U
38	D	124	U
38	D	125	C
38	D	126	C
38	D	127	U
38	D	128	C
38	D	129	C
38	D	130	C
38	D	148	A
38	D	150	C
38	D	153	C
38	D	156	U
39	E	7	G
39	E	19	C
39	E	22	A
39	E	23	A
39	E	24	C
39	E	27	G
39	E	30	C
39	E	33	U
39	E	38	U
39	E	48	G
39	E	53	U
39	E	59	G
39	E	64	G
39	E	74	A
39	E	76	U
39	E	88	A
39	E	97	G

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Mol	Chain	Res	Type
39	E	98	G
39	E	103	A
39	E	104	C
39	E	110	G
79	t	9	C
79	t	15	A
79	t	18	C
79	t	25	A
79	t	30	C
79	t	32	G
79	t	39	A
79	t	42	A
79	t	48	G
79	t	49	U
79	t	59	A
79	t	64	A
79	t	65	A
79	t	71	C
79	t	72	C
79	t	73	A
79	t	74	G
79	t	91	G
79	t	98	A
79	t	108	A
79	t	119	G
79	t	120	A
79	t	131	C
79	t	132	G
79	t	134	G
79	t	135	G
79	t	137	G
79	t	138	C
79	t	144	A
79	t	148	G
79	t	149	U
79	t	156	C
79	t	157	G
79	t	163	C
79	t	169	C
79	t	171	C
79	t	173	G
79	t	181	U

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Mol	Chain	Res	Type
79	t	182	C
79	t	183	G
79	t	184	U
79	t	185	G
79	t	193	C
79	t	196	G
79	t	205	A
79	t	206	U
79	t	208	G
79	t	212	C
79	t	213	C
79	t	214	C
79	t	215	A
79	t	228	U
79	t	229	G
79	t	230	U
79	t	233	G
79	t	234	G
79	t	235	C
79	t	236	C
79	t	237	G
79	t	250	G
79	t	251	G
79	t	252	C
79	t	253	G
79	t	256	C
79	t	260	C
79	t	267	U
79	t	272	G
79	t	289	A
79	t	291	U
79	t	300	A
79	t	304	G
79	t	309	G
79	t	310	U
79	t	311	A
79	t	323	A
79	t	334	C
79	t	338	A
79	t	339	C
79	t	343	A
79	t	351	U

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Mol	Chain	Res	Type
79	t	357	A
79	t	367	G
79	t	370	A
79	t	375	U
79	t	377	A
79	t	381	G
79	t	390	A
79	t	404	A
79	t	405	G
79	t	406	G
79	t	407	G
79	t	409	G
79	t	425	G
79	t	426	U
79	t	434	U
79	t	443	C
79	t	444	G
79	t	446	A
79	t	447	G
79	t	448	U
79	t	449	C
79	t	451	G
79	t	456	G
79	t	458	G
79	t	463	C
79	t	473	G
79	t	474	C
79	t	479	C
79	t	481	G
79	t	482	G
79	t	483	C
79	t	486	U
79	t	487	G
79	t	489	C
79	t	492	C
79	t	493	G
79	t	494	G
79	t	495	C
79	t	496	C
79	t	497	C
79	t	498	G
79	t	504	U

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Mol	Chain	Res	Type
79	t	507	U
79	t	508	U
79	t	509	C
79	t	511	C
79	t	512	G
79	t	516	C
79	t	631	G
79	t	633	U
79	t	634	C
79	t	635	G
79	t	636	G
79	t	643	A
79	t	645	C
79	t	647	U
79	t	649	C
79	t	654	G
79	t	658	G
79	t	661	G
79	t	662	A
79	t	663	C
79	t	674	C
79	t	676	G
79	t	677	G
79	t	678	C
79	t	679	G
79	t	680	C
79	t	684	U
79	t	690	C
79	t	692	G
79	t	693	U
79	t	695	C
79	t	698	C
79	t	703	C
79	t	709	C
79	t	714	A
79	t	719	U
79	t	720	G
79	t	721	G
79	t	724	A
79	t	727	C
79	t	728	C
79	t	730	G

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Mol	Chain	Res	Type
79	t	737	A
79	t	738	A
79	t	739	G
79	t	743	G
79	t	749	G
79	t	899	G
79	t	902	A
79	t	904	A
79	t	905	G
79	t	906	C
79	t	907	C
79	t	912	C
79	t	914	G
79	t	917	G
79	t	918	C
79	t	919	A
79	t	920	G
79	t	921	C
79	t	922	A
79	t	923	C
79	t	924	U
79	t	925	C
79	t	926	G
79	t	927	C
79	t	932	U
79	t	933	C
79	t	940	C
79	t	944	G
79	t	947	A
79	t	948	G
79	t	949	C
79	t	950	G
79	t	952	G
79	t	953	A
79	t	954	C
79	t	957	G
79	t	958	U
79	t	959	C
79	t	976	U
79	t	1055	C
79	t	1058	G
79	t	1061	A

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Mol	Chain	Res	Type
79	t	1063	C
79	t	1065	C
79	t	1068	C
79	t	1083	U
79	t	1086	C
79	t	1087	C
79	t	1149	G
79	t	1150	C
79	t	1152	G
79	t	1156	G
79	t	1157	G
79	t	1162	U
79	t	1165	C
79	t	1174	C
79	t	1176	C
79	t	1179	G
79	t	1188	G
79	t	1192	U
79	t	1193	C
79	t	1196	G
79	t	1197	C
79	t	1198	C
79	t	1199	C
79	t	1201	G
79	t	1220	C
79	t	1221	A
79	t	1222	C
79	t	1223	G
79	t	1224	C
79	t	1225	G
79	t	1226	C
79	t	1228	C
79	t	1236	G
79	t	1238	A
79	t	1239	G
79	t	1240	G
79	t	1242	G
79	t	1248	G
79	t	1249	G
79	t	1250	C
79	t	1251	G
79	t	1253	A

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Mol	Chain	Res	Type
79	t	1258	G
79	t	1259	C
79	t	1265	G
79	t	1268	U
79	t	1269	C
79	t	1271	G
79	t	1277	A
79	t	1279	G
79	t	1280	U
79	t	1285	U
79	t	1286	A
79	t	1301	C
79	t	1309	A
79	t	1322	U
79	t	1337	A
79	t	1341	G
79	t	1342	G
79	t	1348	C
79	t	1349	G
79	t	1350	C
79	t	1351	A
79	t	1353	G
79	t	1360	G
79	t	1361	C
79	t	1362	C
79	t	1364	U
79	t	1370	A
79	t	1380	A
79	t	1381	A
79	t	1387	G
79	t	1391	G
79	t	1392	C
79	t	1393	U
79	t	1394	C
79	t	1395	G
79	t	1401	C
79	t	1403	A
79	t	1420	C
79	t	1421	U
79	t	1423	U
79	t	1424	C
79	t	1426	A

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Mol	Chain	Res	Type
79	t	1438	G
79	t	1439	G
79	t	1440	C
79	t	1453	U
79	t	1463	C
79	t	1464	G
79	t	1465	C
79	t	1466	G
79	t	1467	C
79	t	1468	C
79	t	1469	G
79	t	1473	A
79	t	1480	G
79	t	1485	A
79	t	1497	A
79	t	1500	A
79	t	1507	A
79	t	1516	A
79	t	1517	C
79	t	1531	G
79	t	1545	A
79	t	1548	C
79	t	1556	G
79	t	1560	U
79	t	1564	U
79	t	1573	U
79	t	1578	U
79	t	1587	G
79	t	1589	C
79	t	1595	A
79	t	1606	G
79	t	1613	A
79	t	1614	A
79	t	1615	G
79	t	1616	A
79	t	1619	A
79	t	1622	C
79	t	1623	G
79	t	1624	A
79	t	1636	G
79	t	1643	C
79	t	1652	G

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Mol	Chain	Res	Type
79	t	1658	C
79	t	1659	U
79	t	1660	C
79	t	1663	G
79	t	1676	C
79	t	1678	C
79	t	1679	G
79	t	1680	C
79	t	1700	C
79	t	1701	A
79	t	1702	C
79	t	1706	G
79	t	1711	A
79	t	1714	C
79	t	1716	G
79	t	1722	C
79	t	1728	A
79	t	1732	G
79	t	1738	U
79	t	1740	G
79	t	1742	G
79	t	1746	G
79	t	1747	A
79	t	1748	A
79	t	1750	C
79	t	1769	A
79	t	1776	A
79	t	1779	G
79	t	1785	G
79	t	1786	A
79	t	1788	G
79	t	1794	C
79	t	1797	G
79	t	1803	G
79	t	1814	G
79	t	1816	G
79	t	1818	A
79	t	1823	G
79	t	1836	G
79	t	1840	C
79	t	1850	G
79	t	1859	G

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Mol	Chain	Res	Type
79	t	1863	U
79	t	1872	A
79	t	1879	C
79	t	1881	C
79	t	1887	U
79	t	1891	G
79	t	1896	C
79	t	1902	C
79	t	1903	G
79	t	1906	G
79	t	1910	A
79	t	1912	C
79	t	1916	C
79	t	1920	A
79	t	1921	G
79	t	1928	U
79	t	1929	G
79	t	1930	U
79	t	1932	G
79	t	1938	U
79	t	1940	U
79	t	1941	A
79	t	1942	G
79	t	1943	A
79	t	1952	C
79	t	1956	G
79	t	1960	A
79	t	1961	U
79	t	1963	G
79	t	1964	A
79	t	1968	C
79	t	1972	A
79	t	1973	U
79	t	1978	U
79	t	1979	A
79	t	1980	A
79	t	1983	A
79	t	1984	G
79	t	1991	A
79	t	1994	A
79	t	2003	C
79	t	2007	A

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Mol	Chain	Res	Type
79	t	2011	A
79	t	2014	A
79	t	2020	G
79	t	2021	A
79	t	2025	U
79	t	2027	G
79	t	2029	U
79	t	2036	G
79	t	2037	G
79	t	2050	A
79	t	2051	U
79	t	2065	C
79	t	2069	G
79	t	2072	G
79	t	2073	A
79	t	2075	A
79	t	2076	G
79	t	2077	U
79	t	2078	G
79	t	2080	A
79	t	2081	C
79	t	2082	G
79	t	2084	G
79	t	2086	G
79	t	2087	C
79	t	2088	G
79	t	2090	C
79	t	2091	G
79	t	2092	G
79	t	2231	G
79	t	2232	A
79	t	2233	G
79	t	2234	C
79	t	2235	C
79	t	2236	C
79	t	2237	C
79	t	2240	G
79	t	2241	G
79	t	2245	C
79	t	2246	U
79	t	2247	A
79	t	2268	C

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Mol	Chain	Res	Type
79	t	2278	G
79	t	2279	A
79	t	2280	G
79	t	2282	C
79	t	2285	G
79	t	2292	A
79	t	2299	G
79	t	2301	G
79	t	2310	G
79	t	2323	U
79	t	2326	A
79	t	2327	G
79	t	2330	C
79	t	2339	A
79	t	2340	G
79	t	2343	G
79	t	2344	C
79	t	2358	A
79	t	2361	A
79	t	2374	A
79	t	2375	A
79	t	2396	A
79	t	2400	G
79	t	2401	C
79	t	2404	U
79	t	2405	U
79	t	2416	C
79	t	2421	G
79	t	2426	U
79	t	2429	G
79	t	2442	G
79	t	2446	U
79	t	2447	U
79	t	2449	C
79	t	2450	G
79	t	2451	A
79	t	2453	G
79	t	2458	G
79	t	2467	C
79	t	2468	C
79	t	2470	C
79	t	2472	G

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Mol	Chain	Res	Type
79	t	2473	U
79	t	2474	U
79	t	2475	G
79	t	2482	G
79	t	2483	C
79	t	2484	C
79	t	2485	G
79	t	2490	A
79	t	2492	A
79	t	2509	U
79	t	2523	G
79	t	2524	U
79	t	2525	G
79	t	2526	G
79	t	2532	A
79	t	2533	U
79	t	2543	G
79	t	2544	A
79	t	2545	G
79	t	2548	G
79	t	2562	C
79	t	2565	G
79	t	2566	A
79	t	2568	C
79	t	2580	A
79	t	2585	G
79	t	2590	A
79	t	2600	A
79	t	2606	C
79	t	2617	G
79	t	2618	U
79	t	2632	C
79	t	2640	U
79	t	2648	C
79	t	2652	G
79	t	2654	G
79	t	2665	G
79	t	2666	U
79	t	2675	A
79	t	2686	U
79	t	2687	U
79	t	2688	C

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Mol	Chain	Res	Type
79	t	2689	C
79	t	2690	G
79	t	2691	G
79	t	2700	G
79	t	2702	U
79	t	2705	G
79	t	2714	G
79	t	2719	U
79	t	2722	A
79	t	2723	A
79	t	2733	G
79	t	2737	G
79	t	2741	G
79	t	2742	U
79	t	2745	A
79	t	2748	U
79	t	2766	A
79	t	2767	U
79	t	2769	U
79	t	2776	C
79	t	2778	G
79	t	2785	A
79	t	2793	C
79	t	2794	A
79	t	2798	U
79	t	2805	U
79	t	2806	G
79	t	2817	G
79	t	2821	G
79	t	2834	G
79	t	2835	C
79	t	2839	C
79	t	2855	G
79	t	2860	A
79	t	2863	G
79	t	2871	C
79	t	2873	A
79	t	2879	U
79	t	2881	G
79	t	3571	G
79	t	3572	C
79	t	3573	C

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Mol	Chain	Res	Type
79	t	3575	A
79	t	3577	U
79	t	3587	U
79	t	3589	C
79	t	3590	G
79	t	3591	G
79	t	3596	G
79	t	3597	G
79	t	3606	A
79	t	3612	U
79	t	3614	A
79	t	3619	A
79	t	3627	A
79	t	3633	A
79	t	3635	G
79	t	3643	G
79	t	3644	C
79	t	3651	U
79	t	3653	A
79	t	3662	G
79	t	3663	A
79	t	3682	A
79	t	3683	A
79	t	3700	U
79	t	3707	A
79	t	3724	G
79	t	3728	G
79	t	3730	A
79	t	3731	A
79	t	3733	U
79	t	3742	C
79	t	3744	U
79	t	3745	A
79	t	3748	G
79	t	3751	G
79	t	3754	A
79	t	3755	A
79	t	3759	C
79	t	3765	C
79	t	3781	C
79	t	3782	G
79	t	3783	C

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Mol	Chain	Res	Type
79	t	3784	A
79	t	3785	U
79	t	3788	A
79	t	3789	U
79	t	3790	G
79	t	3795	A
79	t	3798	G
79	t	3799	A
79	t	3809	U
79	t	3810	G
79	t	3811	U
79	t	3822	U
79	t	3838	A
79	t	3848	A
79	t	3849	C
79	t	3850	G
79	t	3851	G
79	t	3852	G
79	t	3860	G
79	t	3863	U
79	t	3866	G
79	t	3868	G
79	t	3872	A
79	t	3876	A
79	t	3877	A
79	t	3878	G
79	t	3879	A
79	t	3880	C
79	t	3886	U
79	t	3894	A
79	t	3909	G
79	t	3917	G
79	t	3918	A
79	t	4046	G
79	t	4054	G
79	t	4061	G
79	t	4062	G
79	t	4064	G
79	t	4065	G
79	t	4066	C
79	t	4067	G
79	t	4069	G

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Mol	Chain	Res	Type
79	t	4070	C
79	t	4071	C
79	t	4072	C
79	t	4074	A
79	t	4079	C
79	t	4080	U
79	t	4083	C
79	t	4084	G
79	t	4086	U
79	t	4088	C
79	t	4101	C
79	t	4106	C
79	t	4107	C
79	t	4108	G
79	t	4109	G
79	t	4110	C
79	t	4119	A
79	t	4124	C
79	t	4126	C
79	t	4132	A
79	t	4145	G
79	t	4146	G
79	t	4153	G
79	t	4158	G
79	t	4167	A
79	t	4176	A
79	t	4187	G
79	t	4190	G
79	t	4191	U
79	t	4195	A
79	t	4213	A
79	t	4215	A
79	t	4216	G
79	t	4217	A
79	t	4228	G
79	t	4230	A
79	t	4234	G
79	t	4235	A
79	t	4236	A
79	t	4242	A
79	t	4243	A
79	t	4253	G

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Mol	Chain	Res	Type
79	t	4259	G
79	t	4266	A
79	t	4267	G
79	t	4276	C
79	t	4292	G
79	t	4294	C
79	t	4300	G
79	t	4311	C
79	t	4316	U
79	t	4320	U
79	t	4322	U
79	t	4326	G
79	t	4333	G
79	t	4334	U
79	t	4338	A
79	t	4339	G
79	t	4340	A
79	t	4342	A
79	t	4343	A
79	t	4349	C
79	t	4353	G
79	t	4356	A
79	t	4358	A
79	t	4360	C
79	t	4367	G
79	t	4377	A
79	t	4384	A
79	t	4388	C
79	t	4392	G
79	t	4402	G
79	t	4405	C
79	t	4406	C
79	t	4410	G
79	t	4414	U
79	t	4426	A
79	t	4437	G
79	t	4450	A
79	t	4455	U
79	t	4464	C
79	t	4472	A
79	t	4474	U
79	t	4475	A

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Mol	Chain	Res	Type
79	t	4477	G
79	t	4480	A
79	t	4481	C
79	t	4486	G
79	t	4490	G
79	t	4510	A
79	t	4517	U
79	t	4518	U
79	t	4522	C
79	t	4529	G
79	t	4531	U
79	t	4532	G
79	t	4537	G
79	t	4546	A
79	t	4551	A
79	t	4552	A
79	t	4561	A
79	t	4562	G
79	t	4570	G
79	t	4579	G
79	t	4586	A
79	t	4591	U
79	t	4593	G
79	t	4595	G
79	t	4597	A
79	t	4598	U
79	t	4599	G
79	t	4601	G
79	t	4611	G
79	t	4618	A
79	t	4619	U
79	t	4626	A
79	t	4632	C
79	t	4633	C
79	t	4634	A
79	t	4640	G
79	t	4649	A
79	t	4656	G
79	t	4657	C
79	t	4662	A
79	t	4671	U
79	t	4674	C

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Mol	Chain	Res	Type
79	t	4683	G
79	t	4692	C
79	t	4693	G
79	t	4694	G
79	t	4695	C
79	t	4696	A
79	t	4697	G
79	t	4703	C
79	t	4704	G
79	t	4706	A
79	t	4714	U
79	t	4715	U
79	t	4716	G
79	t	4718	C
79	t	4720	U
79	t	4722	G
79	t	4726	A
79	t	4727	G
79	t	4732	U
79	t	4736	C
79	t	4737	G
79	t	4816	C
79	t	4817	G
79	t	4824	C
79	t	4827	U
79	t	4828	G
79	t	4831	G
79	t	4832	A
79	t	4833	G
79	t	4834	U
79	t	4838	C
79	t	4840	U
79	t	4841	C
79	t	4847	G
79	t	4853	C
79	t	4854	G
79	t	4855	G
79	t	4856	G
79	t	4858	C
79	t	4859	G
79	t	4864	C
79	t	4865	G

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Mol	Chain	Res	Type
79	t	4866	G
79	t	4867	A
79	t	4868	A
79	t	4869	A
79	t	4870	G
79	t	4871	G
79	t	4872	C
79	t	4881	C
79	t	4882	C
79	t	4883	U
79	t	4885	G
79	t	4886	C
79	t	4894	G
79	t	4895	C
79	t	4896	A
79	t	4901	A
79	t	4902	C
79	t	4903	G
79	t	4909	G
79	t	4914	A
79	t	4915	C
79	t	4921	G
79	t	4924	A
79	t	4926	A
79	t	4933	G
79	t	4934	U
79	t	4943	U
79	t	4946	U
79	t	4947	U
79	t	4949	U
79	t	4950	G
79	t	4957	G
79	t	4971	C
79	t	4972	A
79	t	4975	G
79	t	4981	C
79	t	4982	C
79	t	4983	C
79	t	4984	U
79	t	4985	C
79	t	4986	G
79	t	4999	G

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Mol	Chain	Res	Type
79	t	5005	C
79	t	5007	G
79	t	5008	C
79	t	5011	U
79	t	5012	C
79	t	5013	G
79	t	5016	A
79	t	5020	G
79	t	5024	U
79	t	5028	C
80	u	4	C
80	u	7	A
80	u	8	U
80	u	11	C
80	u	17	C
80	u	18	G
80	u	19	G
80	u	20	U
80	u	21	A
80	u	23	A
80	u	24	G
80	u	25	C
80	u	38	A
80	u	40	C
80	u	44	G
80	u	46	G
80	u	47	U
80	u	48	C
80	u	50	U
80	u	52	G
80	u	56	C
80	u	59	U
80	u	60	U
80	u	61	C
80	u	62	C
80	u	64	A
80	u	69	G
80	u	72	C
80	u	74	C
80	u	76	A
81	v	2	G
81	v	7	G

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Mol	Chain	Res	Type
81	v	8	U
81	v	10	G
81	v	12	C
81	v	15	G
81	v	16	A
81	v	17	A
81	v	19	G
81	v	20	U
81	v	21	A
81	v	29	G
81	v	30	G
81	v	46	G
81	v	47	U
81	v	48	C
81	v	49	C
81	v	51	U
81	v	54	U
81	v	55	U
81	v	56	C
81	v	57	G
81	v	58	A
81	v	61	C
81	v	62	C
81	v	69	G
81	v	70	G
81	v	71	G
81	v	72	C
81	v	75	C
81	v	76	A
82	w	17	G
82	w	18	G
82	w	20	G
82	w	21	G

All (31) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	S2	42	A
1	S2	53	C
1	S2	60	A
1	S2	79	A
1	S2	196	C

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Mol	Chain	Res	Type
1	S2	205	G
1	S2	292	A
1	S2	304	C
1	S2	317	C
1	S2	386	C
1	S2	417	C
1	S2	445	A
1	S2	536	A
1	S2	559	G
1	S2	563	G
1	S2	670	A
1	S2	814	5MU
1	S2	872	A
1	S2	1261	C
1	S2	1375	G
1	S2	1396	A
1	S2	1567	G
1	S2	1572	C
1	S2	1600	G
1	S2	1661	A
1	S2	1681	U
1	S2	1802	C
1	S2	1813	A
1	S2	1814	G
1	S2	1815	A
1	S2	1828	C

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

34 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	PSU	S2	119	1	18,21,22	4.41	7 (38%)	21,30,33	1.92	5 (23%)
1	OMC	S2	517	1	19,22,23	3.47	8 (42%)	25,31,34	0.72	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MA6	S2	1850	1	19,26,27	1.61	2 (10%)	18,38,41	3.79	4 (22%)
1	A2M	S2	166	1	18,25,26	4.29	6 (33%)	20,36,39	3.48	5 (25%)
1	4AC	S2	1337	1	21,24,25	3.33	9 (42%)	28,34,37	1.21	3 (10%)
1	OMU	S2	121	1	19,22,23	3.13	6 (31%)	25,31,34	1.82	6 (24%)
1	OMU	S2	116	1	19,22,23	3.13	6 (31%)	25,31,34	1.66	6 (24%)
1	OMC	S2	1710	1	19,22,23	3.54	8 (42%)	25,31,34	0.75	0
1	A2M	S2	27	1	18,25,26	4.17	5 (27%)	20,36,39	3.66	5 (25%)
1	B8Q	S2	1219	1	18,22,23	4.78	7 (38%)	21,32,35	1.87	4 (19%)
1	PSU	S2	822	1	18,21,22	4.51	8 (44%)	21,30,33	1.91	4 (19%)
1	5MC	S2	1374	1	19,22,23	3.58	8 (42%)	26,32,35	0.94	2 (7%)
1	PSU	S2	823	1	18,21,22	4.45	8 (44%)	21,30,33	2.47	5 (23%)
1	OMG	S2	509	1	19,26,27	2.47	8 (42%)	21,38,41	1.46	4 (19%)
1	PSU	S2	612	1	18,21,22	4.42	8 (44%)	21,30,33	2.34	6 (28%)
1	A2M	S2	668	1	18,25,26	4.14	5 (27%)	20,36,39	3.78	7 (35%)
1	OMG	S2	644	1	19,26,27	2.45	8 (42%)	21,38,41	1.48	4 (19%)
1	A2M	S2	159	1	18,25,26	4.32	5 (27%)	20,36,39	3.59	7 (35%)
1	4AC	S2	1842	1	21,24,25	3.16	9 (42%)	28,34,37	1.20	5 (17%)
1	UR3	S2	1830	1	19,22,23	2.86	7 (36%)	26,32,35	2.98	8 (30%)
1	E3C	S2	568	1	19,23,24	3.51	7 (36%)	21,33,36	2.66	6 (28%)
1	B8N	S2	1248	1	25,29,30	3.13	7 (28%)	28,42,45	2.09	8 (28%)
1	A2M	S2	1678	1	18,25,26	4.34	5 (27%)	20,36,39	3.52	5 (25%)
1	A2M	S2	1031	1	18,25,26	4.13	5 (27%)	20,36,39	3.63	5 (25%)
1	PSU	S2	1243	1	18,21,22	4.38	7 (38%)	21,30,33	1.90	5 (23%)
1	PSU	S2	1081	1	18,21,22	4.27	8 (44%)	21,30,33	1.75	3 (14%)
1	OMC	S2	1703	1	19,22,23	3.47	8 (42%)	25,31,34	0.75	1 (4%)
1	6MZ	S2	1832	1	17,25,26	1.41	3 (17%)	15,36,39	2.26	3 (20%)
1	M7A	S2	1806	1	19,25,26	1.64	2 (10%)	25,37,40	3.66	8 (32%)
1	OMC	S2	174	1	19,22,23	3.55	8 (42%)	25,31,34	0.77	0
1	A2M	S2	484	1	18,25,26	4.15	6 (33%)	20,36,39	3.61	7 (35%)
1	5MU	S2	814	1	19,22,23	7.71	8 (42%)	27,32,35	3.49	12 (44%)
1	OMG	S2	683	1	19,26,27	2.45	8 (42%)	21,38,41	1.43	3 (14%)
1	MA6	S2	1851	1	19,26,27	1.60	2 (10%)	18,38,41	3.71	4 (22%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.
'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	S2	119	1	-	2/7/25/26	0/2/2/2
1	OMC	S2	517	1	-	0/9/27/28	0/2/2/2
1	MA6	S2	1850	1	-	2/7/29/30	0/3/3/3
1	A2M	S2	166	1	-	0/5/27/28	0/3/3/3
1	4AC	S2	1337	1	-	0/11/29/30	0/2/2/2
1	OMU	S2	121	1	-	3/9/27/28	0/2/2/2
1	OMU	S2	116	1	-	3/9/27/28	0/2/2/2
1	OMC	S2	1710	1	-	0/9/27/28	0/2/2/2
1	A2M	S2	27	1	-	1/5/27/28	0/3/3/3
1	B8Q	S2	1219	1	-	2/7/42/43	0/2/2/2
1	PSU	S2	822	1	-	2/7/25/26	0/2/2/2
1	5MC	S2	1374	1	-	0/7/25/26	0/2/2/2
1	PSU	S2	823	1	-	3/7/25/26	0/2/2/2
1	OMG	S2	509	1	-	1/5/27/28	0/3/3/3
1	PSU	S2	612	1	-	1/7/25/26	0/2/2/2
1	A2M	S2	668	1	-	2/5/27/28	0/3/3/3
1	OMG	S2	644	1	-	1/5/27/28	0/3/3/3
1	A2M	S2	159	1	-	3/5/27/28	0/3/3/3
1	4AC	S2	1842	1	-	0/11/29/30	0/2/2/2
1	UR3	S2	1830	1	-	4/7/25/26	0/2/2/2
1	E3C	S2	568	1	-	4/9/44/45	0/2/2/2
1	B8N	S2	1248	1	-	0/16/34/35	0/2/2/2
1	A2M	S2	1678	1	-	1/5/27/28	0/3/3/3
1	A2M	S2	1031	1	-	1/5/27/28	0/3/3/3
1	PSU	S2	1243	1	-	2/7/25/26	0/2/2/2
1	PSU	S2	1081	1	-	0/7/25/26	0/2/2/2
1	OMC	S2	1703	1	-	2/9/27/28	0/2/2/2
1	6MZ	S2	1832	1	-	2/5/27/28	0/3/3/3
1	M7A	S2	1806	1	-	3/7/37/38	0/3/3/3
1	OMC	S2	174	1	-	0/9/27/28	0/2/2/2
1	A2M	S2	484	1	-	0/5/27/28	0/3/3/3
1	5MU	S2	814	1	-	0/7/25/26	0/2/2/2
1	OMG	S2	683	1	-	2/5/27/28	0/3/3/3
1	MA6	S2	1851	1	-	4/7/29/30	0/3/3/3

All (222) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	S2	814	5MU	C4-C5	22.66	1.81	1.44
1	S2	814	5MU	C6-N1	17.25	1.67	1.38
1	S2	823	PSU	C6-C5	11.94	1.48	1.35
1	S2	814	5MU	C6-C5	-11.90	1.15	1.34
1	S2	159	A2M	O4'-C1'	11.88	1.56	1.40
1	S2	822	PSU	C6-C5	11.70	1.48	1.35
1	S2	166	A2M	O4'-C1'	11.68	1.56	1.40
1	S2	1243	PSU	C6-C5	11.56	1.48	1.35
1	S2	1678	A2M	O4'-C1'	11.55	1.56	1.40
1	S2	612	PSU	C6-C5	11.42	1.47	1.35
1	S2	119	PSU	C6-C5	11.38	1.47	1.35
1	S2	27	A2M	O4'-C1'	11.34	1.55	1.40
1	S2	1219	B8Q	C4-N3	11.20	1.65	1.48
1	S2	484	A2M	O4'-C1'	11.09	1.55	1.40
1	S2	1219	B8Q	C6-C5	11.01	1.56	1.33
1	S2	1031	A2M	O4'-C1'	10.99	1.55	1.40
1	S2	814	5MU	C4-N3	-10.98	1.18	1.38
1	S2	1081	PSU	C6-C5	10.87	1.47	1.35
1	S2	668	A2M	O4'-C1'	10.74	1.55	1.40
1	S2	668	A2M	C3'-C4'	-10.30	1.26	1.53
1	S2	166	A2M	C3'-C4'	-10.17	1.27	1.53
1	S2	1678	A2M	C3'-C4'	-10.14	1.27	1.53
1	S2	1031	A2M	C3'-C4'	-10.13	1.27	1.53
1	S2	484	A2M	C3'-C4'	-9.93	1.27	1.53
1	S2	1219	B8Q	C2-N1	9.93	1.52	1.38
1	S2	159	A2M	C3'-C4'	-9.91	1.27	1.53
1	S2	27	A2M	C3'-C4'	-9.87	1.28	1.53
1	S2	612	PSU	C2-N1	9.73	1.49	1.36
1	S2	822	PSU	C2-N1	9.53	1.49	1.36
1	S2	119	PSU	C2-N1	9.52	1.49	1.36
1	S2	1243	PSU	C2-N1	9.16	1.48	1.36
1	S2	1081	PSU	C2-N1	9.07	1.48	1.36
1	S2	823	PSU	C2-N1	8.81	1.48	1.36
1	S2	1374	5MC	C6-C5	8.69	1.48	1.34
1	S2	174	OMC	C4-N4	8.40	1.54	1.33
1	S2	116	OMU	C2-N1	8.36	1.51	1.38
1	S2	1710	OMC	C4-N4	8.32	1.54	1.33
1	S2	1703	OMC	C4-N4	8.28	1.54	1.33
1	S2	121	OMU	C2-N1	8.20	1.51	1.38
1	S2	517	OMC	C4-N4	8.11	1.53	1.33
1	S2	823	PSU	C2-N3	7.98	1.50	1.37
1	S2	568	E3C	C6-C5	7.97	1.49	1.33
1	S2	568	E3C	C2-N3	7.96	1.47	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	S2	1248	B8N	C4-N3	-7.93	1.26	1.40
1	S2	1830	UR3	C2-N1	7.71	1.49	1.38
1	S2	568	E3C	C2-N1	7.62	1.49	1.38
1	S2	1337	4AC	C4-N3	7.48	1.45	1.32
1	S2	1248	B8N	C6-N1	7.43	1.54	1.36
1	S2	822	PSU	C2-N3	7.26	1.49	1.37
1	S2	1842	4AC	C4-N3	7.23	1.45	1.32
1	S2	119	PSU	C2-N3	7.08	1.49	1.37
1	S2	1243	PSU	C2-N3	7.05	1.49	1.37
1	S2	612	PSU	C2-N3	6.98	1.49	1.37
1	S2	1248	B8N	C4-C5	6.93	1.63	1.47
1	S2	174	OMC	C2-N3	6.76	1.49	1.36
1	S2	1710	OMC	C2-N3	6.73	1.49	1.36
1	S2	174	OMC	C6-C5	6.66	1.50	1.35
1	S2	1703	OMC	C6-C5	6.66	1.50	1.35
1	S2	1081	PSU	C2-N3	6.61	1.48	1.37
1	S2	517	OMC	C2-N3	6.59	1.49	1.36
1	S2	1710	OMC	C6-C5	6.59	1.50	1.35
1	S2	1703	OMC	C2-N3	6.58	1.49	1.36
1	S2	121	OMU	C2-N3	6.54	1.49	1.38
1	S2	116	OMU	C2-N3	6.47	1.49	1.38
1	S2	517	OMC	C6-C5	6.42	1.50	1.35
1	S2	1374	5MC	C4-N3	6.31	1.44	1.34
1	S2	1678	A2M	C3'-C2'	6.17	1.66	1.53
1	S2	1337	4AC	C6-C5	6.12	1.49	1.35
1	S2	517	OMC	C4-N3	6.06	1.46	1.34
1	S2	174	OMC	C4-N3	6.05	1.46	1.34
1	S2	1710	OMC	C4-N3	6.05	1.46	1.34
1	S2	121	OMU	C6-C5	6.00	1.49	1.35
1	S2	116	OMU	C6-C5	6.00	1.49	1.35
1	S2	159	A2M	C3'-C2'	5.97	1.66	1.53
1	S2	668	A2M	C3'-C2'	5.95	1.66	1.53
1	S2	1374	5MC	C2-N3	5.84	1.47	1.36
1	S2	1337	4AC	C2-N3	5.79	1.47	1.36
1	S2	1842	4AC	C6-C5	5.77	1.48	1.35
1	S2	166	A2M	C3'-C2'	5.74	1.65	1.53
1	S2	1703	OMC	C4-N3	5.70	1.45	1.34
1	S2	1830	UR3	C6-C5	5.69	1.48	1.35
1	S2	1248	B8N	C2-N1	5.66	1.55	1.39
1	S2	1374	5MC	C5-C4	5.60	1.48	1.44
1	S2	509	OMG	C2-N3	5.54	1.46	1.33
1	S2	1842	4AC	C2-N3	5.50	1.47	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	S2	27	A2M	C3'-C2'	5.41	1.64	1.53
1	S2	1031	A2M	C3'-C2'	5.39	1.64	1.53
1	S2	484	A2M	C3'-C2'	5.38	1.64	1.53
1	S2	814	5MU	C2-N3	5.32	1.47	1.38
1	S2	1219	B8Q	C2-N3	-5.25	1.25	1.35
1	S2	683	OMG	C2-N3	5.22	1.45	1.33
1	S2	644	OMG	C2-N3	5.22	1.45	1.33
1	S2	823	PSU	O2-C2	-5.07	1.12	1.23
1	S2	568	E3C	C4-N3	5.07	1.56	1.48
1	S2	1081	PSU	O2-C2	-5.05	1.12	1.23
1	S2	683	OMG	C4-N3	5.01	1.49	1.37
1	S2	1081	PSU	O4-C4	-4.99	1.14	1.23
1	S2	612	PSU	O2-C2	-4.99	1.12	1.23
1	S2	509	OMG	C4-N3	4.98	1.49	1.37
1	S2	1243	PSU	O2-C2	-4.96	1.12	1.23
1	S2	1851	MA6	C6-C5	-4.94	1.37	1.44
1	S2	1678	A2M	O4'-C4'	4.94	1.56	1.45
1	S2	822	PSU	O2-C2	-4.90	1.13	1.23
1	S2	159	A2M	O4'-C4'	4.90	1.55	1.45
1	S2	1830	UR3	C2-N3	4.85	1.48	1.39
1	S2	166	A2M	O4'-C4'	4.84	1.55	1.45
1	S2	612	PSU	O4-C4	-4.83	1.14	1.23
1	S2	119	PSU	O2-C2	-4.83	1.13	1.23
1	S2	644	OMG	C2-N2	4.83	1.45	1.34
1	S2	1248	B8N	C6-C5	4.82	1.42	1.35
1	S2	644	OMG	C4-N3	4.81	1.48	1.37
1	S2	27	A2M	O4'-C4'	4.77	1.55	1.45
1	S2	1243	PSU	O4-C4	-4.76	1.14	1.23
1	S2	1850	MA6	C6-C5	-4.76	1.37	1.44
1	S2	119	PSU	O4-C4	-4.72	1.14	1.23
1	S2	484	A2M	O4'-C4'	4.72	1.55	1.45
1	S2	822	PSU	O4-C4	-4.71	1.14	1.23
1	S2	1678	A2M	C6-N6	4.70	1.50	1.34
1	S2	509	OMG	C2-N2	4.67	1.45	1.34
1	S2	1806	M7A	C6-N6	4.67	1.46	1.34
1	S2	683	OMG	C2-N2	4.67	1.45	1.34
1	S2	1337	4AC	C2-N1	4.62	1.49	1.40
1	S2	1337	4AC	C4-N4	4.62	1.46	1.39
1	S2	1337	4AC	C7-N4	4.61	1.46	1.37
1	S2	1031	A2M	O4'-C4'	4.59	1.55	1.45
1	S2	121	OMU	C4-N3	4.58	1.46	1.38
1	S2	1219	B8Q	C4-C5	-4.58	1.39	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	S2	1842	4AC	C2-N1	4.51	1.49	1.40
1	S2	116	OMU	C4-N3	4.48	1.46	1.38
1	S2	1374	5MC	C4-N4	4.39	1.45	1.34
1	S2	1842	4AC	C7-N4	4.37	1.46	1.37
1	S2	1337	4AC	C5-C4	4.34	1.50	1.41
1	S2	668	A2M	O4'-C4'	4.33	1.54	1.45
1	S2	1374	5MC	C6-N1	4.23	1.45	1.38
1	S2	1710	OMC	C2-N1	4.16	1.48	1.40
1	S2	822	PSU	C6-N1	4.15	1.43	1.36
1	S2	166	A2M	C6-N6	4.05	1.48	1.34
1	S2	159	A2M	C6-N6	4.03	1.48	1.34
1	S2	174	OMC	C2-N1	4.03	1.48	1.40
1	S2	814	5MU	C2-N1	4.02	1.44	1.38
1	S2	119	PSU	C6-N1	4.02	1.42	1.36
1	S2	1850	MA6	C6-N6	4.01	1.46	1.37
1	S2	484	A2M	C6-N6	4.01	1.48	1.34
1	S2	1243	PSU	C6-N1	4.00	1.42	1.36
1	S2	517	OMC	C2-N1	3.98	1.48	1.40
1	S2	1842	4AC	C4-N4	3.98	1.45	1.39
1	S2	668	A2M	C6-N6	3.96	1.48	1.34
1	S2	1031	A2M	C6-N6	3.96	1.48	1.34
1	S2	1374	5MC	C2-N1	3.96	1.48	1.40
1	S2	612	PSU	C6-N1	3.93	1.42	1.36
1	S2	1337	4AC	C6-N1	3.93	1.47	1.38
1	S2	1842	4AC	C6-N1	3.92	1.47	1.38
1	S2	27	A2M	C6-N6	3.91	1.48	1.34
1	S2	1806	M7A	C5-N7	3.91	1.48	1.39
1	S2	1842	4AC	C5-C4	3.90	1.49	1.41
1	S2	1703	OMC	C2-N1	3.90	1.48	1.40
1	S2	1081	PSU	C6-N1	3.88	1.42	1.36
1	S2	174	OMC	C6-N1	3.82	1.47	1.38
1	S2	1851	MA6	C6-N6	3.74	1.46	1.37
1	S2	1710	OMC	C6-N1	3.73	1.47	1.38
1	S2	517	OMC	C6-N1	3.73	1.47	1.38
1	S2	823	PSU	C4-N3	3.72	1.45	1.38
1	S2	1832	6MZ	C6-C5	-3.64	1.39	1.44
1	S2	1703	OMC	C6-N1	3.59	1.46	1.38
1	S2	1830	UR3	C5-C4	3.51	1.52	1.43
1	S2	1830	UR3	C4-N3	3.35	1.47	1.40
1	S2	823	PSU	C6-N1	3.27	1.41	1.36
1	S2	644	OMG	C6-N1	3.12	1.42	1.37
1	S2	683	OMG	C5-C6	3.07	1.53	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	S2	509	OMG	C6-N1	3.04	1.42	1.37
1	S2	683	OMG	C6-N1	3.03	1.42	1.37
1	S2	644	OMG	C5-C4	-3.03	1.35	1.43
1	S2	822	PSU	C4-N3	3.03	1.44	1.38
1	S2	509	OMG	C5-C6	2.98	1.53	1.47
1	S2	119	PSU	C4-N3	2.94	1.44	1.38
1	S2	1219	B8Q	C31-N3	2.93	1.52	1.46
1	S2	568	E3C	C6-N1	2.91	1.45	1.38
1	S2	823	PSU	O4-C4	-2.90	1.18	1.23
1	S2	1374	5MC	O2-C2	-2.86	1.18	1.23
1	S2	644	OMG	C5-C6	2.81	1.53	1.47
1	S2	1830	UR3	O2-C2	-2.81	1.17	1.22
1	S2	683	OMG	C5-C4	-2.75	1.36	1.43
1	S2	121	OMU	C6-N1	2.75	1.44	1.38
1	S2	509	OMG	C5-C4	-2.74	1.36	1.43
1	S2	568	E3C	C31-N3	2.72	1.54	1.47
1	S2	116	OMU	C6-N1	2.71	1.44	1.38
1	S2	1081	PSU	C4-N3	2.70	1.43	1.38
1	S2	1243	PSU	C4-N3	2.68	1.43	1.38
1	S2	1703	OMC	O2-C2	-2.62	1.18	1.23
1	S2	612	PSU	C4-N3	2.61	1.43	1.38
1	S2	683	OMG	C2-N1	2.57	1.43	1.37
1	S2	644	OMG	C2-N1	2.52	1.43	1.37
1	S2	1830	UR3	C6-N1	2.51	1.44	1.38
1	S2	823	PSU	O4'-C1'	-2.49	1.40	1.43
1	S2	1219	B8Q	C6-N1	-2.44	1.32	1.38
1	S2	1832	6MZ	C2-N3	2.43	1.35	1.32
1	S2	509	OMG	C2-N1	2.42	1.43	1.37
1	S2	568	E3C	C4-C5	-2.42	1.44	1.49
1	S2	1710	OMC	O2-C2	-2.41	1.19	1.23
1	S2	484	A2M	C2-N3	2.41	1.35	1.32
1	S2	1248	B8N	O4-C4	-2.37	1.18	1.23
1	S2	814	5MU	O4-C4	-2.35	1.19	1.23
1	S2	517	OMC	O2-C2	-2.34	1.19	1.23
1	S2	174	OMC	C5-C4	2.29	1.48	1.42
1	S2	814	5MU	O2-C2	-2.29	1.19	1.23
1	S2	174	OMC	O2-C2	-2.29	1.19	1.23
1	S2	822	PSU	O4'-C1'	-2.28	1.40	1.43
1	S2	1710	OMC	C5-C4	2.27	1.48	1.42
1	S2	1842	4AC	O2-C2	-2.23	1.19	1.23
1	S2	166	A2M	C2-N3	2.22	1.35	1.32
1	S2	1703	OMC	C5-C4	2.18	1.48	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	S2	1832	6MZ	C9-N6	2.17	1.48	1.45
1	S2	1081	PSU	O4'-C1'	-2.15	1.40	1.43
1	S2	1248	B8N	O4'-C1'	-2.15	1.40	1.43
1	S2	121	OMU	O4-C4	-2.13	1.20	1.24
1	S2	683	OMG	O6-C6	-2.11	1.18	1.23
1	S2	1337	4AC	O2-C2	-2.09	1.19	1.23
1	S2	644	OMG	O6-C6	-2.08	1.18	1.23
1	S2	509	OMG	O6-C6	-2.08	1.18	1.23
1	S2	116	OMU	O4-C4	-2.06	1.20	1.24
1	S2	517	OMC	C5-C4	2.04	1.47	1.42
1	S2	612	PSU	O4'-C1'	-2.01	1.41	1.43

All (160) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	S2	1851	MA6	N1-C6-N6	-12.87	101.97	116.83
1	S2	1850	MA6	N1-C6-N6	-12.61	102.27	116.83
1	S2	1806	M7A	C5-C6-N6	10.71	141.95	123.75
1	S2	814	5MU	C5-C4-N3	9.71	123.76	115.32
1	S2	668	A2M	C1'-N9-C4	-9.42	110.09	126.64
1	S2	1806	M7A	N6-C6-N1	-9.37	97.51	118.38
1	S2	1031	A2M	C1'-N9-C4	-9.09	110.67	126.64
1	S2	27	A2M	C1'-N9-C4	-8.73	111.30	126.64
1	S2	484	A2M	C1'-N9-C4	-8.72	111.33	126.64
1	S2	668	A2M	C5-C6-N6	8.70	133.57	120.31
1	S2	1678	A2M	C5-C6-N6	8.65	133.49	120.31
1	S2	1678	A2M	C1'-N9-C4	-8.53	111.65	126.64
1	S2	484	A2M	C5-C6-N6	8.31	132.98	120.31
1	S2	159	A2M	C5-C6-N6	8.28	132.93	120.31
1	S2	166	A2M	C5-C6-N6	8.14	132.71	120.31
1	S2	27	A2M	C5-C6-N6	8.09	132.64	120.31
1	S2	1031	A2M	C5-C6-N6	8.03	132.54	120.31
1	S2	159	A2M	C1'-N9-C4	-7.99	112.61	126.64
1	S2	166	A2M	C1'-N9-C4	-7.97	112.63	126.64
1	S2	1830	UR3	C1'-N1-C2	7.62	129.52	117.04
1	S2	568	E3C	C1'-N1-C2	7.53	129.36	117.04
1	S2	1031	A2M	N3-C2-N1	-7.16	118.96	128.67
1	S2	814	5MU	C5-C6-N1	-7.12	115.57	123.31
1	S2	27	A2M	N3-C2-N1	-7.11	119.01	128.67
1	S2	814	5MU	C4-N3-C2	-7.01	118.15	127.34
1	S2	1830	UR3	C6-N1-C2	-6.99	116.09	121.80
1	S2	668	A2M	N3-C2-N1	-6.90	119.31	128.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	S2	159	A2M	N3-C2-N1	-6.64	119.66	128.67
1	S2	1850	MA6	N3-C2-N1	-6.63	119.67	128.67
1	S2	1832	6MZ	N3-C2-N1	-6.47	119.89	128.67
1	S2	1830	UR3	O2-C2-N3	-6.42	112.45	121.33
1	S2	1851	MA6	N3-C2-N1	-6.37	120.03	128.67
1	S2	166	A2M	N3-C2-N1	-6.34	120.07	128.67
1	S2	484	A2M	N3-C2-N1	-6.16	120.32	128.67
1	S2	823	PSU	O2-C2-N1	-6.15	116.45	122.79
1	S2	1678	A2M	N3-C2-N1	-6.07	120.43	128.67
1	S2	1806	M7A	N3-C4-N9	5.94	134.31	126.88
1	S2	166	A2M	C4'-O4'-C1'	-5.73	104.68	109.92
1	S2	27	A2M	C4'-O4'-C1'	-5.71	104.70	109.92
1	S2	1806	M7A	N3-C2-N1	-5.67	120.00	128.58
1	S2	668	A2M	N6-C6-N1	-5.67	106.23	118.33
1	S2	814	5MU	N3-C2-N1	5.54	122.11	114.89
1	S2	484	A2M	N6-C6-N1	-5.51	106.56	118.33
1	S2	159	A2M	N6-C6-N1	-5.51	106.57	118.33
1	S2	612	PSU	N1-C2-N3	5.49	120.96	115.17
1	S2	568	E3C	O2-C2-N3	-5.40	115.19	122.10
1	S2	823	PSU	C6-N1-C2	-5.37	117.71	122.69
1	S2	1248	B8N	C5-C4-N3	5.31	125.80	116.15
1	S2	612	PSU	C4-N3-C2	-5.30	119.07	126.37
1	S2	27	A2M	N6-C6-N1	-5.30	107.01	118.33
1	S2	166	A2M	N6-C6-N1	-5.30	107.01	118.33
1	S2	1832	6MZ	C2-N1-C6	5.28	120.70	116.60
1	S2	1850	MA6	C1'-N9-C4	5.28	135.92	126.64
1	S2	1031	A2M	C4'-O4'-C1'	-5.27	105.10	109.92
1	S2	1806	M7A	C4-N9-C1'	-5.17	114.58	126.63
1	S2	823	PSU	N1-C2-N3	5.16	120.61	115.17
1	S2	1830	UR3	C3U-N3-C4	5.04	124.85	117.87
1	S2	814	5MU	C5M-C5-C6	-4.99	116.10	122.85
1	S2	1031	A2M	N6-C6-N1	-4.98	107.69	118.33
1	S2	1678	A2M	N6-C6-N1	-4.91	107.84	118.33
1	S2	1248	B8N	C4-N3-C2	-4.84	119.66	125.62
1	S2	121	OMU	C4-N3-C2	-4.77	120.69	126.61
1	S2	484	A2M	C4'-O4'-C1'	-4.74	105.59	109.92
1	S2	1219	B8Q	N3-C2-N1	4.69	123.69	117.16
1	S2	1850	MA6	C2-N1-C6	4.58	121.33	116.84
1	S2	1219	B8Q	C31-N3-C4	4.56	122.66	114.76
1	S2	116	OMU	C4-N3-C2	-4.54	120.97	126.61
1	S2	119	PSU	N1-C2-N3	4.52	119.94	115.17
1	S2	668	A2M	C4'-O4'-C1'	-4.49	105.81	109.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	S2	1243	PSU	C4-N3-C2	-4.48	120.19	126.37
1	S2	1678	A2M	C4'-O4'-C1'	-4.48	105.82	109.92
1	S2	159	A2M	C4'-O4'-C1'	-4.47	105.83	109.92
1	S2	119	PSU	C4-N3-C2	-4.43	120.26	126.37
1	S2	822	PSU	N1-C2-N3	4.42	119.83	115.17
1	S2	1830	UR3	C4-N3-C2	-4.38	121.05	124.58
1	S2	1243	PSU	N1-C2-N3	4.38	119.78	115.17
1	S2	822	PSU	C4-N3-C2	-4.37	120.35	126.37
1	S2	568	E3C	C6-N1-C2	-4.35	118.24	121.80
1	S2	1081	PSU	C4-N3-C2	-4.32	120.42	126.37
1	S2	1851	MA6	C2-N1-C6	4.17	120.93	116.84
1	S2	814	5MU	C5M-C5-C4	4.05	123.10	118.78
1	S2	612	PSU	C6-C5-C4	4.04	120.90	118.17
1	S2	612	PSU	C6-N1-C2	-4.03	118.95	122.69
1	S2	823	PSU	C4-N3-C2	-4.00	120.85	126.37
1	S2	1081	PSU	N1-C2-N3	3.98	119.36	115.17
1	S2	1248	B8N	C1'-C5-C4	3.95	123.60	117.61
1	S2	568	E3C	C1'-N1-C6	-3.94	112.36	120.78
1	S2	121	OMU	N3-C2-N1	3.80	119.84	114.89
1	S2	814	5MU	O4-C4-C5	-3.78	120.60	124.92
1	S2	119	PSU	C6-N1-C2	-3.74	119.22	122.69
1	S2	822	PSU	C6-N1-C2	-3.73	119.23	122.69
1	S2	1219	B8Q	O2-C2-N3	-3.72	117.73	122.95
1	S2	1851	MA6	C1'-N9-C4	3.64	133.04	126.64
1	S2	1248	B8N	N3-C2-N1	3.59	121.11	116.72
1	S2	116	OMU	N3-C2-N1	3.57	119.54	114.89
1	S2	1243	PSU	C6-N1-C2	-3.57	119.38	122.69
1	S2	644	OMG	C8-N7-C5	3.45	108.43	102.55
1	S2	509	OMG	C2-N1-C6	-3.41	118.87	125.11
1	S2	1248	B8N	C31-N3-C4	3.38	121.97	117.18
1	S2	814	5MU	C6-C5-C4	3.37	120.80	118.02
1	S2	121	OMU	C5-C4-N3	3.36	119.50	114.80
1	S2	509	OMG	C5-C6-N1	3.32	120.41	114.07
1	S2	509	OMG	C8-N7-C5	3.32	108.20	102.55
1	S2	1806	M7A	C71-N7-C5	-3.28	109.77	123.44
1	S2	1830	UR3	C1'-N1-C6	-3.27	113.79	120.78
1	S2	1806	M7A	C2-N3-C4	3.24	119.75	111.83
1	S2	116	OMU	C5-C4-N3	3.24	119.33	114.80
1	S2	568	E3C	C31-N3-C2	3.22	121.53	117.49
1	S2	683	OMG	C8-N7-C5	3.20	107.99	102.55
1	S2	1081	PSU	C6-N1-C2	-3.16	119.76	122.69
1	S2	121	OMU	C1'-N1-C2	3.14	123.23	117.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	S2	568	E3C	C4-N3-C2	-3.13	116.36	122.00
1	S2	644	OMG	C5-C6-N1	3.12	120.02	114.07
1	S2	644	OMG	C2-N1-C6	-3.11	119.42	125.11
1	S2	683	OMG	C5-C6-N1	3.09	119.96	114.07
1	S2	683	OMG	C2-N1-C6	-3.02	119.59	125.11
1	S2	121	OMU	O4-C4-C5	-3.00	119.98	125.16
1	S2	823	PSU	C6-C5-C4	3.00	120.20	118.17
1	S2	159	A2M	O2'-C2'-C1'	2.97	114.75	109.00
1	S2	814	5MU	O3'-C3'-C2'	2.87	121.03	111.82
1	S2	822	PSU	O2-C2-N1	-2.86	119.83	122.79
1	S2	1337	4AC	C6-C5-C4	2.79	120.36	117.00
1	S2	668	A2M	C3'-C2'-C1'	2.79	108.15	102.81
1	S2	1219	B8Q	C31-N3-C2	2.77	122.05	117.70
1	S2	1337	4AC	C5-C4-N3	-2.71	118.36	122.60
1	S2	1806	M7A	C5-C4-N3	-2.71	120.29	126.56
1	S2	1243	PSU	O2-C2-N1	-2.66	120.04	122.79
1	S2	612	PSU	O2-C2-N1	-2.66	120.05	122.79
1	S2	1248	B8N	O4-C4-C5	-2.62	118.05	122.58
1	S2	116	OMU	O4-C4-C5	-2.59	120.70	125.16
1	S2	484	A2M	C3'-C2'-C1'	2.58	107.74	102.81
1	S2	1374	5MC	C5-C6-N1	-2.55	120.54	123.31
1	S2	1842	4AC	C6-C5-C4	2.53	120.05	117.00
1	S2	119	PSU	O2-C2-N1	-2.52	120.19	122.79
1	S2	814	5MU	O2-C2-N1	-2.51	119.53	122.80
1	S2	121	OMU	C6-N1-C2	-2.48	117.98	121.00
1	S2	484	A2M	O3'-C3'-C2'	-2.43	104.38	111.19
1	S2	1842	4AC	C5-C4-N3	-2.42	118.81	122.60
1	S2	814	5MU	O4-C4-N3	-2.38	115.64	120.11
1	S2	1248	B8N	O4-C4-N3	-2.36	116.15	119.99
1	S2	119	PSU	C6-C5-C4	2.26	119.70	118.17
1	S2	1830	UR3	O4-C4-N3	2.25	122.40	119.66
1	S2	1842	4AC	O2-C2-N3	-2.24	118.79	122.33
1	S2	116	OMU	C1'-N1-C2	2.23	121.60	117.59
1	S2	116	OMU	C6-N1-C2	-2.23	118.28	121.00
1	S2	814	5MU	O3'-C3'-C4'	2.20	117.41	111.08
1	S2	509	OMG	O6-C6-C5	-2.19	119.97	124.32
1	S2	1248	B8N	O4'-C1'-C2'	2.18	108.16	105.15
1	S2	612	PSU	O4'-C1'-C2'	2.14	108.12	105.15
1	S2	1830	UR3	C6-C5-C4	2.14	124.83	120.73
1	S2	1842	4AC	C5-C4-N4	2.14	126.55	122.94
1	S2	644	OMG	O6-C6-C5	-2.14	120.08	124.32
1	S2	1374	5MC	CM5-C5-C6	-2.14	119.96	122.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	S2	668	A2M	C2'-C3'-C4'	2.10	106.51	101.99
1	S2	1832	6MZ	C6-C5-C4	2.08	119.88	117.68
1	S2	159	A2M	C3'-C2'-C1'	2.06	106.74	102.81
1	S2	1703	OMC	O2-C2-N3	-2.04	119.11	122.33
1	S2	1243	PSU	C6-C5-C4	2.04	119.55	118.17
1	S2	1337	4AC	O2-C2-N3	-2.00	119.17	122.33
1	S2	1842	4AC	O7-C7-CM7	-2.00	118.49	122.05

There are no chirality outliers.

All (51) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	S2	27	A2M	C1'-C2'-O2'-CM'
1	S2	116	OMU	O4'-C4'-C5'-O5'
1	S2	121	OMU	O4'-C4'-C5'-O5'
1	S2	159	A2M	C1'-C2'-O2'-CM'
1	S2	509	OMG	C1'-C2'-O2'-CM2
1	S2	568	E3C	O4'-C1'-N1-C2
1	S2	568	E3C	O4'-C1'-N1-C6
1	S2	568	E3C	C3'-C4'-C5'-O5'
1	S2	568	E3C	O4'-C4'-C5'-O5'
1	S2	822	PSU	O4'-C4'-C5'-O5'
1	S2	1031	A2M	C1'-C2'-O2'-CM'
1	S2	1678	A2M	C1'-C2'-O2'-CM'
1	S2	1830	UR3	O4'-C1'-N1-C6
1	S2	1830	UR3	O4'-C1'-N1-C2
1	S2	1832	6MZ	C5-C6-N6-C9
1	S2	1832	6MZ	N1-C6-N6-C9
1	S2	1850	MA6	O4'-C4'-C5'-O5'
1	S2	1850	MA6	C3'-C4'-C5'-O5'
1	S2	1851	MA6	O4'-C4'-C5'-O5'
1	S2	116	OMU	C3'-C4'-C5'-O5'
1	S2	119	PSU	O4'-C4'-C5'-O5'
1	S2	121	OMU	C3'-C4'-C5'-O5'
1	S2	159	A2M	O4'-C4'-C5'-O5'
1	S2	668	A2M	C3'-C4'-C5'-O5'
1	S2	683	OMG	C3'-C4'-C5'-O5'
1	S2	1830	UR3	O4'-C4'-C5'-O5'
1	S2	822	PSU	C3'-C4'-C5'-O5'
1	S2	668	A2M	O4'-C4'-C5'-O5'
1	S2	823	PSU	C3'-C4'-C5'-O5'
1	S2	1219	B8Q	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
1	S2	683	OMG	O4'-C4'-C5'-O5'
1	S2	823	PSU	O4'-C4'-C5'-O5'
1	S2	1851	MA6	C3'-C4'-C5'-O5'
1	S2	119	PSU	C3'-C4'-C5'-O5'
1	S2	159	A2M	C3'-C4'-C5'-O5'
1	S2	1703	OMC	O4'-C4'-C5'-O5'
1	S2	1830	UR3	C3'-C4'-C5'-O5'
1	S2	1806	M7A	C3'-C4'-C5'-O5'
1	S2	1243	PSU	O4'-C4'-C5'-O5'
1	S2	1243	PSU	C3'-C4'-C5'-O5'
1	S2	1851	MA6	C5-C6-N6-C9
1	S2	1806	M7A	C2'-C1'-N9-C8
1	S2	1806	M7A	O4'-C4'-C5'-O5'
1	S2	116	OMU	C3'-C2'-O2'-CM2
1	S2	121	OMU	C4'-C5'-O5'-P
1	S2	612	PSU	O4'-C1'-C5-C4
1	S2	823	PSU	O4'-C1'-C5-C4
1	S2	644	OMG	C4'-C5'-O5'-P
1	S2	1851	MA6	C4'-C5'-O5'-P
1	S2	1219	B8Q	C3'-C4'-C5'-O5'
1	S2	1703	OMC	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 38 ligands modelled in this entry, 37 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
86	MVM	y	101	-	32,35,35	1.67	5 (15%)	39,49,49	2.21	13 (33%)

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
86	MVM	y	101	-	-	1/20/28/28	0/5/5/5

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	y	101	MVM	C5-N1	5.54	1.45	1.37
86	y	101	MVM	N5-N4	-3.98	1.31	1.37
86	y	101	MVM	C6-N1	2.28	1.44	1.39
86	y	101	MVM	C20-C19	2.10	1.41	1.36
86	y	101	MVM	O1-C5	-2.10	1.18	1.22

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	y	101	MVM	C21-N7-C22	5.16	122.98	116.81
86	y	101	MVM	C1-C9-N1	-4.39	105.14	116.16
86	y	101	MVM	C6-N1-C5	-4.19	117.92	122.94
86	y	101	MVM	C15-N4-C22	-4.15	124.76	130.09
86	y	101	MVM	C6-N1-C9	3.90	124.19	118.40
86	y	101	MVM	C19-C18-N6	3.33	135.62	130.19
86	y	101	MVM	C15-N4-N5	3.26	125.17	119.95
86	y	101	MVM	C20-C21-N7	-3.26	119.19	123.97
86	y	101	MVM	C8-N3-C6	3.24	122.38	115.05
86	y	101	MVM	N6-N5-N4	3.23	109.96	106.37
86	y	101	MVM	C12-C5-N1	3.20	122.60	118.36
86	y	101	MVM	N3-C6-N1	2.43	118.95	116.35
86	y	101	MVM	C10-C8-N3	-2.37	119.67	123.42

There are no chirality outliers.

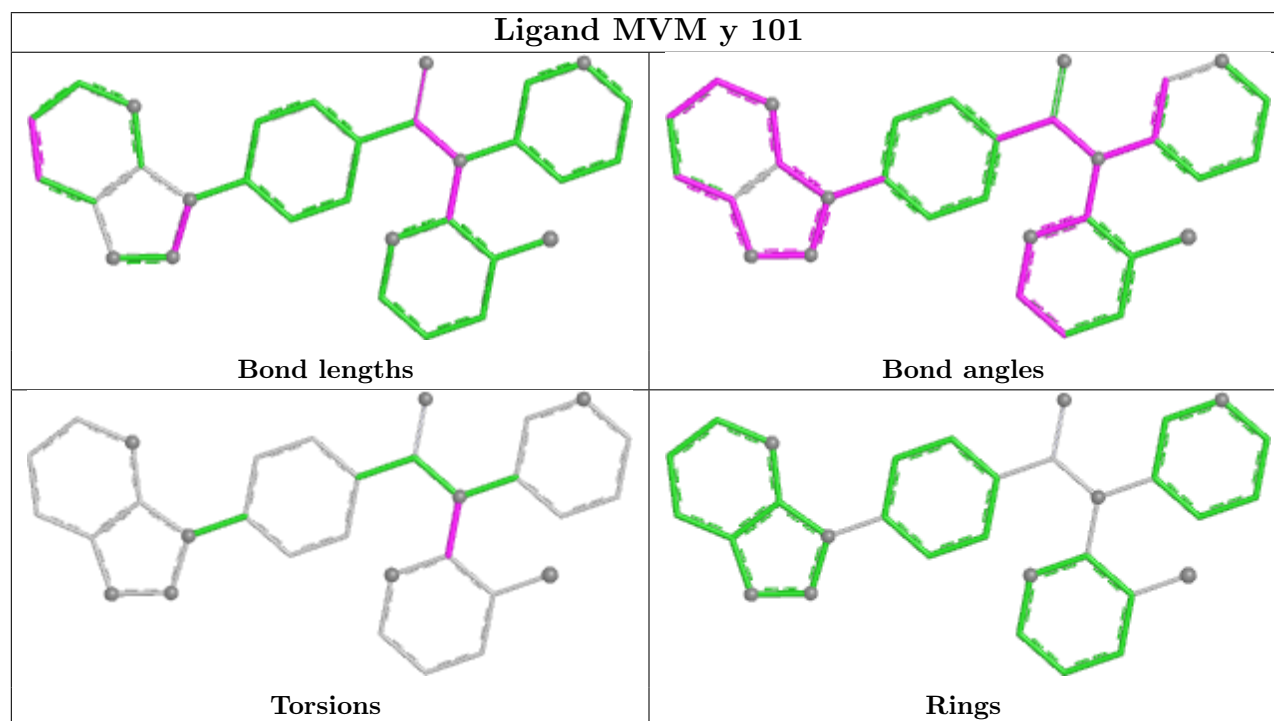
All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
86	y	101	MVM	C2-C6-N1-C5

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

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Mol	Chain	Number of breaks
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Mol	Chain	Number of breaks
79	t	16
1	S2	5
81	v	4
63	c	1
80	u	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	S2	753:C	O3'	785:C	P	26.07
1	t	750:G	O3'	890:C	P	19.83
1	t	3919:C	O3'	4035:G	P	18.64
1	t	517:C	O3'	629:G	P	17.24
1	t	1680:C	O3'	1699:C	P	16.67
1	t	4737:G	O3'	4815:C	P	16.14
1	t	976:U	O3'	1047:G	P	16.09
1	S2	1752:C	O3'	1779:G	P	15.93
1	t	1089:A	O3'	1145:G	P	15.88
1	t	1202:G	O3'	1216:G	P	15.83
1	t	2881:G	O3'	3569:C	P	15.53
1	t	2093:C	O3'	2228:C	P	14.20
1	S2	698:G	O3'	730:C	P	12.55
1	t	1253:A	O3'	1256:G	P	12.43
1	S2	739:C	O3'	746:C	P	11.53
1	S2	225:G	O3'	287:U	P	7.17
1	c	119:CYS	C	120:ARG	N	6.89
1	t	945:G	O3'	946:G	P	6.52
1	v	17:A	O3'	18:G	P	5.45
1	t	4734:C	O3'	4735:C	P	4.84
1	v	10:G	O3'	11:C	P	4.62
1	u	54:U	O3'	55:U	P	4.13
1	v	21:A	O3'	22:G	P	3.75
1	t	964:C	O3'	965:G	P	3.41
1	t	1938:U	O3'	1939:A	P	3.38
1	t	4817:G	O3'	4818:G	P	3.31
1	v	41:C	O3'	42:C	P	3.22

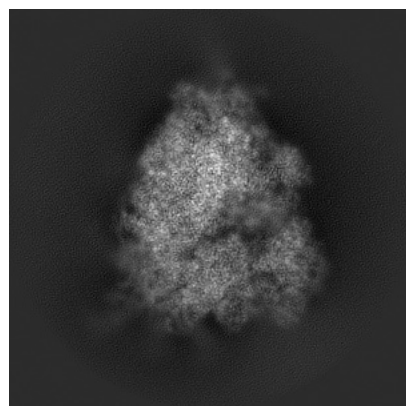
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0600. These allow visual inspection of the internal detail of the map and identification of artifacts.

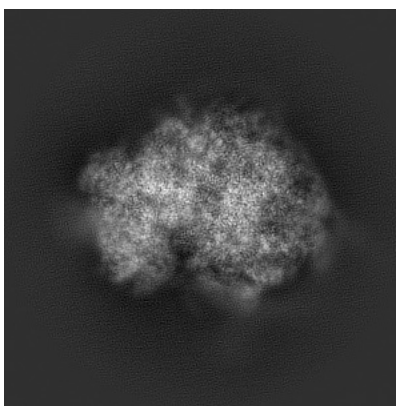
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

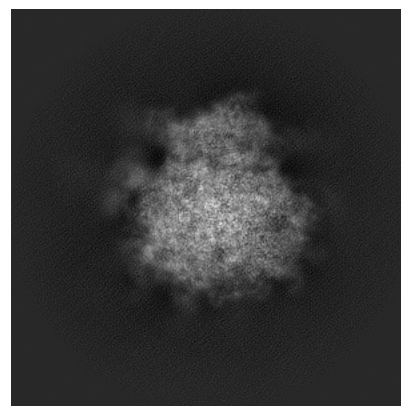
6.1.1 Primary map



X

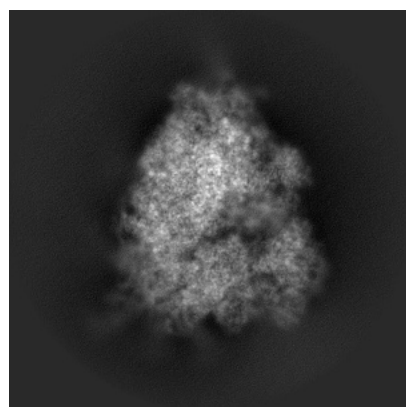


Y

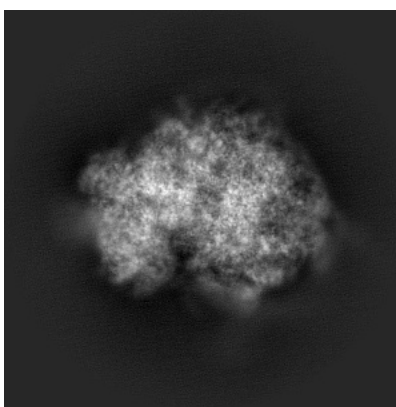


Z

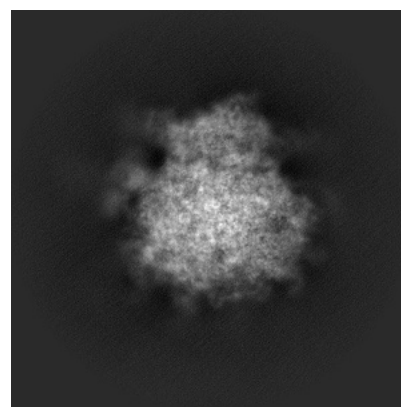
6.1.2 Raw map



X



Y

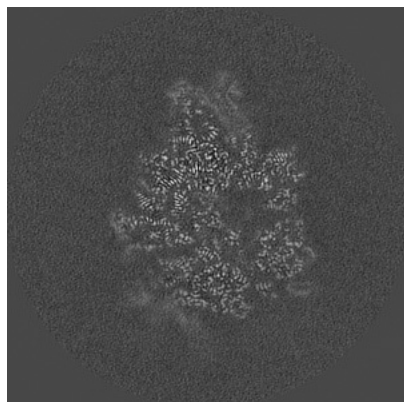


Z

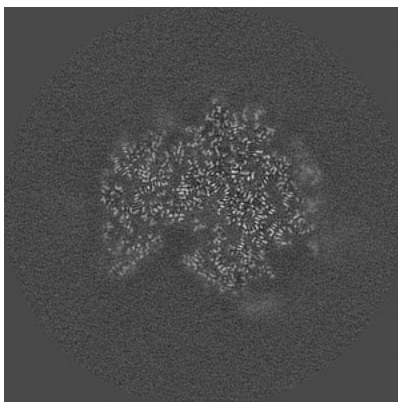
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

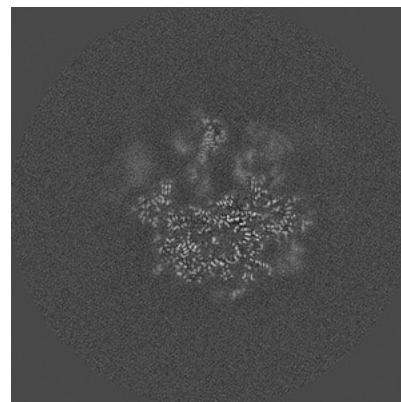
6.2.1 Primary map



X Index: 200

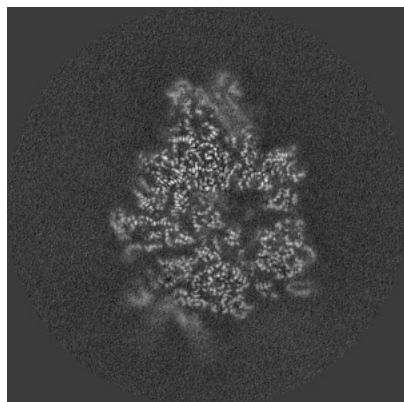


Y Index: 200

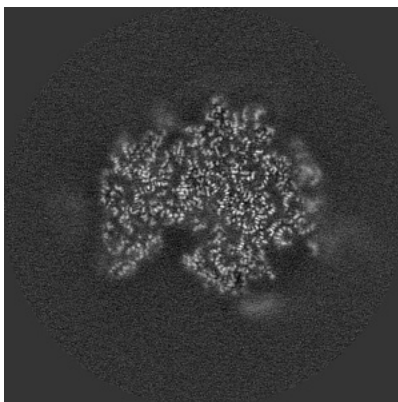


Z Index: 200

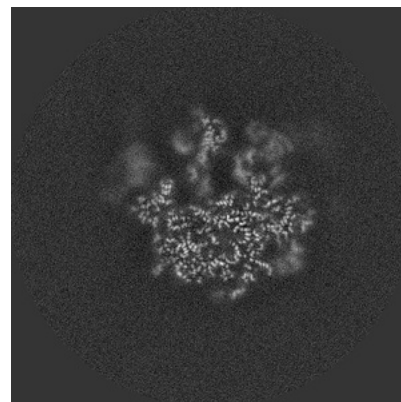
6.2.2 Raw map



X Index: 200



Y Index: 200

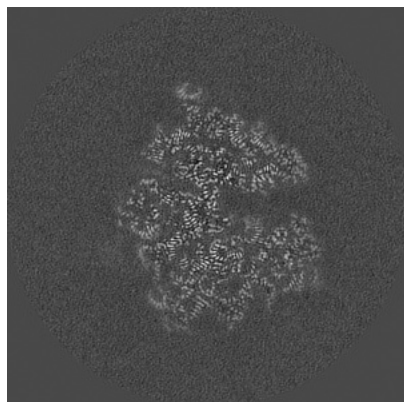


Z Index: 200

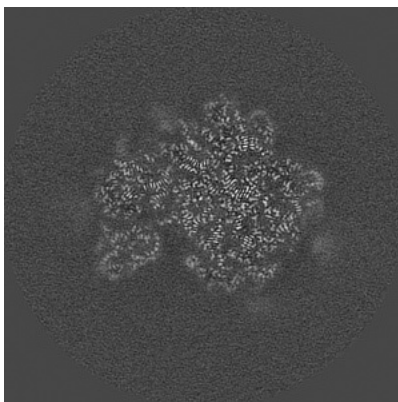
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

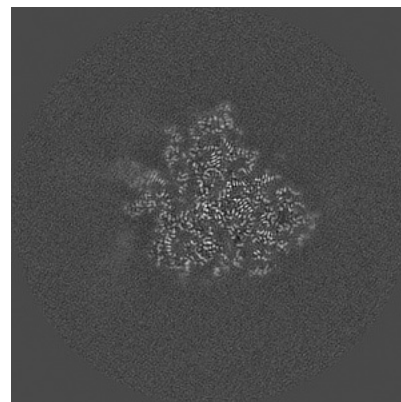
6.3.1 Primary map



X Index: 219

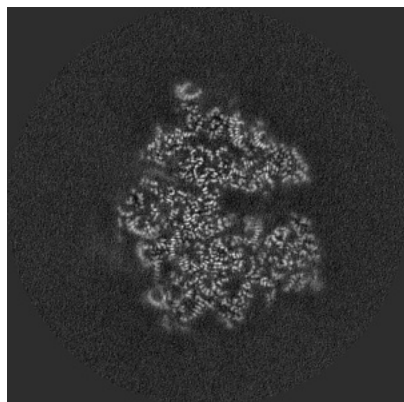


Y Index: 193

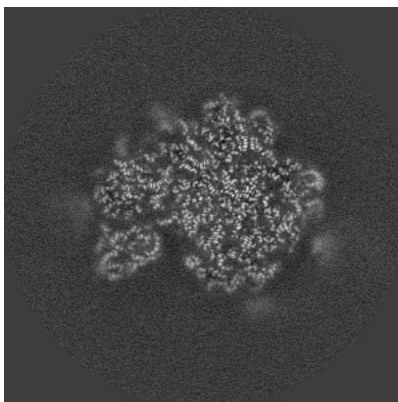


Z Index: 229

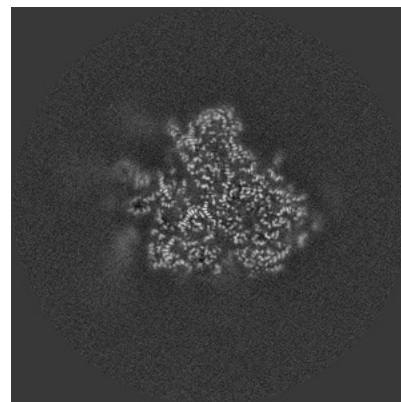
6.3.2 Raw map



X Index: 218



Y Index: 193

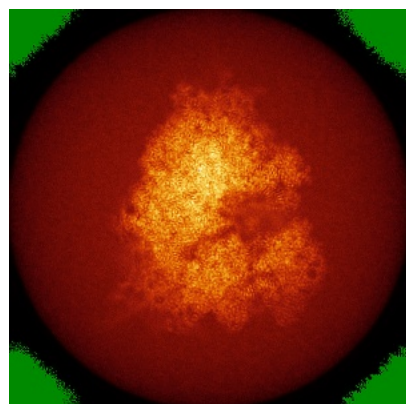


Z Index: 234

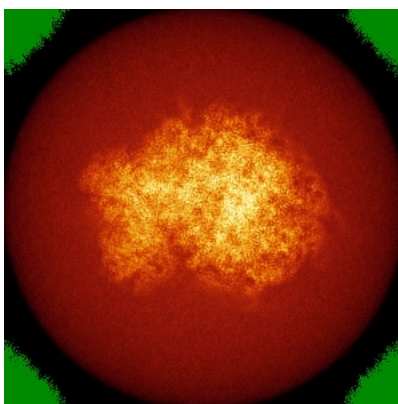
The images above show the largest variance slices of the map in three orthogonal directions.

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

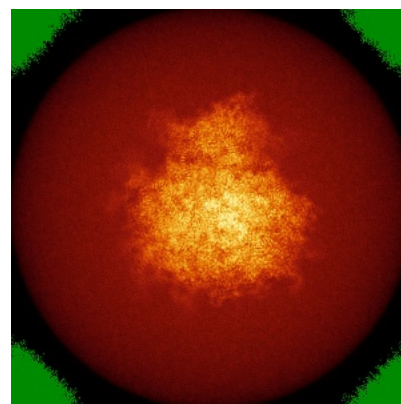
6.4.1 Primary map



X

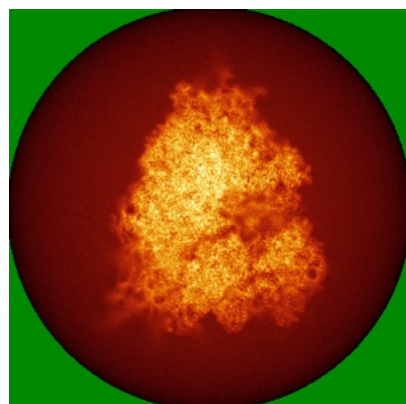


Y

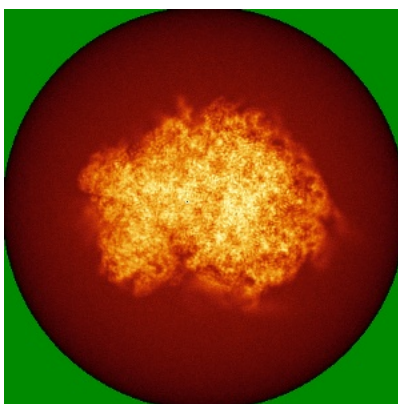


Z

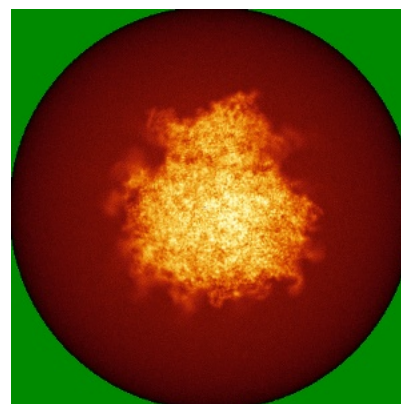
6.4.2 Raw map



X



Y

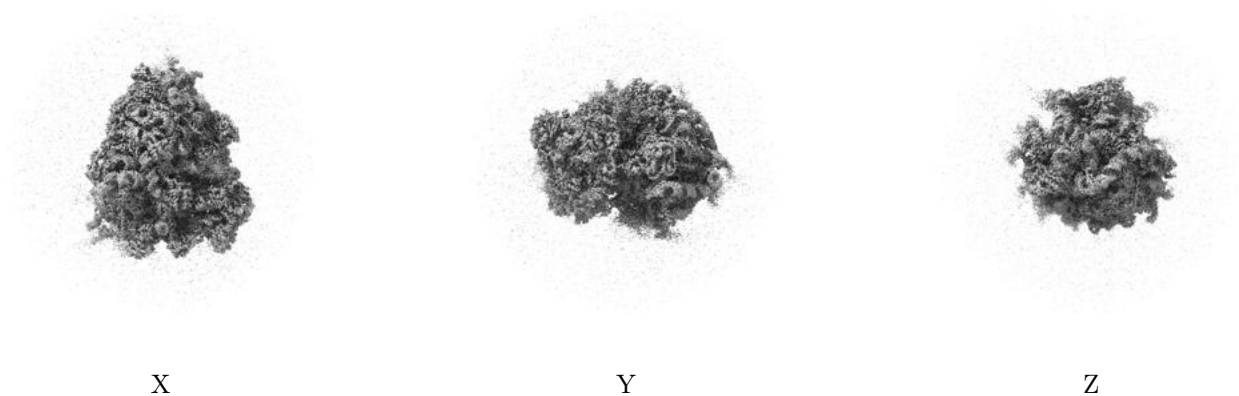


Z

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.

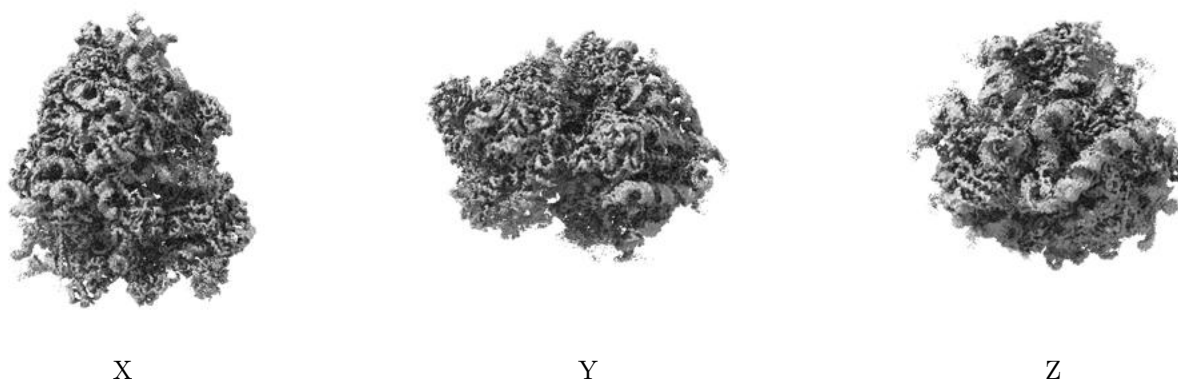
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. 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.

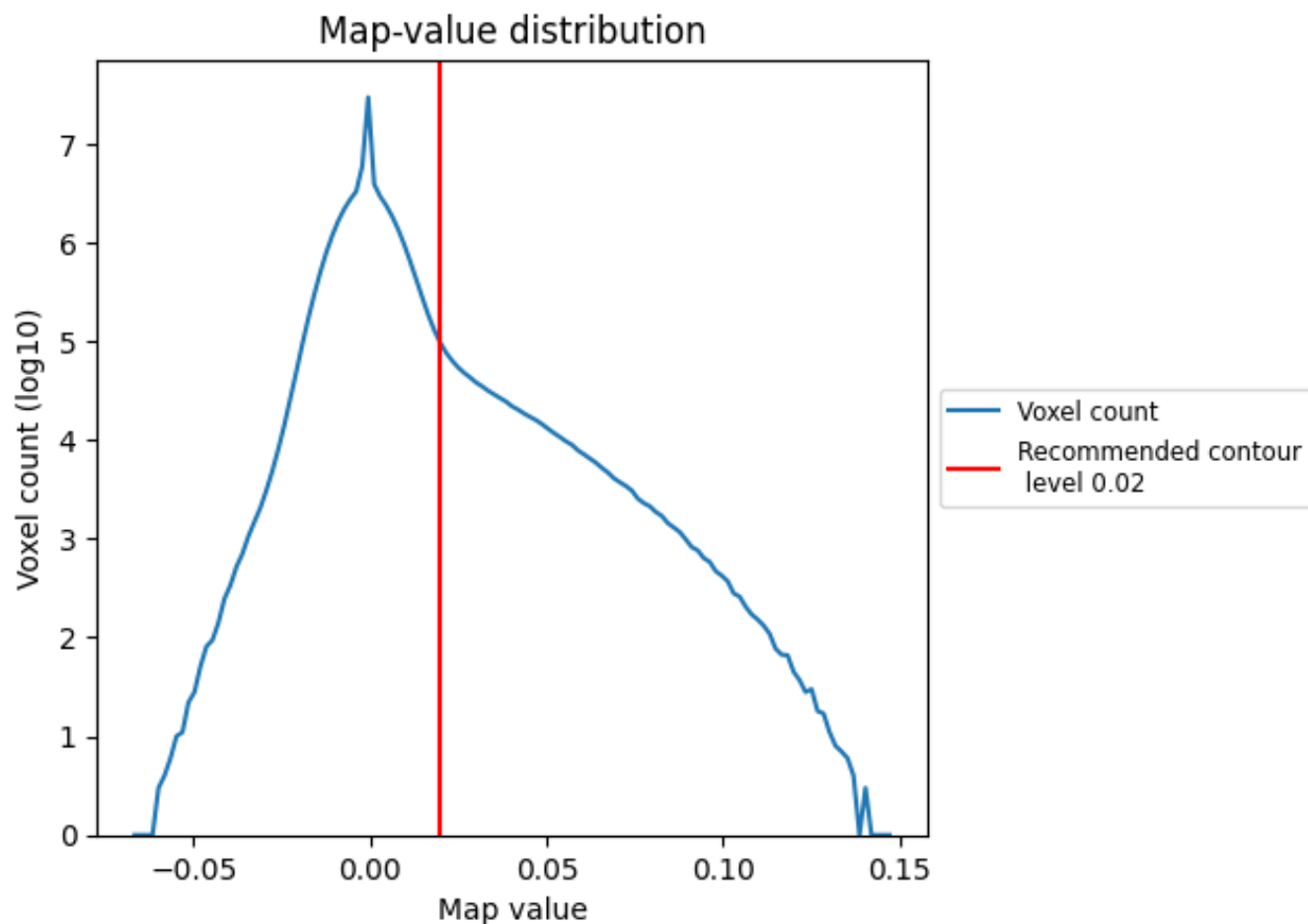
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

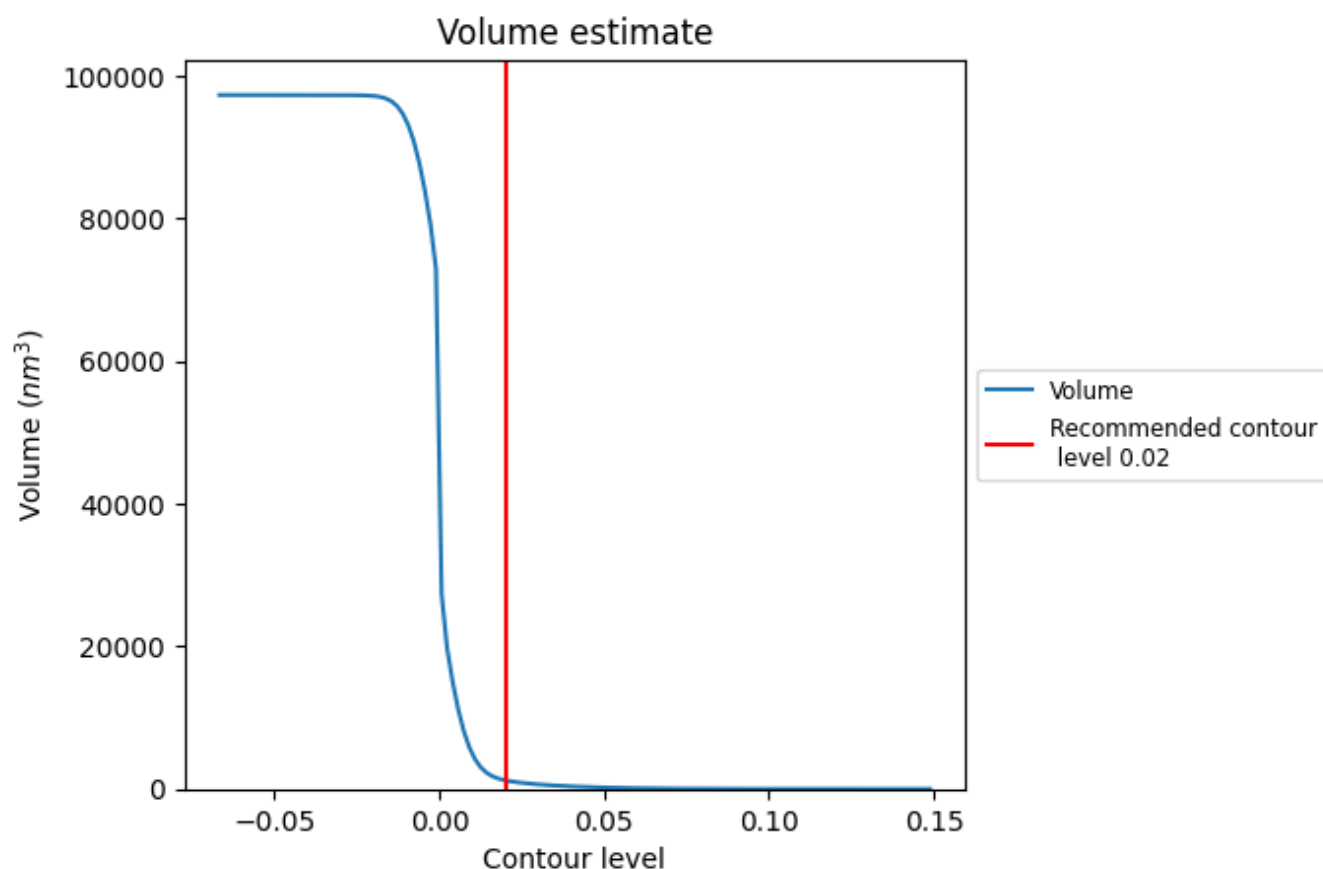
This section contains the results of statistical analysis of the map.

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.

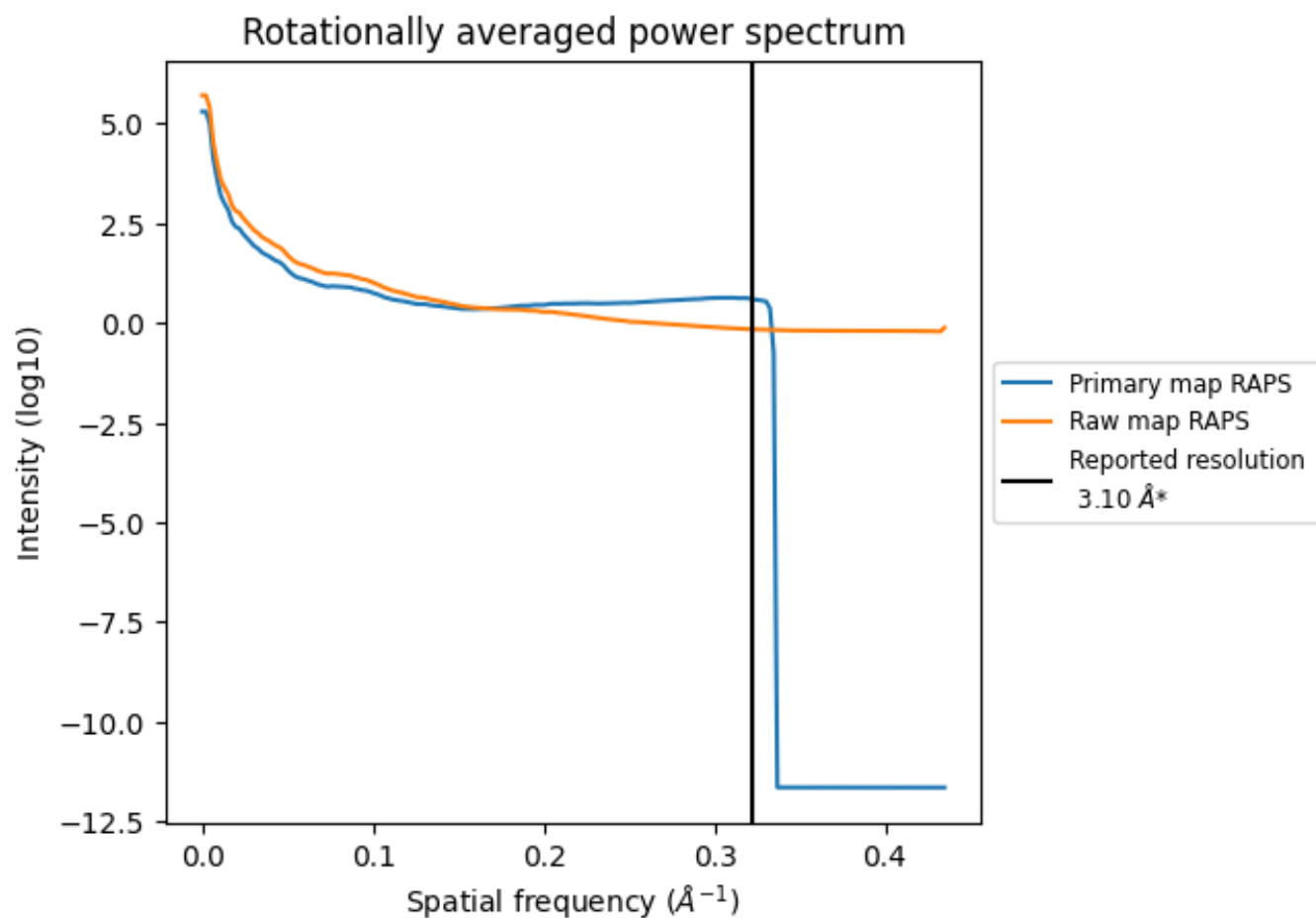
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1213 nm^3 ; this corresponds to an approximate mass of 1096 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 ⓘ

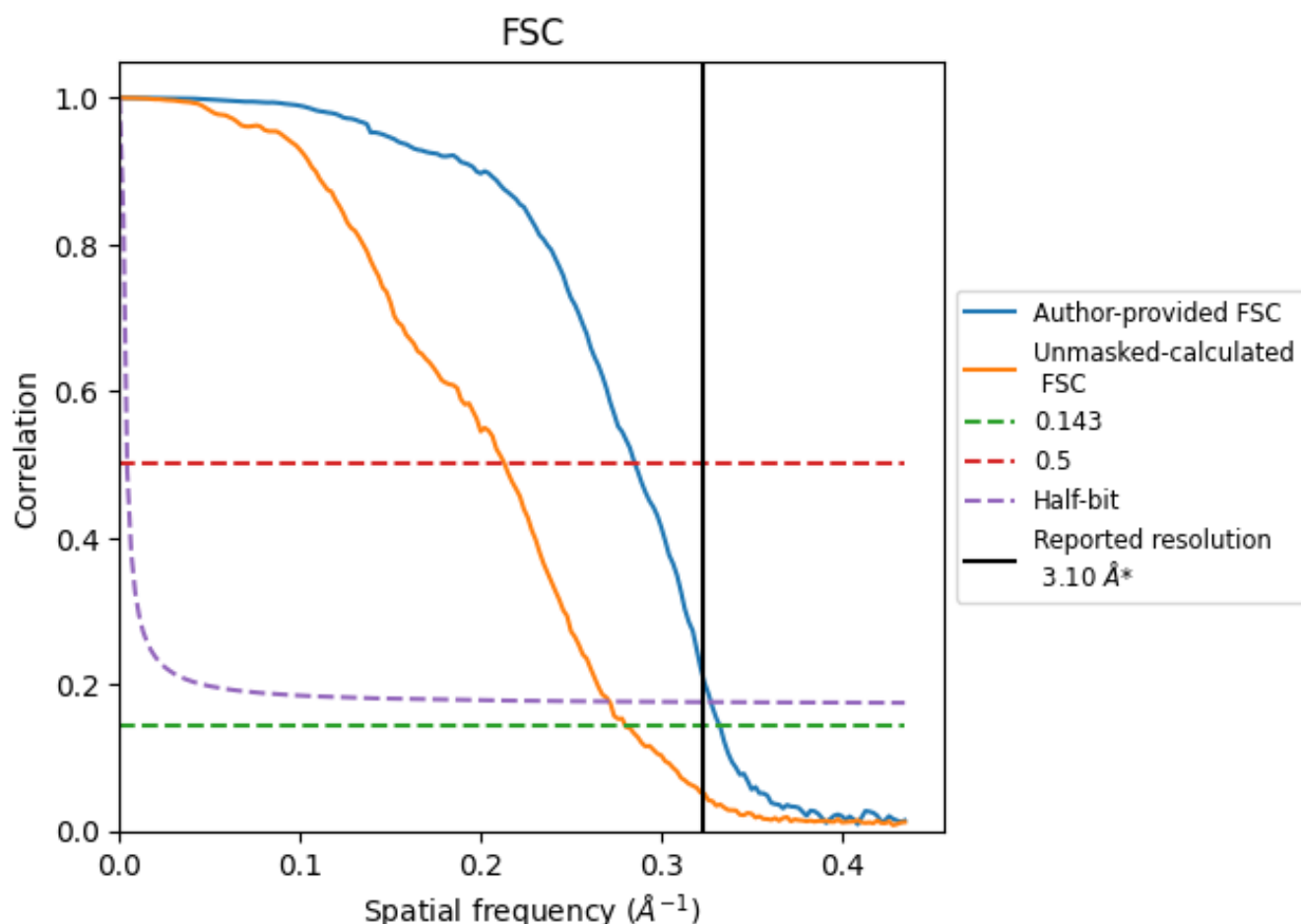


*Reported resolution corresponds to spatial frequency of 0.323 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.323 \AA^{-1}

8.2 Resolution estimates [i](#)

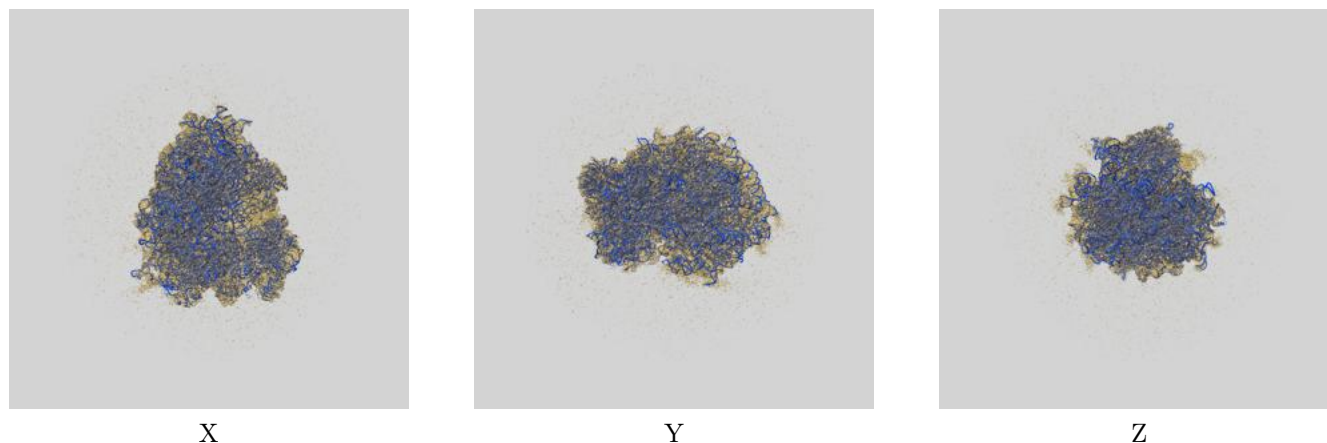
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.01	3.50	3.05
Unmasked-calculated*	3.57	4.69	3.69

*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 3.57 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

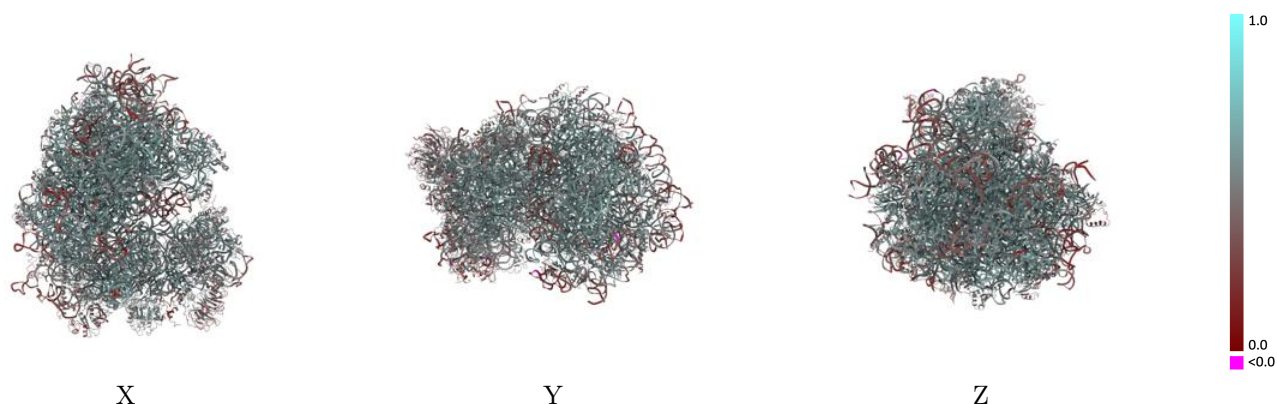
This section contains information regarding the fit between EMDB map EMD-0600 and PDB model 6OLE. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)



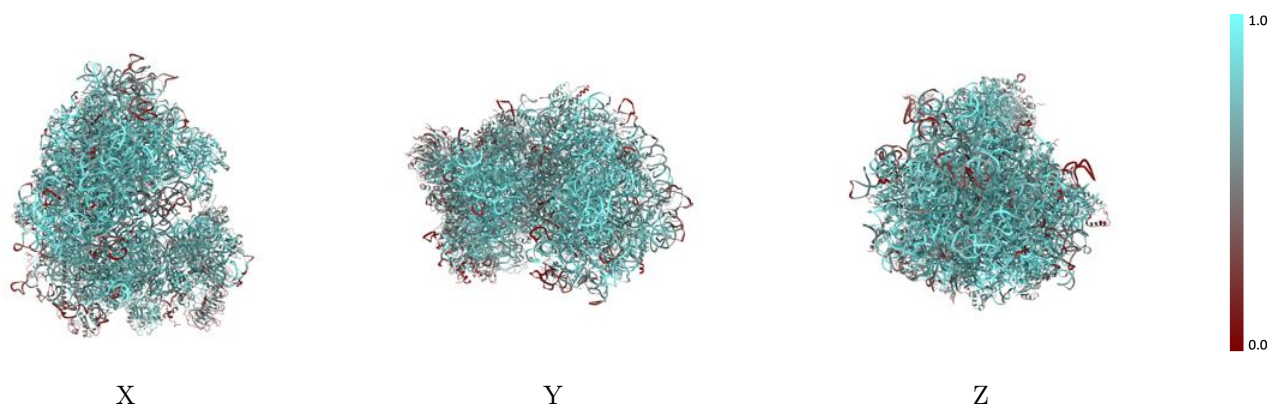
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



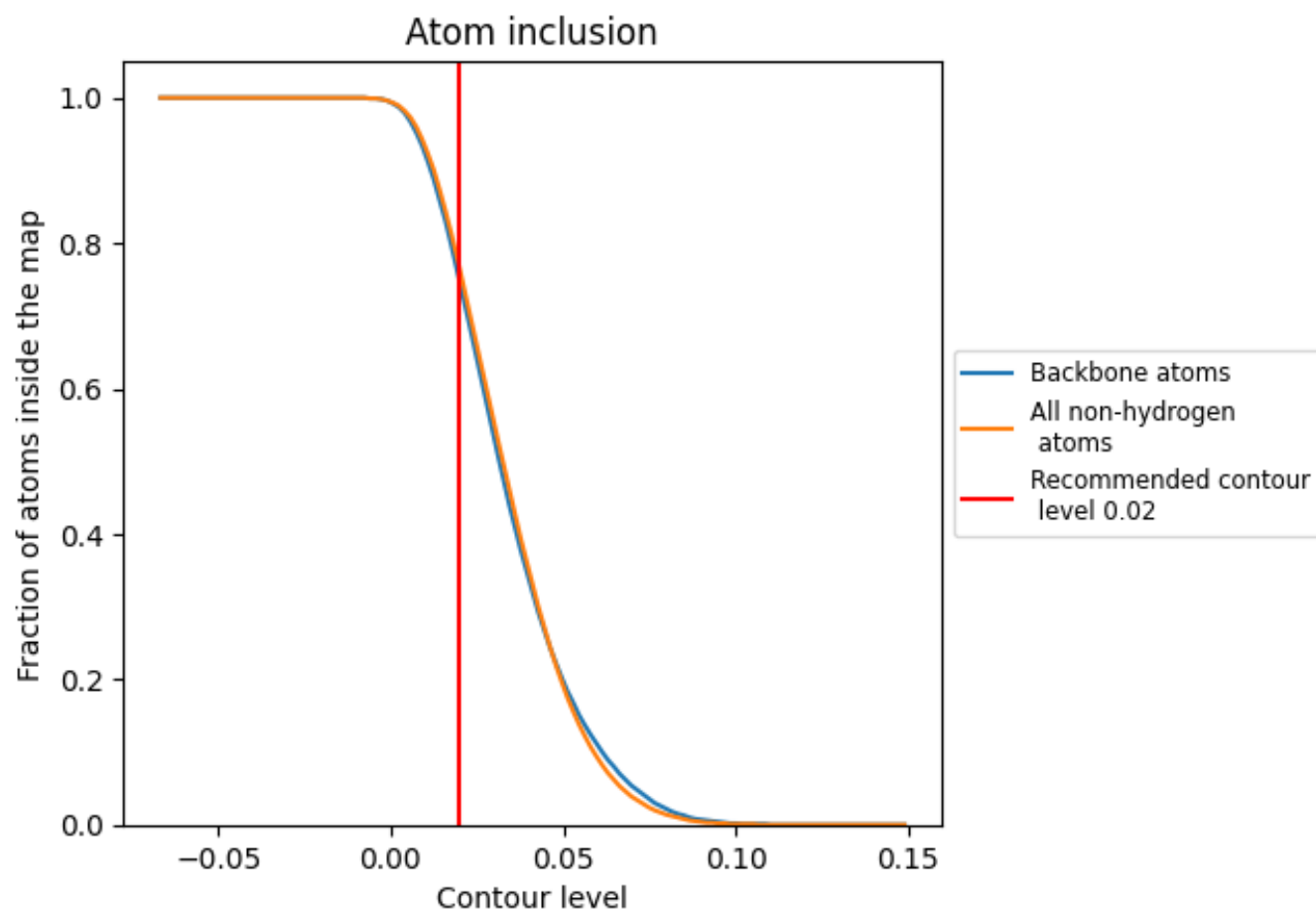
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 76% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7650	 0.5170
A	 0.8030	 0.5710
B	 0.7590	 0.5310
C	 0.7770	 0.5430
D	 0.8550	 0.5510
E	 0.9530	 0.5950
F	 0.7520	 0.5090
G	 0.6690	 0.4730
H	 0.7890	 0.5430
I	 0.6550	 0.4930
J	 0.6830	 0.5080
K	 0.7530	 0.5200
L	 0.7130	 0.5080
M	 0.7050	 0.4980
N	 0.7490	 0.5310
O	 0.8480	 0.5680
P	 0.7960	 0.5420
Q	 0.7780	 0.5510
R	 0.7910	 0.5480
S	 0.7110	 0.5020
S2	 0.8250	 0.5270
SA	 0.6690	 0.4920
SB	 0.6600	 0.5040
SC	 0.6890	 0.5100
SD	 0.5400	 0.4490
SE	 0.6470	 0.4970
SF	 0.6070	 0.4620
SG	 0.5020	 0.4070
SH	 0.4950	 0.4080
SI	 0.6050	 0.4500
SJ	 0.6350	 0.4690
SK	 0.5780	 0.4440
SL	 0.6350	 0.4970
SM	 0.1990	 0.2760
SN	 0.7010	 0.5180

















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Chain	Atom inclusion	Q-score
SO	 0.6720	 0.5010
SP	 0.6470	 0.4870
SQ	 0.6310	 0.4750
SR	 0.5550	 0.4360
SS	 0.6470	 0.4780
ST	 0.6820	 0.4940
SU	 0.5090	 0.4390
SV	 0.6740	 0.5050
SW	 0.7450	 0.5410
SX	 0.7140	 0.5250
SY	 0.5830	 0.4490
SZ	 0.5510	 0.4370
Sa	 0.7160	 0.5100
Sb	 0.6150	 0.4880
Sc	 0.5100	 0.4360
Sd	 0.7530	 0.5100
Se	 0.5630	 0.4540
Sf	 0.2420	 0.3010
Sg	 0.4400	 0.3760
T	 0.8050	 0.5430
U	 0.7610	 0.5260
V	 0.6350	 0.4560
W	 0.7630	 0.5510
X	 0.7700	 0.5350
Y	 0.7500	 0.5310
Z	 0.7550	 0.5230
a	 0.7290	 0.5190
b	 0.8050	 0.5580
c	 0.6690	 0.4850
d	 0.6610	 0.4840
e	 0.7220	 0.5230
f	 0.7960	 0.5550
g	 0.8400	 0.5610
h	 0.7200	 0.5240
i	 0.7190	 0.5120
j	 0.6780	 0.4860
k	 0.8480	 0.5720
l	 0.6120	 0.4730
m	 0.7750	 0.5440
n	 0.7930	 0.5320
o	 0.7170	 0.5130
p	 0.7060	 0.5150

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Chain	Atom inclusion	Q-score
q	 0.7550	 0.5420
r	 0.7710	 0.5300
t	 0.8450	 0.5350
u	 0.5430	 0.4010
v	 0.6080	 0.4040
w	 0.8830	 0.5620
y	 0.1840	 0.3040