



Full wwPDB EM Validation Report ⓘ

Nov 6, 2022 – 04:20 PM EST

PDB ID : 6D9J
EMDB ID : EMD-7836
Title : Mammalian 80S ribosome with a double translocated CrPV-IRES, P-sitetRNA and eRF1.
Authors : Pisareva, V.P.; Pisarev, A.V.; Fernandez, I.S.
Deposited on : 2018-04-30
Resolution : 3.20 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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

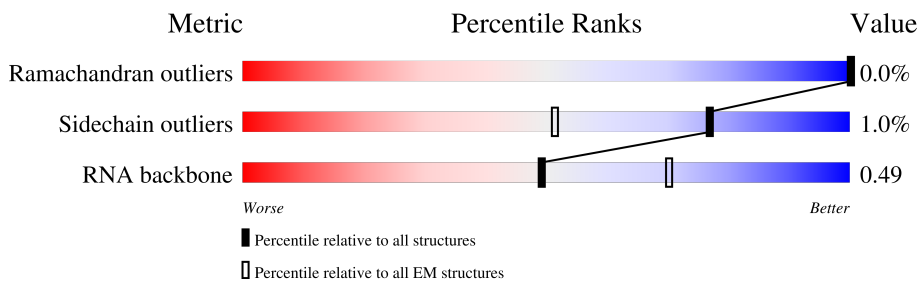
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	A	257	
2	B	403	
3	C	392	
4	D	297	
5	E	291	
6	F	249	
7	G	242	
8	H	192	

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Mol	Chain	Length	Quality of chain
9	I	214	95%
10	J	178	95%
11	L	211	99%
12	M	198	69% 31%
13	N	204	100%
14	O	198	98%
15	P	187	81% 18%
16	Q	187	99%
17	R	181	98%
18	S	176	100%
19	T	160	98%
20	U	99	100%
21	V	140	91% 8%
22	W	157	68% 32%
23	X	156	76% 24%
24	Y	145	92% 8%
25	Z	136	99%
26	a	148	98%
27	b	226	45% 54%
28	c	115	85% 15%
29	d	125	84% 14%
30	e	135	95% 5%
31	f	110	96%
32	g	126	90% 10%
33	h	123	99%

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Mol	Chain	Length	Quality of chain
34	i	105	96%
35	j	97	88% 11%
36	k	69	100%
37	l	51	94%
38	m	52	8% 98%
39	n	25	100%
40	o	106	95%
41	p	92	99%
42	r	137	90% 9%
43	s	303	7% 64% 35%
44	t	195	21% 78% 22%
45	5	3594	72% 26%
46	7	119	84% 16%
47	8	151	72% 27%
48	K	217	35% 96%
49	2	1697	72% 26%
50	BB	217	8% 98%
51	CC	264	79% 19%
52	DD	221	100%
53	EE	281	7% 79% 19%
54	FF	262	100%
55	GG	204	90% 9%
56	HH	249	95% 5%
57	II	194	7% 95% 5%
58	JJ	206	100%

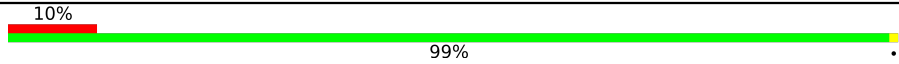

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Mol	Chain	Length	Quality of chain
59	KK	194	94% 5% 5%
60	LL	149	64% 5% 36%
61	MM	158	89% 7% 9%
62	NN	132	52% 88% 11%
63	OO	151	97%
64	PP	151	90% 6% 10%
65	QQ	145	79% 6% 21%
66	RR	172	82% 17%
67	SS	135	24% 96%
68	TT	152	12% 93% 5%
69	UU	145	97%
70	VV	119	83% 8% 16%
71	WW	83	98% 5%
72	XX	130	98%
73	YY	143	97%
74	ZZ	134	91% 7%
75	aa	125	60% 6% 40%
76	bb	101	100%
77	cc	84	99% 6%
78	dd	69	13% 90% 10%
79	ee	56	98%
80	ff	133	41% 19% 57%
81	gg	156	19% 43% 56%
82	hh	317	98% 5%
83	3	87	70% 7% 30%

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Mol	Chain	Length	Quality of chain
84	9	856	 <p>10% 99%</p>
85	4	190	 <p>41% 33% 46% 14% 7%</p>

2 Entry composition [i](#)

There are 87 unique types of molecules in this entry. The entry contains 227188 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	239	1777	1110	361	300	6	0	0

- Molecule 2 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	394	3172	2020	597	542	13	0	0

- Molecule 3 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	362	2883	1812	577	480	14	0	0

- Molecule 4 is a protein called uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	293	2391	1512	438	427	14	0	0

- Molecule 5 is a protein called eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	216	1729	1115	329	282	3	0	0

- Molecule 6 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	225	1875	1205	358	303	9	0	0

- Molecule 7 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	233	1879	1199	361	315	4	0	0

- Molecule 8 is a protein called uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	190	1516	954	284	272	6	0	0

- Molecule 9 is a protein called uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	I	205	1664	1056	321	274	13	0	0

- Molecule 10 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	170	1362	861	254	241	6	0	0

- Molecule 11 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	L	210	1702	1065	354	279	4	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	46	ILE	-	insertion	UNP G1TPV0
L	47	ALA	-	insertion	UNP G1TPV0
L	48	PRO	-	insertion	UNP G1TPV0
L	49	ARG	-	insertion	UNP G1TPV0
L	50	PRO	-	insertion	UNP G1TPV0
L	51	ALA	-	insertion	UNP G1TPV0
L	52	ALA	-	insertion	UNP G1TPV0
L	53	GLY	-	insertion	UNP G1TPV0
L	54	PRO	-	insertion	UNP G1TPV0

- Molecule 12 is a protein called eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	M	137	1130	722	220	181	7	0	0

- Molecule 13 is a protein called eL15.

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

- Molecule 14 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	O	198	1623	1046	318	254	5	0	0

- Molecule 15 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	P	153	1242	777	241	215	9	0	0

- Molecule 16 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	Q	187	1515	946	315	250	4	0	0

- Molecule 17 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	R	180	1508	933	328	238	9	0	0

- Molecule 18 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	S	176	1462	930	285	236	11	0	0

- Molecule 19 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 20 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	99	Total	C	N	O	S	0	0
			809	519	141	147	2		

- Molecule 21 is a protein called uL14.

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

- Molecule 22 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	106	Total	C	N	O	S	0	0
			860	538	174	144	4		

- Molecule 23 is a protein called eL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 24 is a protein called uL24.

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

- Molecule 25 is a protein called eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 26 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	a	147	1162	734	239	185	4	0	0

- Molecule 27 is a protein called eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	b	104	848	527	189	129	3	0	0

- Molecule 28 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	c	98	761	481	134	140	6	0	0

- Molecule 29 is a protein called eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	d	107	888	560	171	155	2	0	0

- Molecule 30 is a protein called eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	e	128	1053	667	216	165	5	0	0

- Molecule 31 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	f	109	876	555	174	143	4	0	0

- Molecule 32 is a protein called eL34.

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

- Molecule 33 is a protein called eL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 34 is a protein called eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 35 is a protein called eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 36 is a protein called eL38.

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

- Molecule 37 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 38 is a protein called eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 39 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 40 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 41 is a protein called eL43.

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

- Molecule 42 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	r	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

- Molecule 43 is a protein called uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

- Molecule 44 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t	153	Total	C	N	O	S	0	0
			1160	722	218	217	3		

- Molecule 45 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	5	3594	Total	C	N	O	P	0	0
			77073	34324	14116	25039	3594		

- Molecule 46 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	7	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

- Molecule 47 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
47	8	151	3208	1432	564	1062	150	0	0

- Molecule 48 is a protein called uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	K	212	1705	1091	306	300	8	0	0

- Molecule 49 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
49	2	1697	36229	16171	6507	11855	1696	0	0

- Molecule 50 is a protein called uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	BB	217	1710	1086	300	316	8	0	0

- Molecule 51 is a protein called eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	CC	213	1729	1098	309	308	14	0	0

- Molecule 52 is a protein called uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	DD	221	1716	1111	295	301	9	0	0

- Molecule 53 is a protein called uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	EE	228	1768	1126	318	316	8	0	0

- Molecule 54 is a protein called eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	FF	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 55 is a protein called uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	GG	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 56 is a protein called eS6.

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

- Molecule 57 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	II	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 58 is a protein called eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	JJ	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
JJ	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 59 is a protein called uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	KK	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 60 is a protein called eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	LL	96	810	530	143	131	6	0	0

- Molecule 61 is a protein called uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	MM	143	1175	749	222	198	6	0	0

- Molecule 62 is a protein called eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	NN	117	908	570	161	169	8	0	0

- Molecule 63 is a protein called uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	OO	149	1202	770	228	203	1	0	0

- Molecule 64 is a protein called uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	PP	136	1016	621	199	190	6	0	0

- Molecule 65 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	QQ	115	956	610	176	163	7	0	0

- Molecule 66 is a protein called uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	RR	142	1128	717	213	195	3	0	0

- Molecule 67 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	SS	132	1068	670	199	195	4	0	0

- Molecule 68 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	TT	144	1190	746	241	202	1	0	0

- Molecule 69 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
69	UU	141	1097	688	211	195	3	0	0

- Molecule 70 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
70	VV	100	795	498	152	141	4	0	0

- Molecule 71 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
71	WW	83	636	393	117	121	5	0	0

- Molecule 72 is a protein called uS8.

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

- Molecule 73 is a protein called uS12.

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

- Molecule 74 is a protein called eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	ZZ	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 75 is a protein called eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	aa	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 76 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	bb	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

- Molecule 77 is a protein called eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	cc	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 78 is a protein called eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	dd	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 79 is a protein called eS29.

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

- Molecule 80 is a protein called eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	ff	57	Total	C	N	O	S	0	0
			457	282	101	73	1		

- Molecule 81 is a protein called eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	gg	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 82 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	hh	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 83 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	3	87	Total	C	N	O	P	0	0
			1860	829	333	612	86		

- Molecule 84 is a protein called eEF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	9	856	Total	C	N	O	S	0	0
			6673	4234	1148	1247	44		

- Molecule 85 is a RNA chain called CrPV IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	4	190	Total	C	N	O	P	0	0
			4020	1802	689	1339	190		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	6217	C	-	insertion	GB 8895506
4	6218	U	-	insertion	GB 8895506
4	6219	U	-	insertion	GB 8895506

- Molecule 86 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
86	p	1	Total	Zn	0
			1	1	
86	2	1	Total	Zn	0
			1	1	
86	bb	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
86	gg	1	Total	Zn	0
			1	1	

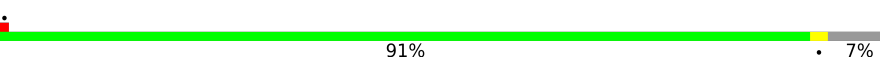
- Molecule 87 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
87	5	2	Total	Mg	0
			2	2	

3 Residue-property plots [i](#)

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: uL2

Chain A:  91% 7%



- Molecule 2: uL3

Chain B:  97% 2%



- Molecule 3: uL4

Chain C:  90% 8%




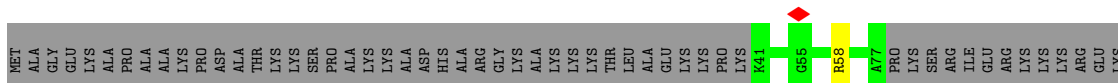
- Molecule 4: uL18

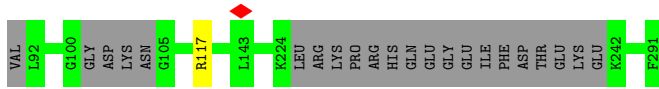
Chain D:  98% 2%



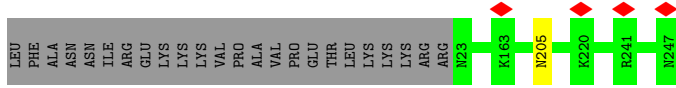
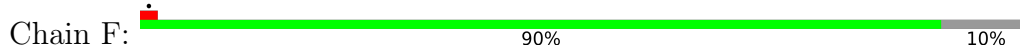
- Molecule 5: eL6

Chain E:  74% 26%

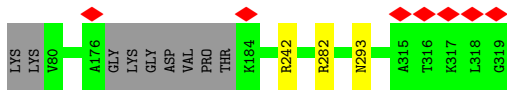




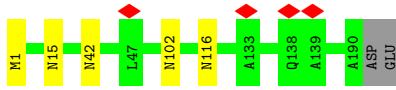
- Molecule 6: uL30



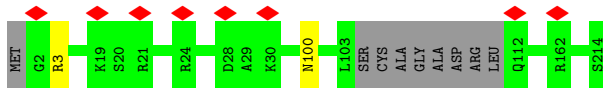
- Molecule 7: eL8



- Molecule 8: uL6



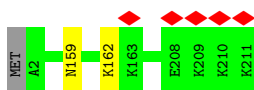
- Molecule 9: uL16



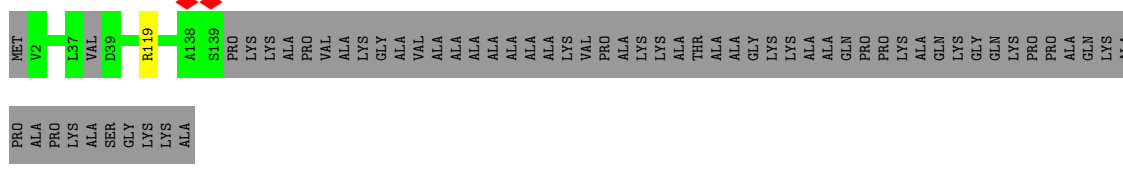
- Molecule 10: uL11



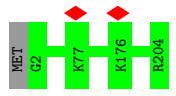
- Molecule 11: eL13



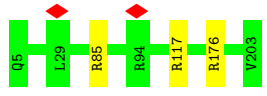
- Molecule 12: eL14



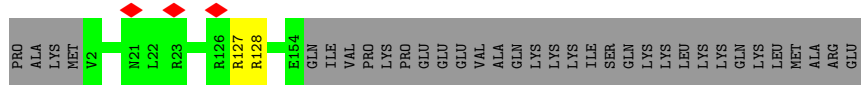
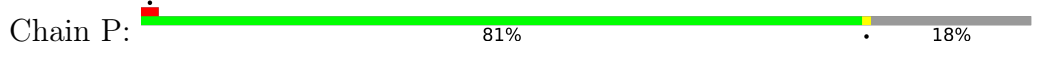
• Molecule 13: eL15



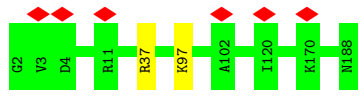
• Molecule 14: uL13



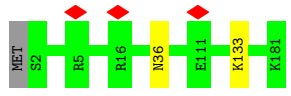
• Molecule 15: uL22



• Molecule 16: eL18

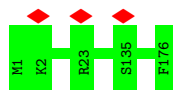


• Molecule 17: eL19

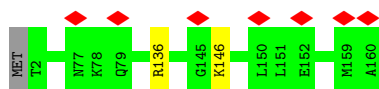


• Molecule 18: eL20

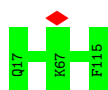




• Molecule 19: eL21



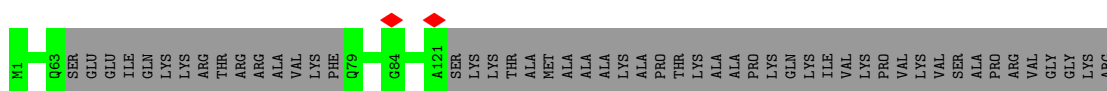
• Molecule 20: eL22



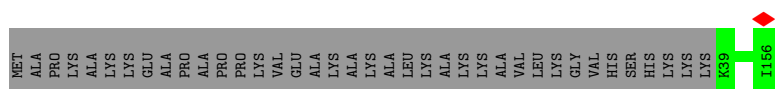
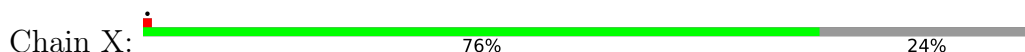
• Molecule 21: uL14



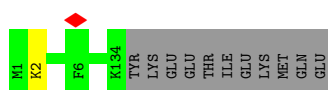
• Molecule 22: eL24



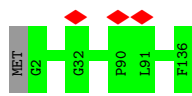
• Molecule 23: eL23



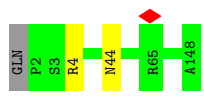
• Molecule 24: uL24



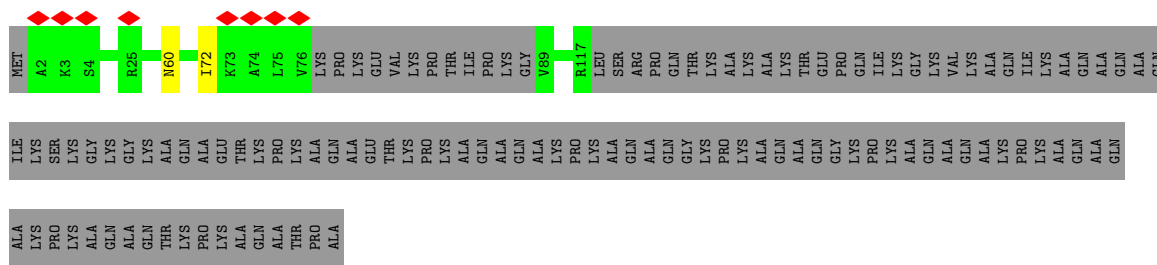
• Molecule 25: eL27



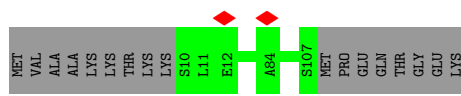
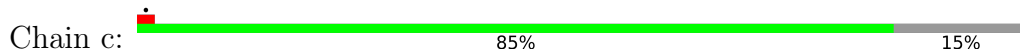
• Molecule 26: uL15



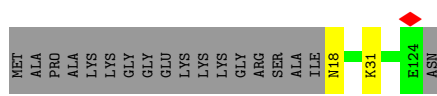
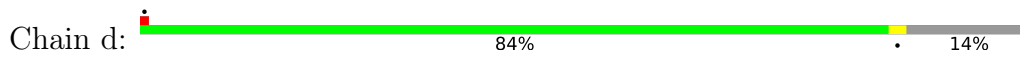
• Molecule 27: eL29



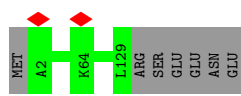
• Molecule 28: eL30



• Molecule 29: eL31



• Molecule 30: eL32




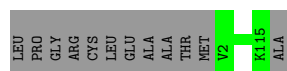
• Molecule 31: eL33

Chain f:  96%



• Molecule 32: eL34

Chain g:  90%



• Molecule 33: eL35

Chain h:  99%




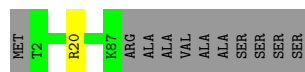
• Molecule 34: eL36

Chain i:  96%



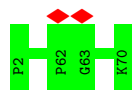
• Molecule 35: eL37

Chain j:  88%



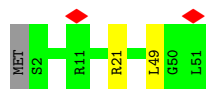
• Molecule 36: eL38

Chain k:  100%

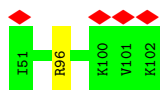


• Molecule 37: eL39

Chain l:  94%



• Molecule 38: eL40

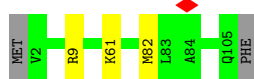


• Molecule 39: eL41



There are no outlier residues recorded for this chain.

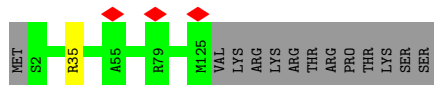
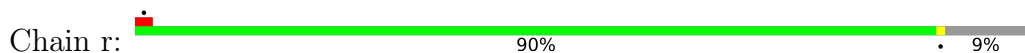
• Molecule 40: eL42



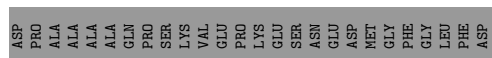
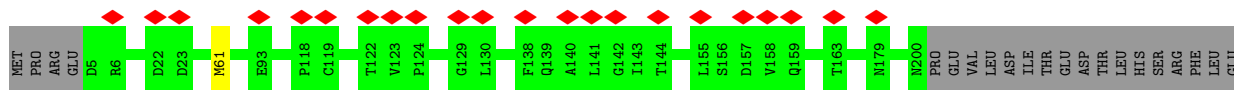
• Molecule 41: eL43



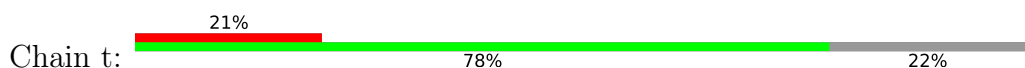
• Molecule 42: eL28

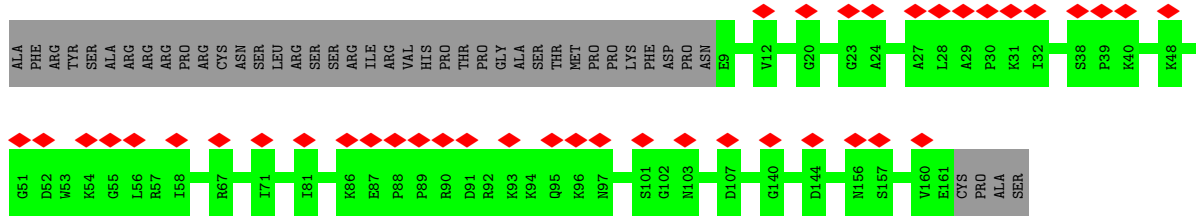


• Molecule 43: uL10

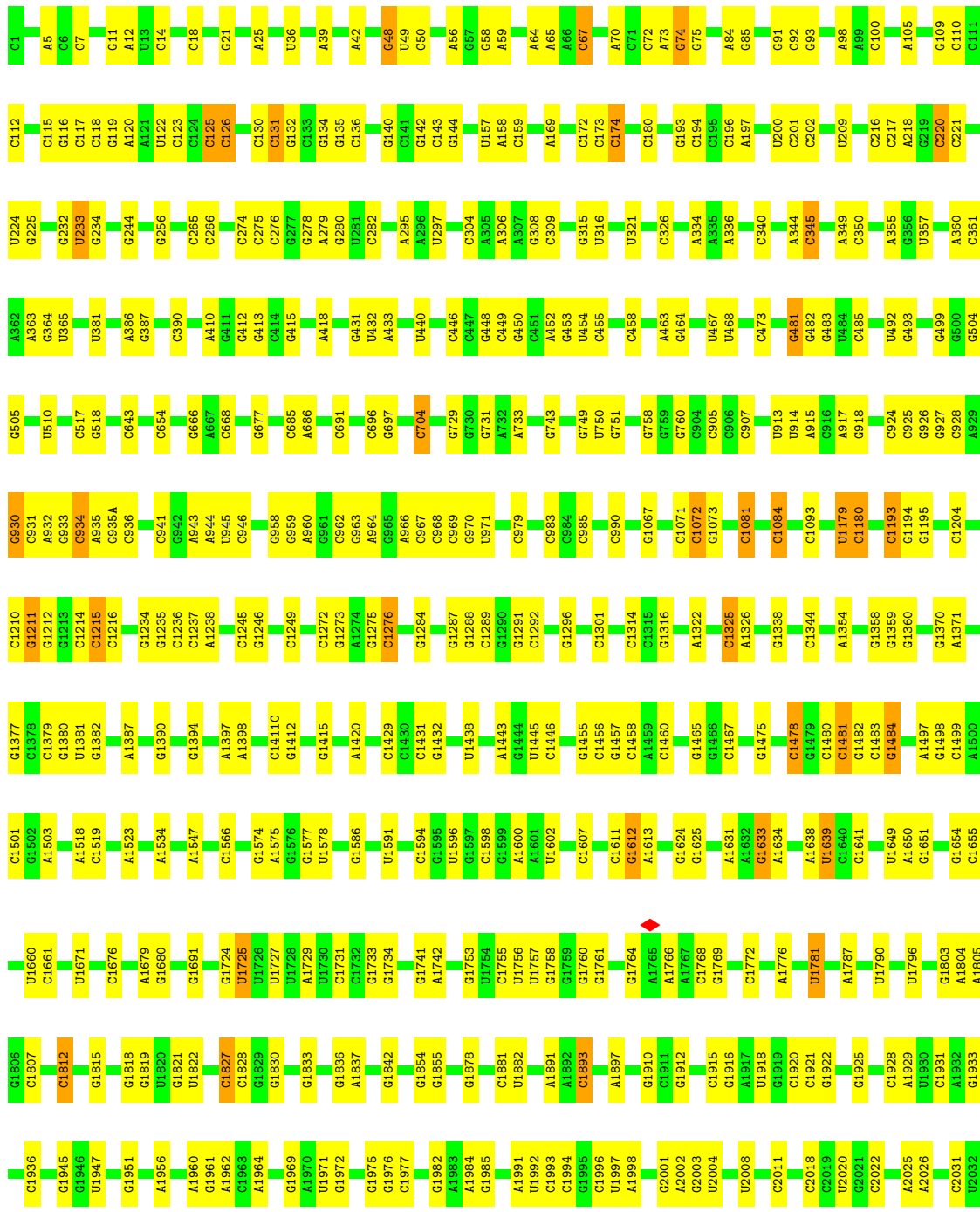


• Molecule 44: uL11



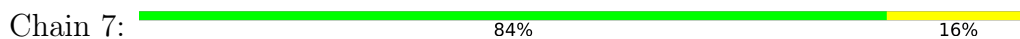


• Molecule 45: 28S rRNA



C4928	C4929	C4930	C4931	C4937	C4942	A4943	C4944	C4947	C4948	C4949	U4950	C4951	A4955	A4956	C4957	C4958	U4965	U4966	C4969	G4975	G4976	U4988	U4989	C4990	G4999	G5005	U5006	A5014	G5017	A4983	U5040	G5041	G5049	C5050	C5054	C5059	A5060	A5061	G5062	U5066	U5069																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
G4754	G4755	C4756	C4757	U4758	C4759	G4765	G4769	U4770	C4771	G4772	C4773	C4774	C4775	G4863	U4864	C4865	C4866	G4867	U4868	C4870	C4871	G4872	G4875	A4876	C4877	C4880	U4881	C4882	C4883	C4884	U4885	G4891	A4892	A4893	A4894	C4895	G4896	A4910	A4911	C4912	G4913	C4914	G4915	C4921	C4924	U4925	C4926	C4927																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
U4419	U4420	C4421	A4422	U4423	A4424	G4425	C4426	G4430	U4436	U4437	U4448	A4449	U4452	A4464	U4465	C4466	C4476	A4477	G4478	U4482	C4483	U4493	U4500	A4511	U4512	A4513	A4518	C4525	U4526	C4527	U4542	A4548	C4560	U4569	C4573	U4574	C4575	C4576	C4577	C4578	C4579	C4580	C4581	C4582	C4583	C4584	C4585																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
U4585	A4590	U4591	C4592	A4599	C4612	A4616	G4617	U4627	U4636	C4637	G4652	U4657	G4658	C4667	C4668	C4669	C4670	C4671	U4672	U4677	G4678	C4687	A4691	G4694	C4695	C4696	C4697	C4698	U4699	A4700	U4709	G4719	C4720	G4721	U4728	C4736	G4737	C4738	C4739	G4745	C4746	C4747																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
U4290	G4291	A4292	U4293	G4297	U4302	C4303	G4304	G4305	A4313	C4314	G4316	A4317	G4326	G4330	G4331	C4332	C4335	A4336	A4339	C4349	C4350	U4354	G4355	U4360	G4373	U4374	C4375	A4376	C4377	A4378	A4381	C4387	G4393	A4394	U4395	C4398	G4401	U4405	C4413	U4419	U4420	U4421	U4422	U4423	U4424	U4425	U4426	U4427	U4428	U4429	U4430	U4431	U4432	U4433	U4434	U4435	U4436	U4437	U4438	U4439	U4440	U4441	U4442	U4443	U4444	U4445	U4446	U4447	U4448	U4449	U4450	U4451	U4452	U4453	U4454	U4455	U4456	U4457	U4458	U4459	U4460	U4461	U4462	U4463	U4464	U4465	U4466	U4467	U4468	U4469	U4470	U4471	U4472	U4473	U4474	U4475	U4476	U4477	U4478	U4479	U4480	U4481	U4482	U4483	U4484	U4485	U4486	U4487	U4488	U4489	U4490	U4491	U4492	U4493	U4494	U4495	U4496	U4497	U4498	U4499	U4500	U4501	U4502	U4503	U4504	U4505	U4506	U4507	U4508	U4509	U4510	U4511	U4512	U4513	U4514	U4515	U4516	U4517	U4518	U4519	U4520	U4521	U4522	U4523	U4524	U4525	U4526	U4527	U4528	U4529	U4530	U4531	U4532	U4533	U4534	U4535	U4536	U4537	U4538	U4539	U4540	U4541	U4542	U4543	U4544	U4545	U4546	U4547	U4548	U4549	U4550	U4551	U4552	U4553	U4554	U4555	U4556	U4557	U4558	U4559	U4560	U4561	U4562	U4563	U4564	U4565	U4566	U4567	U4568	U4569	U4570	U4571	U4572	U4573	U4574	U4575	U4576	U4577	U4578	U4579	U4580	U4581	U4582	U4583	U4584	U4585	U4586	U4587	U4588	U4589	U4590	U4591	U4592	U4593	U4594	U4595	U4596	U4597	U4598	U4599	U4600	U4601	U4602	U4603	U4604	U4605	U4606	U4607	U4608	U4609	U4610	U4611	U4612	U4613	U4614	U4615	U4616	U4617	U4618	U4619	U4620	U4621	U4622	U4623	U4624	U4625	U4626	U4627	U4628	U4629	U4630	U4631	U4632	U4633	U4634	U4635	U4636	U4637	U4638	U4639	U4640	U4641	U4642	U4643	U4644	U4645	U4646	U4647	U4648	U4649	U4650	U4651	U4652	U4653	U4654	U4655	U4656	U4657	U4658	U4659	U4660	U4661	U4662	U4663	U4664	U4665	U4666	U4667	U4668	U4669	U4670	U4671	U4672	U4673	U4674	U4675	U4676	U4677	U4678	U4679	U4680	U4681	U4682	U4683	U4684	U4685	U4686	U4687	U4688	U4689	U4690	U4691	U4692	U4693	U4694	U4695	U4696	U4697	U4698	U4699	U4700	U4701	U4702	U4703	U4704	U4705	U4706	U4707	U4708	U4709	U4710	U4711	U4712	U4713	U4714	U4715	U4716	U4717	U4718	U4719	U4720	U4721	U4722	U4723	U4724	U4725	U4726	U4727	U4728	U4729	U4730	U4731	U4732	U4733	U4734	U4735	U4736	U4737	U4738	U4739	U4740	U4741	U4742	U4743	U4744	U4745	U4746	U4747	U4748	U4749	U4750	U4751	U4752	U4753	U4754	U4755	U4756	U4757	U4758	U4759	U4760	U4761	U4762	U4763	U4764	U4765	U4766	U4767	U4768	U4769	U4770	U4771	U4772	U4773	U4774	U4775	U4776	U4777	U4778	U4779	U4780	U4781	U4782	U4783	U4784	U4785	U4786	U4787	U4788	U4789	U4790	U4791	U4792	U4793	U4794	U4795	U4796	U4797	U4798	U4799	U4800	U4801	U4802	U4803	U4804	U4805	U4806	U4807	U4808	U4809	U4810	U4811	U4812	U4813	U4814	U4815	U4816	U4817	U4818	U4819	U4820	U4821	U4822	U4823	U4824	U4825	U4826	U4827	U4828	U4829	U4830	U4831	U4832	U4833	U4834	U4835	U4836	U4837	U4838	U4839	U4840	U4841	U4842	U4843	U4844	U4845	U4846	U4847	U4848	U4849	U4850	U4851	U4852	U4853	U4854	U4855	U4856	U4857	U4858	U4859	U4860	U4861	U4862	U4863	U4864	U4865	U4866	U4867	U4868	U4869	U4870	U4871	U4872	U4873	U4874	U4875	U4876	U4877	U4878	U4879	U4880	U4881	U4882	U4883	U4884	U4885	U4886	U4887	U4888	U4889	U4890	U4891	U4892	U4893	U4894	U4895	U4896	U4897	U4898	U4899	U4900	U4901	U4902	U4903	U4904	U4905	U4906	U4907	U4908	U4909	U4910	U4911	U4912	U4913	U4914	U4915	U4916	U4917	U4918	U4919	U4920	U4921	U4922	U4923	U4924	U4925	U4926	U4927	U4928	U4929	U4930	U4931	U4932	U4933	U4934	U4935	U4936	U4937	U4938	U4939	U4940	U4941	U4942	U4943	U4944	U4945	U4946	U4947	U4948	U4949	U4950	U4951	U4952	U4953	U4954	U4955	U4956	U4957	U4958	U4959	U4960	U4961	U4962	U4963	U4964	U4965	U4966	U4967	U4968	U4969	U4970	U4971	U4972	U4973	U4974	U4975	U4976	U4977	U4978	U4979	U4980	U4981	U4982	U4983	U4984	U4985	U4986	U4987	U4988	U4989	U4990	U4991	U4992	U4993	U4994	U4995	U4996	U4997	U4998	U4999	U5000	U5001	U5002	U5003	U5004	U5005	U5006	U5007	U5008	U5009	U5010	U5011	U5012	U5013	U5014	U5015	U5016	U5017	U5018	U5019	U5020	U5021	U5022	U5023	U5024	U5025	U5026	U5027	U5028	U5029	U5030	U5031	U5032	U5033	U5034	U5035	U5036	U5037	U5038	U5039	U5040	U5041	U5042	U5043	U5044	U5045	U5046	U5047	U5048	U5049	U5050	U5051	U5052	U5053	U5054	U5055	U5056	U5057	U5058	U5059	U5060	U5061	U5062	U5063	U5064	U5065	U5066	U5067	U5068	U5069	U5070	U5071	U5072	U5073	U5074	U5075	U5076	U5077	U5078	U5079	U5080	U5081	U5082	U5083	U5084	U5085	U5086	U5087	U5088	U5089	U5090	U5091	U5092	U5093	U5094	U5095	U5096	U5097	U5098	U5099	U5100	U5101	U5102	U5103	U5104	U5105	U5106	U5107	U5108	U5109	U5110	U5111	U5112	U5113	U5114	U5115	U5116	U5117	U5118	U5119	U5120	U5121	U5122	U5123	U5124	U5125	U5126	U5127	U5128	U5129	U5130	U5131	U5132	U5133	U5134	U5135	U5136	U5137	U5138	U5139	U5140	U5141	U5142	U5143	U5144	U5145	U5146	U5147	U5148	U5149	U5150	U5151	U5152	U5153	U5154	U5155	U5156	U5157	U5158	U5159	U5160	U5161	U5162	U5163	U5164	U5165	U5166	U5167	U5168	U5169	U5170	U5171	U5172	U5173	U5174	U5175	U5176	U5177	U5178	U5179	U5180	U5181	U5182	U5183	U5184	U5185	U5186	U5187	U5188	U5189	U5190	U5191	U5192	U5193	U5194	U5195	U5196	U5197	U5198	U5199	U5200	U5201	U5202	U5203	U5204	U5205	U5206	U5207	U5208	U5209	U5210	U5211	U5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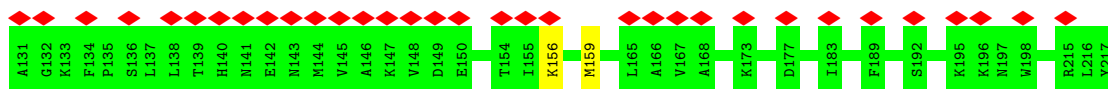
• Molecule 46: 5S rRNA



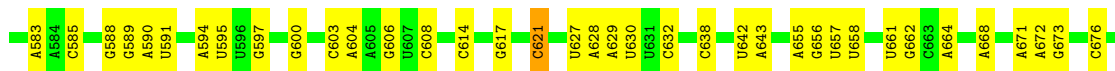
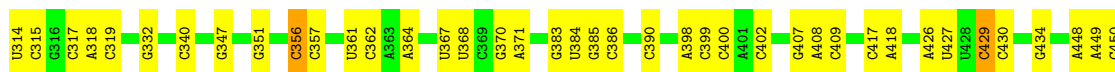
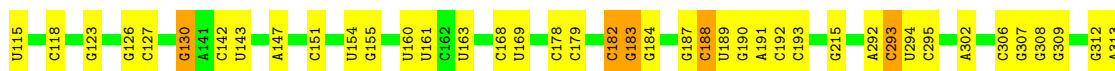
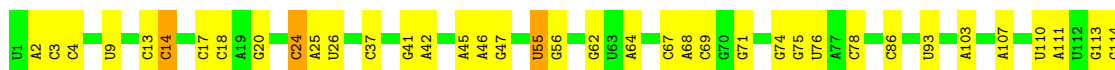
• Molecule 47: 5.8S rRNA

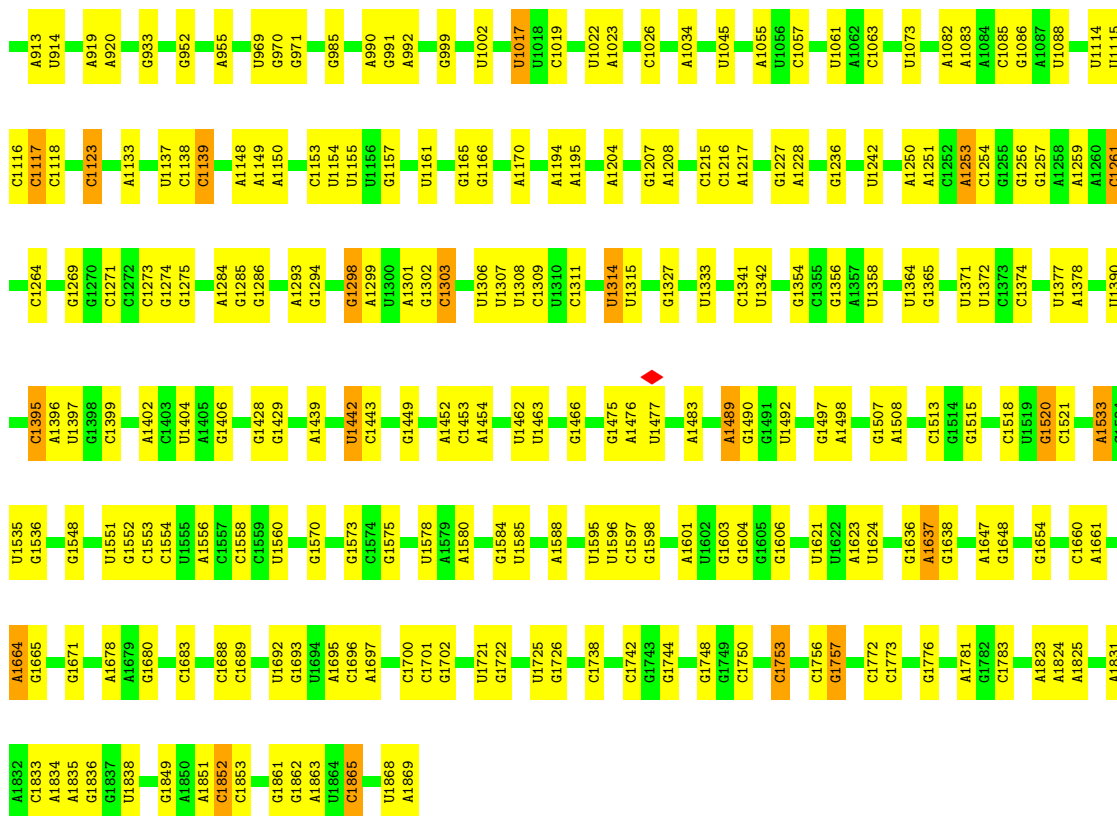


• Molecule 48: uL1

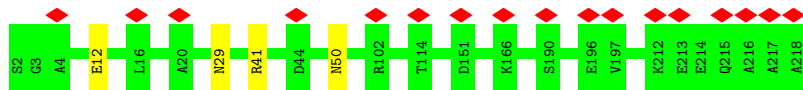


• Molecule 49: 18S rRNA

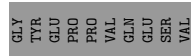
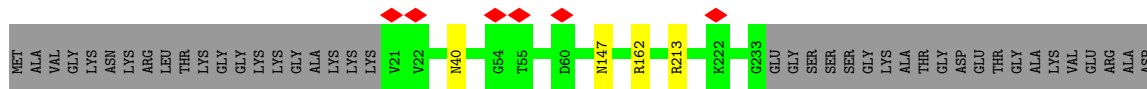
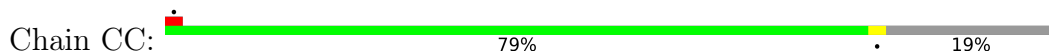




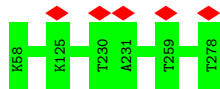
• Molecule 50: uS2



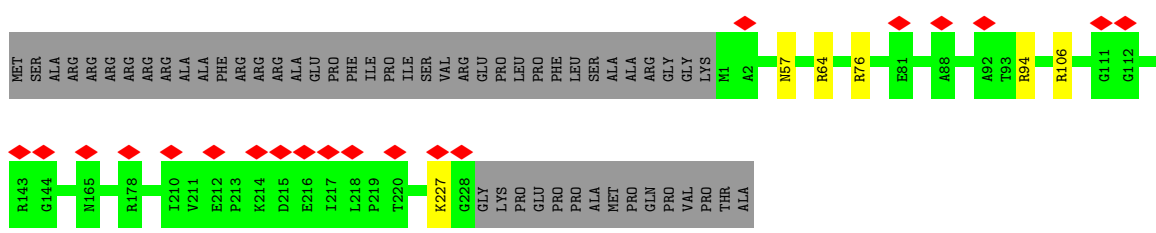
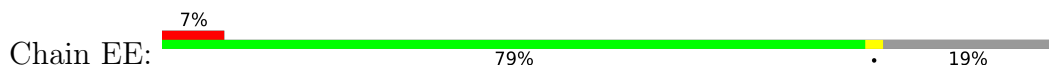
• Molecule 51: eS1



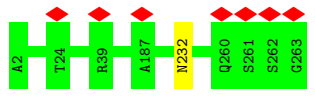
• Molecule 52: uS5



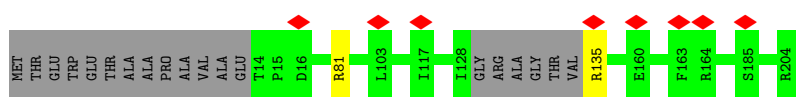
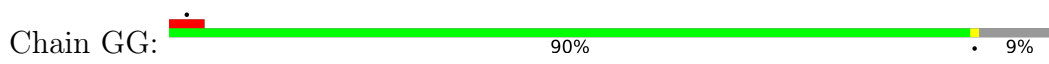
• Molecule 53: uS3



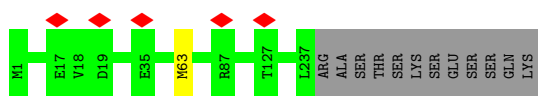
• Molecule 54: eS4



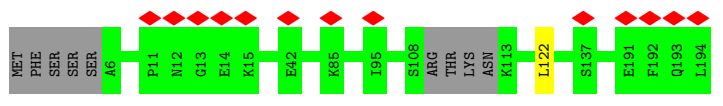
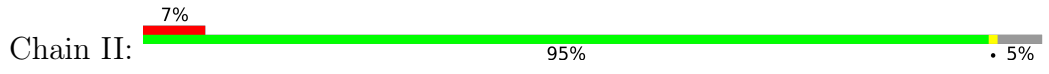
• Molecule 55: uS7



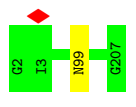
• Molecule 56: eS6



• Molecule 57: eS7

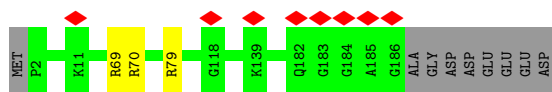


• Molecule 58: eS8

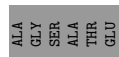
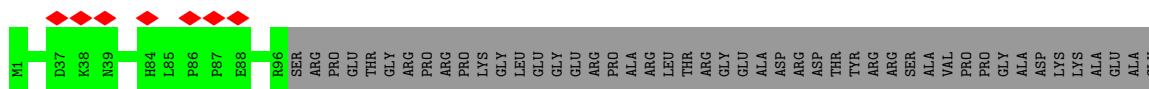


• Molecule 59: uS4

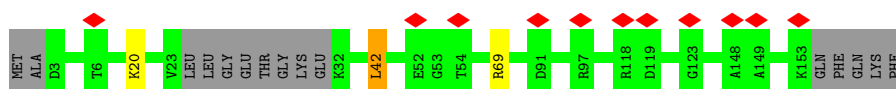




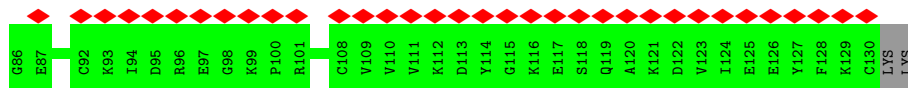
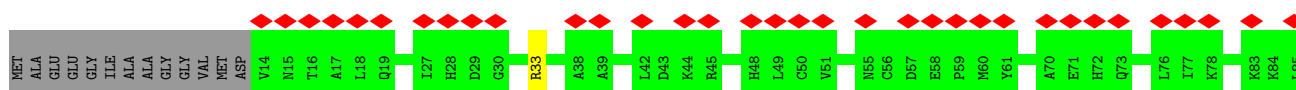
• Molecule 60: eS10



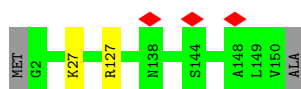
• Molecule 61: uS17



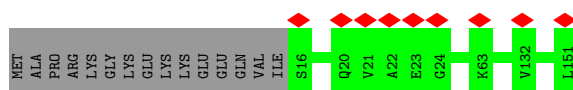
• Molecule 62: eS12



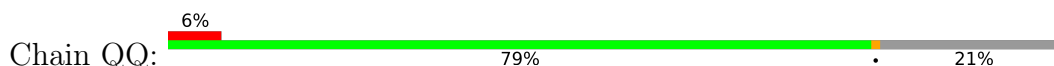
• Molecule 63: uS15

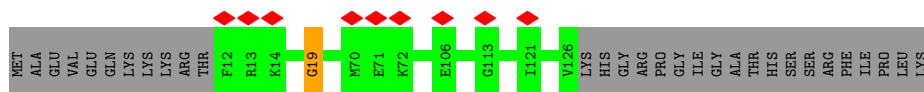


• Molecule 64: uS11

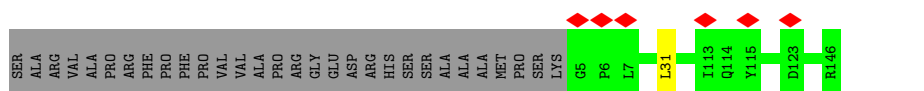
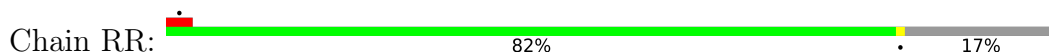


• Molecule 65: uS19

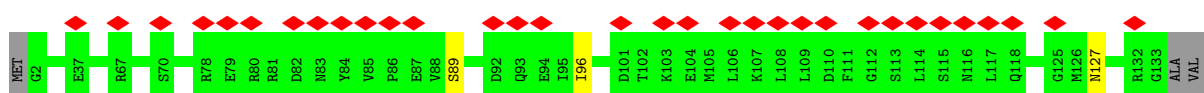




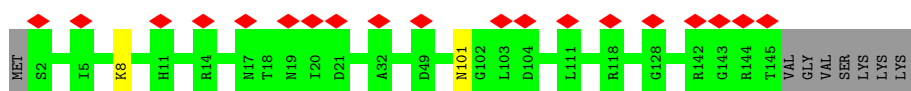
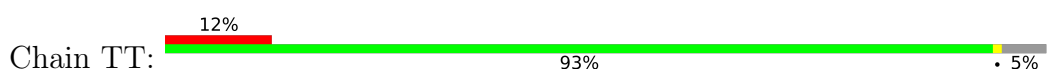
• Molecule 66: uS9



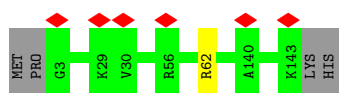
• Molecule 67: eS17



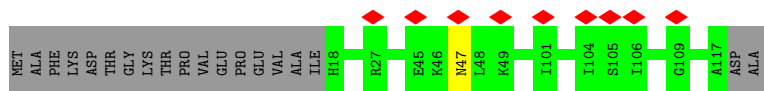
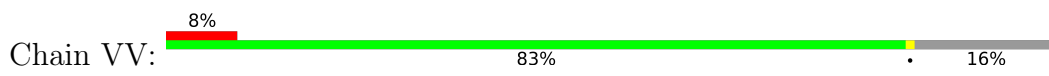
• Molecule 68: uS13



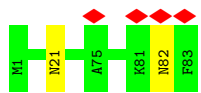
• Molecule 69: eS19



• Molecule 70: uS10

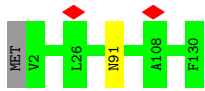


• Molecule 71: eS21



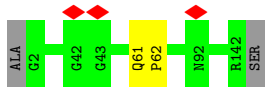
• Molecule 72: uS8

Chain XX:  98%

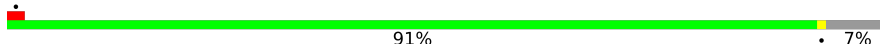


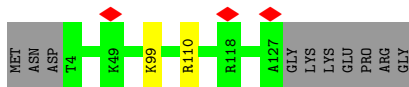
- Molecule 73: uS12

Chain YY:  97%



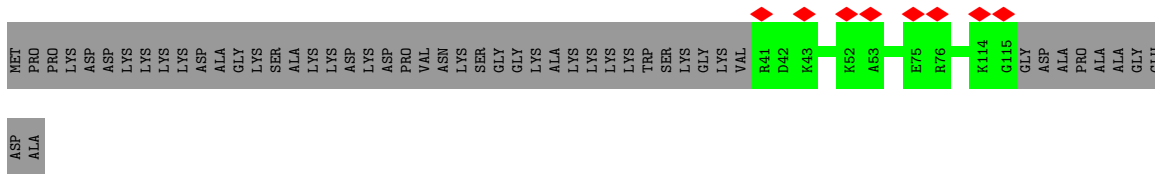
- Molecule 74: eS24

Chain ZZ:  91%



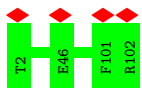
- Molecule 75: eS25

Chain aa:  60%



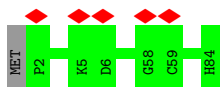
- Molecule 76: eS26

Chain bb:  100%



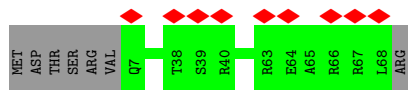
- Molecule 77: eS27

Chain cc:  99%

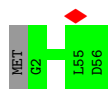


- Molecule 78: eS28

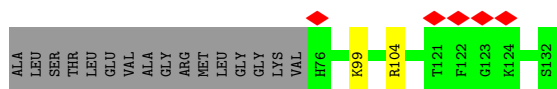
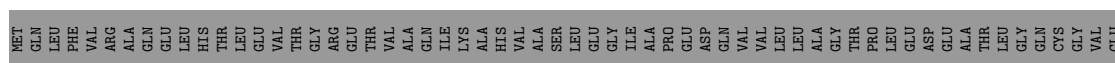
Chain dd:  90%



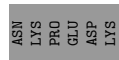
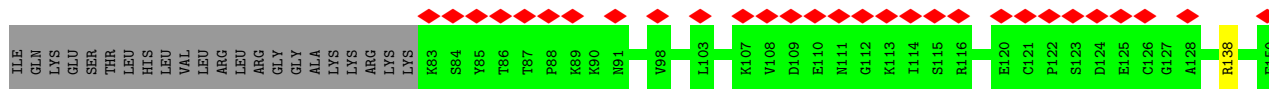
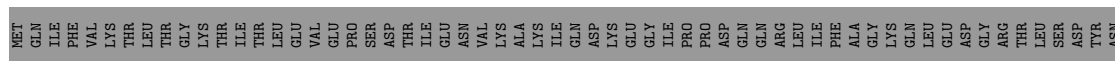
• Molecule 79: eS29



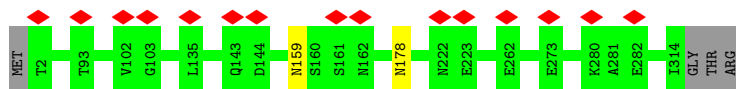
• Molecule 80: eS30



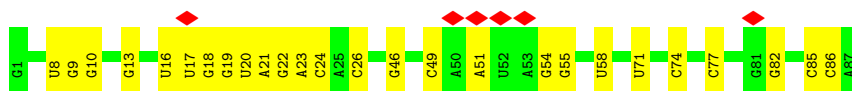
• Molecule 81: eS31



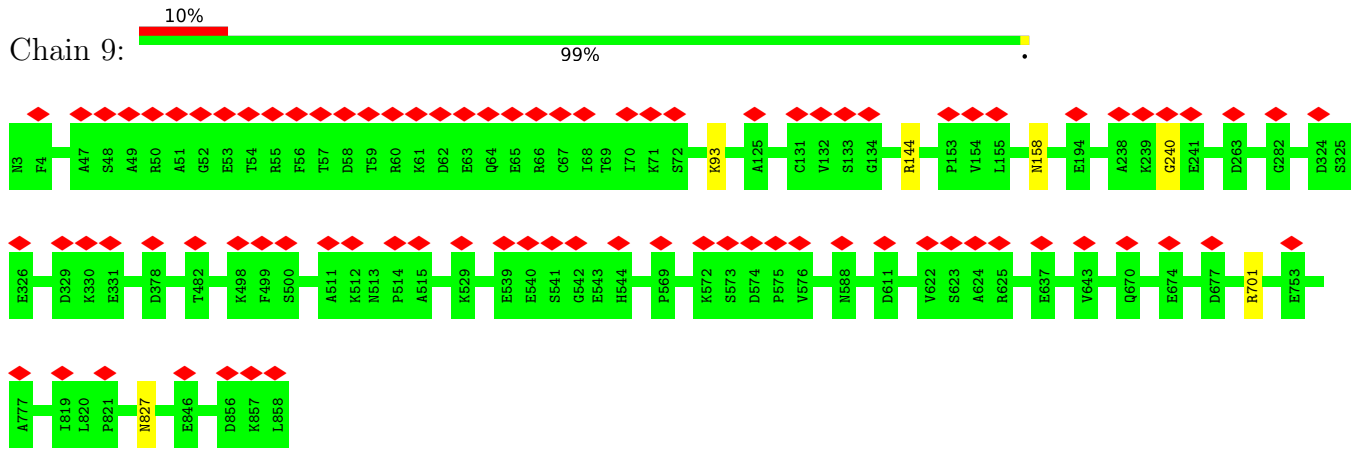
• Molecule 82: RACK1



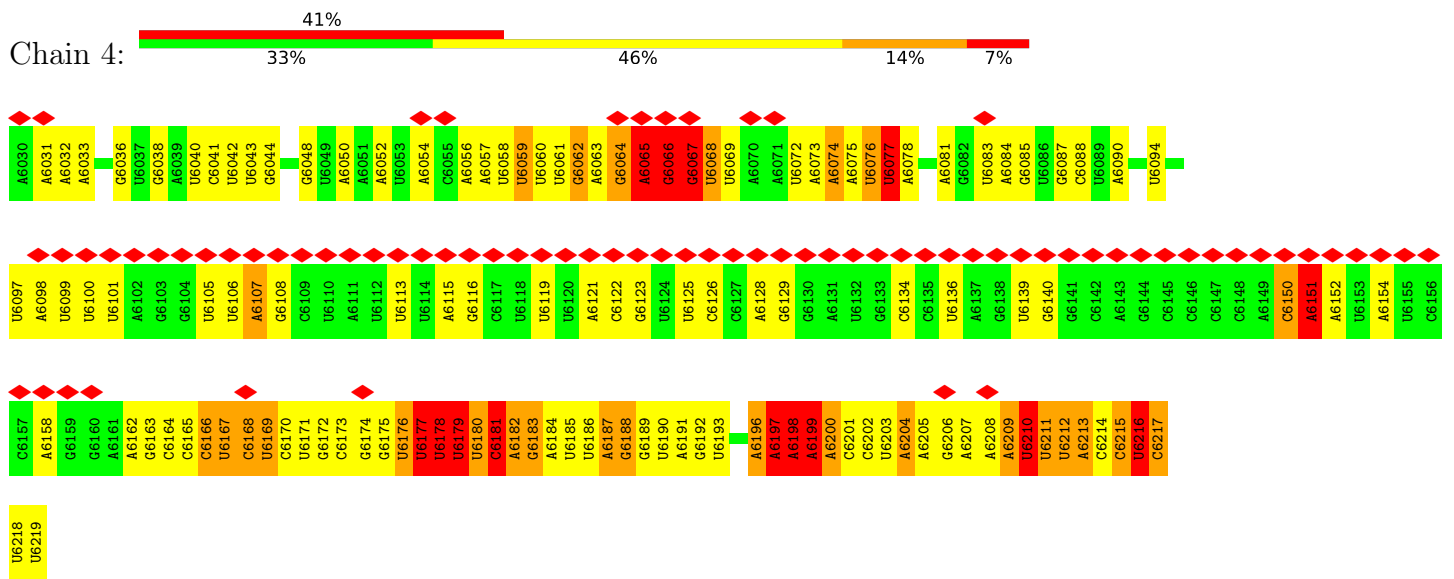
• Molecule 83: P-site tRNA



• Molecule 84: eEF2



• Molecule 85: CrPV IRES



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	75654	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 ($e^-/\text{\AA}^2$)	64	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	0.076	Depositor
Minimum map value	-0.013	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.02	Depositor
Map size (\AA)	432.00003, 432.00003, 432.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.08, 1.08, 1.08	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.26	0/1812	0.50	1/2439 (0.0%)
2	B	0.25	0/3240	0.51	2/4339 (0.0%)
3	C	0.24	0/2936	0.45	0/3943
4	D	0.26	0/2437	0.44	0/3264
5	E	0.25	0/1762	0.48	0/2362
6	F	0.25	0/1911	0.44	0/2549
7	G	0.25	0/1910	0.49	0/2569
8	H	0.25	0/1535	0.50	0/2063
9	I	0.26	0/1702	0.45	0/2272
10	J	0.25	0/1385	0.47	0/1852
11	L	0.27	0/1733	0.46	0/2316
12	M	0.25	0/1150	0.44	0/1534
13	N	0.24	0/1746	0.43	0/2338
14	O	0.25	0/1653	0.44	0/2206
15	P	0.24	0/1268	0.47	0/1700
16	Q	0.24	0/1539	0.48	0/2054
17	R	0.24	0/1524	0.44	0/2013
18	S	0.25	0/1501	0.48	0/2012
19	T	0.25	0/1326	0.44	0/1770
20	U	0.26	0/823	0.45	0/1104
21	V	0.26	0/983	0.46	0/1319
22	W	0.25	0/873	0.43	0/1158
23	X	0.24	0/984	0.46	0/1323
24	Y	0.24	0/1132	0.44	0/1504
25	Z	0.26	0/1130	0.46	0/1507
26	a	0.23	0/1191	0.42	0/1590
27	b	0.24	0/861	0.40	0/1138
28	c	0.25	0/771	0.45	0/1034
29	d	0.26	0/903	0.49	0/1216
30	e	0.24	0/1071	0.47	0/1429
31	f	0.25	0/895	0.49	0/1198
32	g	0.25	0/916	0.48	0/1220

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.25	0/1021	0.42	0/1348
34	i	0.25	0/841	0.43	0/1112
35	j	0.26	0/720	0.45	0/952
36	k	0.24	0/575	0.47	0/761
37	l	0.24	0/459	0.47	1/608 (0.2%)
38	m	0.25	0/435	0.46	0/575
39	n	0.23	0/240	0.40	0/305
40	o	0.24	0/864	0.46	0/1140
41	p	0.24	0/718	0.44	0/953
42	r	0.24	0/1010	0.47	0/1354
43	s	0.27	0/1530	0.47	0/2064
44	t	0.25	0/1174	0.52	0/1582
45	5	0.27	1/86202 (0.0%)	1.01	331/134412 (0.2%)
46	7	0.27	0/2836	1.00	5/4421 (0.1%)
47	8	0.27	0/3581	1.00	10/5577 (0.2%)
48	K	0.28	0/1730	0.55	0/2315
49	2	0.28	0/40500	1.03	194/63092 (0.3%)
50	BB	0.26	0/1747	0.51	0/2374
51	CC	0.26	0/1756	0.50	0/2350
52	DD	0.25	0/1753	0.48	0/2369
53	EE	0.26	0/1796	0.51	0/2417
54	FF	0.25	0/2118	0.47	0/2849
55	GG	0.25	0/1492	0.46	0/2005
56	HH	0.25	0/1946	0.48	0/2590
57	II	0.26	0/1510	0.50	1/2022 (0.0%)
58	JJ	0.25	0/1715	0.46	0/2287
59	KK	0.25	0/1550	0.48	0/2069
60	LL	0.25	0/834	0.48	0/1125
61	MM	0.25	0/1195	0.51	1/1597 (0.1%)
62	NN	0.26	0/918	0.54	0/1233
63	OO	0.24	0/1226	0.45	0/1649
64	PP	0.25	0/1029	0.49	0/1380
65	QQ	0.25	0/974	0.49	0/1301
66	RR	0.25	0/1146	0.48	1/1534 (0.1%)
67	SS	0.25	0/1082	0.50	1/1452 (0.1%)
68	TT	0.25	0/1208	0.47	0/1618
69	UU	0.25	0/1115	0.44	0/1493
70	VV	0.24	0/805	0.48	0/1081
71	WW	0.26	0/643	0.48	0/860
72	XX	0.26	0/1051	0.49	0/1406
73	YY	0.26	0/1116	0.48	0/1490
74	ZZ	0.25	0/1028	0.47	0/1366
75	aa	0.24	0/604	0.50	0/810

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	bb	0.24	0/828	0.44	0/1109
77	cc	0.24	0/665	0.47	0/891
78	dd	0.23	0/490	0.45	0/656
79	ee	0.25	0/470	0.41	0/623
80	ff	0.25	0/462	0.44	0/607
81	gg	0.24	0/567	0.46	0/753
82	hh	0.25	0/2492	0.52	0/3391
83	3	0.26	0/2077	0.96	2/3238 (0.1%)
84	9	0.26	0/6804	0.52	0/9189
85	4	0.69	16/4490 (0.4%)	1.54	125/6984 (1.8%)
All	All	0.28	17/243741 (0.0%)	0.86	675/357074 (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
3	C	0	1
50	BB	0	1
65	QQ	0	1
67	SS	0	1
73	YY	0	1
84	9	0	1
85	4	1	14
All	All	1	20

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	4	6178	U	C2-O2	9.15	1.30	1.22
85	4	6065	A	O3'-P	8.59	1.71	1.61
85	4	6078	A	O3'-P	-8.35	1.51	1.61
85	4	6217	C	O3'-P	8.15	1.71	1.61
85	4	6187	A	O3'-P	7.84	1.70	1.61
85	4	6077	U	C4-O4	7.79	1.29	1.23
85	4	6210	U	O3'-P	7.62	1.70	1.61
85	4	6166	C	O3'-P	7.58	1.70	1.61
85	4	6181	C	O3'-P	7.49	1.70	1.61
85	4	6218	U	C1'-N1	6.91	1.59	1.48
85	4	6219	U	C1'-N1	6.85	1.59	1.48
85	4	6212	U	O3'-P	6.57	1.69	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	4	6218	U	O3'-P	-5.81	1.54	1.61
85	4	6217	C	C3'-O3'	5.80	1.50	1.42
85	4	6197	A	O3'-P	5.37	1.67	1.61
45	5	4893	A	N9-C4	5.19	1.41	1.37
85	4	6181	C	C1'-N1	5.11	1.56	1.48

All (675) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	4	6068	U	OP1-P-O3'	25.71	161.75	105.20
85	4	6068	U	O3'-P-O5'	-20.16	65.70	104.00
85	4	6218	U	O3'-P-O5'	-18.73	68.41	104.00
85	4	6188	G	O5'-P-OP2	16.39	130.37	110.70
85	4	6218	U	P-O3'-C3'	15.72	138.56	119.70
85	4	6215	C	C4'-C3'-O3'	14.53	142.05	113.00
85	4	6188	G	O5'-P-OP1	-14.40	92.74	105.70
85	4	6065	A	O4'-C1'-N9	14.02	119.42	108.20
85	4	6204	A	O3'-P-O5'	-13.97	77.46	104.00
85	4	6077	U	C5-C4-O4	-13.70	117.68	125.90
85	4	6212	U	N1-C1'-C2'	12.71	130.52	114.00
85	4	6210	U	O4'-C1'-N1	12.54	118.23	108.20
85	4	6068	U	OP2-P-O3'	-12.18	78.40	105.20
85	4	6218	U	OP1-P-O3'	11.97	131.53	105.20
85	4	6077	U	N1-C1'-C2'	-11.54	99.00	114.00
85	4	6197	A	N9-C1'-C2'	11.49	128.93	114.00
85	4	6177	U	N1-C1'-C2'	11.39	128.80	114.00
85	4	6176	U	C1'-C2'-O2'	-11.23	76.91	110.60
85	4	6211	U	N1-C1'-C2'	11.11	128.44	114.00
85	4	6199	A	C4-N9-C1'	-10.68	107.08	126.30
85	4	6199	A	O4'-C1'-N9	10.67	116.73	108.20
85	4	6179	U	N1-C1'-C2'	10.64	127.83	114.00
85	4	6166	C	C4'-C3'-O3'	10.44	133.87	113.00
85	4	6181	C	C6-N1-C1'	-10.29	108.45	120.80
49	2	1852	C	N1-C2-O2	9.99	124.89	118.90
85	4	6211	U	O4'-C1'-N1	9.89	116.11	108.20
85	4	6181	C	C3'-C2'-C1'	9.87	109.40	101.50
85	4	6199	A	C8-N9-C1'	9.85	145.43	127.70
85	4	6168	C	N1-C1'-C2'	9.78	126.71	114.00
85	4	6065	A	C8-N9-C1'	-9.73	110.18	127.70
49	2	1261	C	N1-C2-O2	9.73	124.74	118.90
85	4	6151	A	O4'-C1'-N9	9.67	115.94	108.20
85	4	6210	U	N1-C1'-C2'	9.46	126.30	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	5	2655	C	N1-C2-O2	9.44	124.56	118.90
85	4	6199	A	N9-C1'-C2'	9.43	126.26	114.00
49	2	1063	C	N1-C2-O2	9.43	124.56	118.90
85	4	6216	U	O4'-C1'-N1	9.42	115.73	108.20
85	4	6064	G	N9-C1'-C2'	-9.35	101.72	112.00
49	2	178	C	N1-C2-O2	9.08	124.35	118.90
45	5	220	C	N1-C2-O2	9.01	124.30	118.90
85	4	6178	U	C4'-C3'-O3'	8.93	130.85	113.00
85	4	6201	C	N1-C1'-C2'	-8.88	102.23	112.00
45	5	2499	C	N1-C2-O2	8.86	124.22	118.90
85	4	6197	A	C8-N9-C1'	-8.84	111.78	127.70
45	5	2819	U	N3-C2-O2	-8.83	116.02	122.20
85	4	6150	C	C2'-C3'-O3'	8.82	128.90	109.50
85	4	6187	A	C1'-C2'-O2'	-8.59	84.84	110.60
49	2	494	C	N1-C2-O2	8.57	124.04	118.90
49	2	1442	U	N1-C2-O2	8.52	128.76	122.80
45	5	3909	C	N1-C2-O2	8.47	123.98	118.90
45	5	4958	C	N1-C2-O2	8.45	123.97	118.90
85	4	6215	C	N1-C1'-C2'	-8.44	102.72	112.00
85	4	6200	A	N9-C1'-C2'	-8.43	102.73	112.00
49	2	1865	C	N1-C2-O2	8.42	123.95	118.90
85	4	6176	U	N1-C1'-C2'	-8.40	102.76	112.00
49	2	1750	C	N1-C2-O2	8.38	123.93	118.90
45	5	112	C	N1-C2-O2	8.38	123.93	118.90
49	2	1261	C	C2-N1-C1'	8.37	128.00	118.80
49	2	1442	U	N3-C2-O2	-8.29	116.40	122.20
45	5	2819	U	N1-C2-O2	8.26	128.58	122.80
85	4	6074	A	N9-C1'-C2'	-8.21	102.97	112.00
45	5	1193	C	C2-N1-C1'	8.20	127.82	118.80
85	4	6181	C	N1-C1'-C2'	8.19	124.64	114.00
45	5	473	C	N1-C2-O2	8.17	123.80	118.90
85	4	6181	C	C1'-C2'-O2'	-8.17	86.10	110.60
49	2	1624	U	C2-N1-C1'	8.07	127.39	117.70
49	2	1261	C	N3-C2-O2	-8.05	116.26	121.90
45	5	2655	C	N3-C2-O2	-7.93	116.35	121.90
85	4	6197	A	C4-N9-C1'	7.92	140.55	126.30
85	4	6151	A	C1'-O4'-C4'	-7.84	103.62	109.90
45	5	1276	C	N1-C2-O2	7.82	123.59	118.90
45	5	282	C	N1-C2-O2	7.81	123.59	118.90
45	5	3810	C	C2-N1-C1'	7.80	127.38	118.80
49	2	632	C	N1-C2-O2	7.79	123.58	118.90
49	2	1688	C	N3-C2-O2	-7.78	116.45	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	5	2499	C	N3-C2-O2	-7.78	116.46	121.90
49	2	1520	G	C4-N9-C1'	7.73	136.55	126.50
47	8	119	C	N1-C2-O2	7.71	123.53	118.90
49	2	1852	C	N3-C2-O2	-7.71	116.50	121.90
49	2	178	C	N3-C2-O2	-7.71	116.50	121.90
85	4	6077	U	N3-C4-O4	-7.71	114.00	119.40
85	4	6062	G	N9-C1'-C2'	-7.71	103.52	112.00
49	2	1865	C	C2-N1-C1'	7.71	127.28	118.80
45	5	2020	U	N3-C2-O2	-7.70	116.81	122.20
45	5	3810	C	N1-C2-O2	7.69	123.51	118.90
85	4	6078	A	P-O3'-C3'	-7.66	110.50	119.70
45	5	2022	C	N3-C2-O2	-7.66	116.54	121.90
45	5	67	C	N1-C2-O2	7.64	123.48	118.90
85	4	6187	A	C4'-C3'-O3'	-7.62	93.41	109.40
85	4	6065	A	C4-N9-C1'	7.61	139.99	126.30
45	5	202	C	N1-C2-O2	7.51	123.41	118.90
49	2	178	C	C6-N1-C2	-7.49	117.30	120.30
49	2	1063	C	N3-C2-O2	-7.49	116.66	121.90
45	5	1429	C	N1-C2-O2	7.47	123.38	118.90
45	5	1827	C	N1-C2-O2	7.46	123.38	118.90
85	4	6067	G	N9-C1'-C2'	7.44	123.68	114.00
49	2	1520	G	N3-C4-N9	7.44	130.46	126.00
85	4	6188	G	P-O5'-C5'	7.44	132.80	120.90
49	2	1261	C	C6-N1-C2	-7.42	117.33	120.30
45	5	2464	C	N1-C2-O2	7.42	123.35	118.90
45	5	18	C	N1-C2-O2	7.38	123.33	118.90
45	5	2020	U	N1-C2-O2	7.38	127.97	122.80
85	4	6151	A	C4-N9-C1'	-7.37	113.03	126.30
85	4	6076	U	N1-C1'-C2'	-7.36	103.90	112.00
45	5	3778	U	N1-C2-O2	7.36	127.95	122.80
45	5	174	C	N3-C2-O2	-7.35	116.76	121.90
49	2	1118	C	C2-N1-C1'	7.34	126.87	118.80
49	2	1597	C	N1-C2-O2	7.33	123.30	118.90
45	5	2022	C	N1-C2-O2	7.31	123.29	118.90
85	4	6166	C	C3'-C2'-C1'	7.30	107.34	101.50
45	5	4266	G	C4-N9-C1'	7.29	135.97	126.50
85	4	6187	A	C2'-C3'-O3'	7.28	125.52	109.50
49	2	178	C	C2-N1-C1'	7.27	126.80	118.80
45	5	233	U	C2-N1-C1'	7.27	126.42	117.70
45	5	3657	U	N1-C2-O2	7.26	127.88	122.80
49	2	429	C	N1-C2-O2	7.24	123.24	118.90
85	4	6216	U	C4'-C3'-O3'	7.24	127.47	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	5	4930	C	C2-N1-C1'	7.21	126.74	118.80
49	2	1742	C	N1-C2-O2	7.21	123.23	118.90
45	5	4232	U	P-O3'-C3'	7.21	128.35	119.70
49	2	1852	C	C2-N1-C1'	7.20	126.72	118.80
85	4	6151	A	C5'-C4'-O4'	7.19	117.72	109.10
49	2	1520	G	N3-C4-C5	-7.17	125.01	128.60
45	5	4261	C	N1-C2-O2	7.17	123.20	118.90
49	2	1315	U	N1-C2-O2	7.16	127.81	122.80
49	2	1442	U	C2-N1-C1'	7.15	126.28	117.70
45	5	220	C	N3-C2-O2	-7.15	116.90	121.90
45	5	2655	C	C2-N1-C1'	7.14	126.65	118.80
85	4	6177	U	C4'-C3'-O3'	7.12	127.25	113.00
49	2	1624	U	N1-C2-O2	7.12	127.78	122.80
49	2	1595	U	N1-C2-O2	7.11	127.78	122.80
49	2	179	C	N1-C2-O2	7.10	123.16	118.90
45	5	18	C	C2-N1-C1'	7.09	126.60	118.80
45	5	2655	C	C6-N1-C2	-7.09	117.47	120.30
49	2	1063	C	C2-N1-C1'	7.09	126.60	118.80
45	5	985	C	N1-C2-O2	7.08	123.14	118.90
49	2	1298	G	N3-C4-C5	-7.07	125.07	128.60
45	5	2695	A	P-O3'-C3'	7.05	128.16	119.70
49	2	585	C	N1-C2-O2	7.05	123.13	118.90
45	5	4925	U	OP2-P-O3'	7.05	120.71	105.20
45	5	4177	C	N1-C2-O2	7.04	123.13	118.90
45	5	2351	C	N1-C2-O2	7.03	123.12	118.90
49	2	1750	C	N3-C2-O2	-7.02	116.98	121.90
49	2	1298	G	N3-C4-N9	7.00	130.20	126.00
85	4	6187	A	O4'-C1'-N9	7.00	113.80	108.20
49	2	1597	C	N3-C2-O2	-7.00	117.00	121.90
45	5	4266	G	N3-C4-C5	-6.98	125.11	128.60
49	2	1118	C	N1-C2-O2	6.98	123.09	118.90
45	5	3909	C	N3-C2-O2	-6.97	117.02	121.90
49	2	1315	U	N3-C2-O2	-6.97	117.32	122.20
49	2	688	U	P-O3'-C3'	6.94	128.03	119.70
85	4	6215	C	C3'-C2'-C1'	6.94	107.05	101.50
49	2	494	C	C2-N1-C1'	6.94	126.43	118.80
45	5	4925	U	P-O3'-C3'	6.93	128.02	119.70
45	5	3657	U	N3-C2-O2	-6.93	117.35	122.20
45	5	390	C	N1-C2-O2	6.92	123.05	118.90
45	5	2820	C	N1-C2-O2	6.92	123.05	118.90
45	5	4266	G	N3-C4-N9	6.90	130.14	126.00
49	2	1123	C	N1-C2-O2	6.89	123.04	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	5	1612	G	C4-N9-C1'	6.89	135.46	126.50
49	2	1298	G	C4-N9-C1'	6.89	135.46	126.50
45	5	3778	U	N3-C2-O2	-6.87	117.39	122.20
45	5	3778	U	C2-N1-C1'	6.84	125.91	117.70
49	2	1624	U	N3-C2-O2	-6.84	117.41	122.20
49	2	1063	C	C6-N1-C2	-6.84	117.56	120.30
45	5	1612	G	N3-C4-N9	6.82	130.09	126.00
45	5	2373	C	N1-C2-O2	6.82	122.99	118.90
85	4	6180	U	C4'-C3'-O3'	-6.80	95.13	109.40
45	5	220	C	C6-N1-C2	-6.79	117.58	120.30
45	5	4627	U	N1-C2-O2	6.79	127.55	122.80
49	2	193	C	N3-C2-O2	-6.78	117.16	121.90
49	2	1772	C	N1-C2-O2	6.77	122.96	118.90
45	5	2089	G	P-O3'-C3'	6.77	127.82	119.70
45	5	4774	C	N1-C2-O2	6.77	122.96	118.90
85	4	6181	C	C2-N1-C1'	6.76	126.23	118.80
49	2	1852	C	C6-N1-C2	-6.75	117.60	120.30
85	4	6151	A	C8-N9-C1'	6.75	139.86	127.70
49	2	494	C	N3-C2-O2	-6.75	117.17	121.90
49	2	1750	C	C6-N1-C2	-6.74	117.61	120.30
47	8	64	U	N3-C2-O2	-6.74	117.48	122.20
45	5	4747	C	N1-C2-O2	6.73	122.94	118.90
85	4	6198	A	C5'-C4'-C3'	6.73	126.77	116.00
45	5	4759	C	N1-C2-O2	6.72	122.93	118.90
49	2	1595	U	N3-C2-O2	-6.70	117.51	122.20
45	5	2046	G	P-O3'-C3'	6.70	127.73	119.70
47	8	64	U	N1-C2-O2	6.69	127.48	122.80
49	2	340	C	N1-C2-O2	6.68	122.91	118.90
49	2	532	C	P-O3'-C3'	6.68	127.71	119.70
85	4	6179	U	C2-N1-C1'	-6.68	109.69	117.70
85	4	6187	A	P-O3'-C3'	6.68	127.71	119.70
45	5	4880	C	C2-N1-C1'	6.67	126.14	118.80
49	2	1139	C	N1-C2-O2	6.66	122.89	118.90
49	2	1271	C	N1-C2-O2	6.66	122.89	118.90
85	4	6065	A	C1'-C2'-O2'	-6.65	90.64	110.60
85	4	6065	A	C2'-C3'-O3'	-6.65	94.87	109.50
49	2	24	C	N1-C2-O2	6.64	122.89	118.90
49	2	1315	U	C2-N1-C1'	6.64	125.67	117.70
45	5	1276	C	C2-N1-C1'	6.64	126.10	118.80
45	5	3851	U	N1-C2-O2	6.64	127.45	122.80
45	5	517	C	N1-C2-O2	6.63	122.88	118.90
45	5	1977	C	N1-C2-O2	6.63	122.88	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	8	129	C	N1-C2-O2	6.62	122.87	118.90
49	2	879	C	N1-C2-O2	6.61	122.87	118.90
45	5	1484	G	C4-N9-C1'	6.61	135.09	126.50
45	5	112	C	N3-C2-O2	-6.60	117.28	121.90
45	5	3831	U	N3-C2-O2	-6.60	117.58	122.20
45	5	4958	C	N3-C2-O2	-6.58	117.29	121.90
49	2	1865	C	N3-C2-O2	-6.57	117.30	121.90
49	2	1057	C	C2-N1-C1'	6.56	126.02	118.80
45	5	50	C	N1-C2-O2	6.54	122.82	118.90
45	5	220	C	C2-N1-C1'	6.53	125.99	118.80
45	5	112	C	C2-N1-C1'	6.53	125.98	118.80
47	8	119	C	N3-C2-O2	-6.53	117.33	121.90
45	5	473	C	N3-C2-O2	-6.52	117.33	121.90
46	7	102	U	N1-C2-O2	6.52	127.36	122.80
45	5	4627	U	N3-C2-O2	-6.51	117.64	122.20
45	5	4948	C	C2-N1-C1'	6.50	125.95	118.80
49	2	1664	A	P-O3'-C3'	6.50	127.50	119.70
85	4	6213	A	O5'-P-OP1	-6.48	99.87	105.70
45	5	4177	C	C2-N1-C1'	6.48	125.92	118.80
45	5	2020	U	C2-N1-C1'	6.47	125.47	117.70
49	2	553	U	P-O3'-C3'	6.47	127.46	119.70
83	3	74	C	C2-N1-C1'	6.46	125.91	118.80
49	2	752	G	P-O3'-C3'	6.45	127.44	119.70
2	B	309	LEU	CA-CB-CG	6.44	130.11	115.30
49	2	1395	C	P-O3'-C3'	6.43	127.42	119.70
49	2	1750	C	C2-N1-C1'	6.43	125.87	118.80
85	4	6198	A	C8-N9-C1'	-6.43	116.13	127.70
45	5	2819	U	C2-N1-C1'	6.42	125.41	117.70
45	5	4054	C	P-O3'-C3'	6.42	127.40	119.70
45	5	3657	U	C2-N1-C1'	6.42	125.40	117.70
45	5	1484	G	N3-C4-C5	-6.41	125.39	128.60
85	4	6065	A	C1'-O4'-C4'	-6.40	104.78	109.90
85	4	6209	A	O4'-C1'-N9	6.40	113.32	108.20
45	5	1612	G	N3-C4-C5	-6.39	125.40	128.60
85	4	6188	G	OP1-P-OP2	-6.38	110.02	119.60
45	5	1725	U	N3-C2-O2	-6.38	117.74	122.20
85	4	6210	U	O4'-C1'-C2'	6.38	113.34	107.60
45	5	481	G	P-O3'-C3'	6.37	127.35	119.70
85	4	6169	U	N1-C1'-C2'	6.37	122.28	114.00
45	5	4958	C	C2-N1-C1'	6.37	125.80	118.80
49	2	1017	U	N1-C2-O2	6.37	127.26	122.80
49	2	1637	A	P-O3'-C3'	6.36	127.34	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	5	1481	C	N1-C2-O2	6.36	122.72	118.90
85	4	6209	A	C8-N9-C1'	6.36	139.15	127.70
45	5	2528	G	C4-N9-C1'	6.36	134.77	126.50
49	2	1520	G	C8-N9-C1'	-6.36	118.73	127.00
45	5	3831	U	N1-C2-O2	6.35	127.25	122.80
85	4	6188	G	C5'-C4'-C3'	-6.35	105.84	116.00
45	5	1072	C	P-O3'-C3'	6.33	127.29	119.70
49	2	1139	C	C6-N1-C2	-6.33	117.77	120.30
49	2	193	C	N1-C2-O2	6.32	122.69	118.90
49	2	1518	C	C2-N1-C1'	6.31	125.74	118.80
49	2	118	C	N1-C2-O2	6.31	122.68	118.90
85	4	6209	A	C4-N9-C1'	-6.31	114.95	126.30
49	2	183	G	C4-N9-C1'	6.30	134.69	126.50
49	2	1303	C	N1-C2-O2	6.30	122.68	118.90
45	5	2661	U	P-O3'-C3'	6.30	127.26	119.70
49	2	14	C	C2-N1-C1'	6.30	125.73	118.80
45	5	704	C	N1-C2-O2	6.29	122.67	118.90
45	5	282	C	N3-C2-O2	-6.29	117.50	121.90
45	5	1725	U	N1-C2-O2	6.29	127.20	122.80
45	5	233	U	N1-C2-O2	6.28	127.19	122.80
45	5	3909	C	C2-N1-C1'	6.28	125.70	118.80
45	5	1276	C	N3-C2-O2	-6.27	117.51	121.90
45	5	131	C	N3-C2-O2	-6.25	117.53	121.90
49	2	1453	C	C2-N1-C1'	6.25	125.67	118.80
45	5	1084	C	N1-C2-O2	6.24	122.64	118.90
45	5	1812	C	N1-C2-O2	6.24	122.64	118.90
45	5	4709	U	N1-C2-O2	6.24	127.17	122.80
85	4	6065	A	C4'-C3'-O3'	6.23	125.47	113.00
45	5	473	C	C2-N1-C1'	6.23	125.66	118.80
45	5	4263	C	N1-C2-O2	6.23	122.64	118.90
85	4	6181	C	C4'-C3'-O3'	6.23	125.46	113.00
45	5	2560	C	N1-C2-O2	6.23	122.64	118.90
45	5	1481	C	C2-N1-C1'	6.22	125.64	118.80
45	5	4759	C	C2-N1-C1'	6.22	125.64	118.80
45	5	1484	G	N3-C4-N9	6.21	129.73	126.00
45	5	1478	C	N1-C2-O2	6.21	122.62	118.90
85	4	6183	G	C4'-C3'-O3'	-6.21	96.36	109.40
45	5	202	C	C2-N1-C1'	6.21	125.63	118.80
45	5	4413	C	C2-N1-C1'	6.21	125.63	118.80
45	5	1781	U	N1-C2-O2	6.20	127.14	122.80
49	2	494	C	C6-N1-C2	-6.19	117.83	120.30
45	5	3855	C	N1-C2-O2	6.19	122.61	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	5	1893	C	N1-C2-O2	6.18	122.61	118.90
85	4	6217	C	C3'-C2'-C1'	6.18	106.44	101.50
49	2	1596	U	N1-C2-O2	6.18	127.12	122.80
45	5	3909	C	C6-N1-C2	-6.17	117.83	120.30
49	2	1596	U	N3-C2-O2	-6.16	117.89	122.20
45	5	704	C	C2-N1-C1'	6.16	125.57	118.80
45	5	2464	C	N3-C2-O2	-6.15	117.59	121.90
45	5	1344	C	N1-C2-O2	6.15	122.59	118.90
49	2	632	C	N3-C2-O2	-6.15	117.60	121.90
85	4	6198	A	C5'-C4'-O4'	6.15	116.47	109.10
46	7	102	U	N3-C2-O2	-6.14	117.90	122.20
85	4	6151	A	O4'-C4'-C3'	-6.13	97.87	104.00
45	5	2627	C	C2-N1-C1'	6.12	125.53	118.80
45	5	3810	C	N3-C2-O2	-6.11	117.62	121.90
45	5	1081	C	N1-C2-O2	6.11	122.57	118.90
45	5	2351	C	N3-C2-O2	-6.10	117.63	121.90
45	5	2499	C	C2-N1-C1'	6.10	125.50	118.80
85	4	6077	U	C4'-C3'-O3'	6.09	125.19	113.00
45	5	1993	C	N1-C2-O2	6.09	122.55	118.90
49	2	86	C	N1-C2-O2	6.09	122.55	118.90
45	5	1807	C	C2-N1-C1'	6.08	125.49	118.80
45	5	390	C	N3-C2-O2	-6.07	117.65	121.90
45	5	4266	G	C8-N9-C1'	-6.07	119.11	127.00
49	2	13	C	C2-N1-C1'	6.07	125.48	118.80
49	2	429	C	N3-C2-O2	-6.07	117.65	121.90
85	4	6198	A	O4'-C1'-N9	6.06	113.05	108.20
85	4	6077	U	N3-C4-C5	-6.06	110.97	114.60
49	2	1017	U	N3-C2-O2	-6.05	117.96	122.20
49	2	568	C	N1-C2-O2	6.05	122.53	118.90
49	2	179	C	N3-C2-O2	-6.04	117.67	121.90
45	5	1467	C	N1-C2-O2	6.03	122.52	118.90
49	2	188	C	C2-N1-C1'	6.03	125.43	118.80
49	2	1443	C	N1-C2-O2	6.02	122.51	118.90
45	5	4958	C	C6-N1-C2	-6.01	117.89	120.30
49	2	1303	C	C2-N1-C1'	6.01	125.42	118.80
45	5	4413	C	N1-C2-O2	6.01	122.50	118.90
45	5	2802	C	C2-N1-C1'	6.00	125.40	118.80
85	4	6107	A	C2'-C3'-O3'	6.00	123.29	113.70
45	5	1081	C	N3-C2-O2	-5.99	117.71	121.90
47	8	119	C	C6-N1-C2	-5.99	117.91	120.30
49	2	632	C	C6-N1-C2	-5.99	117.91	120.30
45	5	3851	U	N3-C2-O2	-5.99	118.01	122.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	5	985	C	N3-C2-O2	-5.98	117.71	121.90
85	4	6212	U	P-O3'-C3'	5.98	126.88	119.70
45	5	4303	C	C2-N1-C1'	5.98	125.38	118.80
49	2	1298	G	C8-N9-C1'	-5.98	119.23	127.00
45	5	4476	C	N1-C2-O2	5.97	122.48	118.90
45	5	4893	A	C2-N3-C4	5.97	113.58	110.60
45	5	2499	C	C6-N1-C2	-5.97	117.91	120.30
45	5	4612	C	N1-C2-O2	5.97	122.48	118.90
47	8	64	U	C2-N1-C1'	5.96	124.86	117.70
45	5	1276	C	C6-N1-C2	-5.96	117.92	120.30
49	2	24	C	P-O3'-C3'	5.95	126.84	119.70
49	2	183	G	O4'-C1'-N9	5.95	112.96	108.20
45	5	112	C	C6-N1-C2	-5.94	117.92	120.30
45	5	1994	C	C2-N1-C1'	5.94	125.33	118.80
49	2	801	U	N1-C2-O2	5.93	126.95	122.80
49	2	1660	C	C2-N1-C1'	5.93	125.33	118.80
45	5	2528	G	N3-C4-C5	-5.93	125.64	128.60
45	5	2614	C	C2-N1-C1'	5.93	125.32	118.80
45	5	4592	C	N1-C2-O2	5.92	122.45	118.90
49	2	801	U	N3-C2-O2	-5.92	118.05	122.20
45	5	1429	C	N3-C2-O2	-5.92	117.76	121.90
45	5	2572	C	N1-C2-O2	5.92	122.45	118.90
49	2	1057	C	N1-C2-O2	5.92	122.45	118.90
49	2	1399	C	N1-C2-O2	5.91	122.45	118.90
45	5	1612	G	C8-N9-C1'	-5.91	119.32	127.00
45	5	3882	C	C2-N1-C1'	5.90	125.29	118.80
45	5	174	C	C6-N1-C2	-5.90	117.94	120.30
45	5	2627	C	N1-C2-O2	5.90	122.44	118.90
49	2	356	C	C2-N1-C1'	5.90	125.29	118.80
45	5	4930	C	C6-N1-C2	-5.88	117.95	120.30
66	RR	31	LEU	CA-CB-CG	5.86	128.78	115.30
45	5	3892	U	N3-C2-O2	-5.86	118.10	122.20
45	5	4928	C	C2-N1-C1'	5.86	125.24	118.80
49	2	1489	A	P-O3'-C3'	5.86	126.73	119.70
45	5	4170	A	P-O3'-C3'	5.85	126.72	119.70
45	5	517	C	C2-N1-C1'	5.85	125.23	118.80
45	5	48	G	P-O3'-C3'	5.84	126.71	119.70
45	5	100	C	C2-N1-C1'	5.84	125.22	118.80
83	3	74	C	C6-N1-C2	-5.84	117.96	120.30
45	5	3855	C	N3-C2-O2	-5.83	117.82	121.90
85	4	6182	A	C4-N9-C1'	-5.82	115.82	126.30
45	5	1431	C	N1-C2-O2	5.82	122.39	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	2	1139	C	N3-C2-O2	-5.82	117.83	121.90
46	7	95	C	N1-C2-O2	5.82	122.39	118.90
45	5	473	C	C6-N1-C2	-5.82	117.97	120.30
45	5	1796	U	N1-C2-O2	5.82	126.87	122.80
45	5	2528	G	N3-C4-N9	5.81	129.49	126.00
45	5	202	C	N3-C2-O2	-5.80	117.84	121.90
45	5	1193	C	C6-N1-C2	-5.79	117.98	120.30
49	2	1852	C	C5-C6-N1	5.79	123.90	121.00
45	5	4709	U	N3-C2-O2	-5.79	118.15	122.20
49	2	853	C	C2-N1-C1'	5.79	125.17	118.80
45	5	2072	C	N1-C2-O2	5.79	122.37	118.90
45	5	3693	U	N1-C2-O2	5.77	126.84	122.80
45	5	2266	C	P-O3'-C3'	5.76	126.62	119.70
45	5	1237	C	C2-N1-C1'	5.76	125.14	118.80
45	5	1210	C	C2-N1-C1'	5.76	125.13	118.80
45	5	282	C	C2-N1-C1'	5.75	125.13	118.80
85	4	6216	U	N1-C1'-C2'	-5.75	105.67	112.00
45	5	67	C	N3-C2-O2	-5.75	117.88	121.90
45	5	2820	C	N3-C2-O2	-5.75	117.88	121.90
45	5	74	G	C4-N9-C1'	5.75	133.97	126.50
85	4	6178	U	O4'-C1'-N1	5.74	112.79	108.20
45	5	1781	U	N3-C2-O2	-5.73	118.19	122.20
49	2	356	C	N1-C2-O2	5.73	122.34	118.90
49	2	553	U	OP1-P-O3'	5.73	117.81	105.20
47	8	124	U	P-O3'-C3'	5.73	126.58	119.70
49	2	1311	C	N1-C2-O2	5.72	122.33	118.90
49	2	1022	U	C2-N1-C1'	5.72	124.57	117.70
45	5	1827	C	N3-C2-O2	-5.72	117.89	121.90
49	2	632	C	C2-N1-C1'	5.72	125.09	118.80
2	B	17	LEU	CA-CB-CG	5.72	128.45	115.30
47	8	119	C	C2-N1-C1'	5.72	125.09	118.80
49	2	1063	C	C5-C6-N1	5.71	123.86	121.00
45	5	1467	C	N3-C2-O2	-5.71	117.91	121.90
45	5	304	C	N1-C2-O2	5.71	122.32	118.90
45	5	233	U	N3-C2-O2	-5.70	118.21	122.20
49	2	1742	C	N3-C2-O2	-5.70	117.91	121.90
49	2	1261	C	C5-C6-N1	5.69	123.85	121.00
45	5	971	U	C2-N1-C1'	5.69	124.53	117.70
45	5	67	C	C2-N1-C1'	5.69	125.05	118.80
45	5	4177	C	N3-C2-O2	-5.69	117.92	121.90
45	5	18	C	N3-C2-O2	-5.68	117.92	121.90
45	5	18	C	C6-N1-C2	-5.68	118.03	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	5	4948	C	N1-C2-O2	5.68	122.31	118.90
85	4	6179	U	O4'-C1'-N1	5.68	112.75	108.20
85	4	6187	A	C3'-C2'-O2'	5.68	129.78	113.30
45	5	4261	C	N3-C2-O2	-5.67	117.93	121.90
45	5	220	C	C5-C6-N1	5.67	123.84	121.00
49	2	1019	C	N1-C2-O2	5.67	122.30	118.90
45	5	3835	C	N1-C2-O2	5.66	122.30	118.90
49	2	1453	C	N1-C2-O2	5.66	122.30	118.90
45	5	2572	C	C2-N1-C1'	5.66	125.02	118.80
45	5	4476	C	C2-N1-C1'	5.66	125.02	118.80
45	5	4747	C	C2-N1-C1'	5.65	125.02	118.80
45	5	115	C	C2-N1-C1'	5.65	125.01	118.80
45	5	1193	C	C6-N1-C1'	-5.64	114.03	120.80
45	5	4525	C	N1-C2-O2	5.64	122.28	118.90
45	5	4360	U	N1-C2-O2	5.63	126.75	122.80
85	4	6059	U	C2'-C3'-O3'	5.63	122.71	113.70
45	5	1193	C	N1-C2-O2	5.62	122.28	118.90
45	5	390	C	C6-N1-C2	-5.62	118.05	120.30
45	5	1827	C	C2-N1-C1'	5.62	124.98	118.80
49	2	1314	U	C2-N1-C1'	5.62	124.45	117.70
49	2	899	U	N1-C2-O2	5.62	126.73	122.80
45	5	1727	U	C2-N1-C1'	5.61	124.43	117.70
45	5	126	C	C2-N1-C1'	5.61	124.97	118.80
49	2	1660	C	N1-C2-O2	5.61	122.27	118.90
49	2	1253	A	P-O3'-C3'	5.60	126.42	119.70
85	4	6215	C	C2'-C3'-O3'	-5.60	97.19	109.50
49	2	801	U	C2-N1-C1'	5.59	124.41	117.70
49	2	178	C	C5-C6-N1	5.59	123.80	121.00
49	2	585	C	N3-C2-O2	-5.59	117.99	121.90
49	2	621	C	N1-C2-O2	5.59	122.25	118.90
45	5	4261	C	C2-N1-C1'	5.59	124.95	118.80
45	5	4560	C	N1-C2-O2	5.59	122.25	118.90
45	5	1781	U	C2-N1-C1'	5.59	124.41	117.70
49	2	1595	U	C2-N1-C1'	5.58	124.40	117.70
45	5	4885	U	N1-C2-O2	5.58	126.70	122.80
49	2	1123	C	N3-C2-O2	-5.58	118.00	121.90
45	5	3693	U	N3-C2-O2	-5.56	118.31	122.20
49	2	130	G	N3-C4-N9	5.56	129.34	126.00
49	2	899	U	N3-C2-O2	-5.55	118.31	122.20
49	2	130	G	N3-C4-C5	-5.55	125.83	128.60
45	5	4885	U	N3-C2-O2	-5.55	118.32	122.20
45	5	1796	U	N3-C2-O2	-5.54	118.32	122.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	5	4052	C	C6-N1-C2	-5.54	118.08	120.30
85	4	6187	A	C4-N9-C1'	-5.54	116.32	126.30
45	5	2351	C	C6-N1-C2	-5.54	118.08	120.30
49	2	183	G	N3-C4-N9	5.54	129.32	126.00
45	5	4880	C	N1-C2-O2	5.53	122.22	118.90
49	2	1753	C	C2-N1-C1'	5.53	124.88	118.80
85	4	6065	A	C5'-C4'-C3'	5.52	124.84	116.00
45	5	4929	C	N1-C2-O2	5.52	122.21	118.90
45	5	4893	A	C4-N9-C1'	5.52	136.24	126.30
49	2	430	C	N1-C2-O2	5.52	122.21	118.90
49	2	1118	C	N3-C2-O2	-5.52	118.04	121.90
85	4	6179	U	C5'-C4'-C3'	5.52	124.83	116.00
49	2	55	U	C2-N1-C1'	5.51	124.31	117.70
45	5	2008	U	C2-N1-C1'	5.51	124.31	117.70
45	5	1458	C	N1-C2-O2	5.51	122.20	118.90
85	4	6182	A	O4'-C1'-N9	5.51	112.61	108.20
85	4	6150	C	C4'-C3'-O3'	5.50	124.01	113.00
45	5	1429	C	C2-N1-C1'	5.50	124.85	118.80
45	5	1478	C	C2-N1-C1'	5.49	124.84	118.80
45	5	2373	C	N3-C2-O2	-5.49	118.06	121.90
49	2	630	U	C2-N1-C1'	5.49	124.29	117.70
49	2	1395	C	OP1-P-O3'	5.49	117.27	105.20
49	2	823	U	N3-C2-O2	-5.48	118.36	122.20
45	5	1179	U	C2-N1-C1'	5.48	124.27	117.70
49	2	24	C	C2-N1-C1'	5.48	124.82	118.80
45	5	3870	C	N1-C2-O2	5.47	122.18	118.90
45	5	4303	C	N1-C2-O2	5.47	122.18	118.90
45	5	985	C	C6-N1-C2	-5.47	118.11	120.30
45	5	4148	C	N1-C2-O2	5.47	122.18	118.90
45	5	130	C	N3-C2-O2	-5.46	118.08	121.90
45	5	180	C	N1-C2-O2	5.46	122.17	118.90
45	5	196	C	N3-C2-O2	-5.46	118.08	121.90
45	5	1484	G	C8-N9-C1'	-5.45	119.91	127.00
47	8	130	C	N1-C2-O2	5.45	122.17	118.90
45	5	282	C	C6-N1-C2	-5.45	118.12	120.30
49	2	1271	C	N3-C2-O2	-5.45	118.09	121.90
49	2	1513	C	N1-C2-O2	5.45	122.17	118.90
49	2	14	C	C5-C6-N1	5.45	123.72	121.00
45	5	1237	C	N1-C2-O2	5.45	122.17	118.90
45	5	1460	C	N1-C2-O2	5.44	122.16	118.90
85	4	6166	C	O4'-C1'-N1	5.44	112.55	108.20
49	2	24	C	N3-C2-O2	-5.44	118.09	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	2	1742	C	C2-N1-C1'	5.44	124.78	118.80
85	4	6182	A	C8-N9-C1'	5.44	137.48	127.70
57	II	122	LEU	CA-CB-CG	5.43	127.78	115.30
45	5	1215	C	N1-C2-O2	5.42	122.15	118.90
45	5	1325	C	N1-C2-O2	5.42	122.15	118.90
45	5	3835	C	N3-C2-O2	-5.42	118.11	121.90
49	2	182	C	P-O3'-C3'	5.42	126.20	119.70
45	5	4709	U	C2-N1-C1'	5.42	124.20	117.70
49	2	183	G	C8-N9-C1'	-5.41	119.96	127.00
49	2	55	U	N1-C2-O2	5.41	126.59	122.80
85	4	6216	U	C2-N1-C1'	-5.41	111.21	117.70
45	5	654	C	N1-C2-O2	5.41	122.14	118.90
45	5	3882	C	N1-C2-O2	5.41	122.14	118.90
49	2	1518	C	N1-C2-O2	5.41	122.14	118.90
45	5	2351	C	C2-N1-C1'	5.40	124.74	118.80
49	2	585	C	C2-N1-C1'	5.40	124.74	118.80
49	2	17	C	N1-C2-O2	5.40	122.14	118.90
49	2	879	C	N3-C2-O2	-5.39	118.13	121.90
85	4	6064	G	C4'-C3'-O3'	5.39	123.78	113.00
1	A	29	LEU	CA-CB-CG	5.38	127.68	115.30
49	2	295	C	N1-C2-O2	5.38	122.13	118.90
45	5	221	C	C2-N1-C1'	5.38	124.72	118.80
45	5	4398	C	N1-C2-O2	5.38	122.13	118.90
49	2	130	G	C4-N9-C1'	5.38	133.49	126.50
45	5	2856	C	N1-C2-O2	5.38	122.13	118.90
45	5	3810	C	C6-N1-C1'	-5.37	114.35	120.80
49	2	1533	A	C2-N3-C4	5.37	113.29	110.60
85	4	6199	A	O4'-C1'-C2'	5.36	112.43	107.60
85	4	6204	A	OP1-P-O3'	5.36	116.98	105.20
45	5	3829	G	N3-C4-C5	-5.35	125.92	128.60
85	4	6169	U	C4'-C3'-O3'	5.35	123.71	113.00
85	4	6187	A	C8-N9-C1'	5.35	137.33	127.70
45	5	934	C	N1-C2-O2	5.35	122.11	118.90
49	2	1853	C	N1-C2-O2	5.34	122.11	118.90
45	5	3762	U	N1-C2-O2	5.34	126.54	122.80
49	2	340	C	N3-C2-O2	-5.34	118.16	121.90
45	5	4127	A	O4'-C1'-N9	5.33	112.47	108.20
45	5	4177	C	C6-N1-C2	-5.33	118.17	120.30
45	5	2528	G	C8-N9-C1'	-5.33	120.07	127.00
45	5	2439	G	C4-N9-C1'	5.32	133.42	126.50
49	2	427	U	C2-N1-C1'	5.32	124.08	117.70
85	4	6197	A	C4'-C3'-O3'	5.32	123.64	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	5	67	C	C6-N1-C2	-5.32	118.17	120.30
45	5	5059	C	N1-C2-O2	5.32	122.09	118.90
49	2	1117	C	N1-C2-O2	5.32	122.09	118.90
45	5	1180	C	N1-C2-O2	5.31	122.09	118.90
49	2	183	G	N3-C4-C5	-5.31	125.94	128.60
49	2	1865	C	C6-N1-C2	-5.31	118.18	120.30
45	5	3892	U	N1-C2-O2	5.31	126.51	122.80
45	5	4942	C	N1-C2-O2	5.31	122.08	118.90
45	5	4360	U	N3-C2-O2	-5.30	118.49	122.20
45	5	1977	C	N3-C2-O2	-5.30	118.19	121.90
45	5	2439	G	N3-C4-C5	-5.29	125.95	128.60
45	5	4774	C	N3-C2-O2	-5.29	118.19	121.90
49	2	142	C	N1-C2-O2	5.29	122.08	118.90
49	2	676	C	N1-C2-O2	5.29	122.07	118.90
85	4	6183	G	O4'-C1'-N9	5.29	112.43	108.20
45	5	4592	C	N3-C2-O2	-5.28	118.20	121.90
85	4	6210	U	P-O3'-C3'	5.28	126.04	119.70
45	5	4774	C	C2-N1-C1'	5.28	124.60	118.80
67	SS	96	ILE	CG1-CB-CG2	-5.28	99.79	111.40
45	5	1893	C	C2-N1-C1'	5.28	124.60	118.80
45	5	1211	G	P-O3'-C3'	5.27	126.03	119.70
45	5	4627	U	C2-N1-C1'	5.27	124.02	117.70
49	2	687	C	N1-C2-O2	5.27	122.06	118.90
45	5	2502	A	P-O3'-C3'	5.27	126.02	119.70
45	5	4405	G	C4-N9-C1'	5.27	133.35	126.50
45	5	1429	C	C6-N1-C2	-5.26	118.19	120.30
45	5	4928	C	N1-C2-O2	5.26	122.06	118.90
49	2	638	C	N1-C2-O2	5.26	122.06	118.90
45	5	345	C	N1-C2-O2	5.26	122.06	118.90
49	2	18	C	N1-C2-O2	5.26	122.06	118.90
85	4	6198	A	N9-C1'-C2'	5.26	120.84	114.00
49	2	1750	C	C5-C6-N1	5.25	123.63	121.00
45	5	4759	C	N3-C2-O2	-5.25	118.22	121.90
45	5	3855	C	C6-N1-C2	-5.25	118.20	120.30
45	5	1639	U	C2-N1-C1'	5.24	123.99	117.70
45	5	2464	C	C6-N1-C2	-5.24	118.20	120.30
45	5	2439	G	N3-C4-N9	5.24	129.14	126.00
85	4	6167	U	C4'-C3'-C2'	5.23	107.83	102.60
37	1	49	LEU	CA-CB-CG	5.23	127.33	115.30
45	5	517	C	C6-N1-C2	-5.23	118.21	120.30
49	2	1017	U	C2-N1-C1'	5.23	123.98	117.70
85	4	6204	A	OP2-P-O3'	5.23	116.70	105.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	7	29	C	N1-C2-O2	5.22	122.03	118.90
49	2	179	C	C6-N1-C2	-5.22	118.21	120.30
49	2	879	C	C2-N1-C1'	5.22	124.54	118.80
45	5	2271	C	N3-C2-O2	-5.22	118.25	121.90
45	5	458	C	N1-C2-O2	5.21	122.03	118.90
49	2	1865	C	C6-N1-C1'	-5.21	114.55	120.80
45	5	4893	A	N3-C4-N9	5.21	131.56	127.40
46	7	102	U	C2-N1-C1'	5.20	123.94	117.70
49	2	1636	G	C4-N9-C1'	5.20	133.26	126.50
85	4	6151	A	P-O3'-C3'	5.20	125.94	119.70
49	2	805	U	N3-C2-O2	-5.20	118.56	122.20
49	2	496	C	C2-N1-C1'	5.19	124.51	118.80
45	5	4405	G	N3-C4-N9	5.19	129.11	126.00
45	5	4930	C	N1-C2-O2	5.18	122.01	118.90
45	5	3831	U	C2-N1-C1'	5.18	123.92	117.70
45	5	4969	C	N1-C2-O2	5.18	122.01	118.90
45	5	1633	G	P-O3'-C3'	5.18	125.91	119.70
45	5	4747	C	N3-C2-O2	-5.17	118.28	121.90
45	5	4775	C	N1-C2-O2	5.17	122.00	118.90
49	2	340	C	C6-N1-C2	-5.17	118.23	120.30
45	5	4930	C	C5-C6-N1	5.17	123.58	121.00
45	5	4958	C	C5-C6-N1	5.17	123.58	121.00
45	5	202	C	C6-N1-C2	-5.16	118.24	120.30
45	5	2655	C	C5-C6-N1	5.16	123.58	121.00
45	5	4696	C	N1-C2-O2	5.16	121.99	118.90
49	2	494	C	C5-C6-N1	5.15	123.58	121.00
49	2	1261	C	C6-N1-C1'	-5.14	114.63	120.80
85	4	6066	G	P-O5'-C5'	5.14	129.12	120.90
49	2	55	U	N3-C2-O2	-5.14	118.60	122.20
45	5	2819	U	C6-N1-C2	-5.14	117.92	121.00
45	5	50	C	N3-C2-O2	-5.13	118.31	121.90
45	5	2073	C	N1-C2-O2	5.13	121.98	118.90
45	5	2470	C	N1-C2-O2	5.13	121.98	118.90
49	2	14	C	C6-N1-C2	-5.13	118.25	120.30
49	2	459	C	N1-C2-O2	5.13	121.98	118.90
45	5	2726	G	N3-C4-C5	-5.13	126.03	128.60
45	5	1478	C	C6-N1-C2	-5.13	118.25	120.30
45	5	4206	C	N1-C2-O2	5.13	121.98	118.90
45	5	930	G	P-O3'-C3'	5.12	125.85	119.70
85	4	6178	U	N3-C2-O2	-5.12	118.61	122.20
49	2	293	C	C2-N1-C1'	5.12	124.43	118.80
45	5	112	C	C5-C6-N1	5.12	123.56	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	4	6198	A	O4'-C4'-C3'	5.12	110.19	106.10
49	2	632	C	C5-C6-N1	5.12	123.56	121.00
45	5	4158	C	N1-C2-O2	5.11	121.97	118.90
45	5	3761	C	N1-C2-O2	5.11	121.97	118.90
49	2	857	U	N3-C2-O2	-5.11	118.62	122.20
45	5	1594	C	N1-C2-O2	5.11	121.97	118.90
49	2	1118	C	C6-N1-C1'	-5.11	114.67	120.80
45	5	3767	C	N1-C2-O2	5.10	121.96	118.90
45	5	74	G	C8-N9-C1'	-5.10	120.37	127.00
45	5	1976	G	C4-N9-C1'	5.10	133.13	126.50
45	5	2532	C	N1-C2-O2	5.10	121.96	118.90
49	2	1518	C	N3-C2-O2	-5.09	118.33	121.90
45	5	3851	U	C2-N1-C1'	5.09	123.81	117.70
45	5	4130	C	C2-N1-C1'	5.09	124.40	118.80
45	5	2817	C	N1-C2-O2	5.09	121.95	118.90
49	2	1442	U	C5-C6-N1	5.09	125.24	122.70
45	5	1084	C	N3-C2-O2	-5.09	118.34	121.90
45	5	126	C	N1-C2-O2	5.08	121.95	118.90
45	5	4423	U	C2-N1-C1'	5.08	123.80	117.70
45	5	517	C	N3-C2-O2	-5.07	118.35	121.90
45	5	1179	U	N1-C2-O2	5.07	126.35	122.80
45	5	3810	C	C6-N1-C2	-5.07	118.27	120.30
45	5	2540	C	C5-C6-N1	5.07	123.53	121.00
45	5	2818	C	N1-C2-O2	5.07	121.94	118.90
49	2	1757	G	N3-C4-C5	-5.07	126.07	128.60
45	5	304	C	N3-C2-O2	-5.07	118.35	121.90
85	4	6169	U	C5'-C4'-C3'	5.07	124.10	116.00
61	MM	42	LEU	CA-CB-CG	5.05	126.92	115.30
45	5	3625	G	P-O3'-C3'	5.05	125.76	119.70
45	5	3690	U	N3-C2-O2	-5.05	118.66	122.20
49	2	1624	U	C6-N1-C1'	-5.05	114.13	121.20
85	4	6196	A	C2'-C3'-O3'	5.05	121.77	113.70
45	5	3673	C	N1-C2-O2	5.04	121.93	118.90
45	5	3762	U	C2-N1-C1'	5.04	123.75	117.70
49	2	1271	C	C2-N1-C1'	5.04	124.35	118.80
49	2	1123	C	C2-N1-C1'	5.04	124.35	118.80
45	5	1812	C	C2-N1-C1'	5.04	124.34	118.80
45	5	125	C	P-O3'-C3'	5.04	125.75	119.70
49	2	1664	A	OP1-P-O3'	5.04	116.28	105.20
49	2	402	C	N1-C2-O2	5.03	121.92	118.90
45	5	4896	G	C4-N9-C1'	5.02	133.03	126.50
49	2	151	C	C2-N1-C1'	5.02	124.32	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	5	4053	A	C8-N9-C4	-5.02	103.79	105.80
49	2	1738	C	N1-C2-O2	5.01	121.91	118.90
49	2	568	C	C2-N1-C1'	5.01	124.31	118.80
45	5	1727	U	N1-C2-O2	5.01	126.31	122.80
45	5	4869	U	C2-N1-C1'	5.01	123.71	117.70
49	2	179	C	C2-N1-C1'	5.01	124.31	118.80
45	5	704	C	N3-C2-O2	-5.00	118.40	121.90
45	5	3709	U	C2-N1-C1'	5.00	123.70	117.70
85	4	6187	A	N9-C1'-C2'	5.00	120.50	114.00
45	5	1210	C	N1-C2-O2	5.00	121.90	118.90
45	5	2072	C	N3-C2-O2	-5.00	118.40	121.90
45	5	2819	U	C5-C6-N1	5.00	125.20	122.70

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
85	4	6210	U	C1'

All (20) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
85	4	6065	A	Sidechain
85	4	6066	G	Sidechain
85	4	6067	G	Sidechain
85	4	6077	U	Sidechain
85	4	6151	A	Sidechain
85	4	6177	U	Sidechain
85	4	6178	U	Sidechain
85	4	6179	U	Sidechain
85	4	6181	C	Sidechain
85	4	6197	A	Sidechain
85	4	6198	A	Sidechain
85	4	6199	A	Sidechain
85	4	6210	U	Sidechain
85	4	6216	U	Sidechain
84	9	240	GLY	Peptide
50	BB	12	GLU	Peptide
3	C	151	PRO	Peptide
65	QQ	19	GLY	Peptide
67	SS	89	SER	Peptide
73	YY	61	GLN	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	
1	A	237/257 (92%)	223 (94%)	14 (6%)	0	100	100
2	B	392/403 (97%)	381 (97%)	11 (3%)	0	100	100
3	C	358/392 (91%)	341 (95%)	17 (5%)	0	100	100
4	D	291/297 (98%)	281 (97%)	10 (3%)	0	100	100
5	E	208/291 (72%)	198 (95%)	10 (5%)	0	100	100
6	F	223/249 (90%)	214 (96%)	9 (4%)	0	100	100
7	G	229/242 (95%)	218 (95%)	11 (5%)	0	100	100
8	H	188/192 (98%)	176 (94%)	12 (6%)	0	100	100
9	I	201/214 (94%)	192 (96%)	9 (4%)	0	100	100
10	J	168/178 (94%)	165 (98%)	3 (2%)	0	100	100
11	L	208/211 (99%)	198 (95%)	10 (5%)	0	100	100
12	M	133/198 (67%)	128 (96%)	5 (4%)	0	100	100
13	N	201/204 (98%)	189 (94%)	12 (6%)	0	100	100
14	O	194/198 (98%)	186 (96%)	8 (4%)	0	100	100
15	P	151/187 (81%)	147 (97%)	4 (3%)	0	100	100
16	Q	185/187 (99%)	179 (97%)	6 (3%)	0	100	100
17	R	178/181 (98%)	174 (98%)	4 (2%)	0	100	100
18	S	174/176 (99%)	167 (96%)	7 (4%)	0	100	100
19	T	157/160 (98%)	150 (96%)	7 (4%)	0	100	100
20	U	97/99 (98%)	96 (99%)	1 (1%)	0	100	100
21	V	127/140 (91%)	123 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	W	102/157 (65%)	99 (97%)	3 (3%)	0	100	100
23	X	116/156 (74%)	109 (94%)	7 (6%)	0	100	100
24	Y	132/145 (91%)	129 (98%)	3 (2%)	0	100	100
25	Z	133/136 (98%)	123 (92%)	10 (8%)	0	100	100
26	a	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
27	b	100/226 (44%)	99 (99%)	1 (1%)	0	100	100
28	c	96/115 (84%)	94 (98%)	2 (2%)	0	100	100
29	d	105/125 (84%)	97 (92%)	8 (8%)	0	100	100
30	e	126/135 (93%)	123 (98%)	3 (2%)	0	100	100
31	f	107/110 (97%)	98 (92%)	9 (8%)	0	100	100
32	g	112/126 (89%)	109 (97%)	3 (3%)	0	100	100
33	h	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
34	i	100/105 (95%)	98 (98%)	2 (2%)	0	100	100
35	j	84/97 (87%)	79 (94%)	5 (6%)	0	100	100
36	k	67/69 (97%)	65 (97%)	2 (3%)	0	100	100
37	l	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
38	m	50/52 (96%)	47 (94%)	3 (6%)	0	100	100
39	n	23/25 (92%)	23 (100%)	0	0	100	100
40	o	102/106 (96%)	97 (95%)	5 (5%)	0	100	100
41	p	89/92 (97%)	86 (97%)	3 (3%)	0	100	100
42	r	122/137 (89%)	119 (98%)	3 (2%)	0	100	100
43	s	194/303 (64%)	186 (96%)	8 (4%)	0	100	100
44	t	151/195 (77%)	135 (89%)	16 (11%)	0	100	100
48	K	204/217 (94%)	182 (89%)	21 (10%)	1 (0%)	29	67
50	BB	215/217 (99%)	202 (94%)	13 (6%)	0	100	100
51	CC	211/264 (80%)	197 (93%)	14 (7%)	0	100	100
52	DD	219/221 (99%)	216 (99%)	3 (1%)	0	100	100
53	EE	226/281 (80%)	217 (96%)	9 (4%)	0	100	100
54	FF	260/262 (99%)	244 (94%)	16 (6%)	0	100	100
55	GG	181/204 (89%)	173 (96%)	8 (4%)	0	100	100
56	HH	235/249 (94%)	227 (97%)	8 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
57	II	181/194 (93%)	173 (96%)	8 (4%)	0	100	100
58	JJ	204/206 (99%)	190 (93%)	14 (7%)	0	100	100
59	KK	183/194 (94%)	181 (99%)	2 (1%)	0	100	100
60	LL	94/149 (63%)	90 (96%)	4 (4%)	0	100	100
61	MM	139/158 (88%)	132 (95%)	7 (5%)	0	100	100
62	NN	115/132 (87%)	107 (93%)	8 (7%)	0	100	100
63	OO	147/151 (97%)	145 (99%)	2 (1%)	0	100	100
64	PP	134/151 (89%)	126 (94%)	8 (6%)	0	100	100
65	QQ	113/145 (78%)	102 (90%)	10 (9%)	1 (1%)	17	56
66	RR	140/172 (81%)	133 (95%)	7 (5%)	0	100	100
67	SS	130/135 (96%)	119 (92%)	11 (8%)	0	100	100
68	TT	142/152 (93%)	133 (94%)	9 (6%)	0	100	100
69	UU	139/145 (96%)	133 (96%)	6 (4%)	0	100	100
70	VV	98/119 (82%)	96 (98%)	2 (2%)	0	100	100
71	WW	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
72	XX	127/130 (98%)	120 (94%)	7 (6%)	0	100	100
73	YY	139/143 (97%)	131 (94%)	7 (5%)	1 (1%)	22	61
74	ZZ	122/134 (91%)	120 (98%)	2 (2%)	0	100	100
75	aa	73/125 (58%)	72 (99%)	1 (1%)	0	100	100
76	bb	99/101 (98%)	92 (93%)	7 (7%)	0	100	100
77	cc	81/84 (96%)	78 (96%)	3 (4%)	0	100	100
78	dd	60/69 (87%)	60 (100%)	0	0	100	100
79	ee	53/56 (95%)	48 (91%)	5 (9%)	0	100	100
80	ff	55/133 (41%)	49 (89%)	6 (11%)	0	100	100
81	gg	66/156 (42%)	63 (96%)	3 (4%)	0	100	100
82	hh	310/317 (98%)	292 (94%)	18 (6%)	0	100	100
84	9	854/856 (100%)	801 (94%)	53 (6%)	0	100	100
All	All	12554/14095 (89%)	11964 (95%)	587 (5%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
48	K	59	PRO

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Mol	Chain	Res	Type
73	YY	62	PRO
65	QQ	19	GLY

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	172/199 (86%)	167 (97%)	5 (3%)	42 74
2	B	342/348 (98%)	341 (100%)	1 (0%)	92 96
3	C	302/323 (94%)	295 (98%)	7 (2%)	50 78
4	D	247/250 (99%)	245 (99%)	2 (1%)	81 93
5	E	190/251 (76%)	188 (99%)	2 (1%)	73 88
6	F	196/218 (90%)	195 (100%)	1 (0%)	88 95
7	G	200/208 (96%)	197 (98%)	3 (2%)	65 85
8	H	169/171 (99%)	164 (97%)	5 (3%)	41 73
9	I	175/181 (97%)	173 (99%)	2 (1%)	73 88
10	J	143/149 (96%)	142 (99%)	1 (1%)	84 94
11	L	175/176 (99%)	173 (99%)	2 (1%)	73 88
12	M	116/151 (77%)	115 (99%)	1 (1%)	78 91
13	N	171/172 (99%)	171 (100%)	0	100 100
14	O	170/170 (100%)	167 (98%)	3 (2%)	59 82
15	P	134/165 (81%)	132 (98%)	2 (2%)	65 85
16	Q	164/164 (100%)	162 (99%)	2 (1%)	71 88
17	R	159/160 (99%)	157 (99%)	2 (1%)	69 87
18	S	157/157 (100%)	157 (100%)	0	100 100
19	T	139/140 (99%)	137 (99%)	2 (1%)	67 86
20	U	89/89 (100%)	89 (100%)	0	100 100
21	V	100/107 (94%)	98 (98%)	2 (2%)	55 80
22	W	86/126 (68%)	86 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	X	106/134 (79%)	106 (100%)	0	100	100
24	Y	124/135 (92%)	123 (99%)	1 (1%)	81	93
25	Z	117/118 (99%)	117 (100%)	0	100	100
26	a	119/120 (99%)	117 (98%)	2 (2%)	60	83
27	b	84/172 (49%)	82 (98%)	2 (2%)	49	77
28	c	84/98 (86%)	84 (100%)	0	100	100
29	d	98/110 (89%)	96 (98%)	2 (2%)	55	80
30	e	114/121 (94%)	114 (100%)	0	100	100
31	f	88/89 (99%)	85 (97%)	3 (3%)	37	70
32	g	98/106 (92%)	98 (100%)	0	100	100
33	h	109/110 (99%)	109 (100%)	0	100	100
34	i	86/89 (97%)	85 (99%)	1 (1%)	71	88
35	j	73/80 (91%)	72 (99%)	1 (1%)	67	86
36	k	64/64 (100%)	64 (100%)	0	100	100
37	l	47/48 (98%)	46 (98%)	1 (2%)	53	79
38	m	48/48 (100%)	47 (98%)	1 (2%)	53	79
39	n	24/24 (100%)	24 (100%)	0	100	100
40	o	92/94 (98%)	89 (97%)	3 (3%)	38	71
41	p	74/75 (99%)	74 (100%)	0	100	100
42	r	108/121 (89%)	107 (99%)	1 (1%)	78	91
43	s	164/258 (64%)	163 (99%)	1 (1%)	86	94
44	t	126/163 (77%)	126 (100%)	0	100	100
48	K	190/196 (97%)	188 (99%)	2 (1%)	73	88
50	BB	180/181 (99%)	177 (98%)	3 (2%)	60	83
51	CC	194/231 (84%)	190 (98%)	4 (2%)	53	79
52	DD	187/187 (100%)	187 (100%)	0	100	100
53	EE	190/232 (82%)	184 (97%)	6 (3%)	39	71
54	FF	224/224 (100%)	223 (100%)	1 (0%)	91	95
55	GG	158/170 (93%)	156 (99%)	2 (1%)	69	87
56	HH	207/218 (95%)	206 (100%)	1 (0%)	88	95
57	II	165/174 (95%)	165 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	JJ	178/178 (100%)	177 (99%)	1 (1%)	86	94
59	KK	161/168 (96%)	158 (98%)	3 (2%)	57	81
60	LL	87/125 (70%)	87 (100%)	0	100	100
61	MM	130/142 (92%)	127 (98%)	3 (2%)	50	78
62	NN	99/108 (92%)	98 (99%)	1 (1%)	76	90
63	OO	130/131 (99%)	128 (98%)	2 (2%)	65	85
64	PP	106/119 (89%)	106 (100%)	0	100	100
65	QQ	105/130 (81%)	105 (100%)	0	100	100
66	RR	117/140 (84%)	117 (100%)	0	100	100
67	SS	119/121 (98%)	118 (99%)	1 (1%)	81	93
68	TT	125/132 (95%)	123 (98%)	2 (2%)	62	84
69	UU	111/116 (96%)	110 (99%)	1 (1%)	78	91
70	VV	92/107 (86%)	91 (99%)	1 (1%)	73	88
71	WW	67/67 (100%)	65 (97%)	2 (3%)	41	73
72	XX	112/113 (99%)	111 (99%)	1 (1%)	78	91
73	YY	113/114 (99%)	113 (100%)	0	100	100
74	ZZ	107/115 (93%)	105 (98%)	2 (2%)	57	81
75	aa	66/103 (64%)	66 (100%)	0	100	100
76	bb	88/88 (100%)	88 (100%)	0	100	100
77	cc	75/76 (99%)	75 (100%)	0	100	100
78	dd	55/62 (89%)	55 (100%)	0	100	100
79	ee	48/49 (98%)	48 (100%)	0	100	100
80	ff	47/106 (44%)	45 (96%)	2 (4%)	29	64
81	gg	61/140 (44%)	60 (98%)	1 (2%)	62	84
82	hh	272/275 (99%)	270 (99%)	2 (1%)	84	94
84	9	728/728 (100%)	723 (99%)	5 (1%)	84	94
All	All	10937/12018 (91%)	10824 (99%)	113 (1%)	77	90

All (113) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	64	ARG
1	A	128	ARG

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Mol	Chain	Res	Type
1	A	140	ASN
1	A	194	ASN
1	A	242	ARG
2	B	10	ARG
3	C	38	ASN
3	C	95	MET
3	C	100	ARG
3	C	188	ARG
3	C	222	ARG
3	C	281	MET
3	C	312	ARG
4	D	111	ASN
4	D	268	ARG
5	E	58	ARG
5	E	117	ARG
6	F	205	ASN
7	G	242	ARG
7	G	282	ARG
7	G	293	ASN
8	H	1	MET
8	H	15	ASN
8	H	42	ASN
8	H	102	ASN
8	H	116	ASN
9	I	3	ARG
9	I	100	ASN
10	J	16	ARG
11	L	159	ASN
11	L	162	LYS
12	M	119	ARG
14	O	85	ARG
14	O	117	ARG
14	O	176	ARG
15	P	127	ARG
15	P	128	ARG
16	Q	37	ARG
16	Q	97	LYS
17	R	36	ASN
17	R	133	LYS
19	T	136	ARG
19	T	146	LYS
21	V	15	ARG

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Mol	Chain	Res	Type
21	V	48	ARG
24	Y	2	LYS
26	a	4	ARG
26	a	44	ASN
27	b	60	ASN
27	b	72	ILE
29	d	18	ASN
29	d	31	LYS
31	f	16	ARG
31	f	76	ARG
31	f	80	ASN
34	i	29	ARG
35	j	20	ARG
37	l	21	ARG
38	m	96	ARG
40	o	9	ARG
40	o	61	LYS
40	o	82	MET
42	r	35	ARG
43	s	61	MET
48	K	156	LYS
48	K	159	MET
50	BB	29	ASN
50	BB	41	ARG
50	BB	50	ASN
51	CC	40	ASN
51	CC	147	ASN
51	CC	162	ARG
51	CC	213	ARG
53	EE	57	ASN
53	EE	64	ARG
53	EE	76	ARG
53	EE	94	ARG
53	EE	106	ARG
53	EE	227	LYS
54	FF	232	ASN
55	GG	81	ARG
55	GG	135	ARG
56	HH	63	MET
58	JJ	99	ASN
59	KK	69	ARG
59	KK	70	ARG

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Mol	Chain	Res	Type
59	KK	79	ARG
61	MM	20	LYS
61	MM	42	LEU
61	MM	69	ARG
62	NN	33	ARG
63	OO	27	LYS
63	OO	127	ARG
67	SS	127	ASN
68	TT	8	LYS
68	TT	101	ASN
69	UU	62	ARG
70	VV	47	ASN
71	WW	21	ASN
71	WW	82	ASN
72	XX	91	ASN
74	ZZ	99	LYS
74	ZZ	110	ARG
80	ff	99	LYS
80	ff	104	ARG
81	gg	138	ARG
82	hh	159	ASN
82	hh	178	ASN
84	9	93	LYS
84	9	144	ARG
84	9	158	ASN
84	9	701	ARG
84	9	827	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (109) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	HIS
1	A	140	ASN
1	A	194	ASN
2	B	42	HIS
2	B	315	ASN
3	C	38	ASN
3	C	203	GLN
3	C	223	ASN
4	D	202	GLN
5	E	193	HIS
5	E	253	GLN

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Mol	Chain	Res	Type
5	E	287	HIS
6	F	109	GLN
6	F	205	ASN
7	G	293	ASN
8	H	42	ASN
8	H	102	ASN
8	H	116	ASN
8	H	163	GLN
9	I	95	HIS
9	I	100	ASN
10	J	104	ASN
10	J	155	HIS
11	L	104	ASN
11	L	159	ASN
14	O	184	ASN
15	P	34	GLN
15	P	64	ASN
15	P	97	ASN
15	P	120	ASN
17	R	36	ASN
17	R	58	HIS
19	T	3	ASN
19	T	58	HIS
21	V	77	HIS
21	V	84	GLN
23	X	111	GLN
25	Z	79	HIS
28	c	51	ASN
29	d	18	ASN
31	f	24	HIS
31	f	80	ASN
32	g	114	GLN
42	r	6	GLN
42	r	121	GLN
43	s	68	HIS
44	t	100	HIS
44	t	137	GLN
48	K	143	ASN
48	K	182	ASN
50	BB	29	ASN
50	BB	50	ASN
50	BB	81	ASN

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Mol	Chain	Res	Type
50	BB	84	GLN
50	BB	141	ASN
51	CC	40	ASN
51	CC	147	ASN
51	CC	232	HIS
52	DD	115	GLN
52	DD	267	GLN
53	EE	57	ASN
54	FF	142	HIS
54	FF	232	ASN
56	HH	13	GLN
56	HH	65	GLN
57	II	91	HIS
57	II	186	ASN
57	II	193	GLN
58	JJ	99	ASN
58	JJ	165	GLN
58	JJ	168	GLN
60	LL	7	ASN
60	LL	61	GLN
61	MM	100	ASN
63	OO	101	HIS
63	OO	105	ASN
64	PP	94	HIS
66	RR	48	GLN
66	RR	86	GLN
68	TT	76	GLN
68	TT	101	ASN
68	TT	120	HIS
68	TT	135	HIS
70	VV	47	ASN
70	VV	81	GLN
71	WW	21	ASN
71	WW	35	ASN
71	WW	82	ASN
72	XX	91	ASN
72	XX	113	HIS
73	YY	20	GLN
74	ZZ	19	GLN
75	aa	46	ASN
80	ff	117	ASN
82	hh	133	ASN

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Mol	Chain	Res	Type
82	hh	159	ASN
82	hh	178	ASN
84	9	21	ASN
84	9	30	HIS
84	9	64	GLN
84	9	101	ASN
84	9	158	ASN
84	9	291	GLN
84	9	306	ASN
84	9	493	ASN
84	9	670	GLN
84	9	696	ASN
84	9	811	GLN
84	9	827	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	5	3558/3594 (98%)	900 (25%)	29 (0%)
46	7	118/119 (99%)	16 (13%)	0
47	8	149/151 (98%)	37 (24%)	1 (0%)
49	2	1676/1697 (98%)	408 (24%)	14 (0%)
83	3	86/87 (98%)	25 (29%)	0
85	4	188/190 (98%)	123 (65%)	48 (25%)
All	All	5775/5838 (98%)	1509 (26%)	92 (1%)

All (1509) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
45	5	5	A
45	5	7	C
45	5	11	G
45	5	12	A
45	5	14	C
45	5	21	G
45	5	25	A
45	5	36	U
45	5	39	A
45	5	42	A
45	5	48	G
45	5	49	U

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Mol	Chain	Res	Type
45	5	56	A
45	5	58	G
45	5	59	A
45	5	64	A
45	5	65	A
45	5	67	C
45	5	70	A
45	5	72	C
45	5	73	A
45	5	74	G
45	5	75	G
45	5	84	A
45	5	85	G
45	5	91	G
45	5	92	C
45	5	93	G
45	5	98	A
45	5	105	A
45	5	109	G
45	5	110	C
45	5	116	G
45	5	117	C
45	5	118	C
45	5	119	G
45	5	120	A
45	5	122	U
45	5	123	C
45	5	126	C
45	5	131	C
45	5	132	G
45	5	134	G
45	5	135	G
45	5	136	C
45	5	140	G
45	5	142	G
45	5	143	C
45	5	144	G
45	5	157	U
45	5	158	A
45	5	159	C
45	5	169	A
45	5	172	C

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Mol	Chain	Res	Type
45	5	173	C
45	5	174	C
45	5	193	G
45	5	194	C
45	5	197	A
45	5	200	U
45	5	201	C
45	5	209	U
45	5	216	C
45	5	217	C
45	5	218	A
45	5	220	C
45	5	224	U
45	5	225	G
45	5	232	G
45	5	233	U
45	5	234	G
45	5	244	G
45	5	256	G
45	5	265	C
45	5	266	C
45	5	274	C
45	5	276	C
45	5	278	G
45	5	279	A
45	5	280	G
45	5	295	A
45	5	297	U
45	5	306	A
45	5	308	G
45	5	309	C
45	5	315	G
45	5	316	U
45	5	321	U
45	5	326	C
45	5	334	A
45	5	336	A
45	5	340	C
45	5	344	A
45	5	345	C
45	5	349	A
45	5	350	C

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Mol	Chain	Res	Type
45	5	355	A
45	5	357	U
45	5	360	A
45	5	361	C
45	5	363	A
45	5	364	G
45	5	365	U
45	5	381	U
45	5	386	A
45	5	387	G
45	5	410	A
45	5	412	G
45	5	413	G
45	5	415	G
45	5	418	A
45	5	431	G
45	5	432	U
45	5	433	A
45	5	440	U
45	5	446	C
45	5	448	G
45	5	449	C
45	5	450	G
45	5	452	A
45	5	453	G
45	5	454	U
45	5	455	C
45	5	463	A
45	5	464	G
45	5	467	U
45	5	468	U
45	5	481	G
45	5	482	G
45	5	483	G
45	5	485	C
45	5	492	U
45	5	493	G
45	5	499	G
45	5	505	G
45	5	510	U
45	5	518	G
45	5	643	C

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Mol	Chain	Res	Type
45	5	666	G
45	5	668	C
45	5	677	G
45	5	685	C
45	5	686	A
45	5	691	C
45	5	696	C
45	5	697	G
45	5	704	C
45	5	729	G
45	5	731	G
45	5	733	A
45	5	743	G
45	5	749	G
45	5	750	U
45	5	751	G
45	5	758	G
45	5	760	G
45	5	905	C
45	5	907	C
45	5	913	U
45	5	914	U
45	5	915	A
45	5	917	A
45	5	918	G
45	5	924	C
45	5	925	C
45	5	926	G
45	5	927	G
45	5	928	C
45	5	931	C
45	5	932	A
45	5	933	G
45	5	934	C
45	5	935	A
45	5	935(A)	G
45	5	936	C
45	5	941	C
45	5	943	A
45	5	944	A
45	5	945	U
45	5	946	C

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Mol	Chain	Res	Type
45	5	958	G
45	5	959	G
45	5	960	A
45	5	962	C
45	5	963	G
45	5	964	A
45	5	966	A
45	5	967	C
45	5	968	C
45	5	969	C
45	5	970	G
45	5	979	C
45	5	983	C
45	5	990	C
45	5	1067	G
45	5	1071	C
45	5	1072	C
45	5	1073	G
45	5	1081	C
45	5	1084	C
45	5	1093	C
45	5	1179	U
45	5	1180	C
45	5	1193	C
45	5	1194	G
45	5	1195	G
45	5	1204	C
45	5	1211	G
45	5	1212	G
45	5	1214	C
45	5	1215	C
45	5	1216	C
45	5	1234	G
45	5	1235	G
45	5	1236	C
45	5	1238	A
45	5	1245	C
45	5	1246	G
45	5	1249	C
45	5	1272	C
45	5	1273	G
45	5	1275	G

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Mol	Chain	Res	Type
45	5	1276	C
45	5	1284	G
45	5	1287	G
45	5	1288	G
45	5	1289	C
45	5	1291	G
45	5	1292	C
45	5	1296	G
45	5	1301	C
45	5	1314	C
45	5	1316	G
45	5	1322	A
45	5	1325	C
45	5	1326	A
45	5	1338	G
45	5	1354	A
45	5	1358	G
45	5	1359	G
45	5	1360	G
45	5	1370	G
45	5	1371	A
45	5	1377	G
45	5	1379	C
45	5	1380	G
45	5	1381	U
45	5	1382	G
45	5	1387	A
45	5	1390	G
45	5	1394	G
45	5	1397	A
45	5	1398	A
45	5	1411(C)	C
45	5	1412	G
45	5	1415	G
45	5	1420	A
45	5	1432	G
45	5	1438	U
45	5	1443	A
45	5	1445	U
45	5	1446	C
45	5	1456	C
45	5	1457	G

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Mol	Chain	Res	Type
45	5	1465	G
45	5	1475	G
45	5	1478	C
45	5	1480	C
45	5	1481	C
45	5	1482	G
45	5	1483	C
45	5	1484	G
45	5	1497	A
45	5	1498	G
45	5	1499	C
45	5	1501	C
45	5	1503	A
45	5	1518	A
45	5	1519	C
45	5	1523	A
45	5	1534	A
45	5	1547	A
45	5	1566	C
45	5	1574	G
45	5	1575	A
45	5	1577	G
45	5	1578	U
45	5	1586	G
45	5	1591	U
45	5	1596	U
45	5	1598	C
45	5	1600	A
45	5	1602	U
45	5	1607	C
45	5	1611	C
45	5	1612	G
45	5	1613	A
45	5	1624	G
45	5	1625	G
45	5	1631	A
45	5	1633	G
45	5	1634	A
45	5	1638	A
45	5	1639	U
45	5	1641	G
45	5	1649	U

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Mol	Chain	Res	Type
45	5	1650	A
45	5	1651	G
45	5	1654	G
45	5	1655	C
45	5	1660	U
45	5	1661	C
45	5	1671	U
45	5	1676	C
45	5	1679	A
45	5	1680	G
45	5	1691	G
45	5	1724	G
45	5	1725	U
45	5	1729	A
45	5	1731	C
45	5	1733	G
45	5	1734	G
45	5	1741	G
45	5	1742	A
45	5	1753	G
45	5	1755	C
45	5	1756	U
45	5	1757	U
45	5	1758	G
45	5	1760	G
45	5	1761	G
45	5	1764	G
45	5	1766	A
45	5	1768	C
45	5	1769	G
45	5	1772	C
45	5	1776	A
45	5	1781	U
45	5	1787	A
45	5	1790	U
45	5	1803	G
45	5	1804	A
45	5	1805	A
45	5	1812	C
45	5	1815	G
45	5	1818	G
45	5	1819	G

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Mol	Chain	Res	Type
45	5	1821	G
45	5	1822	U
45	5	1827	C
45	5	1828	C
45	5	1830	G
45	5	1833	G
45	5	1836	G
45	5	1837	A
45	5	1842	G
45	5	1854	G
45	5	1855	G
45	5	1878	G
45	5	1881	C
45	5	1882	U
45	5	1891	A
45	5	1893	C
45	5	1897	A
45	5	1910	G
45	5	1912	G
45	5	1915	C
45	5	1916	G
45	5	1918	U
45	5	1920	C
45	5	1921	C
45	5	1922	G
45	5	1925	G
45	5	1928	C
45	5	1929	A
45	5	1931	C
45	5	1933	G
45	5	1936	C
45	5	1945	G
45	5	1947	U
45	5	1951	G
45	5	1956	A
45	5	1960	A
45	5	1961	G
45	5	1962	A
45	5	1964	A
45	5	1969	G
45	5	1971	U
45	5	1972	G

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Mol	Chain	Res	Type
45	5	1975	G
45	5	1982	G
45	5	1984	A
45	5	1985	G
45	5	1991	A
45	5	1992	U
45	5	1996	C
45	5	1997	U
45	5	1998	A
45	5	2001	G
45	5	2002	A
45	5	2003	G
45	5	2004	U
45	5	2011	C
45	5	2018	C
45	5	2025	A
45	5	2026	A
45	5	2031	C
45	5	2033	A
45	5	2034	G
45	5	2041	A
45	5	2042	A
45	5	2044	U
45	5	2045	G
45	5	2047	A
45	5	2048	U
45	5	2055	G
45	5	2056	G
45	5	2062	C
45	5	2069	A
45	5	2070	U
45	5	2073	C
45	5	2084	U
45	5	2085	G
45	5	2088	A
45	5	2090	U
45	5	2093	G
45	5	2094	C
45	5	2097	A
45	5	2099	C
45	5	2100	G
45	5	2102	G

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Mol	Chain	Res	Type
45	5	2104	A
45	5	2105	A
45	5	2107	A
45	5	2108	G
45	5	2259	G
45	5	2260	C
45	5	2267	U
45	5	2268	A
45	5	2289	C
45	5	2300	A
45	5	2301	G
45	5	2306	G
45	5	2313	A
45	5	2314	G
45	5	2316	G
45	5	2318	G
45	5	2325	C
45	5	2331	G
45	5	2333	G
45	5	2348	G
45	5	2351	C
45	5	2360	A
45	5	2369	U
45	5	2382	A
45	5	2395	A
45	5	2402	G
45	5	2410	C
45	5	2416	G
45	5	2422	C
45	5	2424	G
45	5	2425	U
45	5	2428	A
45	5	2432	U
45	5	2433	G
45	5	2442	G
45	5	2467	U
45	5	2469	C
45	5	2475	G
45	5	2483	G
45	5	2485	U
45	5	2486	G
45	5	2488	C

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Mol	Chain	Res	Type
45	5	2489	C
45	5	2490	U
45	5	2491	C
45	5	2492	C
45	5	2493	G
45	5	2494	U
45	5	2503	G
45	5	2504	C
45	5	2505	C
45	5	2506	G
45	5	2513	A
45	5	2516	G
45	5	2517	A
45	5	2520	C
45	5	2529	A
45	5	2530	U
45	5	2537	A
45	5	2544	G
45	5	2546	G
45	5	2547	G
45	5	2551	A
45	5	2552	G
45	5	2553	A
45	5	2560	C
45	5	2569	G
45	5	2572	C
45	5	2575	U
45	5	2576	G
45	5	2582	A
45	5	2583	C
45	5	2589	C
45	5	2600	A
45	5	2602	G
45	5	2623	A
45	5	2628	U
45	5	2632	U
45	5	2638	G
45	5	2647	A
45	5	2654	C
45	5	2657	G
45	5	2658	G
45	5	2660	A

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Mol	Chain	Res	Type
45	5	2661	U
45	5	2662	G
45	5	2669	C
45	5	2675	G
45	5	2681	G
45	5	2683	C
45	5	2687	U
45	5	2694	G
45	5	2695	A
45	5	2696	A
45	5	2700	G
45	5	2708	U
45	5	2709	C
45	5	2710	C
45	5	2711	G
45	5	2712	G
45	5	2714	G
45	5	2719	C
45	5	2726	G
45	5	2740	U
45	5	2743	A
45	5	2752	G
45	5	2753	G
45	5	2754	G
45	5	2756	G
45	5	2758	G
45	5	2761	U
45	5	2764	A
45	5	2768	C
45	5	2769	U
45	5	2772	C
45	5	2787	A
45	5	2788	U
45	5	2789	A
45	5	2790	U
45	5	2794	C
45	5	2795	A
45	5	2796	G
45	5	2798	A
45	5	2799	G
45	5	2807	A
45	5	2811	G

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Mol	Chain	Res	Type
45	5	2814	C
45	5	2825	A
45	5	2826	U
45	5	2827	G
45	5	2828	U
45	5	2833	A
45	5	2835	A
45	5	2837	U
45	5	2839	U
45	5	2842	G
45	5	2849	A
45	5	2853	C
45	5	2855	G
45	5	2857	A
45	5	2874	U
45	5	2875	C
45	5	2876	G
45	5	2880	U
45	5	2883	G
45	5	2884	G
45	5	2888	G
45	5	2897	G
45	5	2898	G
45	5	3598	C
45	5	3599	A
45	5	3603	G
45	5	3604	A
45	5	3616	U
45	5	3618	C
45	5	3619	G
45	5	3620	G
45	5	3621	A
45	5	3625	G
45	5	3626	G
45	5	3635	A
45	5	3639	U
45	5	3643	A
45	5	3646	A
45	5	3647	A
45	5	3657	U
45	5	3662	A
45	5	3664	G

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Mol	Chain	Res	Type
45	5	3673	C
45	5	3678	G
45	5	3680	U
45	5	3688	U
45	5	3692	A
45	5	3698	G
45	5	3711	A
45	5	3727	A
45	5	3729	U
45	5	3747	A
45	5	3748	A
45	5	3753	G
45	5	3759	A
45	5	3760	A
45	5	3763	A
45	5	3772	U
45	5	3773	U
45	5	3775	A
45	5	3776	G
45	5	3777	G
45	5	3778	U
45	5	3783	A
45	5	3784	A
45	5	3785	A
45	5	3790	U
45	5	3791	C
45	5	3793	U
45	5	3795	A
45	5	3798	U
45	5	3802	U
45	5	3808	C
45	5	3810	C
45	5	3812	C
45	5	3814	U
45	5	3817	A
45	5	3818	U
45	5	3819	G
45	5	3825	A
45	5	3828	A
45	5	3829	G
45	5	3830	A
45	5	3839	G

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Mol	Chain	Res	Type
45	5	3840	U
45	5	3843	C
45	5	3851	U
45	5	3852	A
45	5	3868	G
45	5	3869	C
45	5	3876	A
45	5	3877	A
45	5	3878	C
45	5	3879	G
45	5	3880	G
45	5	3889	G
45	5	3890	A
45	5	3897	G
45	5	3898	G
45	5	3901	A
45	5	3905	A
45	5	3906	A
45	5	3907	G
45	5	3914	U
45	5	3915	U
45	5	3917	A
45	5	3924	C
45	5	3926	C
45	5	3927	U
45	5	3938	G
45	5	3939	G
45	5	3956	G
45	5	3957	U
45	5	3958	G
45	5	3964	U
45	5	3965	A
45	5	3966	A
45	5	3968	U
45	5	3970	G
45	5	3972	A
45	5	3973	G
45	5	3975	C
45	5	4036	G
45	5	4040	C
45	5	4041	C
45	5	4045	G

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Mol	Chain	Res	Type
45	5	4048	A
45	5	4049	U
45	5	4050	A
45	5	4052	C
45	5	4053	A
45	5	4055	U
45	5	4063	U
45	5	4064	C
45	5	4065	G
45	5	4072	C
45	5	4073	A
45	5	4074	C
45	5	4075	U
45	5	4076	G
45	5	4085	A
45	5	4086	G
45	5	4116	C
45	5	4119	C
45	5	4120	U
45	5	4125	C
45	5	4127	A
45	5	4131	G
45	5	4148	C
45	5	4157	A
45	5	4158	C
45	5	4162	C
45	5	4163	U
45	5	4164	C
45	5	4170	A
45	5	4171	C
45	5	4183	G
45	5	4184	G
45	5	4191	G
45	5	4194	U
45	5	4197	G
45	5	4203	A
45	5	4205	A
45	5	4213	A
45	5	4225	G
45	5	4229	U
45	5	4233	A
45	5	4234	A

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Mol	Chain	Res	Type
45	5	4235	G
45	5	4249	G
45	5	4251	A
45	5	4253	A
45	5	4254	G
45	5	4260	U
45	5	4263	C
45	5	4265	U
45	5	4266	G
45	5	4268	A
45	5	4271	A
45	5	4273	A
45	5	4281	A
45	5	4282	A
45	5	4290	U
45	5	4291	G
45	5	4293	U
45	5	4297	G
45	5	4302	U
45	5	4304	A
45	5	4305	G
45	5	4313	A
45	5	4315	A
45	5	4317	A
45	5	4326	G
45	5	4330	G
45	5	4332	C
45	5	4335	C
45	5	4336	A
45	5	4339	A
45	5	4349	C
45	5	4350	C
45	5	4354	U
45	5	4355	G
45	5	4360	U
45	5	4373	G
45	5	4375	C
45	5	4376	A
45	5	4377	G
45	5	4378	A
45	5	4381	A
45	5	4387	C

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Mol	Chain	Res	Type
45	5	4393	G
45	5	4394	A
45	5	4395	U
45	5	4398	C
45	5	4401	G
45	5	4419	U
45	5	4421	C
45	5	4422	A
45	5	4424	A
45	5	4426	C
45	5	4430	G
45	5	4436	U
45	5	4437	U
45	5	4448	G
45	5	4449	A
45	5	4452	U
45	5	4464	A
45	5	4466	C
45	5	4477	A
45	5	4478	G
45	5	4482	U
45	5	4483	C
45	5	4493	U
45	5	4500	U
45	5	4511	A
45	5	4512	U
45	5	4513	A
45	5	4518	A
45	5	4525	C
45	5	4527	G
45	5	4542	U
45	5	4548	A
45	5	4560	C
45	5	4569	U
45	5	4573	G
45	5	4574	U
45	5	4575	G
45	5	4577	U
45	5	4581	G
45	5	4585	U
45	5	4590	A
45	5	4592	C

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Mol	Chain	Res	Type
45	5	4599	A
45	5	4616	A
45	5	4617	G
45	5	4636	U
45	5	4637	G
45	5	4652	G
45	5	4657	U
45	5	4658	G
45	5	4667	C
45	5	4670	C
45	5	4672	A
45	5	4677	U
45	5	4678	G
45	5	4687	A
45	5	4691	A
45	5	4694	G
45	5	4698	C
45	5	4700	A
45	5	4709	U
45	5	4719	G
45	5	4720	C
45	5	4721	G
45	5	4728	U
45	5	4736	C
45	5	4738	C
45	5	4739	C
45	5	4745	G
45	5	4754	G
45	5	4756	C
45	5	4757	C
45	5	4759	C
45	5	4765	G
45	5	4769	G
45	5	4771	C
45	5	4773	C
45	5	4775	C
45	5	4863	G
45	5	4865	C
45	5	4867	G
45	5	4870	G
45	5	4871	C
45	5	4872	G

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Mol	Chain	Res	Type
45	5	4875	G
45	5	4876	A
45	5	4877	G
45	5	4882	U
45	5	4883	C
45	5	4885	U
45	5	4891	G
45	5	4895	C
45	5	4896	G
45	5	4910	A
45	5	4911	A
45	5	4912	G
45	5	4914	G
45	5	4915	G
45	5	4921	C
45	5	4924	C
45	5	4926	C
45	5	4931	G
45	5	4937	C
45	5	4943	A
45	5	4944	C
45	5	4947	U
45	5	4948	C
45	5	4949	G
45	5	4951	G
45	5	4955	A
45	5	4956	A
45	5	4958	C
45	5	4965	U
45	5	4966	A
45	5	4975	G
45	5	4976	U
45	5	4988	U
45	5	4989	U
45	5	4990	C
45	5	4999	G
45	5	5005	G
45	5	5006	U
45	5	5014	A
45	5	5017	G
45	5	5040	U
45	5	5041	G

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Mol	Chain	Res	Type
45	5	5049	G
45	5	5050	C
45	5	5054	C
45	5	5061	A
45	5	5062	G
45	5	5066	U
46	7	7	G
46	7	33	U
46	7	41	G
46	7	50	A
46	7	53	U
46	7	54	A
46	7	63	C
46	7	64	G
46	7	74	A
46	7	76	U
46	7	84	U
46	7	85	G
46	7	97	G
46	7	100	A
46	7	110	G
46	7	117	G
47	8	2	G
47	8	3	A
47	8	14	U
47	8	16	G
47	8	23	C
47	8	34	U
47	8	35	C
47	8	38	U
47	8	46	G
47	8	51	U
47	8	52	A
47	8	59	A
47	8	62	A
47	8	63	U
47	8	71	A
47	8	72	A
47	8	78	G
47	8	86	U
47	8	87	G
47	8	88	A

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Mol	Chain	Res	Type
47	8	90	C
47	8	94	G
47	8	95	A
47	8	103	A
47	8	105	C
47	8	110	U
47	8	111	U
47	8	114	G
47	8	123	U
47	8	125	C
47	8	126	C
47	8	127	U
47	8	135	C
47	8	137	A
47	8	147	G
47	8	150	C
47	8	151	G
49	2	2	A
49	2	3	C
49	2	4	C
49	2	9	U
49	2	14	C
49	2	20	G
49	2	25	A
49	2	26	U
49	2	37	C
49	2	41	G
49	2	42	A
49	2	45	A
49	2	46	A
49	2	47	G
49	2	55	U
49	2	56	G
49	2	62	G
49	2	64	A
49	2	67	C
49	2	68	A
49	2	69	C
49	2	71	G
49	2	74	G
49	2	75	G
49	2	76	U

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Mol	Chain	Res	Type
49	2	78	C
49	2	93	U
49	2	103	A
49	2	107	A
49	2	110	U
49	2	111	A
49	2	113	G
49	2	114	G
49	2	115	U
49	2	123	G
49	2	126	G
49	2	127	C
49	2	130	G
49	2	143	U
49	2	147	A
49	2	154	U
49	2	155	G
49	2	160	U
49	2	161	U
49	2	163	U
49	2	168	C
49	2	169	U
49	2	183	G
49	2	184	G
49	2	187	G
49	2	188	C
49	2	189	U
49	2	190	G
49	2	191	A
49	2	192	C
49	2	215	G
49	2	292	A
49	2	293	C
49	2	294	U
49	2	302	A
49	2	306	C
49	2	307	G
49	2	308	G
49	2	309	G
49	2	312	G
49	2	313	A
49	2	314	U

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Mol	Chain	Res	Type
49	2	315	C
49	2	317	C
49	2	318	A
49	2	319	C
49	2	332	G
49	2	347	G
49	2	351	G
49	2	356	C
49	2	357	C
49	2	361	U
49	2	362	C
49	2	364	A
49	2	367	U
49	2	368	U
49	2	370	G
49	2	371	A
49	2	383	G
49	2	384	U
49	2	385	G
49	2	386	C
49	2	390	C
49	2	398	A
49	2	399	C
49	2	400	C
49	2	407	G
49	2	408	A
49	2	409	C
49	2	417	C
49	2	418	A
49	2	426	A
49	2	429	C
49	2	434	G
49	2	448	A
49	2	449	A
49	2	450	C
49	2	452	G
49	2	465	A
49	2	466	G
49	2	471	G
49	2	472	C
49	2	473	A
49	2	474	G

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Mol	Chain	Res	Type
49	2	476	A
49	2	487	U
49	2	492	C
49	2	493	A
49	2	500	A
49	2	502	C
49	2	509	G
49	2	516	A
49	2	525	A
49	2	530	U
49	2	531	A
49	2	532	C
49	2	533	A
49	2	542	U
49	2	547	G
49	2	548	C
49	2	549	C
49	2	550	C
49	2	552	G
49	2	554	A
49	2	555	A
49	2	556	U
49	2	559	G
49	2	560	A
49	2	562	U
49	2	569	A
49	2	576	A
49	2	583	A
49	2	588	G
49	2	589	G
49	2	590	A
49	2	591	U
49	2	594	A
49	2	595	U
49	2	597	G
49	2	600	G
49	2	603	C
49	2	604	A
49	2	606	G
49	2	608	C
49	2	614	C
49	2	617	G

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Mol	Chain	Res	Type
49	2	621	C
49	2	627	U
49	2	628	A
49	2	629	A
49	2	642	U
49	2	643	A
49	2	655	A
49	2	656	G
49	2	657	U
49	2	658	U
49	2	661	U
49	2	662	G
49	2	664	A
49	2	668	A
49	2	671	A
49	2	672	A
49	2	673	G
49	2	684	G
49	2	688	U
49	2	689	U
49	2	696	G
49	2	752	G
49	2	753	C
49	2	754	G
49	2	811	A
49	2	821	G
49	2	822	U
49	2	824	C
49	2	827	A
49	2	830	A
49	2	847	A
49	2	852	G
49	2	853	C
49	2	870	A
49	2	871	U
49	2	872	A
49	2	873	G
49	2	875	A
49	2	879	C
49	2	882	U
49	2	886	A
49	2	888	U

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Mol	Chain	Res	Type
49	2	890	U
49	2	891	G
49	2	893	U
49	2	894	G
49	2	897	U
49	2	898	U
49	2	913	A
49	2	914	U
49	2	919	A
49	2	920	A
49	2	933	G
49	2	952	G
49	2	955	A
49	2	969	U
49	2	970	G
49	2	971	G
49	2	985	G
49	2	990	A
49	2	991	G
49	2	992	A
49	2	999	G
49	2	1002	U
49	2	1017	U
49	2	1023	A
49	2	1026	C
49	2	1034	A
49	2	1045	U
49	2	1055	A
49	2	1061	U
49	2	1073	U
49	2	1082	A
49	2	1083	A
49	2	1085	C
49	2	1086	G
49	2	1088	U
49	2	1114	U
49	2	1115	U
49	2	1116	C
49	2	1117	C
49	2	1123	C
49	2	1133	A
49	2	1138	C

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Mol	Chain	Res	Type
49	2	1139	C
49	2	1148	A
49	2	1149	A
49	2	1150	A
49	2	1153	C
49	2	1154	U
49	2	1155	U
49	2	1157	G
49	2	1161	U
49	2	1165	G
49	2	1166	G
49	2	1170	A
49	2	1194	A
49	2	1195	A
49	2	1204	A
49	2	1207	G
49	2	1208	A
49	2	1215	C
49	2	1216	C
49	2	1217	A
49	2	1227	G
49	2	1228	A
49	2	1236	G
49	2	1242	U
49	2	1250	A
49	2	1251	A
49	2	1253	A
49	2	1254	C
49	2	1256	G
49	2	1257	G
49	2	1259	A
49	2	1261	C
49	2	1264	C
49	2	1269	G
49	2	1273	C
49	2	1274	G
49	2	1275	G
49	2	1284	A
49	2	1285	G
49	2	1286	G
49	2	1293	A
49	2	1294	G

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Mol	Chain	Res	Type
49	2	1298	G
49	2	1299	A
49	2	1301	A
49	2	1302	G
49	2	1303	C
49	2	1306	U
49	2	1307	U
49	2	1308	U
49	2	1309	C
49	2	1314	U
49	2	1327	G
49	2	1333	U
49	2	1341	C
49	2	1342	U
49	2	1354	G
49	2	1356	G
49	2	1358	U
49	2	1364	U
49	2	1365	G
49	2	1371	U
49	2	1372	U
49	2	1374	C
49	2	1377	U
49	2	1378	A
49	2	1390	U
49	2	1396	A
49	2	1397	U
49	2	1402	A
49	2	1404	U
49	2	1406	G
49	2	1428	G
49	2	1429	G
49	2	1439	A
49	2	1442	U
49	2	1449	G
49	2	1452	A
49	2	1454	A
49	2	1462	U
49	2	1463	U
49	2	1466	G
49	2	1475	G
49	2	1476	A

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Mol	Chain	Res	Type
49	2	1477	U
49	2	1483	A
49	2	1489	A
49	2	1490	G
49	2	1492	U
49	2	1497	G
49	2	1498	A
49	2	1507	G
49	2	1508	A
49	2	1515	G
49	2	1520	G
49	2	1521	C
49	2	1533	A
49	2	1535	U
49	2	1536	G
49	2	1548	G
49	2	1551	U
49	2	1552	G
49	2	1553	C
49	2	1554	C
49	2	1556	A
49	2	1558	C
49	2	1560	U
49	2	1570	G
49	2	1573	G
49	2	1575	G
49	2	1578	U
49	2	1580	A
49	2	1584	G
49	2	1585	U
49	2	1588	A
49	2	1598	G
49	2	1601	A
49	2	1603	G
49	2	1604	G
49	2	1606	G
49	2	1621	U
49	2	1623	A
49	2	1637	A
49	2	1638	G
49	2	1647	A
49	2	1648	G

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Mol	Chain	Res	Type
49	2	1654	G
49	2	1661	A
49	2	1665	G
49	2	1671	G
49	2	1678	A
49	2	1680	G
49	2	1683	C
49	2	1689	C
49	2	1692	U
49	2	1693	G
49	2	1695	A
49	2	1696	C
49	2	1697	A
49	2	1700	C
49	2	1701	C
49	2	1702	G
49	2	1721	U
49	2	1722	G
49	2	1725	U
49	2	1726	G
49	2	1744	G
49	2	1748	G
49	2	1753	C
49	2	1756	C
49	2	1757	G
49	2	1773	C
49	2	1776	G
49	2	1781	A
49	2	1783	C
49	2	1823	A
49	2	1824	A
49	2	1825	A
49	2	1831	A
49	2	1833	C
49	2	1834	A
49	2	1835	A
49	2	1836	G
49	2	1838	U
49	2	1849	G
49	2	1851	A
49	2	1852	C
49	2	1861	G

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Mol	Chain	Res	Type
49	2	1862	G
49	2	1863	A
49	2	1865	C
49	2	1868	U
49	2	1869	A
83	3	8	U
83	3	9	G
83	3	10	G
83	3	13	G
83	3	16	U
83	3	17	U
83	3	18	G
83	3	19	G
83	3	20	U
83	3	21	A
83	3	22	G
83	3	23	A
83	3	24	C
83	3	26	C
83	3	46	G
83	3	49	C
83	3	51	A
83	3	54	G
83	3	55	G
83	3	58	U
83	3	71	U
83	3	77	C
83	3	82	G
83	3	85	C
83	3	86	C
85	4	6031	A
85	4	6032	A
85	4	6033	A
85	4	6036	G
85	4	6038	G
85	4	6040	U
85	4	6041	C
85	4	6042	U
85	4	6043	U
85	4	6044	G
85	4	6048	G
85	4	6050	A

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Mol	Chain	Res	Type
85	4	6052	A
85	4	6054	A
85	4	6056	A
85	4	6057	A
85	4	6058	U
85	4	6059	U
85	4	6060	U
85	4	6061	U
85	4	6062	G
85	4	6063	A
85	4	6064	G
85	4	6065	A
85	4	6066	G
85	4	6067	G
85	4	6068	U
85	4	6069	U
85	4	6072	U
85	4	6073	A
85	4	6074	A
85	4	6075	A
85	4	6076	U
85	4	6077	U
85	4	6081	A
85	4	6083	U
85	4	6084	A
85	4	6085	G
85	4	6087	G
85	4	6088	C
85	4	6090	A
85	4	6094	U
85	4	6097	U
85	4	6098	A
85	4	6099	U
85	4	6100	U
85	4	6101	U
85	4	6105	U
85	4	6106	U
85	4	6107	A
85	4	6108	G
85	4	6113	U
85	4	6115	A
85	4	6116	G

Continued on next page...

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Mol	Chain	Res	Type
85	4	6119	U
85	4	6121	A
85	4	6122	C
85	4	6123	G
85	4	6125	U
85	4	6126	C
85	4	6128	A
85	4	6129	G
85	4	6134	C
85	4	6136	U
85	4	6139	U
85	4	6140	G
85	4	6150	C
85	4	6151	A
85	4	6152	A
85	4	6154	A
85	4	6158	A
85	4	6162	A
85	4	6163	G
85	4	6164	C
85	4	6165	C
85	4	6166	C
85	4	6167	U
85	4	6168	C
85	4	6169	U
85	4	6170	C
85	4	6171	U
85	4	6172	G
85	4	6173	C
85	4	6174	G
85	4	6175	G
85	4	6176	U
85	4	6177	U
85	4	6178	U
85	4	6179	U
85	4	6180	U
85	4	6181	C
85	4	6182	A
85	4	6183	G
85	4	6185	U
85	4	6186	U
85	4	6187	A

Continued on next page...

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Mol	Chain	Res	Type
85	4	6188	G
85	4	6189	G
85	4	6190	U
85	4	6191	A
85	4	6192	G
85	4	6193	U
85	4	6196	A
85	4	6197	A
85	4	6198	A
85	4	6199	A
85	4	6200	A
85	4	6202	C
85	4	6203	U
85	4	6204	A
85	4	6205	A
85	4	6206	G
85	4	6207	A
85	4	6208	A
85	4	6209	A
85	4	6210	U
85	4	6211	U
85	4	6212	U
85	4	6213	A
85	4	6214	C
85	4	6215	C
85	4	6216	U
85	4	6217	C

All (92) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
45	5	48	G
45	5	125	C
45	5	275	C
45	5	481	G
45	5	504	G
45	5	930	G
45	5	1072	C
45	5	1211	G
45	5	1291	G
45	5	1445	U
45	5	1455	G

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Mol	Chain	Res	Type
45	5	1633	G
45	5	2046	G
45	5	2089	G
45	5	2266	C
45	5	2502	A
45	5	2661	U
45	5	2695	A
45	5	3603	G
45	5	3625	G
45	5	4054	C
45	5	4170	A
45	5	4232	U
45	5	4448	G
45	5	4699	U
45	5	4719	G
45	5	4884	G
45	5	4925	U
45	5	4947	U
47	8	124	U
49	2	24	C
49	2	110	U
49	2	182	C
49	2	532	C
49	2	553	U
49	2	561	A
49	2	688	U
49	2	752	G
49	2	1137	U
49	2	1253	A
49	2	1395	C
49	2	1489	A
49	2	1637	A
49	2	1664	A
85	4	6057	A
85	4	6058	U
85	4	6059	U
85	4	6060	U
85	4	6061	U
85	4	6066	G
85	4	6067	G
85	4	6068	U
85	4	6072	U

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Mol	Chain	Res	Type
85	4	6073	A
85	4	6076	U
85	4	6107	A
85	4	6150	C
85	4	6151	A
85	4	6163	G
85	4	6164	C
85	4	6165	C
85	4	6166	C
85	4	6167	U
85	4	6170	C
85	4	6171	U
85	4	6172	G
85	4	6173	C
85	4	6174	G
85	4	6175	G
85	4	6176	U
85	4	6179	U
85	4	6180	U
85	4	6181	C
85	4	6182	A
85	4	6183	G
85	4	6184	A
85	4	6185	U
85	4	6186	U
85	4	6187	A
85	4	6188	G
85	4	6189	G
85	4	6190	U
85	4	6196	A
85	4	6199	A
85	4	6206	G
85	4	6208	A
85	4	6209	A
85	4	6210	U
85	4	6211	U
85	4	6212	U
85	4	6213	A
85	4	6214	C

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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:

Mol	Chain	Number of breaks
45	5	36
49	2	20
48	K	3
47	8	1
82	hh	1
14	O	1
3	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	2113:G	O3'	2258:C	P	41.98

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	1252:C	O3'	1271:G	P	33.40
1	5	1696:C	O3'	1720:C	P	19.99
1	5	1219:G	O3'	1233:G	P	18.35
1	5	523:C	O3'	638:G	P	18.12
1	5	990:C	O3'	1064:G	P	18.08
1	2	756:C	O3'	788:G	P	17.83
1	5	4101:C	O3'	4107:G	P	17.76
1	5	4138:C	O3'	4146:G	P	17.64
1	2	834:C	O3'	841:G	P	17.63
1	2	697:G	O3'	729:C	P	17.51
1	5	3977:C	O3'	4034:G	P	17.44
1	2	1417:C	O3'	1423:C	P	15.35
1	5	5022:U	O3'	5028:G	P	14.94
1	2	1761:U	O3'	1771:G	P	14.63
1	5	4777:C	O3'	4859:C	P	14.47
1	5	760:G	O3'	904:C	P	14.39
1	2	130:G	O3'	141:A	P	13.98
1	5	1364:U	O3'	1368:A	P	13.51
1	2	323:C	O3'	329:G	P	12.90
1	5	1405:C	O3'	1411(A):G	P	12.67
1	5	4045:G	O3'	4047:A	P	12.53
1	5	2901:G	O3'	3597:G	P	11.66
1	5	182:G	O3'	189:G	P	10.37
1	5	4729:A	O3'	4735:G	P	9.24
1	5	1180:C	O3'	1183:C	P	8.44
1	5	971(A):G	O3'	972:C	P	8.39
1	2	689:U	O3'	690:G	P	8.38
1	8	79:G	O3'	85:U	P	7.62
1	hh	2:THR	C	3:GLU	N	7.52
1	K	194:LEU	C	195:LYS	N	7.40
1	5	737:C	O3'	738(A):C	P	7.09
1	5	970:G	O3'	971:U	P	6.80
1	5	500:G	O3'	504:G	P	6.70
1	2	736:C	O3'	743:U	P	6.55
1	5	1957:U	O3'	1958:A	P	6.11
1	2	225:G	O3'	287:U	P	5.99
1	5	751:G	O3'	752:G	P	5.86
1	5	4740:G	O3'	4743:G	P	5.52
1	5	971:U	O3'	971(A):G	P	5.18
1	K	9:THR	C	10:LEU	N	5.03
1	2	1432:U	O3'	1438:A	P	4.80
1	5	1239:C	O3'	1244:G	P	4.77

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	322:C	O3'	323:C	P	4.73
1	5	512:U	O3'	515:C	P	4.66
1	K	172:VAL	C	173:LYS	N	4.60
1	5	1438:U	O3'	1440:U	P	4.48
1	5	170:C	O3'	171:U	P	4.34
1	2	745:C	O3'	749:U	P	4.21
1	2	1697:A	O3'	1698:C	P	4.16
1	2	886:A	O3'	887:U	P	4.06
1	2	304:C	O3'	305:U	P	4.01
1	O	109:PRO	C	111:PRO	N	3.99
1	2	903:A	O3'	904:A	P	3.93
1	5	4899:G	O3'	4902:C	P	3.53
1	2	798:G	O3'	799:U	P	3.35
1	5	1100:U	O3'	1168:G	P	3.34
1	5	738(A):C	O3'	739:G	P	3.31
1	5	267:G	O3'	268:G	P	3.29
1	2	902:G	O3'	903:A	P	3.29
1	2	1201:U	O3'	1202:U	P	3.27
1	5	5020:G	O3'	5021:C	P	3.24
1	C	132:ALA	C	133:LEU	N	3.22

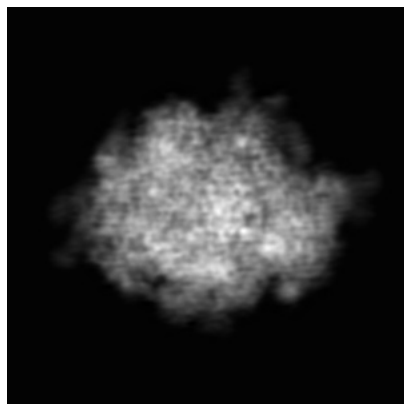
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7836. These allow visual inspection of the internal detail of the map and identification of artifacts.

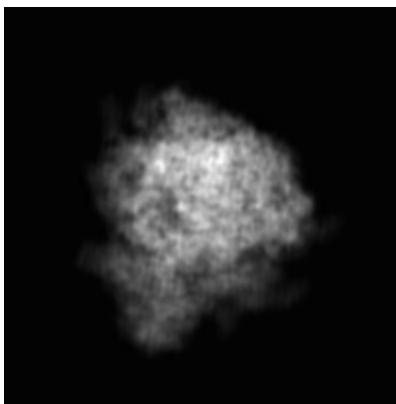
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

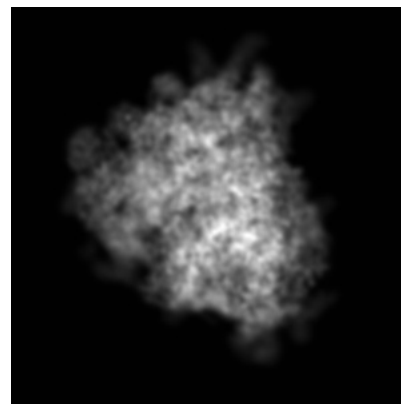
6.1.1 Primary map



X

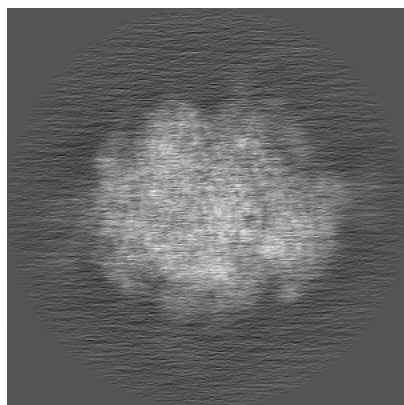


Y

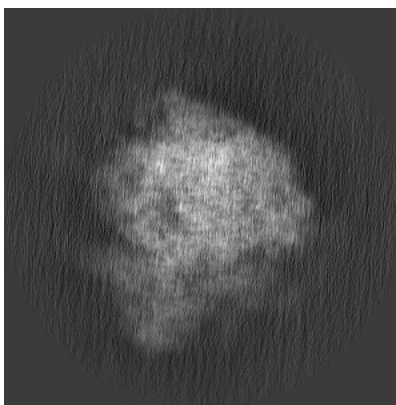


Z

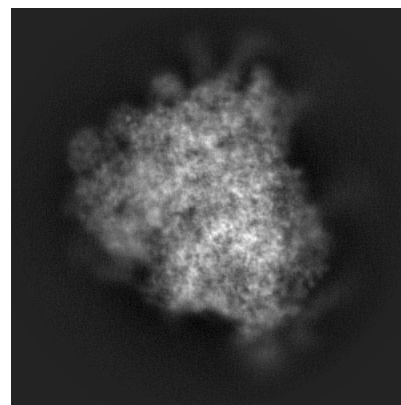
6.1.2 Raw map



X



Y

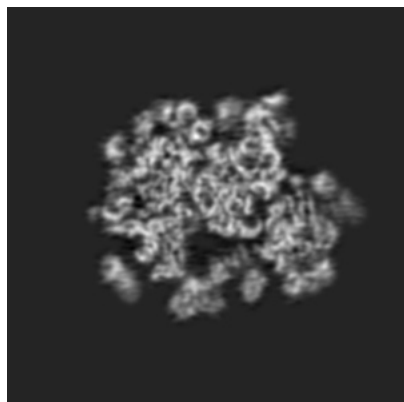


Z

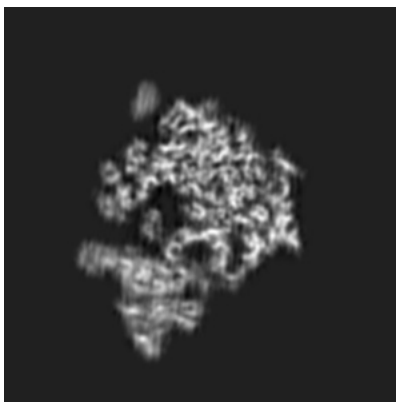
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

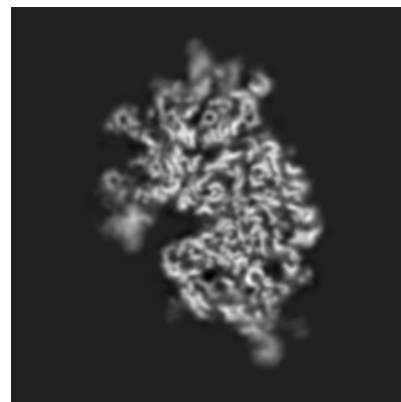
6.2.1 Primary map



X Index: 200

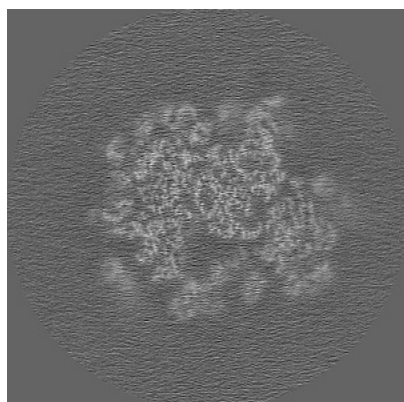


Y Index: 200

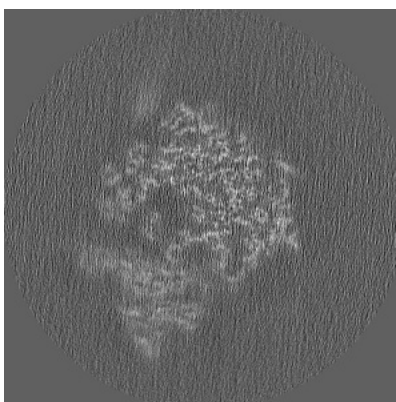


Z Index: 200

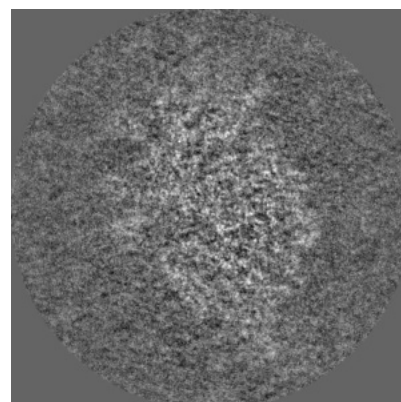
6.2.2 Raw map



X Index: 200



Y Index: 200

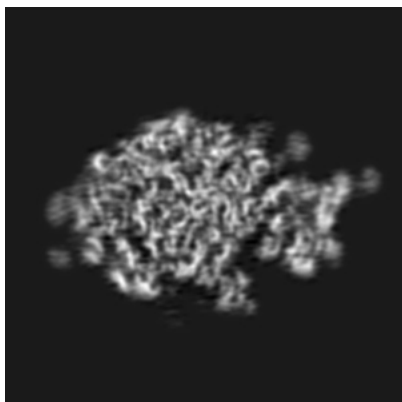


Z Index: 200

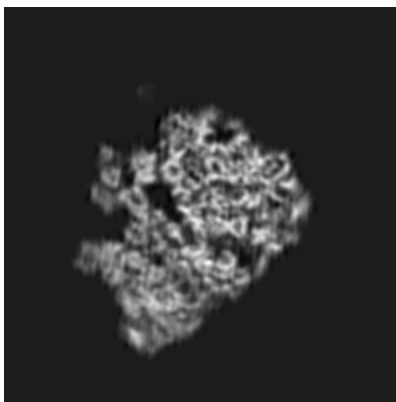
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

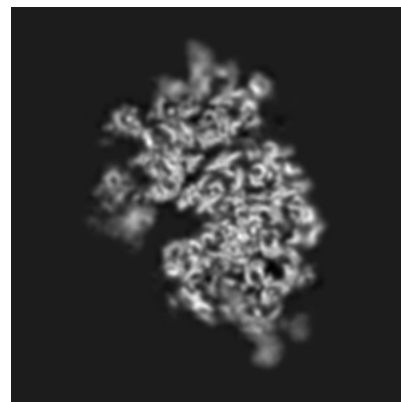
6.3.1 Primary map



X Index: 248

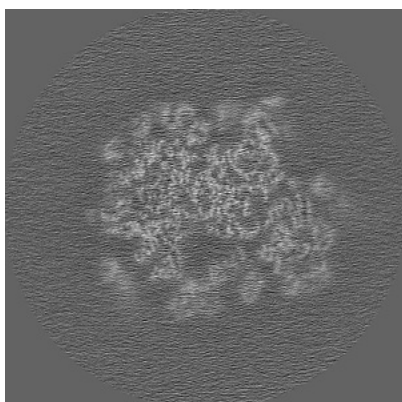


Y Index: 213

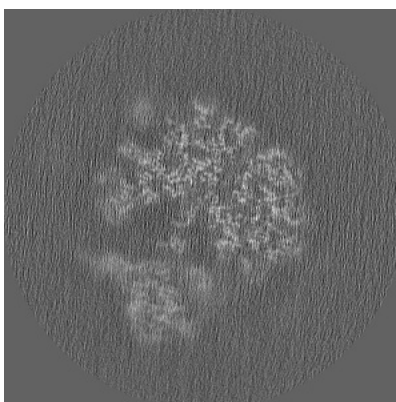


Z Index: 197

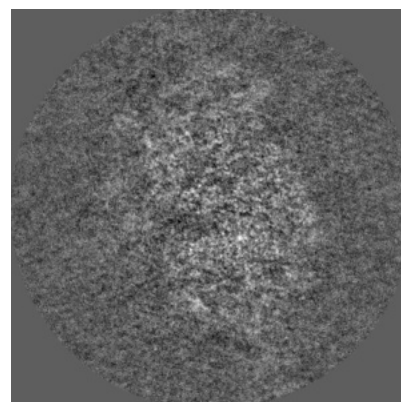
6.3.2 Raw map



X Index: 201



Y Index: 189

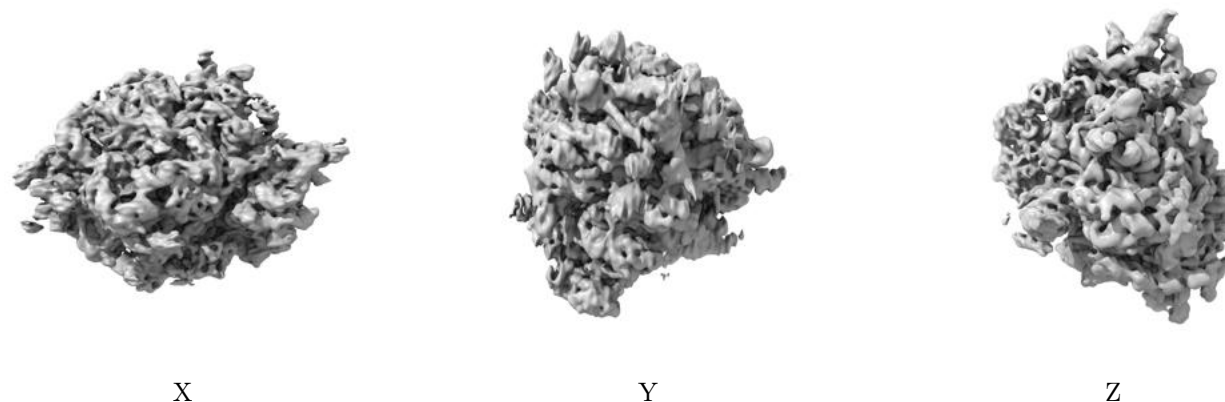


Z Index: 198

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

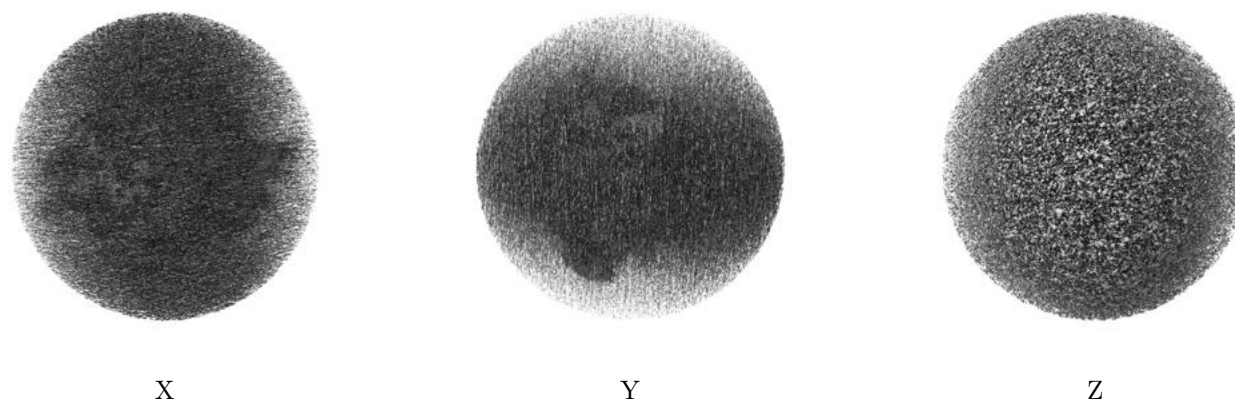
6.4 Orthogonal surface views [i](#)

6.4.1 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.

6.4.2 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.

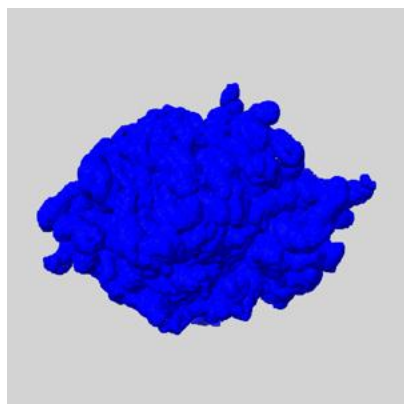
6.5 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

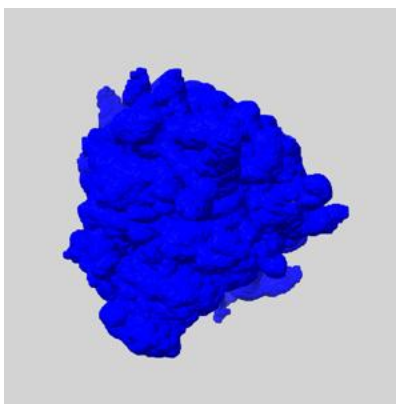
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

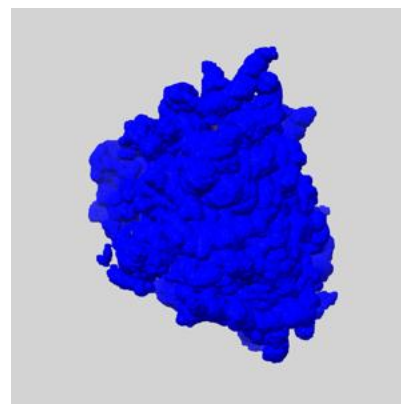
6.5.1 emd_7836_msk_1.map [i](#)



X



Y

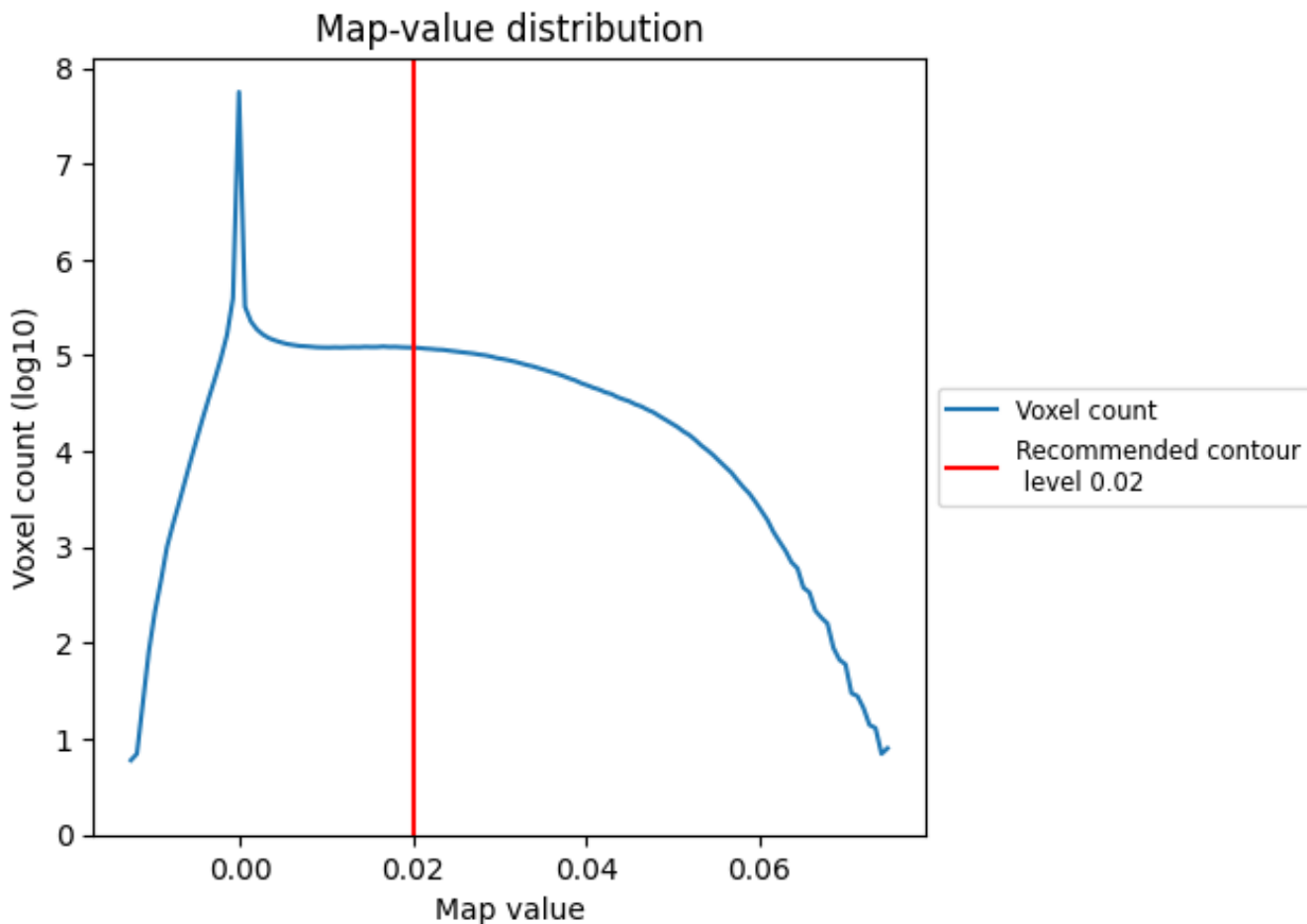


Z

7 Map analysis [i](#)

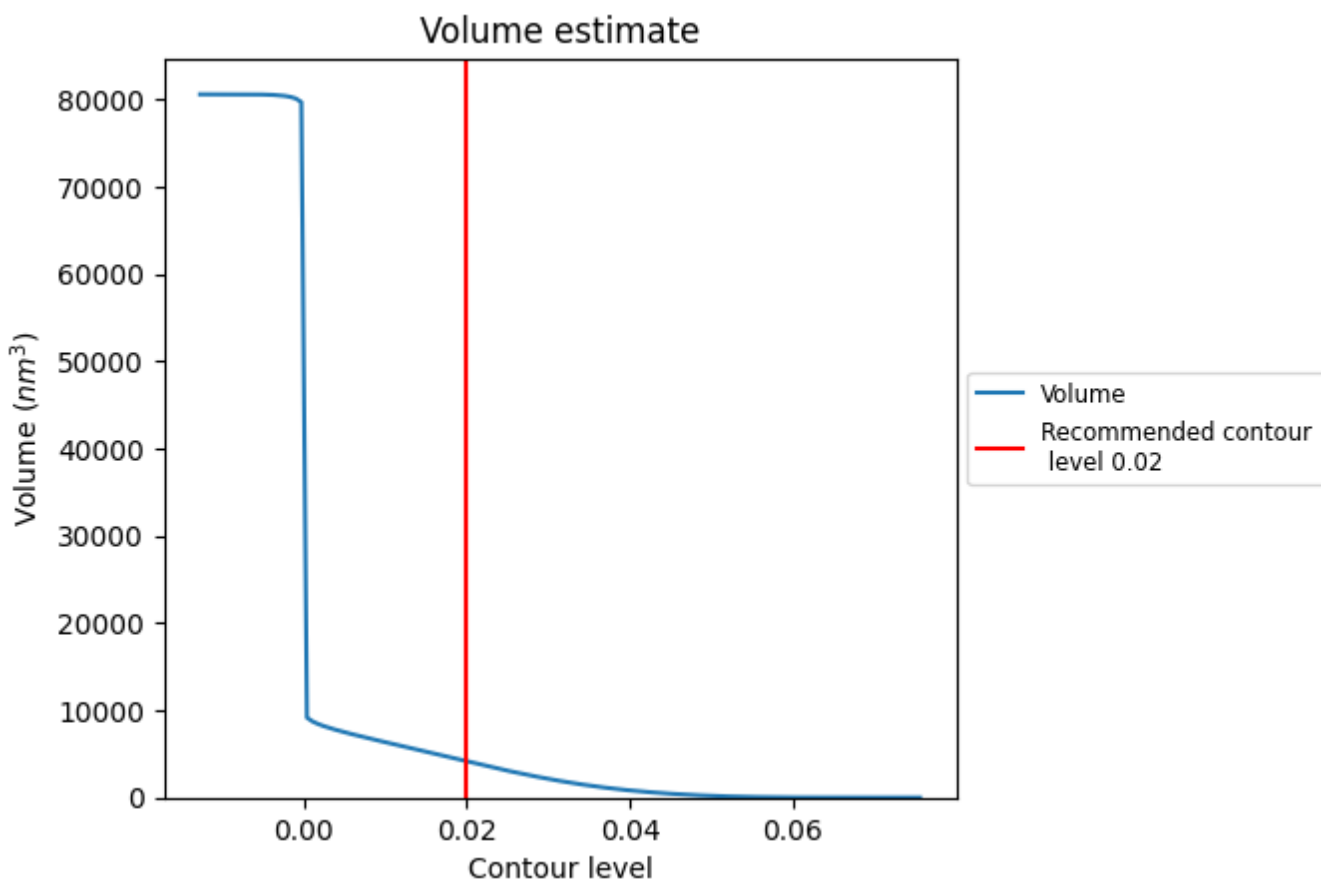
This section contains the results of statistical analysis of the map.

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.

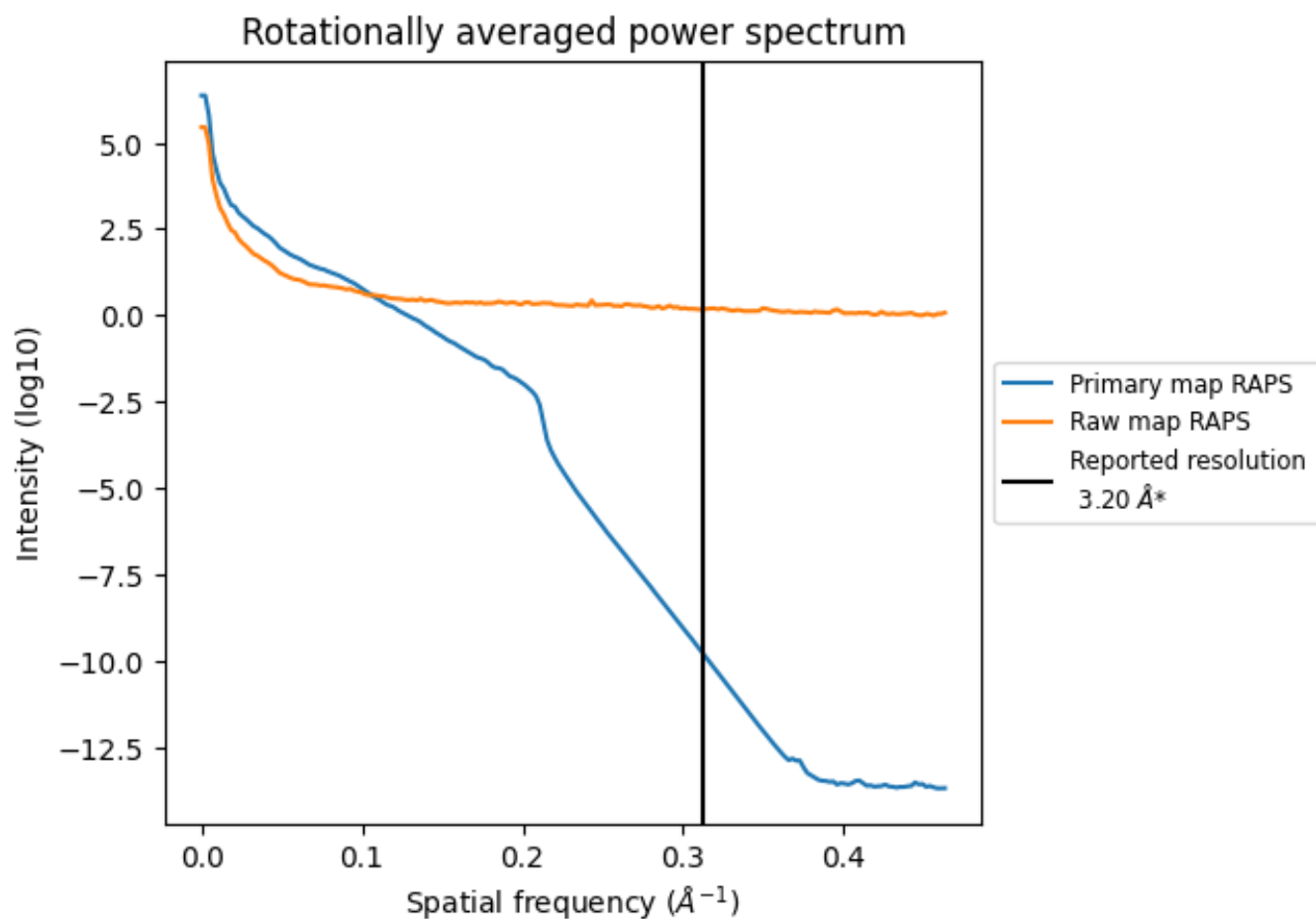
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4136 nm³; this corresponds to an approximate mass of 3736 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 [i](#)

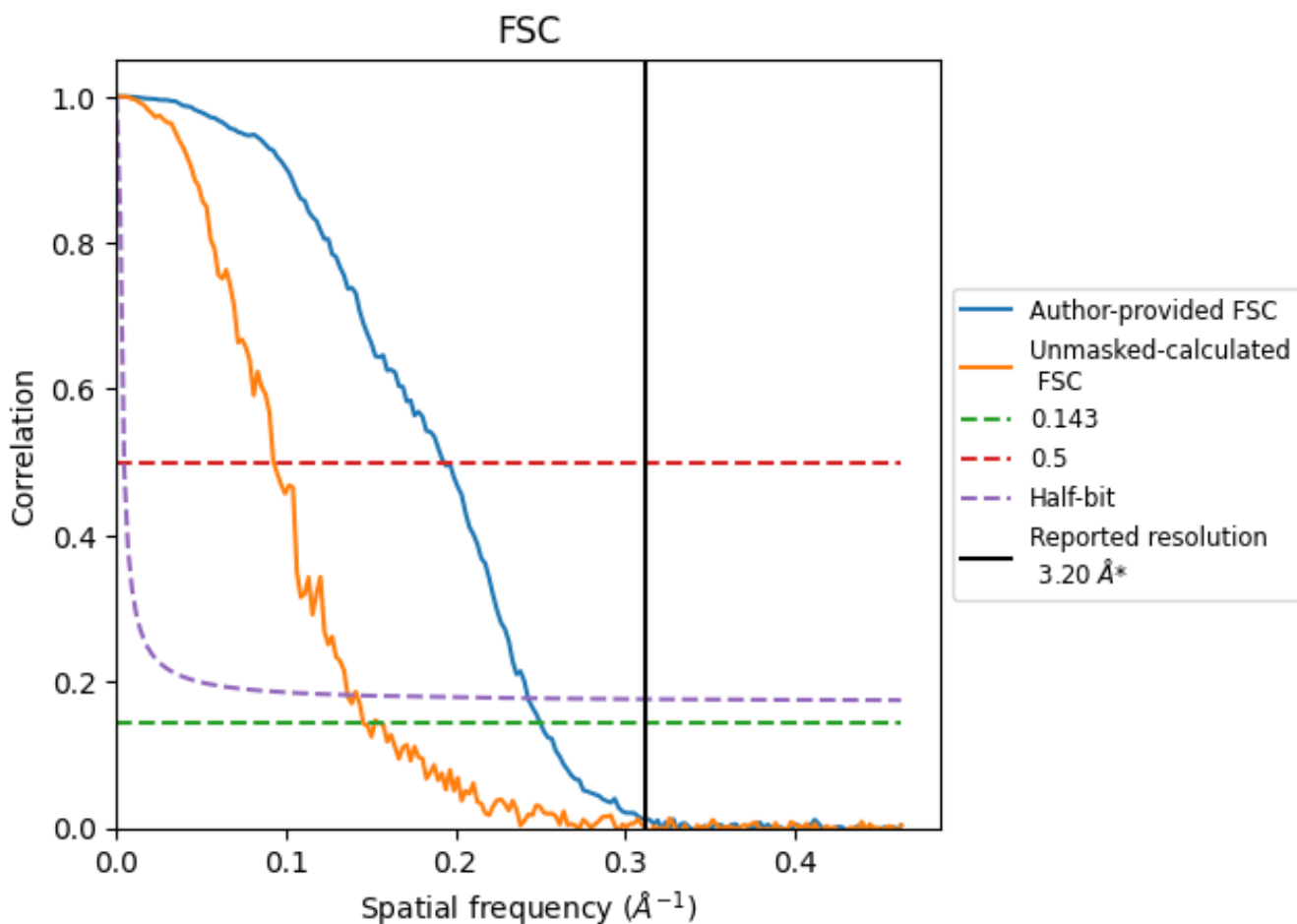


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	4.00	5.17	4.12
Unmasked-calculated*	6.86	10.79	7.33

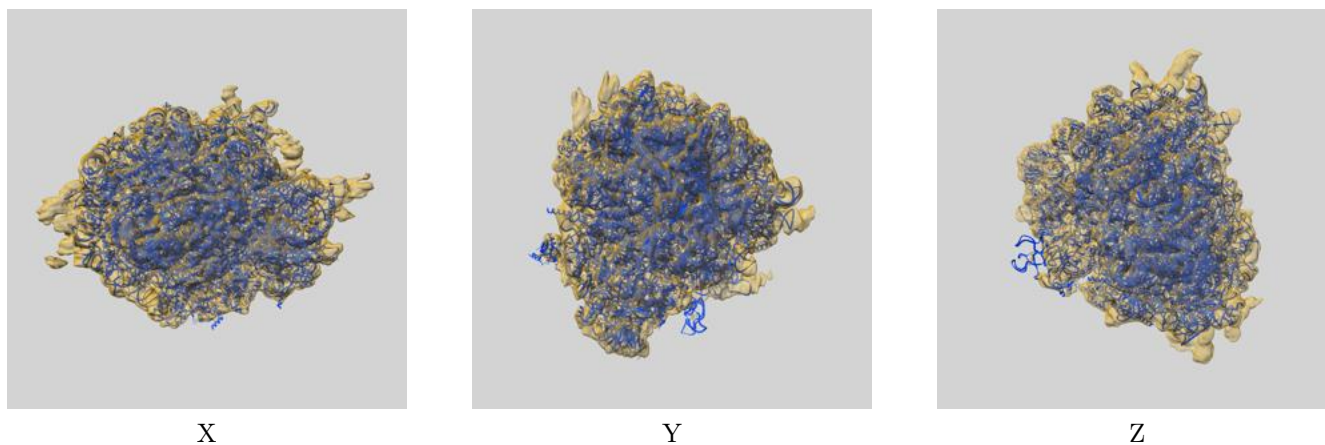
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 4.00 differs from the reported value 3.2 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.86 differs from the reported value 3.2 by more than 10 %

9 Map-model fit [i](#)

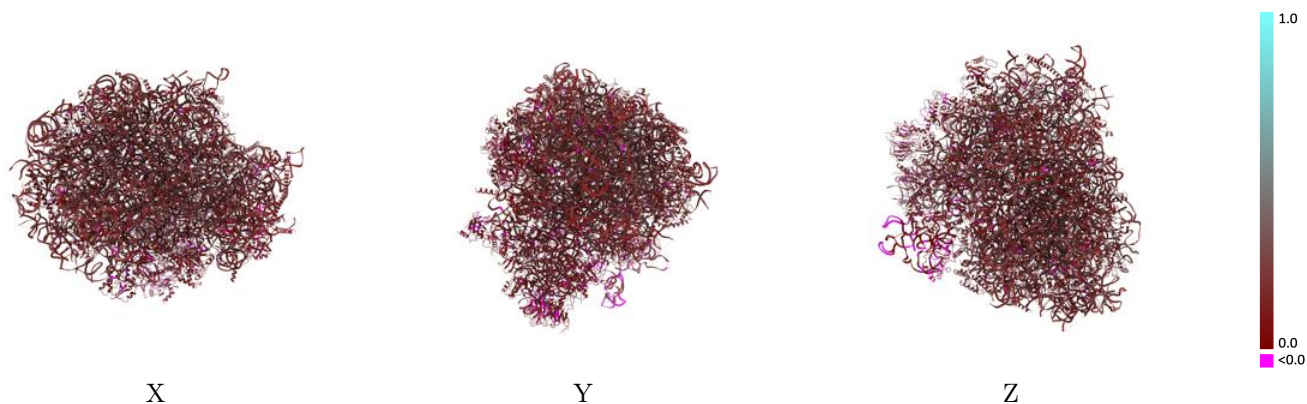
This section contains information regarding the fit between EMDB map EMD-7836 and PDB model 6D9J. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)



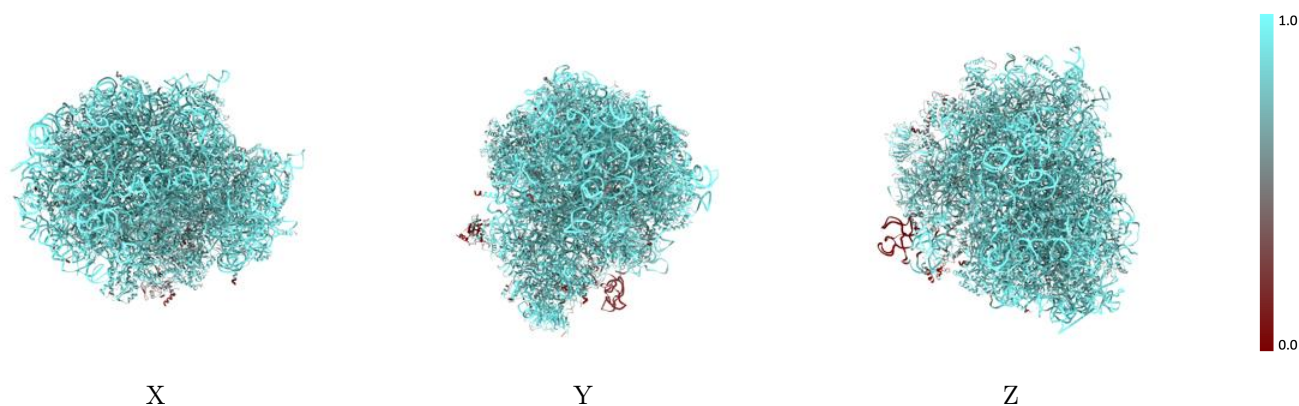
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



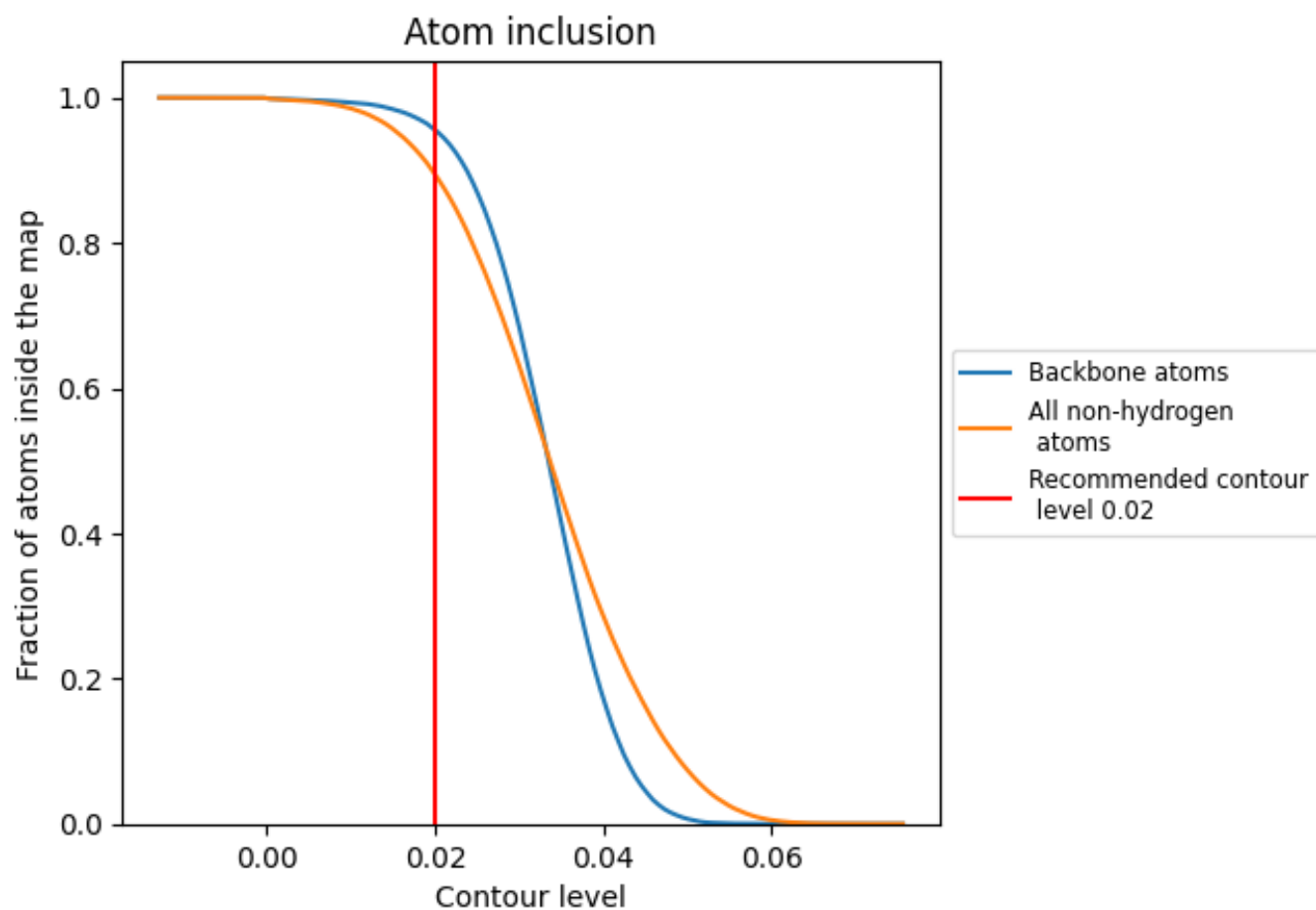
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 96% of all backbone atoms, 89% 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	 0.8948	 0.1880
2	 0.9769	 0.2060
3	 0.7774	 0.1720
4	 0.5296	 0.0620
5	 0.9830	 0.2280
7	 0.9961	 0.2340
8	 0.9804	 0.2140
9	 0.7334	 0.1480
A	 0.8352	 0.1770
B	 0.8227	 0.1750
BB	 0.7879	 0.1530
C	 0.8351	 0.1610
CC	 0.8570	 0.1640
D	 0.8944	 0.1680
DD	 0.8005	 0.1630
E	 0.8523	 0.1690
EE	 0.7809	 0.1540
F	 0.7993	 0.1610
FF	 0.8578	 0.1500
G	 0.8268	 0.1690
GG	 0.8031	 0.1470
H	 0.8072	 0.1740
HH	 0.8571	 0.1460
I	 0.8203	 0.1700
II	 0.7960	 0.1670
J	 0.8448	 0.1570
JJ	 0.8494	 0.1540
K	 0.5691	 0.0670
KK	 0.8150	 0.1510
L	 0.8354	 0.1780
LL	 0.8608	 0.1400
M	 0.9020	 0.1660
MM	 0.8123	 0.1870
N	 0.8414	 0.1420
NN	 0.3300	 0.0790





















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Chain	Atom inclusion	Q-score
O	0.8032	0.1710
OO	0.8122	0.1750
P	0.8723	0.1570
PP	0.8460	0.1530
Q	0.8000	0.1630
QQ	0.8197	0.1090
R	0.8244	0.1720
RR	0.8205	0.1110
S	0.8487	0.1750
SS	0.5973	0.0840
T	0.8036	0.1790
TT	0.7459	0.1390
U	0.8407	0.1780
UU	0.8594	0.1220
V	0.7687	0.1790
VV	0.7842	0.1220
W	0.8387	0.1680
WW	0.7910	0.1510
X	0.8170	0.1620
XX	0.8149	0.1770
Y	0.8822	0.1560
YY	0.7554	0.1600
Z	0.8910	0.1650
ZZ	0.8787	0.1410
a	0.8812	0.1550
aa	0.7496	0.1480
b	0.8074	0.1590
bb	0.8248	0.1560
c	0.8669	0.1750
cc	0.8138	0.1780
d	0.8483	0.1750
dd	0.7404	0.1430
e	0.8279	0.1830
ee	0.9048	0.1340
f	0.8302	0.1700
ff	0.7841	0.1470
g	0.8481	0.1460
gg	0.5009	0.0810
h	0.8315	0.1750
hh	0.8708	0.1260
i	0.8128	0.1780
j	0.8720	0.1320

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Chain	Atom inclusion	Q-score
k	 0.8259	 0.1720
l	 0.8337	 0.1610
m	 0.8072	 0.1570
n	 0.7661	 0.1230
o	 0.8752	 0.1730
p	 0.8200	 0.1710
r	 0.8454	 0.1740
s	 0.7697	 0.1380
t	 0.6520	 0.0890