Full wwPDB EM Validation Report ⓘ

Nov 9, 2022 – 10:42 AM EST

PDB ID	:	6OSK
EMDB ID	:	EMD-20184
Title	:	RF1 accommodated 70S complex at 60 ms
Authors	:	Fu, Z.; Indrisiunaite, G.; Kaledhonkar, S.; Shah, B.; Sun, M.; Chen, B.; Grassucci, R.A.; Ehrenberg, M.; Frank, J.
Deposited on	:	2019-05-01
Resolution	:	3.60 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:

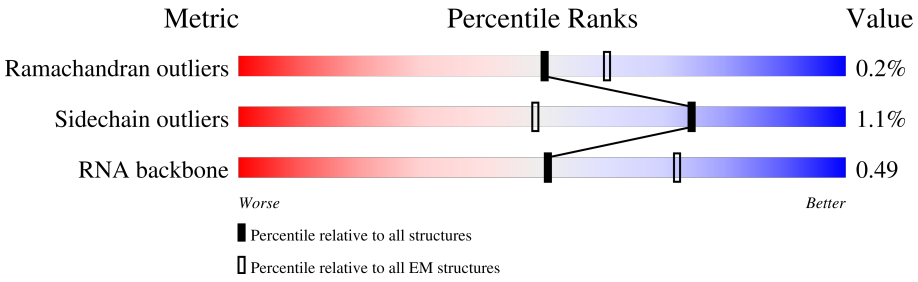
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (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 3.60 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 <=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	1	2903	7% 79% 21%
2	2	1534	5% 80% 20%
3	3	120	81% 19%
4	4	9	67% 33%
5	B	271	99%
6	C	209	98%
7	D	201	6% 99%
8	E	177	35% 100%

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Mol	Chain	Length	Quality of chain
9	F	175	16% 99%
10	G	149	74% 98%
11	J	142	100%
12	K	123	7% 99%
13	L	144	99%
14	M	136	99%
15	N	119	99%
16	O	116	16% 98%
17	P	114	8% 98%
18	Q	117	99%
19	R	103	5% 97%
20	S	110	99%
21	T	94	11% 99%
22	U	103	12% 100%
23	V	94	18% 99%
24	W	76	100%
25	X	77	8% 99%
26	Y	62	10% 100%
27	Z	58	5% 98%
28	a	66	100% 97%
29	b	56	98%
30	c	52	6% 98%
31	d	46	98%
32	e	64	6% 97%
33	f	38	5% 100%

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Mol	Chain	Length	Quality of chain
34	g	225	27% 100%
35	h	208	15% 99%
36	i	205	48% 100%
37	j	156	99%
38	k	104	18% 100%
39	l	151	40% 99%
40	m	129	5% 100%
41	n	127	20% 98%
42	o	99	37% 99%
43	p	117	15% 99%
44	q	123	13% 98%
45	r	116	31% 100%
46	s	100	15% 100%
47	t	88	11% 99%
48	u	82	18% 99%
49	v	80	24% 99%
50	w	66	27% 100%
51	x	83	28% 98%
52	y	86	15% 100%
53	z	70	39% 100%
54	A	259	36% 98%
55	5	76	18% 71% 26%
56	6	3	67% 67% 33%

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 146659 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	2903	62336	27816	11470	20147	2903	0	0

- Molecule 2 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	1534	32929	14693	6041	10661	1534	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	3	120	2569	1144	468	837	120	0	0

- Molecule 4 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	4	9	184	83	26	66	9	0	0

- Molecule 5 is a protein called 50S ribosomal protein L2.

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

- Molecule 6 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	C	209	1565	979	288	294	4	0	0

- Molecule 7 is a protein called 50S ribosomal protein L4.

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

- Molecule 8 is a protein called 50S ribosomal protein L5.

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

- Molecule 9 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 10 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 11 is a protein called 50S ribosomal protein L13.

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

- Molecule 12 is a protein called 50S ribosomal protein L14.

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

- Molecule 13 is a protein called 50S ribosomal protein L15.

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

- Molecule 14 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 15 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	119	Total	C	N	O	S	0	0
			951	588	195	163	5		

- Molecule 16 is a protein called 50S ribosomal protein L18.

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

- Molecule 17 is a protein called 50S ribosomal protein L19.

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

- Molecule 18 is a protein called 50S ribosomal protein L20.

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

- Molecule 19 is a protein called 50S ribosomal protein L21.

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

- Molecule 20 is a protein called 50S ribosomal protein L22.

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

- Molecule 21 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	94	Total	C	N	O	S	0	0
			746	470	140	134	2		

- Molecule 22 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	U	103	Total	C	N	O	0	0
			788	498	148	142		

- Molecule 23 is a protein called 50S ribosomal protein L25.

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

- Molecule 24 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	76	Total	C	N	O	S	0	0
			582	360	117	104	1		

- Molecule 25 is a protein called 50S ribosomal protein L28.

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

- Molecule 26 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 27 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 28 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 29 is a protein called 50S ribosomal protein L32.

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

- Molecule 30 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	c	52	Total	C	N	O	0	0
			426	275	78	73		

- Molecule 31 is a protein called 50S ribosomal protein L34.

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

- Molecule 32 is a protein called 50S ribosomal protein L35.

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

- Molecule 33 is a protein called 50S ribosomal protein L36.

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

- Molecule 34 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	225	Total	C	N	O	S	0	0
			1760	1113	316	323	8		

- Molecule 35 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	208	Total	C	N	O	S	0	0
			1636	1036	307	290	3		

- Molecule 36 is a protein called 30S ribosomal protein S4.

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

- Molecule 37 is a protein called 30S ribosomal protein S5.

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

- Molecule 38 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	k	104	Total	C	N	O	S	0	0
			848	536	153	152	7		

- Molecule 39 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	l	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 40 is a protein called 30S ribosomal protein S8.

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

- Molecule 41 is a protein called 30S ribosomal protein S9.

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

- Molecule 42 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	o	99	Total 790	C 495	N 151	O 143	S 1	0	0

- Molecule 43 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	p	117	Total 877	C 540	N 174	O 160	S 3	0	0

- Molecule 44 is a protein called 30S ribosomal protein S12.

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

- Molecule 45 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	116	Total 900	C 558	N 181	O 158	S 3	0	0

- Molecule 46 is a protein called 30S ribosomal protein S14.

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

- Molecule 47 is a protein called 30S ribosomal protein S15.

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

- Molecule 48 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	u	82	Total 649	C 406	N 128	O 114	S 1	0	0

- Molecule 49 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	v	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 50 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	w	66	Total	C	N	O	S	0	0
			544	344	102	97	1		

- Molecule 51 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	x	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 52 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	y	86	Total	C	N	O	S	0	0
			669	414	138	114	3		

- Molecule 53 is a protein called 30S ribosomal protein S21.

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

- Molecule 54 is a protein called Peptide chain release factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	A	259	Total	C	N	O	S	0	0
			2014	1235	382	389	8		

- Molecule 55 is a RNA chain called P-tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	5	76	Total	C	N	O	P	S	0	0
			1627	727	296	527	76	1		

- Molecule 56 is a protein called FME-PHE-PHE.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	6	3	Total	C	N	O	S	0	0
			32	24	3	4	1		

- Molecule 57 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
57	1	292	Total	Mg	0
			292	292	
57	2	1	Total	Mg	0
			1	1	
57	3	8	Total	Mg	0
			8	8	
57	C	1	Total	Mg	0
			1	1	
57	b	1	Total	Mg	0
			1	1	
57	f	1	Total	Mg	0
			1	1	
57	i	1	Total	Mg	0
			1	1	
57	5	2	Total	Mg	0
			2	2	

- Molecule 58 is ZINC ION (three-letter code: ZN) (formula: Zn).

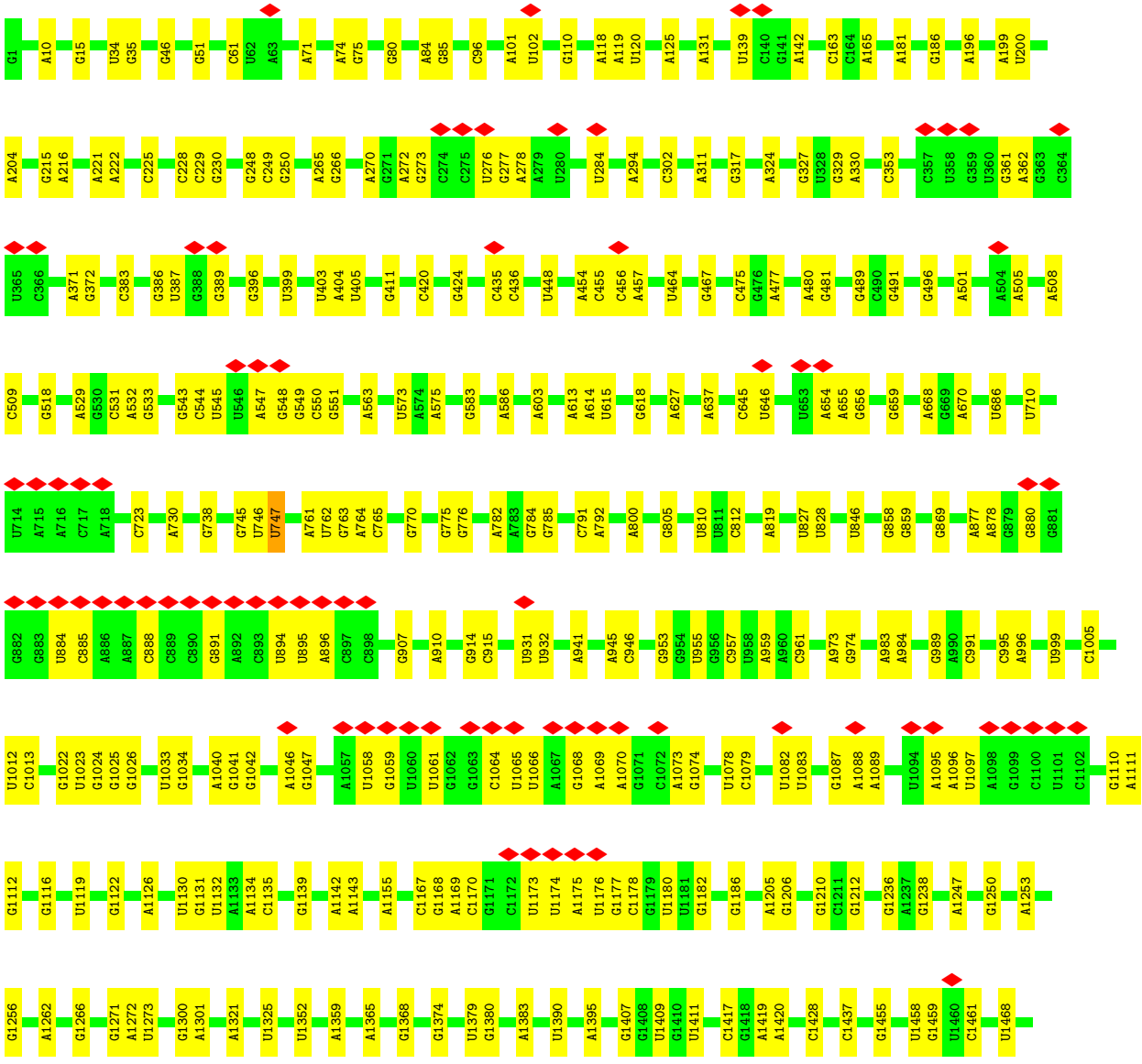
Mol	Chain	Residues	Atoms		AltConf
58	a	1	Total	Zn	0
			1	1	
58	f	1	Total	Zn	0
			1	1	

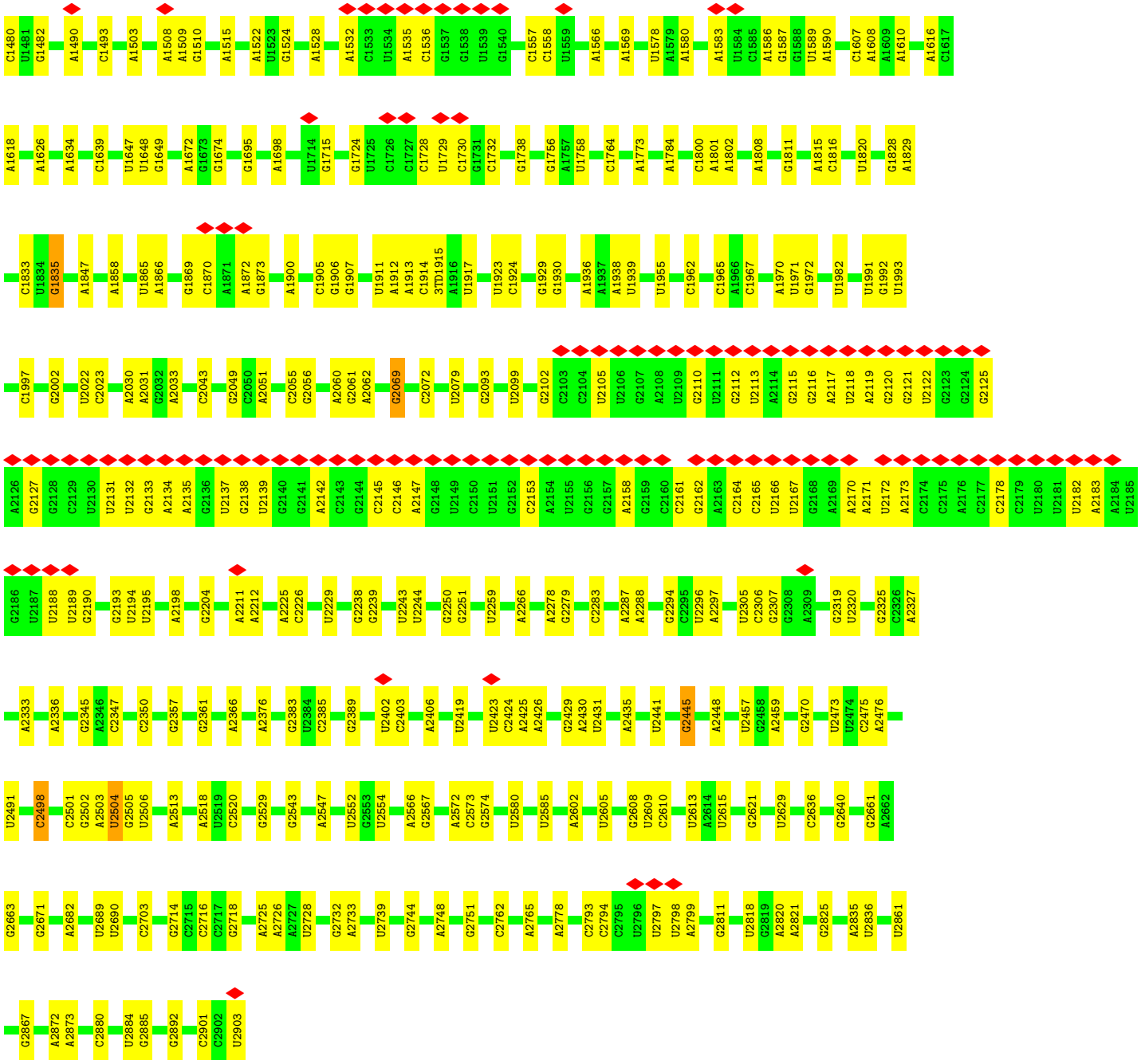
3 Residue-property plots (i)

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: 23S ribosomal RNA

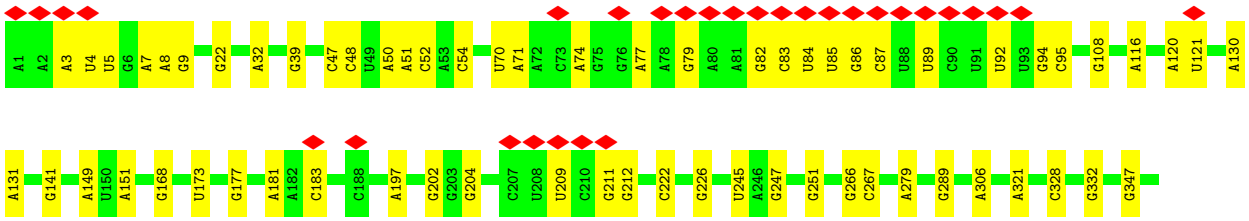
Chain 1:

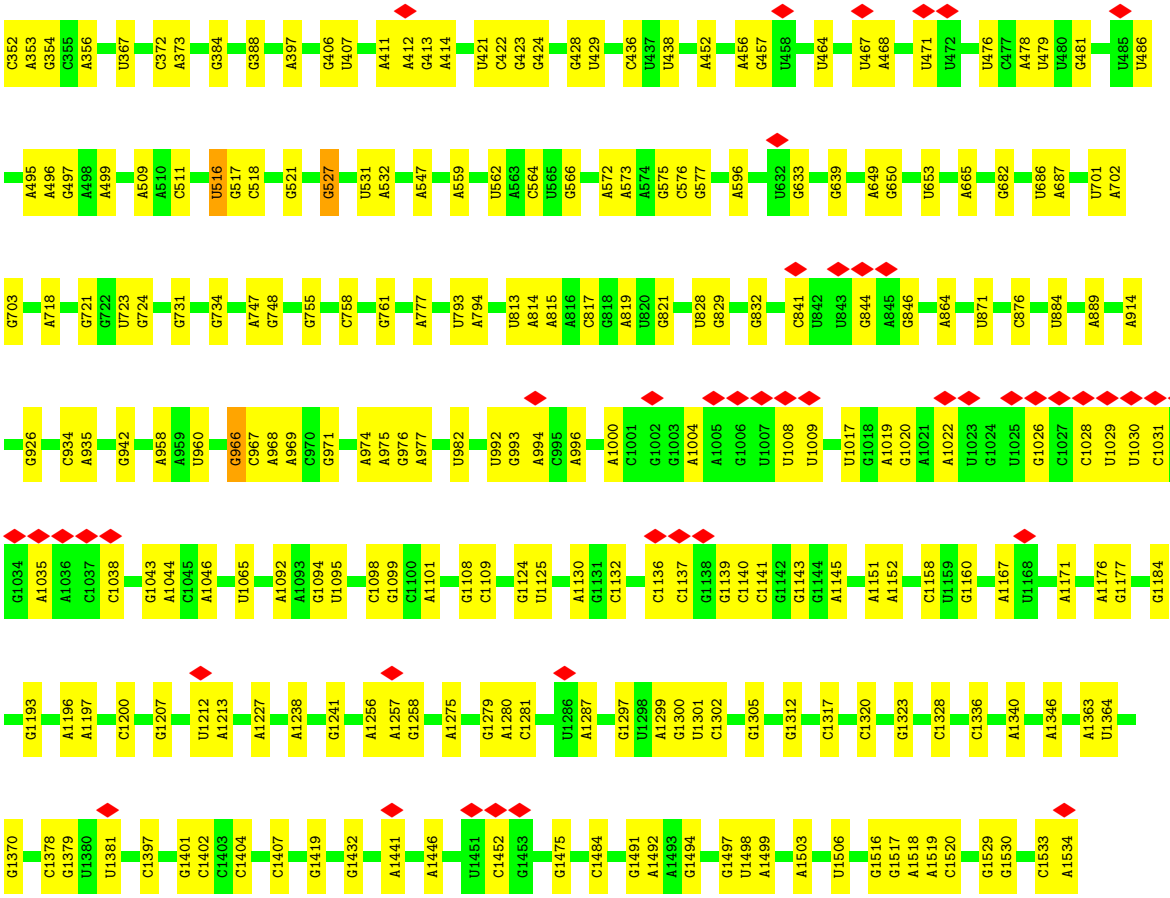




• Molecule 2: 16S ribosomal RNA

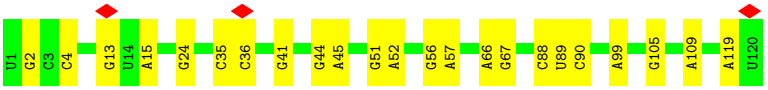
Chain 2:





• Molecule 3: 5S ribosomal RNA

Chain 3:

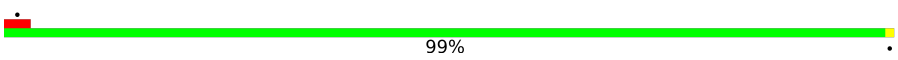


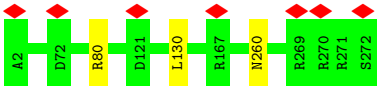
• Molecule 4: mRNA

Chain 4:

• Molecule 5: 50S ribosomal protein L2

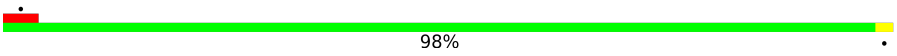
Chain B:

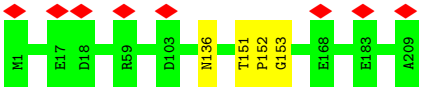




• Molecule 6: 50S ribosomal protein L3

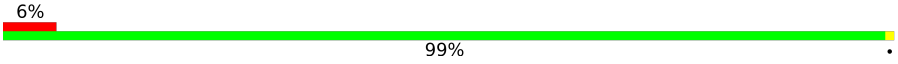
Chain C:

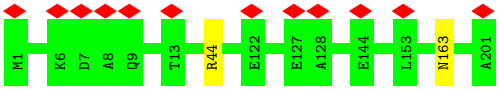




• Molecule 7: 50S ribosomal protein L4

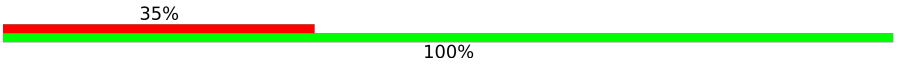
Chain D:

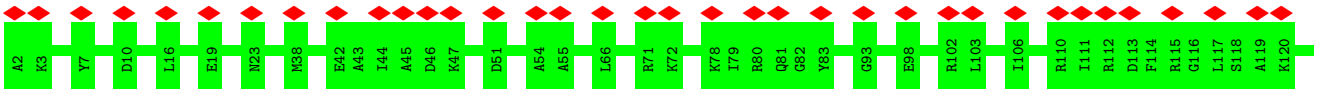


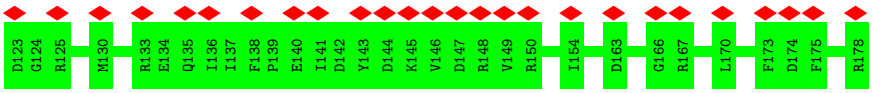


• Molecule 8: 50S ribosomal protein L5

Chain E:

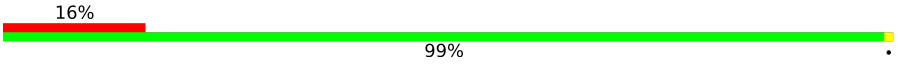


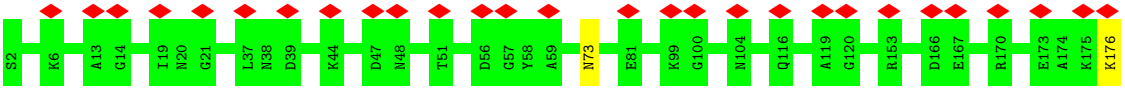




• Molecule 9: 50S ribosomal protein L6

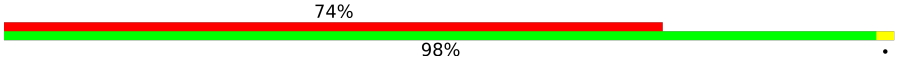
Chain F:

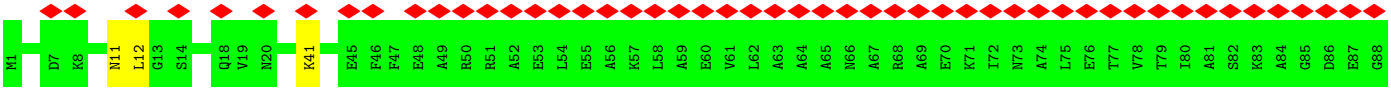


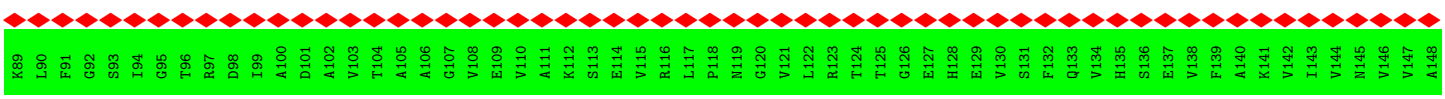


• Molecule 10: 50S ribosomal protein L9

Chain G:

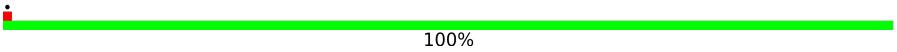






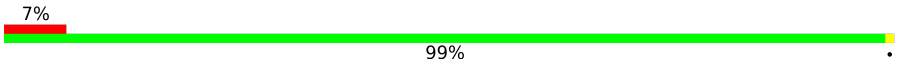
• Molecule 11: 50S ribosomal protein L13

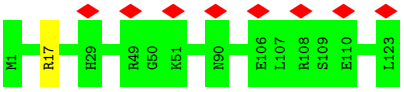
Chain J:



• Molecule 12: 50S ribosomal protein L14

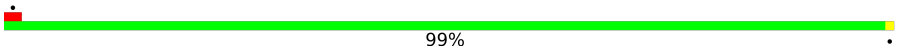
Chain K:

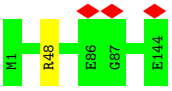




• Molecule 13: 50S ribosomal protein L15

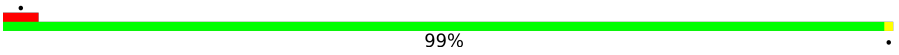
Chain L:

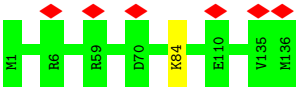




• Molecule 14: 50S ribosomal protein L16

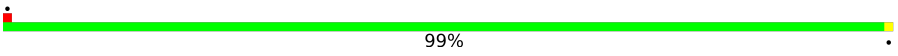
Chain M:

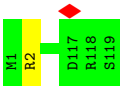




• Molecule 15: 50S ribosomal protein L17

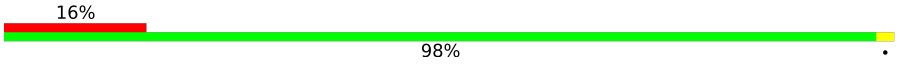
Chain N:

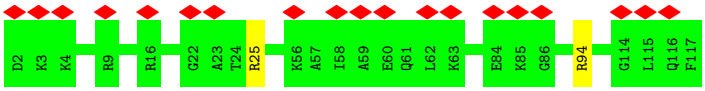




• Molecule 16: 50S ribosomal protein L18

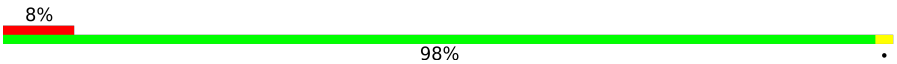
Chain O:

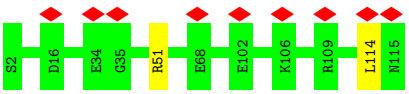




• Molecule 17: 50S ribosomal protein L19

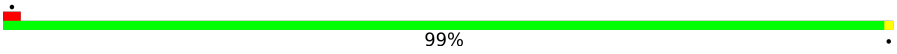
Chain P:

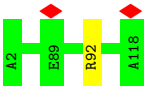




• Molecule 18: 50S ribosomal protein L20

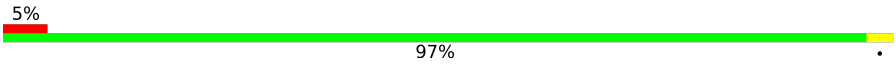
Chain Q:

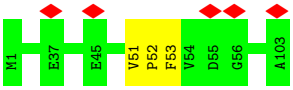




• Molecule 19: 50S ribosomal protein L21

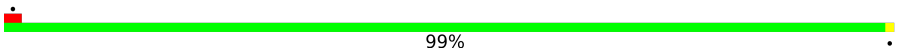
Chain R:

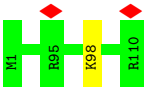




• Molecule 20: 50S ribosomal protein L22

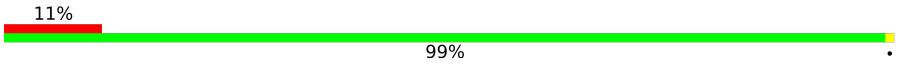
Chain S:

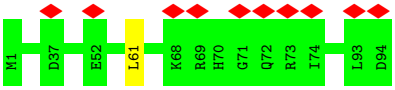




• Molecule 21: 50S ribosomal protein L23

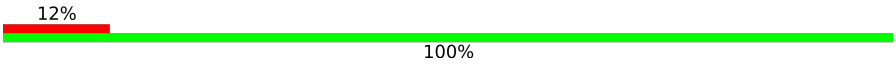
Chain T:

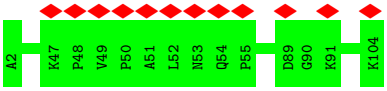




• Molecule 22: 50S ribosomal protein L24

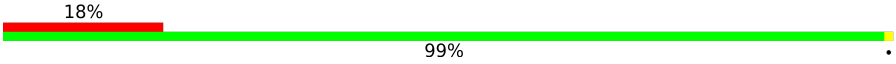
Chain U:

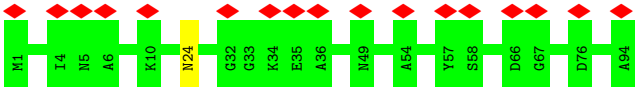




• Molecule 23: 50S ribosomal protein L25

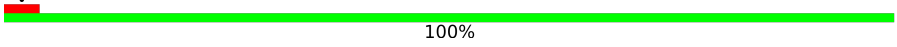
Chain V:





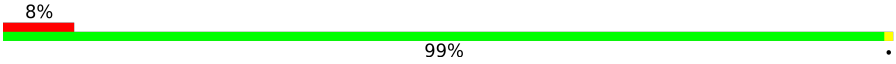
• Molecule 24: 50S ribosomal protein L27

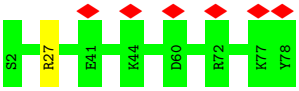
Chain W:



• Molecule 25: 50S ribosomal protein L28

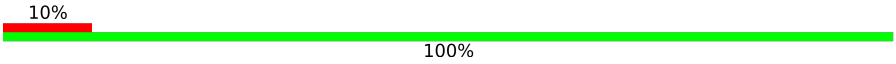
Chain X:

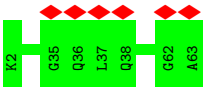




• Molecule 26: 50S ribosomal protein L29

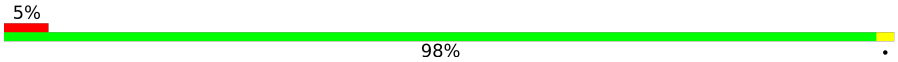
Chain Y:

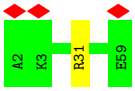




• Molecule 27: 50S ribosomal protein L30

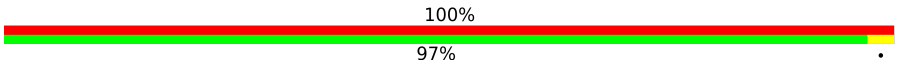
Chain Z:

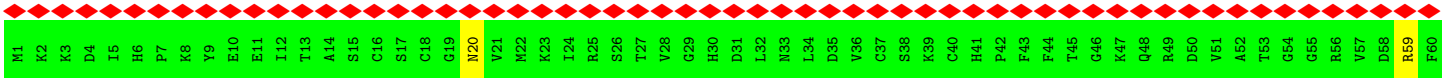


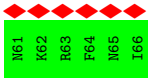


• Molecule 28: 50S ribosomal protein L31

Chain a:

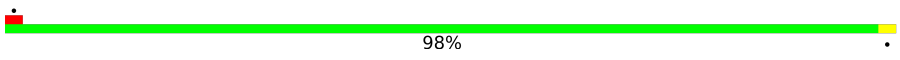


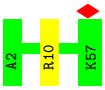




• Molecule 29: 50S ribosomal protein L32

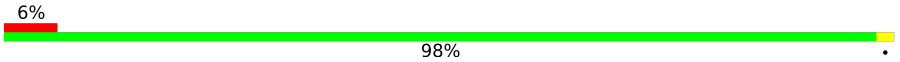
Chain b:

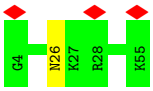




• Molecule 30: 50S ribosomal protein L33

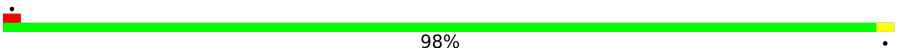
Chain c:

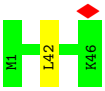




• Molecule 31: 50S ribosomal protein L34

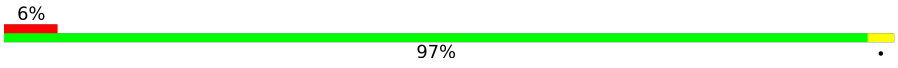
Chain d:

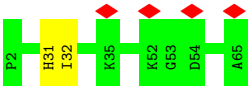




• Molecule 32: 50S ribosomal protein L35

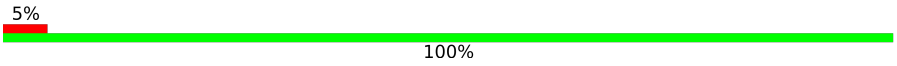
Chain e:

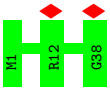




• Molecule 33: 50S ribosomal protein L36

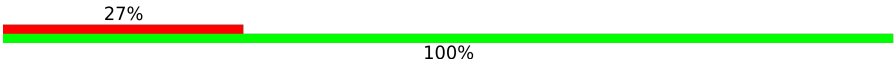
Chain f:

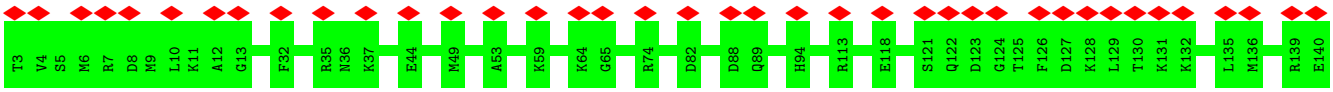


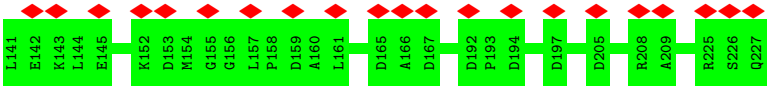


• Molecule 34: 30S ribosomal protein S2

Chain g:

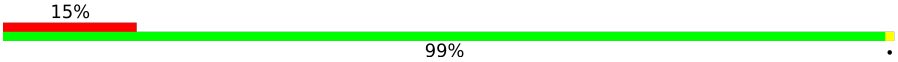


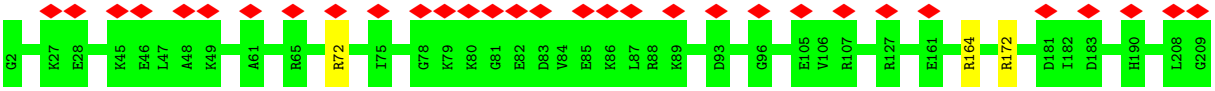




• Molecule 35: 30S ribosomal protein S3

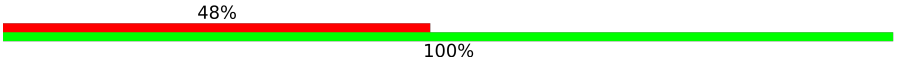
Chain h:

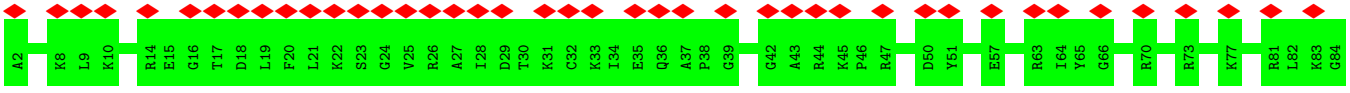


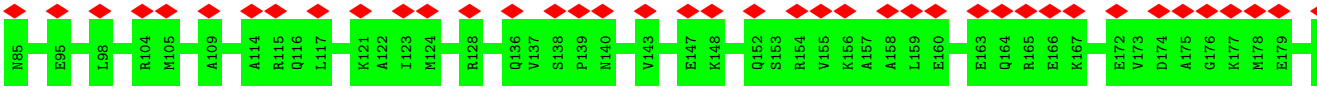


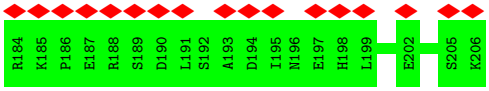
• Molecule 36: 30S ribosomal protein S4

Chain i:



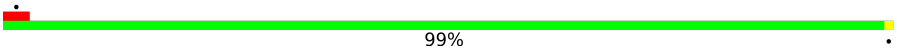


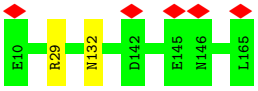




• Molecule 37: 30S ribosomal protein S5

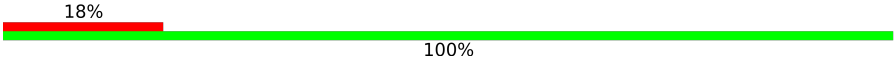
Chain j:

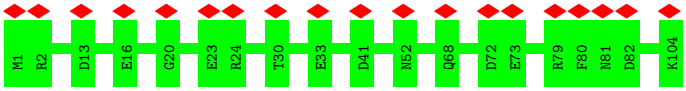




• Molecule 38: 30S ribosomal protein S6

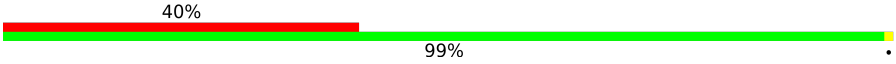
Chain k:

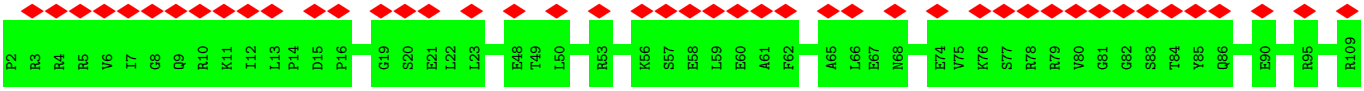


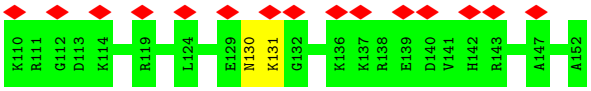


• Molecule 39: 30S ribosomal protein S7

Chain l:

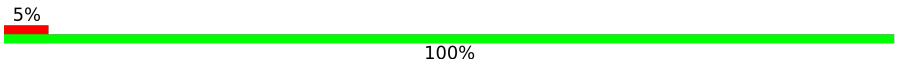


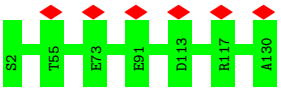




• Molecule 40: 30S ribosomal protein S8

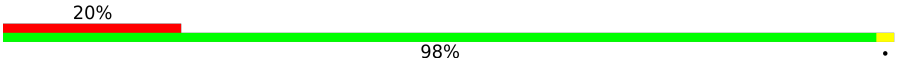
Chain m:

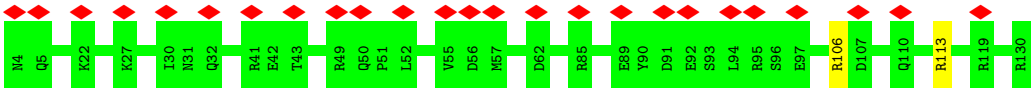




• Molecule 41: 30S ribosomal protein S9

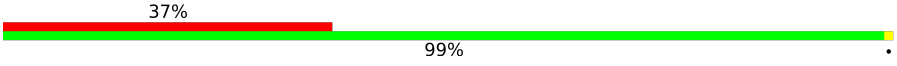
Chain n:

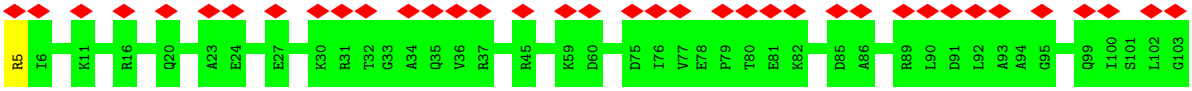




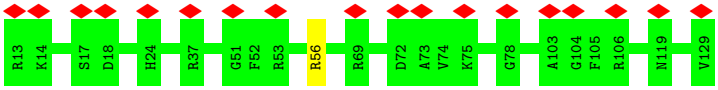
• Molecule 42: 30S ribosomal protein S10

Chain o:

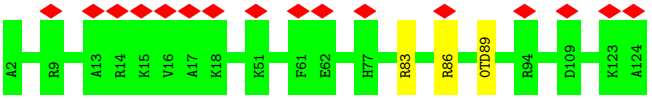




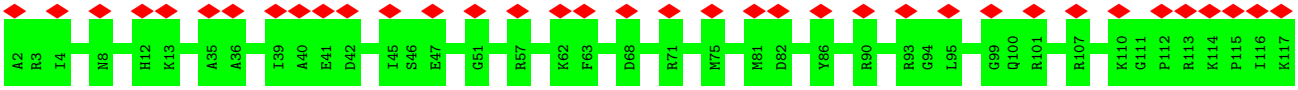
• Molecule 43: 30S ribosomal protein S11



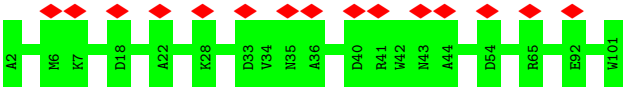
• Molecule 44: 30S ribosomal protein S12



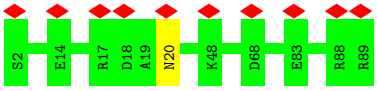
• Molecule 45: 30S ribosomal protein S13



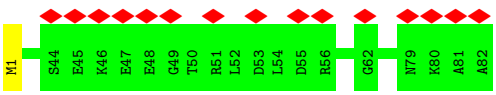
• Molecule 46: 30S ribosomal protein S14



• Molecule 47: 30S ribosomal protein S15

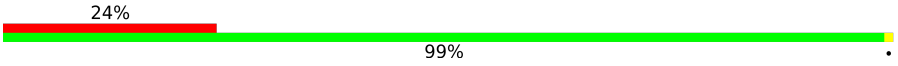


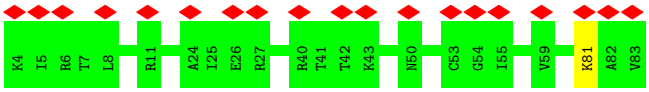
• Molecule 48: 30S ribosomal protein S16



• Molecule 49: 30S ribosomal protein S17

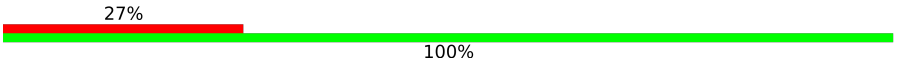
Chain v:

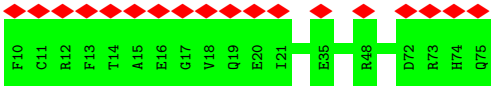




• Molecule 50: 30S ribosomal protein S18

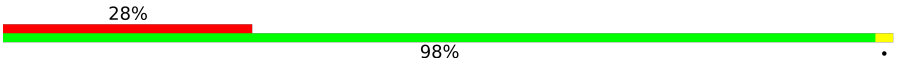
Chain w:

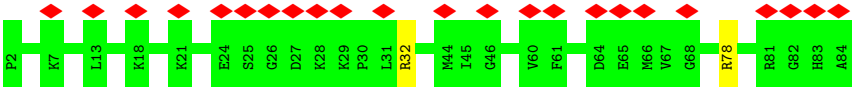




• Molecule 51: 30S ribosomal protein S19

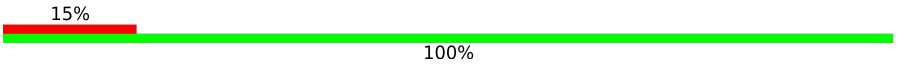
Chain x:

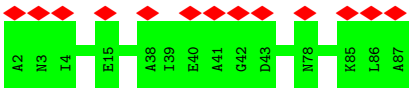




• Molecule 52: 30S ribosomal protein S20

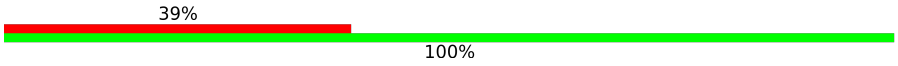
Chain y:

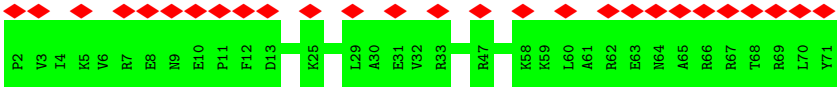




• Molecule 53: 30S ribosomal protein S21

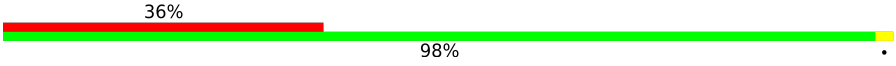
Chain z:

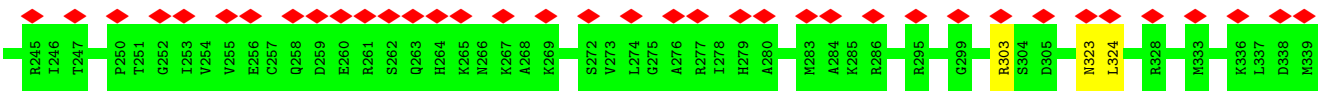


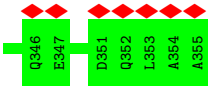


• Molecule 54: Peptide chain release factor 1

Chain A:

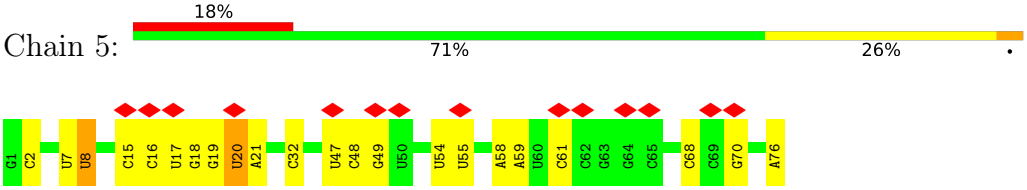






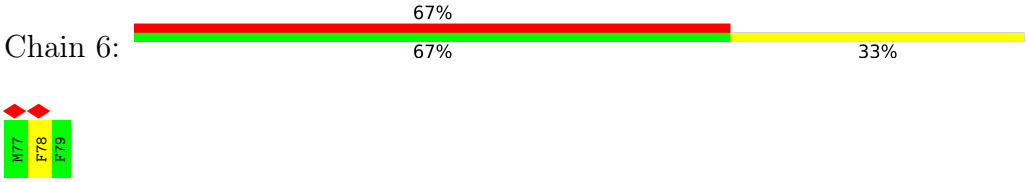
• Molecule 55: P-tRNA

Chain 5:



• Molecule 56: FME-PHE-PHE

Chain 6:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	202103	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	41.6	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	0.421	Depositor
Minimum map value	-0.221	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	421.12, 421.12, 421.12	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.645, 1.645, 1.645	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: G7M, 0TD, 2MG, OMG, 5MU, OMU, 3TD, 1MG, 4SU, 4OC, H2U, 5MC, MG, ZN, 2MA, 6MZ, UR3, PSU, OMC, MA6, FME

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	1	0.91	0/69286	0.97	0/108087
2	2	0.67	0/36590	0.93	0/57074
3	3	0.58	0/2872	0.94	0/4478
4	4	0.78	0/203	1.04	0/312
5	B	0.52	0/2121	0.61	0/2852
6	C	0.50	0/1586	0.61	0/2134
7	D	0.47	0/1571	0.57	0/2113
8	E	0.34	0/1434	0.55	0/1926
9	F	0.33	0/1333	0.53	0/1805
10	G	0.33	0/1122	0.56	0/1515
11	J	0.50	0/1152	0.56	0/1551
12	K	0.51	0/955	0.61	0/1279
13	L	0.45	0/1062	0.62	0/1413
14	M	0.45	0/1093	0.57	0/1460
15	N	0.50	0/964	0.63	0/1289
16	O	0.33	0/902	0.55	0/1209
17	P	0.47	0/929	0.57	0/1242
18	Q	0.60	0/960	0.58	0/1278
19	R	0.50	0/829	0.62	0/1107
20	S	0.50	0/864	0.58	0/1156
21	T	0.42	0/752	0.56	0/1005
22	U	0.43	0/796	0.54	0/1062
23	V	0.36	0/766	0.54	0/1025
24	W	0.48	0/589	0.55	0/779
25	X	0.42	0/635	0.54	0/848
26	Y	0.34	0/502	0.51	0/667
27	Z	0.42	0/452	0.60	0/605
28	a	0.28	0/531	0.50	0/709
29	b	0.46	0/450	0.63	0/599
30	c	0.40	0/433	0.59	0/576
31	d	0.55	0/380	0.62	0/498

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
32	e	0.47	0/513	0.62	0/676
33	f	0.46	0/303	0.58	0/397
34	g	0.34	0/1791	0.54	0/2413
35	h	0.36	0/1663	0.54	0/2241
36	i	0.32	0/1665	0.51	0/2227
37	j	0.42	0/1165	0.59	0/1568
38	k	0.37	0/867	0.58	0/1171
39	l	0.32	0/1195	0.53	0/1602
40	m	0.39	0/989	0.55	0/1326
41	n	0.34	0/1034	0.57	0/1375
42	o	0.36	0/800	0.59	0/1082
43	p	0.36	0/893	0.51	0/1205
44	q	0.43	0/960	0.65	0/1286
45	r	0.32	0/909	0.57	0/1215
46	s	0.33	0/817	0.48	0/1088
47	t	0.34	0/722	0.55	0/964
48	u	0.37	0/659	0.58	0/884
49	v	0.34	0/657	0.57	0/881
50	w	0.36	0/553	0.54	0/743
51	x	0.32	0/680	0.51	0/915
52	y	0.31	0/675	0.48	0/895
53	z	0.33	0/597	0.52	0/792
54	A	0.39	0/2046	0.61	0/2759
55	5	0.52	0/1704	0.95	0/2654
56	6	0.72	0/23	0.73	0/29
All	All	0.73	0/157994	0.87	0/236041

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	B	269/271 (99%)	254 (94%)	15 (6%)	0	100	100
6	C	207/209 (99%)	195 (94%)	10 (5%)	2 (1%)	15	55
7	D	199/201 (99%)	190 (96%)	9 (4%)	0	100	100
8	E	175/177 (99%)	163 (93%)	12 (7%)	0	100	100
9	F	173/175 (99%)	163 (94%)	10 (6%)	0	100	100
10	G	147/149 (99%)	135 (92%)	12 (8%)	0	100	100
11	J	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
12	K	121/123 (98%)	116 (96%)	5 (4%)	0	100	100
13	L	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
14	M	134/136 (98%)	131 (98%)	3 (2%)	0	100	100
15	N	117/119 (98%)	111 (95%)	6 (5%)	0	100	100
16	O	114/116 (98%)	110 (96%)	4 (4%)	0	100	100
17	P	112/114 (98%)	104 (93%)	8 (7%)	0	100	100
18	Q	115/117 (98%)	112 (97%)	3 (3%)	0	100	100
19	R	101/103 (98%)	90 (89%)	9 (9%)	2 (2%)	7	41
20	S	108/110 (98%)	100 (93%)	8 (7%)	0	100	100
21	T	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
22	U	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
23	V	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
24	W	74/76 (97%)	71 (96%)	3 (4%)	0	100	100
25	X	75/77 (97%)	71 (95%)	4 (5%)	0	100	100
26	Y	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
27	Z	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
28	a	64/66 (97%)	60 (94%)	4 (6%)	0	100	100
29	b	54/56 (96%)	52 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	c	50/52 (96%)	50 (100%)	0	0	100	100
31	d	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
32	e	62/64 (97%)	56 (90%)	5 (8%)	1 (2%)	9	46
33	f	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
34	g	223/225 (99%)	211 (95%)	12 (5%)	0	100	100
35	h	206/208 (99%)	193 (94%)	13 (6%)	0	100	100
36	i	203/205 (99%)	194 (96%)	9 (4%)	0	100	100
37	j	154/156 (99%)	144 (94%)	10 (6%)	0	100	100
38	k	102/104 (98%)	100 (98%)	2 (2%)	0	100	100
39	l	149/151 (99%)	143 (96%)	6 (4%)	0	100	100
40	m	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
41	n	125/127 (98%)	115 (92%)	10 (8%)	0	100	100
42	o	97/99 (98%)	88 (91%)	9 (9%)	0	100	100
43	p	115/117 (98%)	108 (94%)	7 (6%)	0	100	100
44	q	120/123 (98%)	108 (90%)	12 (10%)	0	100	100
45	r	114/116 (98%)	106 (93%)	8 (7%)	0	100	100
46	s	98/100 (98%)	96 (98%)	2 (2%)	0	100	100
47	t	86/88 (98%)	82 (95%)	4 (5%)	0	100	100
48	u	80/82 (98%)	76 (95%)	4 (5%)	0	100	100
49	v	78/80 (98%)	71 (91%)	7 (9%)	0	100	100
50	w	64/66 (97%)	60 (94%)	4 (6%)	0	100	100
51	x	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
52	y	84/86 (98%)	83 (99%)	1 (1%)	0	100	100
53	z	68/70 (97%)	68 (100%)	0	0	100	100
54	A	257/259 (99%)	236 (92%)	18 (7%)	3 (1%)	13	51
56	6	1/3 (33%)	0	0	1 (100%)	0	0
All	All	5866/5969 (98%)	5551 (95%)	306 (5%)	9 (0%)	50	79

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
19	R	53	PHE
54	A	213	GLU

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Mol	Chain	Res	Type
54	A	323	ASN
54	A	324	LEU
19	R	52	PRO
56	6	78	PHE
6	C	153	GLY
32	e	32	ILE
6	C	152	PRO

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
5	B	216/216 (100%)	213 (99%)	3 (1%)	67 85
6	C	164/164 (100%)	162 (99%)	2 (1%)	71 87
7	D	165/165 (100%)	163 (99%)	2 (1%)	71 87
8	E	148/148 (100%)	148 (100%)	0	100 100
9	F	136/136 (100%)	134 (98%)	2 (2%)	65 84
10	G	114/114 (100%)	111 (97%)	3 (3%)	46 74
11	J	116/116 (100%)	116 (100%)	0	100 100
12	K	104/104 (100%)	103 (99%)	1 (1%)	76 88
13	L	103/103 (100%)	102 (99%)	1 (1%)	76 88
14	M	109/109 (100%)	108 (99%)	1 (1%)	78 90
15	N	99/99 (100%)	98 (99%)	1 (1%)	76 88
16	O	86/86 (100%)	84 (98%)	2 (2%)	50 76
17	P	99/99 (100%)	97 (98%)	2 (2%)	55 79
18	Q	89/89 (100%)	88 (99%)	1 (1%)	73 88
19	R	84/84 (100%)	83 (99%)	1 (1%)	71 87
20	S	93/93 (100%)	92 (99%)	1 (1%)	73 88
21	T	81/81 (100%)	80 (99%)	1 (1%)	71 87
22	U	84/84 (100%)	84 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
23	V	78/78 (100%)	77 (99%)	1 (1%)	69 86
24	W	58/58 (100%)	58 (100%)	0	100 100
25	X	67/67 (100%)	66 (98%)	1 (2%)	65 84
26	Y	54/54 (100%)	54 (100%)	0	100 100
27	Z	48/48 (100%)	47 (98%)	1 (2%)	53 78
28	a	59/59 (100%)	57 (97%)	2 (3%)	37 69
29	b	47/47 (100%)	46 (98%)	1 (2%)	53 78
30	c	47/47 (100%)	46 (98%)	1 (2%)	53 78
31	d	38/38 (100%)	37 (97%)	1 (3%)	46 74
32	e	51/51 (100%)	50 (98%)	1 (2%)	55 79
33	f	34/34 (100%)	34 (100%)	0	100 100
34	g	187/187 (100%)	187 (100%)	0	100 100
35	h	171/171 (100%)	168 (98%)	3 (2%)	59 81
36	i	172/172 (100%)	172 (100%)	0	100 100
37	j	119/119 (100%)	117 (98%)	2 (2%)	60 82
38	k	91/91 (100%)	91 (100%)	0	100 100
39	l	124/124 (100%)	122 (98%)	2 (2%)	62 83
40	m	104/104 (100%)	104 (100%)	0	100 100
41	n	105/105 (100%)	103 (98%)	2 (2%)	57 80
42	o	86/86 (100%)	85 (99%)	1 (1%)	71 87
43	p	90/90 (100%)	89 (99%)	1 (1%)	73 88
44	q	102/102 (100%)	100 (98%)	2 (2%)	55 79
45	r	94/94 (100%)	94 (100%)	0	100 100
46	s	83/83 (100%)	83 (100%)	0	100 100
47	t	76/76 (100%)	75 (99%)	1 (1%)	69 86
48	u	65/65 (100%)	64 (98%)	1 (2%)	65 84
49	v	74/74 (100%)	73 (99%)	1 (1%)	67 85
50	w	57/57 (100%)	57 (100%)	0	100 100
51	x	72/72 (100%)	70 (97%)	2 (3%)	43 72
52	y	65/65 (100%)	65 (100%)	0	100 100
53	z	60/60 (100%)	60 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
54	A	210/210 (100%)	208 (99%)	2 (1%)	76 88
56	6	2/2 (100%)	2 (100%)	0	100 100
All	All	4880/4880 (100%)	4827 (99%)	53 (1%)	74 88

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	B	80	ARG
5	B	130	LEU
5	B	260	ASN
6	C	136	ASN
6	C	151	THR
7	D	44	ARG
7	D	163	ASN
9	F	73	ASN
9	F	176	LYS
10	G	11	ASN
10	G	12	LEU
10	G	41	LYS
12	K	17	ARG
13	L	48	ARG
14	M	84	LYS
15	N	2	ARG
16	O	25	ARG
16	O	94	ARG
17	P	51	ARG
17	P	114	LEU
18	Q	92	ARG
19	R	51	VAL
20	S	98	LYS
21	T	61	LEU
23	V	24	ASN
25	X	27	ARG
27	Z	31	ARG
28	a	20	ASN
28	a	59	ARG
29	b	10	ARG
30	c	26	ASN
31	d	42	LEU
32	e	31	HIS
35	h	72	ARG

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Mol	Chain	Res	Type
35	h	164	ARG
35	h	172	ARG
37	j	29	ARG
37	j	132	ASN
39	l	130	ASN
39	l	131	LYS
41	n	106	ARG
41	n	113	ARG
42	o	5	ARG
43	p	56	ARG
44	q	83	ARG
44	q	86	ARG
47	t	20	ASN
48	u	1	MET
49	v	81	LYS
51	x	32	ARG
51	x	78	ARG
54	A	218	ASN
54	A	303	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (39) such sidechains are listed below:

Mol	Chain	Res	Type
5	B	58	HIS
5	B	86	ASN
5	B	260	ASN
6	C	32	ASN
6	C	49	GLN
6	C	136	ASN
7	D	115	GLN
7	D	163	ASN
9	F	88	GLN
10	G	11	ASN
12	K	29	HIS
15	N	31	HIS
16	O	38	GLN
17	P	12	GLN
18	Q	44	GLN
18	Q	72	ASN
19	R	6	GLN
23	V	24	ASN
24	W	46	HIS

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Mol	Chain	Res	Type
28	a	20	ASN
30	c	26	ASN
34	g	39	HIS
34	g	177	ASN
37	j	12	GLN
37	j	132	ASN
38	k	46	GLN
38	k	63	ASN
39	l	130	ASN
41	n	50	GLN
43	p	22	HIS
45	r	14	HIS
47	t	20	ASN
47	t	80	GLN
51	x	52	HIS
52	y	21	ASN
52	y	52	ASN
52	y	61	GLN
54	A	218	ASN
54	A	279	HIS

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2898/2903 (99%)	596 (20%)	9 (0%)
2	2	1529/1534 (99%)	293 (19%)	4 (0%)
3	3	119/120 (99%)	23 (19%)	0
4	4	8/9 (88%)	3 (37%)	0
55	5	74/76 (97%)	19 (25%)	2 (2%)
All	All	4628/4642 (99%)	934 (20%)	15 (0%)

All (934) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	A
1	1	15	G
1	1	34	U
1	1	35	G
1	1	46	G
1	1	51	G
1	1	61	C

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Mol	Chain	Res	Type
1	1	71	A
1	1	74	A
1	1	75	G
1	1	80	G
1	1	84	A
1	1	85	G
1	1	96	C
1	1	101	A
1	1	102	U
1	1	110	G
1	1	118	A
1	1	119	A
1	1	120	U
1	1	125	A
1	1	131	A
1	1	139	U
1	1	142	A
1	1	163	C
1	1	165	A
1	1	181	A
1	1	186	G
1	1	196	A
1	1	199	A
1	1	200	U
1	1	204	A
1	1	215	G
1	1	216	A
1	1	221	A
1	1	222	A
1	1	225	C
1	1	228	C
1	1	229	C
1	1	230	G
1	1	248	G
1	1	249	C
1	1	250	G
1	1	265	A
1	1	266	G
1	1	270	A
1	1	272	A
1	1	273	G
1	1	276	U

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Mol	Chain	Res	Type
1	1	277	G
1	1	278	A
1	1	284	U
1	1	294	A
1	1	302	C
1	1	311	A
1	1	317	G
1	1	324	A
1	1	327	G
1	1	329	G
1	1	330	A
1	1	353	C
1	1	361	G
1	1	362	A
1	1	371	A
1	1	372	G
1	1	383	C
1	1	386	G
1	1	387	U
1	1	389	G
1	1	396	G
1	1	399	U
1	1	403	U
1	1	404	A
1	1	405	U
1	1	411	G
1	1	420	C
1	1	424	G
1	1	435	C
1	1	436	C
1	1	448	U
1	1	454	A
1	1	455	C
1	1	456	C
1	1	457	A
1	1	464	U
1	1	467	G
1	1	475	C
1	1	477	A
1	1	480	A
1	1	481	G
1	1	489	G

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Mol	Chain	Res	Type
1	1	491	G
1	1	496	G
1	1	501	A
1	1	505	A
1	1	508	A
1	1	509	C
1	1	518	G
1	1	529	A
1	1	531	C
1	1	532	A
1	1	533	G
1	1	543	G
1	1	544	C
1	1	545	U
1	1	547	A
1	1	548	G
1	1	549	G
1	1	550	C
1	1	551	G
1	1	563	A
1	1	573	U
1	1	575	A
1	1	583	G
1	1	586	A
1	1	603	A
1	1	613	A
1	1	614	A
1	1	615	U
1	1	618	G
1	1	627	A
1	1	637	A
1	1	645	C
1	1	646	U
1	1	654	A
1	1	655	A
1	1	656	G
1	1	659	G
1	1	668	A
1	1	670	A
1	1	686	U
1	1	710	U
1	1	723	C

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Mol	Chain	Res	Type
1	1	730	A
1	1	738	G
1	1	747	5MU
1	1	761	A
1	1	762	U
1	1	763	G
1	1	764	A
1	1	765	C
1	1	770	G
1	1	775	G
1	1	776	G
1	1	782	A
1	1	784	G
1	1	785	G
1	1	791	C
1	1	792	A
1	1	800	A
1	1	805	G
1	1	810	U
1	1	812	C
1	1	819	A
1	1	827	U
1	1	828	U
1	1	846	U
1	1	858	G
1	1	859	G
1	1	869	G
1	1	877	A
1	1	878	A
1	1	880	G
1	1	884	U
1	1	885	C
1	1	888	C
1	1	891	G
1	1	894	U
1	1	895	U
1	1	896	A
1	1	907	G
1	1	910	A
1	1	914	G
1	1	915	C
1	1	931	U

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Mol	Chain	Res	Type
1	1	932	U
1	1	941	A
1	1	945	A
1	1	946	C
1	1	953	G
1	1	957	C
1	1	959	A
1	1	961	C
1	1	973	A
1	1	974	G
1	1	983	A
1	1	984	A
1	1	989	G
1	1	991	C
1	1	995	C
1	1	996	A
1	1	999	U
1	1	1005	C
1	1	1012	U
1	1	1013	C
1	1	1022	G
1	1	1023	U
1	1	1024	G
1	1	1025	G
1	1	1026	G
1	1	1033	U
1	1	1034	G
1	1	1040	A
1	1	1041	G
1	1	1042	G
1	1	1046	A
1	1	1047	G
1	1	1058	U
1	1	1059	G
1	1	1061	U
1	1	1064	C
1	1	1065	U
1	1	1066	U
1	1	1068	G
1	1	1069	A
1	1	1070	A
1	1	1073	A

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Mol	Chain	Res	Type
1	1	1074	G
1	1	1078	U
1	1	1079	C
1	1	1082	U
1	1	1083	U
1	1	1087	G
1	1	1088	A
1	1	1089	A
1	1	1095	A
1	1	1096	A
1	1	1097	U
1	1	1110	G
1	1	1111	A
1	1	1112	G
1	1	1116	G
1	1	1119	U
1	1	1122	G
1	1	1126	A
1	1	1130	U
1	1	1131	G
1	1	1132	U
1	1	1134	A
1	1	1135	C
1	1	1139	G
1	1	1142	A
1	1	1143	A
1	1	1155	A
1	1	1167	C
1	1	1168	G
1	1	1169	A
1	1	1170	C
1	1	1173	U
1	1	1174	U
1	1	1175	A
1	1	1176	U
1	1	1177	G
1	1	1178	C
1	1	1180	U
1	1	1182	G
1	1	1186	G
1	1	1205	A
1	1	1206	G

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Mol	Chain	Res	Type
1	1	1210	G
1	1	1212	G
1	1	1236	G
1	1	1238	G
1	1	1247	A
1	1	1250	G
1	1	1253	A
1	1	1256	G
1	1	1262	A
1	1	1266	G
1	1	1271	G
1	1	1272	A
1	1	1273	U
1	1	1300	G
1	1	1301	A
1	1	1321	A
1	1	1325	U
1	1	1352	U
1	1	1359	A
1	1	1365	A
1	1	1368	G
1	1	1374	G
1	1	1379	U
1	1	1380	G
1	1	1383	A
1	1	1390	U
1	1	1395	A
1	1	1407	G
1	1	1409	U
1	1	1411	U
1	1	1417	C
1	1	1419	A
1	1	1420	A
1	1	1428	C
1	1	1437	C
1	1	1455	G
1	1	1458	U
1	1	1459	G
1	1	1461	C
1	1	1468	U
1	1	1480	C
1	1	1482	G

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Mol	Chain	Res	Type
1	1	1490	A
1	1	1493	C
1	1	1503	A
1	1	1508	A
1	1	1509	A
1	1	1510	G
1	1	1515	A
1	1	1522	A
1	1	1524	G
1	1	1528	A
1	1	1532	A
1	1	1535	A
1	1	1536	C
1	1	1557	C
1	1	1558	C
1	1	1566	A
1	1	1569	A
1	1	1578	U
1	1	1580	A
1	1	1583	A
1	1	1586	A
1	1	1587	G
1	1	1589	U
1	1	1590	A
1	1	1607	C
1	1	1608	A
1	1	1610	A
1	1	1616	A
1	1	1626	A
1	1	1634	A
1	1	1639	C
1	1	1647	U
1	1	1648	U
1	1	1649	G
1	1	1672	A
1	1	1674	G
1	1	1695	G
1	1	1698	A
1	1	1715	G
1	1	1724	G
1	1	1728	C
1	1	1729	U

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Mol	Chain	Res	Type
1	1	1730	C
1	1	1732	C
1	1	1738	G
1	1	1756	G
1	1	1758	U
1	1	1764	C
1	1	1773	A
1	1	1784	A
1	1	1800	C
1	1	1801	A
1	1	1802	A
1	1	1808	A
1	1	1811	G
1	1	1815	A
1	1	1816	C
1	1	1820	U
1	1	1828	G
1	1	1829	A
1	1	1833	C
1	1	1835	2MG
1	1	1847	A
1	1	1858	A
1	1	1865	U
1	1	1866	A
1	1	1869	G
1	1	1870	C
1	1	1872	A
1	1	1873	G
1	1	1900	A
1	1	1905	C
1	1	1906	G
1	1	1907	G
1	1	1912	A
1	1	1913	A
1	1	1914	C
1	1	1923	U
1	1	1924	C
1	1	1929	G
1	1	1930	G
1	1	1936	A
1	1	1938	A
1	1	1955	U

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Mol	Chain	Res	Type
1	1	1965	C
1	1	1967	C
1	1	1970	A
1	1	1971	U
1	1	1972	G
1	1	1982	U
1	1	1991	U
1	1	1992	G
1	1	1993	U
1	1	1997	C
1	1	2002	G
1	1	2022	U
1	1	2023	C
1	1	2031	A
1	1	2033	A
1	1	2043	C
1	1	2049	G
1	1	2051	A
1	1	2055	C
1	1	2056	G
1	1	2060	A
1	1	2061	G
1	1	2062	A
1	1	2069	G7M
1	1	2072	C
1	1	2079	U
1	1	2093	G
1	1	2099	U
1	1	2102	G
1	1	2105	U
1	1	2110	G
1	1	2112	G
1	1	2113	U
1	1	2115	G
1	1	2116	G
1	1	2117	A
1	1	2118	U
1	1	2119	A
1	1	2120	G
1	1	2121	G
1	1	2122	U
1	1	2125	G

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Mol	Chain	Res	Type
1	1	2127	G
1	1	2131	U
1	1	2132	U
1	1	2133	G
1	1	2134	A
1	1	2135	A
1	1	2137	U
1	1	2138	G
1	1	2139	U
1	1	2142	A
1	1	2145	C
1	1	2146	C
1	1	2147	A
1	1	2153	C
1	1	2158	A
1	1	2161	C
1	1	2162	G
1	1	2164	C
1	1	2165	C
1	1	2166	U
1	1	2167	U
1	1	2170	A
1	1	2171	A
1	1	2172	U
1	1	2173	A
1	1	2178	C
1	1	2182	U
1	1	2183	A
1	1	2188	U
1	1	2189	U
1	1	2190	G
1	1	2193	G
1	1	2194	U
1	1	2195	U
1	1	2198	A
1	1	2204	G
1	1	2211	A
1	1	2212	A
1	1	2225	A
1	1	2226	C
1	1	2229	U
1	1	2238	G

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Mol	Chain	Res	Type
1	1	2239	G
1	1	2243	U
1	1	2244	U
1	1	2250	G
1	1	2259	U
1	1	2266	A
1	1	2278	A
1	1	2279	G
1	1	2283	C
1	1	2287	A
1	1	2288	A
1	1	2294	G
1	1	2296	U
1	1	2297	A
1	1	2305	U
1	1	2306	C
1	1	2307	G
1	1	2319	G
1	1	2320	U
1	1	2325	G
1	1	2327	A
1	1	2333	A
1	1	2336	A
1	1	2345	G
1	1	2347	C
1	1	2350	C
1	1	2357	G
1	1	2361	G
1	1	2366	A
1	1	2376	A
1	1	2383	G
1	1	2385	C
1	1	2389	G
1	1	2402	U
1	1	2403	C
1	1	2406	A
1	1	2419	U
1	1	2423	U
1	1	2424	C
1	1	2425	A
1	1	2426	A
1	1	2429	G

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Mol	Chain	Res	Type
1	1	2430	A
1	1	2431	U
1	1	2435	A
1	1	2441	U
1	1	2445	2MG
1	1	2448	A
1	1	2459	A
1	1	2470	G
1	1	2473	U
1	1	2475	C
1	1	2476	A
1	1	2491	U
1	1	2498	OMC
1	1	2501	C
1	1	2502	G
1	1	2504	PSU
1	1	2505	G
1	1	2506	U
1	1	2513	A
1	1	2518	A
1	1	2520	C
1	1	2529	G
1	1	2543	G
1	1	2547	A
1	1	2554	U
1	1	2566	A
1	1	2567	G
1	1	2572	A
1	1	2573	C
1	1	2574	G
1	1	2585	U
1	1	2602	A
1	1	2608	G
1	1	2609	U
1	1	2610	C
1	1	2613	U
1	1	2615	U
1	1	2621	G
1	1	2629	U
1	1	2636	C
1	1	2640	G
1	1	2661	G

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Mol	Chain	Res	Type
1	1	2663	G
1	1	2671	G
1	1	2682	A
1	1	2689	U
1	1	2690	U
1	1	2703	C
1	1	2714	G
1	1	2716	C
1	1	2718	G
1	1	2725	A
1	1	2726	A
1	1	2728	U
1	1	2732	G
1	1	2733	A
1	1	2739	U
1	1	2744	G
1	1	2748	A
1	1	2751	G
1	1	2762	C
1	1	2765	A
1	1	2778	A
1	1	2793	C
1	1	2794	C
1	1	2797	U
1	1	2798	U
1	1	2799	A
1	1	2811	G
1	1	2818	U
1	1	2820	A
1	1	2821	A
1	1	2825	G
1	1	2835	A
1	1	2836	U
1	1	2861	U
1	1	2867	G
1	1	2872	A
1	1	2873	A
1	1	2880	C
1	1	2884	U
1	1	2885	G
1	1	2892	G
1	1	2901	C

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Mol	Chain	Res	Type
1	1	2903	U
2	2	3	A
2	2	4	U
2	2	5	U
2	2	7	A
2	2	8	A
2	2	9	G
2	2	22	G
2	2	32	A
2	2	39	G
2	2	47	C
2	2	48	C
2	2	50	A
2	2	51	A
2	2	52	C
2	2	54	C
2	2	70	U
2	2	71	A
2	2	74	A
2	2	77	A
2	2	79	G
2	2	82	G
2	2	83	C
2	2	84	U
2	2	85	U
2	2	86	G
2	2	87	C
2	2	89	U
2	2	92	U
2	2	94	G
2	2	95	C
2	2	108	G
2	2	116	A
2	2	120	A
2	2	121	U
2	2	130	A
2	2	131	A
2	2	141	G
2	2	149	A
2	2	151	A
2	2	168	G
2	2	173	U

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Mol	Chain	Res	Type
2	2	177	G
2	2	181	A
2	2	183	C
2	2	197	A
2	2	202	G
2	2	204	G
2	2	209	U
2	2	211	G
2	2	212	G
2	2	222	C
2	2	226	G
2	2	245	U
2	2	247	G
2	2	251	G
2	2	266	G
2	2	267	C
2	2	279	A
2	2	289	G
2	2	306	A
2	2	321	A
2	2	328	C
2	2	332	G
2	2	347	G
2	2	352	C
2	2	353	A
2	2	354	G
2	2	356	A
2	2	367	U
2	2	372	C
2	2	373	A
2	2	384	G
2	2	388	G
2	2	397	A
2	2	406	G
2	2	407	U
2	2	411	A
2	2	412	A
2	2	413	G
2	2	414	A
2	2	421	U
2	2	422	C
2	2	423	G

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Mol	Chain	Res	Type
2	2	424	G
2	2	428	G
2	2	429	U
2	2	436	C
2	2	438	U
2	2	452	A
2	2	456	A
2	2	457	G
2	2	464	U
2	2	467	U
2	2	468	A
2	2	471	U
2	2	476	U
2	2	478	A
2	2	479	U
2	2	481	G
2	2	486	U
2	2	495	A
2	2	496	A
2	2	497	G
2	2	499	A
2	2	509	A
2	2	511	C
2	2	517	G
2	2	518	C
2	2	521	G
2	2	527	G7M
2	2	531	U
2	2	532	A
2	2	547	A
2	2	559	A
2	2	562	U
2	2	564	C
2	2	566	G
2	2	572	A
2	2	573	A
2	2	575	G
2	2	576	C
2	2	577	G
2	2	596	A
2	2	633	G
2	2	639	G

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Mol	Chain	Res	Type
2	2	649	A
2	2	650	G
2	2	653	U
2	2	665	A
2	2	682	G
2	2	686	U
2	2	687	A
2	2	701	U
2	2	702	A
2	2	703	G
2	2	718	A
2	2	721	G
2	2	723	U
2	2	724	G
2	2	731	G
2	2	734	G
2	2	747	A
2	2	748	G
2	2	755	G
2	2	758	C
2	2	761	G
2	2	777	A
2	2	793	U
2	2	794	A
2	2	813	U
2	2	814	A
2	2	815	A
2	2	817	C
2	2	819	A
2	2	821	G
2	2	828	U
2	2	829	G
2	2	832	G
2	2	841	C
2	2	844	G
2	2	846	G
2	2	864	A
2	2	871	U
2	2	876	C
2	2	884	U
2	2	889	A
2	2	914	A

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Mol	Chain	Res	Type
2	2	926	G
2	2	934	C
2	2	935	A
2	2	942	G
2	2	958	A
2	2	960	U
2	2	966	2MG
2	2	968	A
2	2	969	A
2	2	971	G
2	2	974	A
2	2	975	A
2	2	976	G
2	2	977	A
2	2	982	U
2	2	992	U
2	2	993	G
2	2	994	A
2	2	996	A
2	2	1000	A
2	2	1004	A
2	2	1008	U
2	2	1009	U
2	2	1017	U
2	2	1019	A
2	2	1020	G
2	2	1022	A
2	2	1026	G
2	2	1028	C
2	2	1029	U
2	2	1030	U
2	2	1031	C
2	2	1033	G
2	2	1035	A
2	2	1038	C
2	2	1043	G
2	2	1044	A
2	2	1046	A
2	2	1065	U
2	2	1092	A
2	2	1094	G
2	2	1095	U

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Mol	Chain	Res	Type
2	2	1098	C
2	2	1099	G
2	2	1101	A
2	2	1108	G
2	2	1124	G
2	2	1125	U
2	2	1130	A
2	2	1132	C
2	2	1136	C
2	2	1137	C
2	2	1139	G
2	2	1140	C
2	2	1141	C
2	2	1143	G
2	2	1145	A
2	2	1151	A
2	2	1152	A
2	2	1158	C
2	2	1160	G
2	2	1167	A
2	2	1171	A
2	2	1176	A
2	2	1177	G
2	2	1184	G
2	2	1193	G
2	2	1196	A
2	2	1197	A
2	2	1200	C
2	2	1212	U
2	2	1213	A
2	2	1227	A
2	2	1238	A
2	2	1241	G
2	2	1256	A
2	2	1257	A
2	2	1258	G
2	2	1275	A
2	2	1279	G
2	2	1280	A
2	2	1281	C
2	2	1287	A
2	2	1297	G

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Mol	Chain	Res	Type
2	2	1299	A
2	2	1300	G
2	2	1301	U
2	2	1302	C
2	2	1305	G
2	2	1312	G
2	2	1317	C
2	2	1320	C
2	2	1323	G
2	2	1328	C
2	2	1336	C
2	2	1340	A
2	2	1346	A
2	2	1363	A
2	2	1364	U
2	2	1370	G
2	2	1378	C
2	2	1379	G
2	2	1381	U
2	2	1397	C
2	2	1401	G
2	2	1404	C
2	2	1419	G
2	2	1432	G
2	2	1441	A
2	2	1446	A
2	2	1452	C
2	2	1475	G
2	2	1484	C
2	2	1491	G
2	2	1492	A
2	2	1494	G
2	2	1497	G
2	2	1499	A
2	2	1503	A
2	2	1506	U
2	2	1517	G
2	2	1520	C
2	2	1529	G
2	2	1530	G
2	2	1533	C
2	2	1534	A

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Mol	Chain	Res	Type
3	3	2	G
3	3	4	C
3	3	13	G
3	3	15	A
3	3	24	G
3	3	35	C
3	3	36	C
3	3	41	G
3	3	44	G
3	3	45	A
3	3	51	G
3	3	52	A
3	3	56	G
3	3	57	A
3	3	66	A
3	3	67	G
3	3	88	C
3	3	89	U
3	3	90	C
3	3	99	A
3	3	105	G
3	3	109	A
3	3	119	A
4	4	19	U
4	4	20	A
4	4	21	A
55	5	2	C
55	5	7	U
55	5	8	4SU
55	5	15	C
55	5	16	C
55	5	17	U
55	5	18	G
55	5	19	G
55	5	20	H2U
55	5	21	A
55	5	47	U
55	5	48	C
55	5	49	G
55	5	58	A
55	5	59	A
55	5	61	C

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Mol	Chain	Res	Type
55	5	68	C
55	5	70	G
55	5	76	A

All (15) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	404	A
1	1	613	A
1	1	784	G
1	1	894	U
1	1	984	A
1	1	1379	U
1	1	2146	C
1	1	2193	G
1	1	2425	A
2	2	328	C
2	2	496	A
2	2	516	PSU
2	2	1109	C
55	5	8	4SU
55	5	17	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	PSU	1	955	1	18,21,22	1.16	2 (11%)	22,30,33	1.91	4 (18%)
1	3TD	1	1915	57,1	18,22,23	4.22	5 (27%)	22,32,35	1.72	2 (9%)
1	PSU	1	2504	57,1	18,21,22	1.14	2 (11%)	22,30,33	2.11	4 (18%)
1	2MA	1	2503	57,1	17,25,26	2.23	4 (23%)	17,37,40	1.41	2 (11%)
1	5MU	1	747	1	19,22,23	4.45	7 (36%)	28,32,35	3.98	12 (42%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
44	0TD	q	89	44	7,9,10	1.55	0	6,11,13	2.33	2 (33%)
1	PSU	1	746	57,1	18,21,22	1.11	3 (16%)	22,30,33	1.89	4 (18%)
2	MA6	2	1518	2	19,26,27	1.05	1 (5%)	18,38,41	2.95	3 (16%)
55	4OC	5	32	55	20,23,24	2.92	8 (40%)	26,32,35	0.92	1 (3%)
1	OMC	1	2498	57,1	19,22,23	2.65	7 (36%)	26,31,34	1.14	2 (7%)
1	OMG	1	2251	1,55	18,26,27	2.41	8 (44%)	19,38,41	1.62	4 (21%)
1	PSU	1	1917	1	18,21,22	1.08	1 (5%)	22,30,33	1.79	3 (13%)
1	PSU	1	2580	1	18,21,22	1.13	3 (16%)	22,30,33	1.91	4 (18%)
55	4SU	5	8	55	18,21,22	3.59	7 (38%)	26,30,33	2.22	5 (19%)
56	FME	6	77	56	8,9,10	0.95	0	7,9,11	0.78	0
2	2MG	2	1207	2	18,26,27	2.56	7 (38%)	16,38,41	1.44	4 (25%)
2	UR3	2	1498	2	19,22,23	2.56	6 (31%)	26,32,35	1.35	2 (7%)
2	MA6	2	1519	2	19,26,27	1.03	1 (5%)	18,38,41	2.76	2 (11%)
1	G7M	1	2069	1	20,26,27	2.23	7 (35%)	17,39,42	1.13	1 (5%)
1	PSU	1	1911	1	18,21,22	1.14	2 (11%)	22,30,33	1.79	4 (18%)
2	5MC	2	1407	2	18,22,23	3.58	7 (38%)	26,32,35	1.10	1 (3%)
55	H2U	5	20	55	18,21,22	3.12	5 (27%)	21,30,33	2.09	5 (23%)
1	PSU	1	2457	1	18,21,22	1.10	3 (16%)	22,30,33	2.39	6 (27%)
1	2MG	1	2445	1	18,26,27	2.44	7 (38%)	16,38,41	1.67	4 (25%)
1	5MU	1	1939	1	19,22,23	4.60	7 (36%)	28,32,35	3.93	9 (32%)
1	PSU	1	2605	1	18,21,22	1.09	1 (5%)	22,30,33	1.91	4 (18%)
2	5MC	2	967	2	18,22,23	3.62	7 (38%)	26,32,35	0.89	1 (3%)
2	G7M	2	527	2	20,26,27	3.86	10 (50%)	17,39,42	1.15	2 (11%)
1	6MZ	1	2030	1	18,25,26	2.17	3 (16%)	16,36,39	2.37	3 (18%)
55	5MU	5	54	55	19,22,23	4.78	7 (36%)	28,32,35	3.79	9 (32%)
2	4OC	2	1402	2	20,23,24	2.83	8 (40%)	26,32,35	1.15	3 (11%)
1	6MZ	1	1618	1	18,25,26	2.11	4 (22%)	16,36,39	2.24	2 (12%)
55	PSU	5	55	55	18,21,22	1.11	1 (5%)	22,30,33	1.76	4 (18%)
2	PSU	2	516	2	18,21,22	1.38	3 (16%)	22,30,33	1.95	6 (27%)
1	OMU	1	2552	57,1	19,22,23	2.77	7 (36%)	26,31,34	1.86	5 (19%)
1	5MC	1	1962	1	18,22,23	3.50	7 (38%)	26,32,35	1.18	2 (7%)
1	2MG	1	1835	1	18,26,27	2.49	7 (38%)	16,38,41	1.56	4 (25%)
1	1MG	1	745	1	18,26,27	2.51	4 (22%)	19,39,42	1.69	6 (31%)
2	2MG	2	1516	2	18,26,27	2.50	7 (38%)	16,38,41	1.56	4 (25%)
2	2MG	2	966	2	18,26,27	2.54	7 (38%)	16,38,41	1.49	3 (18%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	1	955	1	-	0/7/25/26	0/2/2/2
1	3TD	1	1915	57,1	-	2/7/25/26	0/2/2/2
1	PSU	1	2504	57,1	-	1/7/25/26	0/2/2/2
1	2MA	1	2503	57,1	-	1/3/25/26	0/3/3/3
1	5MU	1	747	1	-	1/7/25/26	0/2/2/2
44	0TD	q	89	44	-	1/7/12/14	-
1	PSU	1	746	57,1	-	2/7/25/26	0/2/2/2
2	MA6	2	1518	2	-	0/7/29/30	0/3/3/3
55	4OC	5	32	55	-	0/9/29/30	0/2/2/2
1	OMC	1	2498	57,1	-	1/9/27/28	0/2/2/2
1	OMG	1	2251	1,55	-	0/5/27/28	0/3/3/3
1	PSU	1	1917	1	-	0/7/25/26	0/2/2/2
1	PSU	1	2580	1	-	0/7/25/26	0/2/2/2
55	4SU	5	8	55	-	2/7/25/26	0/2/2/2
56	FME	6	77	56	-	5/7/9/11	-
2	2MG	2	1207	2	-	0/5/27/28	0/3/3/3
2	UR3	2	1498	2	-	0/7/25/26	0/2/2/2
2	MA6	2	1519	2	-	4/7/29/30	0/3/3/3
1	G7M	1	2069	1	-	1/3/25/26	0/3/3/3
1	PSU	1	1911	1	-	0/7/25/26	0/2/2/2
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
55	H2U	5	20	55	-	4/7/38/39	0/2/2/2
1	PSU	1	2457	1	-	0/7/25/26	0/2/2/2
1	2MG	1	2445	1	-	2/5/27/28	0/3/3/3
1	5MU	1	1939	1	-	0/7/25/26	0/2/2/2
1	PSU	1	2605	1	-	0/7/25/26	0/2/2/2
2	5MC	2	967	2	-	0/7/25/26	0/2/2/2
2	G7M	2	527	2	-	3/3/25/26	0/3/3/3
1	6MZ	1	2030	1	-	2/5/27/28	0/3/3/3
55	5MU	5	54	55	-	0/7/25/26	0/2/2/2
2	4OC	2	1402	2	-	2/9/29/30	0/2/2/2
1	6MZ	1	1618	1	-	1/5/27/28	0/3/3/3
55	PSU	5	55	55	-	0/7/25/26	0/2/2/2
2	PSU	2	516	2	-	3/7/25/26	0/2/2/2
1	OMU	1	2552	57,1	-	0/9/27/28	0/2/2/2
1	5MC	1	1962	1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	2MG	1	1835	1	-	2/5/27/28	0/3/3/3
1	1MG	1	745	1	-	0/3/25/26	0/3/3/3
2	2MG	2	1516	2	-	0/5/27/28	0/3/3/3
2	2MG	2	966	2	-	2/5/27/28	0/3/3/3

All (193) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	1915	3TD	C6-C5	12.88	1.50	1.35
55	5	54	5MU	C2-N1	11.16	1.56	1.38
55	5	54	5MU	C6-N1	10.35	1.55	1.38
1	1	1939	5MU	C6-N1	9.96	1.55	1.38
55	5	20	H2U	C2-N1	9.76	1.49	1.35
2	2	527	G7M	C8-N7	9.74	1.50	1.33
1	1	747	5MU	C2-N1	9.74	1.54	1.38
55	5	54	5MU	C4-C5	9.67	1.60	1.44
1	1	1939	5MU	C2-N1	9.36	1.53	1.38
1	1	1939	5MU	C4-C5	9.31	1.60	1.44
1	1	747	5MU	C4-C5	9.28	1.60	1.44
2	2	1407	5MC	C6-C5	9.28	1.49	1.34
2	2	527	G7M	C8-N9	9.26	1.50	1.33
1	1	1915	3TD	C2-N1	9.21	1.49	1.37
1	1	747	5MU	C6-N1	9.18	1.53	1.38
2	2	967	5MC	C6-C5	9.05	1.49	1.34
1	1	1939	5MU	C4-N3	-8.73	1.22	1.38
1	1	1962	5MC	C6-C5	8.64	1.48	1.34
1	1	747	5MU	C4-N3	-8.42	1.23	1.38
55	5	8	4SU	C4-N3	7.78	1.46	1.37
55	5	8	4SU	C2-N1	7.75	1.50	1.38
55	5	54	5MU	C4-N3	-7.74	1.24	1.38
1	1	1618	6MZ	C6-N6	7.30	1.47	1.35
1	1	2030	6MZ	C6-N6	7.14	1.46	1.35
1	1	745	1MG	C2-N2	6.86	1.46	1.34
2	2	967	5MC	C4-N3	6.86	1.45	1.34
1	1	1962	5MC	C4-N3	6.79	1.45	1.34
55	5	32	4OC	C4-N3	6.77	1.44	1.32
1	1	2503	2MA	C2-N3	6.58	1.45	1.31
55	5	20	H2U	C2-N3	6.40	1.49	1.38
2	2	1498	UR3	C2-N1	6.29	1.47	1.38
2	2	1407	5MC	C4-N3	6.27	1.44	1.34
2	2	966	2MG	C2-N2	6.15	1.47	1.33
1	1	2552	OMU	C2-N1	6.14	1.48	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1207	2MG	C2-N2	6.09	1.46	1.33
1	1	2552	OMU	C2-N3	6.09	1.48	1.38
2	2	967	5MC	C2-N3	6.06	1.48	1.36
2	2	1402	4OC	C4-N3	6.02	1.43	1.32
2	2	1498	UR3	C6-C5	6.00	1.49	1.35
2	2	1402	4OC	C6-C5	5.94	1.48	1.35
2	2	1407	5MC	C2-N3	5.94	1.48	1.36
1	1	1962	5MC	C2-N3	5.93	1.48	1.36
2	2	1516	2MG	C2-N2	5.86	1.46	1.33
1	1	1835	2MG	C2-N2	5.85	1.46	1.33
55	5	8	4SU	C6-C5	5.82	1.48	1.35
2	2	527	G7M	C2-N3	5.78	1.47	1.33
55	5	32	4OC	C2-N3	5.75	1.48	1.36
55	5	54	5MU	C6-C5	5.70	1.44	1.34
1	1	2498	OMC	C2-N3	5.65	1.47	1.36
1	1	2445	2MG	C2-N2	5.64	1.45	1.33
55	5	32	4OC	C6-C5	5.62	1.48	1.35
55	5	8	4SU	C2-N3	5.60	1.47	1.38
1	1	1939	5MU	C6-C5	5.59	1.43	1.34
1	1	1915	3TD	C6-N1	5.58	1.45	1.36
1	1	2498	OMC	C6-C5	5.56	1.48	1.35
1	1	2552	OMU	C6-C5	5.42	1.47	1.35
55	5	8	4SU	C4-S4	-5.19	1.58	1.68
2	2	1402	4OC	C2-N3	5.13	1.46	1.36
2	2	966	2MG	C4-N3	5.12	1.49	1.37
1	1	2251	OMG	C2-N3	5.02	1.45	1.33
1	1	2498	OMC	C4-N3	4.97	1.44	1.34
1	1	1835	2MG	C4-N3	4.95	1.49	1.37
55	5	20	H2U	C4-N3	4.92	1.46	1.37
1	1	2069	G7M	C2-N3	4.91	1.45	1.33
1	1	745	1MG	C2-N3	4.88	1.43	1.34
2	2	967	5MC	C4-N4	4.75	1.46	1.34
1	1	2069	G7M	C4-N3	4.70	1.48	1.37
2	2	1407	5MC	C4-N4	4.67	1.46	1.34
1	1	2251	OMG	C4-N3	4.66	1.48	1.37
2	2	527	G7M	C2-N2	4.66	1.45	1.34
1	1	1915	3TD	C2-N3	4.65	1.48	1.38
1	1	1962	5MC	C4-N4	4.65	1.46	1.34
2	2	1207	2MG	C4-N3	4.63	1.48	1.37
1	1	747	5MU	C6-C5	4.63	1.42	1.34
2	2	1498	UR3	C2-N3	4.61	1.47	1.39
2	2	1516	2MG	C4-N3	4.49	1.48	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1207	2MG	C2-N1	4.47	1.43	1.36
1	1	2503	2MA	C4-N3	4.45	1.48	1.37
2	2	1407	5MC	C6-N1	4.41	1.45	1.38
1	1	745	1MG	C4-N3	4.38	1.48	1.37
1	1	2251	OMG	C2-N2	4.34	1.44	1.34
1	1	2445	2MG	C4-N3	4.34	1.47	1.37
2	2	967	5MC	C6-N1	4.26	1.45	1.38
2	2	1516	2MG	C2-N1	4.22	1.43	1.36
55	5	32	4OC	C4-N4	4.15	1.44	1.35
2	2	527	G7M	C6-N1	3.97	1.43	1.37
1	1	1835	2MG	C2-N1	3.96	1.43	1.36
2	2	966	2MG	C2-N1	3.94	1.43	1.36
1	1	2069	G7M	C2-N2	3.92	1.43	1.34
2	2	527	G7M	C4-N3	3.91	1.46	1.37
1	1	1962	5MC	C6-N1	3.89	1.44	1.38
2	2	1402	4OC	C4-N4	3.87	1.43	1.35
2	2	1402	4OC	C2-N1	3.86	1.48	1.40
2	2	967	5MC	C2-N1	3.81	1.48	1.40
1	1	2445	2MG	C2-N1	3.77	1.42	1.36
55	5	32	4OC	C2-N1	3.70	1.48	1.40
2	2	1407	5MC	C2-N1	3.69	1.48	1.40
1	1	2030	6MZ	C5-C4	-3.66	1.31	1.40
1	1	1962	5MC	C2-N1	3.61	1.47	1.40
1	1	2498	OMC	C4-N4	3.58	1.42	1.33
55	5	55	PSU	C6-C5	3.56	1.39	1.35
2	2	516	PSU	C6-C5	3.50	1.39	1.35
2	2	1402	4OC	C5-C4	3.50	1.48	1.40
1	1	2445	2MG	C5-C4	-3.49	1.34	1.43
2	2	1207	2MG	C6-N1	3.48	1.43	1.37
1	1	1962	5MC	O2-C2	-3.47	1.17	1.23
1	1	2552	OMU	C4-N3	3.42	1.44	1.38
55	5	32	4OC	C5-C4	3.42	1.48	1.40
1	1	1911	PSU	C6-C5	3.38	1.39	1.35
2	2	1407	5MC	O2-C2	-3.38	1.17	1.23
1	1	2498	OMC	O2-C2	-3.32	1.17	1.23
1	1	745	1MG	C5-C4	-3.28	1.34	1.43
2	2	967	5MC	O2-C2	-3.28	1.17	1.23
1	1	1618	6MZ	C5-C4	-3.27	1.32	1.40
2	2	527	G7M	C2-N1	3.26	1.45	1.37
2	2	1516	2MG	C5-C4	-3.19	1.34	1.43
1	1	2069	G7M	C6-N1	3.19	1.42	1.37
1	1	2498	OMC	C2-N1	3.18	1.46	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2552	OMU	O4-C4	-3.17	1.18	1.24
1	1	2445	2MG	O6-C6	-3.17	1.16	1.23
2	2	1516	2MG	C6-N1	3.17	1.42	1.37
1	1	1835	2MG	O6-C6	-3.15	1.16	1.23
1	1	1939	5MU	O4-C4	-3.14	1.17	1.23
1	1	1835	2MG	C5-C4	-3.13	1.35	1.43
2	2	966	2MG	O6-C6	-3.12	1.17	1.23
1	1	2251	OMG	C6-N1	3.11	1.42	1.37
2	2	1402	4OC	O2-C2	-3.09	1.18	1.23
1	1	2605	PSU	C6-C5	3.07	1.38	1.35
2	2	1516	2MG	O6-C6	-3.06	1.17	1.23
1	1	2503	2MA	C5-C4	-3.04	1.35	1.43
1	1	2251	OMG	C5-C4	-3.01	1.35	1.43
2	2	1207	2MG	C5-C4	-2.98	1.35	1.43
2	2	966	2MG	C5-C4	-2.97	1.35	1.43
1	1	955	PSU	C6-C5	2.97	1.38	1.35
1	1	1939	5MU	O2-C2	-2.97	1.17	1.23
1	1	2498	OMC	C6-N1	2.95	1.45	1.38
1	1	1835	2MG	C6-N1	2.94	1.42	1.37
2	2	1207	2MG	O6-C6	-2.93	1.17	1.23
1	1	2069	G7M	C5-C6	2.91	1.53	1.45
55	5	32	4OC	O2-C2	-2.89	1.18	1.23
55	5	8	4SU	C5-C4	2.89	1.46	1.42
1	1	1917	PSU	C6-C5	2.89	1.38	1.35
1	1	747	5MU	O2-C2	-2.87	1.17	1.23
2	2	1518	MA6	C5-C4	-2.86	1.33	1.40
1	1	2580	PSU	C6-C5	2.82	1.38	1.35
2	2	1402	4OC	C6-N1	2.81	1.44	1.38
1	1	2504	PSU	C6-C5	2.80	1.38	1.35
2	2	966	2MG	C6-N1	2.79	1.42	1.37
1	1	746	PSU	C6-C5	2.78	1.38	1.35
1	1	2552	OMU	O2-C2	-2.78	1.18	1.23
55	5	54	5MU	O4-C4	-2.78	1.18	1.23
1	1	2445	2MG	C6-N1	2.75	1.42	1.37
1	1	747	5MU	O4-C4	-2.72	1.18	1.23
2	2	1207	2MG	C5-C6	2.69	1.52	1.47
1	1	1915	3TD	C4-N3	2.64	1.46	1.40
2	2	1519	MA6	C5-C4	-2.64	1.33	1.40
2	2	527	G7M	C5-C6	2.62	1.52	1.45
2	2	966	2MG	C5-C6	2.62	1.52	1.47
2	2	1516	2MG	C5-C6	2.59	1.52	1.47
1	1	2069	G7M	O6-C6	-2.58	1.18	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	5	32	4OC	C6-N1	2.56	1.44	1.38
2	2	1498	UR3	O4-C4	-2.56	1.18	1.23
55	5	20	H2U	O2-C2	-2.52	1.18	1.23
2	2	527	G7M	O6-C6	-2.45	1.18	1.23
1	1	1835	2MG	C5-C6	2.45	1.52	1.47
1	1	2251	OMG	C5-C6	2.44	1.52	1.47
2	2	516	PSU	C4-N3	-2.43	1.34	1.38
55	5	8	4SU	O2-C2	-2.41	1.18	1.23
2	2	1498	UR3	C6-N1	2.39	1.43	1.38
1	1	2030	6MZ	C6-N1	-2.38	1.30	1.34
55	5	54	5MU	O2-C2	-2.38	1.18	1.23
1	1	2457	PSU	O4'-C1'	-2.37	1.40	1.43
1	1	2251	OMG	O6-C6	-2.35	1.18	1.23
1	1	2552	OMU	C6-N1	2.32	1.43	1.38
2	2	1498	UR3	O2-C2	-2.30	1.18	1.22
1	1	2445	2MG	C5-C6	2.30	1.52	1.47
1	1	2580	PSU	O4'-C1'	-2.23	1.40	1.43
1	1	2457	PSU	C6-C5	2.23	1.37	1.35
1	1	1618	6MZ	C2-N3	2.20	1.35	1.32
55	5	20	H2U	O4-C4	-2.20	1.18	1.23
1	1	1911	PSU	C4-C5	-2.19	1.37	1.44
1	1	2251	OMG	C2-N1	2.19	1.43	1.37
1	1	2457	PSU	C4-C5	-2.18	1.37	1.44
1	1	2504	PSU	C4-C5	-2.18	1.38	1.44
1	1	955	PSU	C4-C5	-2.17	1.38	1.44
1	1	2580	PSU	C4-C5	-2.11	1.38	1.44
2	2	516	PSU	C4-C5	2.09	1.50	1.44
1	1	746	PSU	O4'-C1'	-2.08	1.40	1.43
1	1	746	PSU	C4-C5	-2.07	1.38	1.44
1	1	2069	G7M	C2-N1	2.06	1.42	1.37
1	1	1618	6MZ	C6-N1	-2.05	1.31	1.34
1	1	2503	2MA	C2-N1	2.02	1.42	1.36
2	2	527	G7M	C5-C4	2.00	1.43	1.39

All (148) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1	1939	5MU	C5-C4-N3	12.94	126.36	115.31
55	5	54	5MU	C5-C4-N3	12.84	126.27	115.31
1	1	747	5MU	C5-C4-N3	11.30	124.96	115.31
1	1	747	5MU	C5-C6-N1	-11.03	111.99	123.34
1	1	1939	5MU	C5-C6-N1	-10.99	112.03	123.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	2	1518	MA6	N1-C6-N6	-10.60	105.90	117.06
55	5	54	5MU	C5-C6-N1	-10.39	112.65	123.34
2	2	1519	MA6	N1-C6-N6	-9.73	106.82	117.06
55	5	20	H2U	C4-N3-C2	-7.27	119.76	125.79
55	5	8	4SU	C4-N3-C2	-7.22	120.33	127.34
1	1	747	5MU	C5M-C5-C6	-6.57	114.07	122.85
1	1	1618	6MZ	C9-N6-C6	-6.48	117.29	122.87
55	5	54	5MU	O4-C4-C5	-6.19	117.72	124.90
2	2	1518	MA6	N3-C2-N1	-6.01	119.29	128.68
1	1	2030	6MZ	N3-C2-N1	-5.98	119.34	128.68
1	1	2457	PSU	N1-C2-N3	5.91	121.83	115.13
2	2	1519	MA6	N3-C2-N1	-5.84	119.55	128.68
1	1	2457	PSU	C4-N3-C2	-5.69	118.14	126.34
1	1	747	5MU	C5M-C5-C4	5.69	125.03	118.77
1	1	1939	5MU	C4-N3-C2	-5.67	120.01	127.35
1	1	2030	6MZ	C9-N6-C6	-5.66	118.00	122.87
1	1	2552	OMU	C4-N3-C2	-5.65	119.12	126.58
1	1	1915	3TD	N1-C2-N3	5.55	120.52	116.14
1	1	1939	5MU	O4-C4-C5	-5.52	118.50	124.90
1	1	747	5MU	C4-N3-C2	-5.45	120.29	127.35
55	5	54	5MU	C4-N3-C2	-5.31	120.48	127.35
1	1	1618	6MZ	N3-C2-N1	-5.25	120.47	128.68
1	1	2504	PSU	N1-C2-N3	5.22	121.05	115.13
55	5	8	4SU	C5-C4-N3	5.18	119.50	114.69
1	1	1939	5MU	N3-C2-N1	5.16	121.74	114.89
1	1	2580	PSU	N1-C2-N3	5.14	120.95	115.13
1	1	746	PSU	C4-N3-C2	-5.11	118.98	126.34
2	2	516	PSU	N1-C2-N3	5.06	120.86	115.13
1	1	747	5MU	O4-C4-C5	-5.00	119.10	124.90
1	1	747	5MU	N3-C2-N1	4.91	121.41	114.89
1	1	2605	PSU	C4-N3-C2	-4.89	119.29	126.34
1	1	2605	PSU	N1-C2-N3	4.86	120.63	115.13
1	1	1917	PSU	N1-C2-N3	4.81	120.58	115.13
2	2	1498	UR3	C4-N3-C2	-4.77	120.07	124.56
55	5	55	PSU	C4-N3-C2	-4.72	119.54	126.34
1	1	746	PSU	N1-C2-N3	4.68	120.44	115.13
1	1	1911	PSU	C4-N3-C2	-4.68	119.59	126.34
1	1	955	PSU	N1-C2-N3	4.67	120.42	115.13
1	1	2504	PSU	C6-N1-C2	-4.66	117.92	122.68
1	1	1917	PSU	C4-N3-C2	-4.62	119.68	126.34
1	1	2580	PSU	C4-N3-C2	-4.58	119.73	126.34
1	1	1911	PSU	N1-C2-N3	4.53	120.26	115.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
44	q	89	0TD	OD2-CG-CB	4.47	122.81	113.15
1	1	2504	PSU	O2-C2-N1	-4.45	117.89	122.79
55	5	55	PSU	N1-C2-N3	4.44	120.17	115.13
1	1	2552	OMU	N3-C2-N1	4.43	120.77	114.89
1	1	2457	PSU	O2-C2-N1	-4.42	117.92	122.79
1	1	955	PSU	C4-N3-C2	-4.30	120.14	126.34
55	5	54	5MU	N3-C2-N1	4.25	120.54	114.89
1	1	2030	6MZ	C1'-N9-C4	-4.24	119.20	126.64
1	1	2504	PSU	C4-N3-C2	-4.17	120.33	126.34
1	1	745	1MG	C5-C6-N1	4.15	120.15	113.90
1	1	1962	5MC	C5-C6-N1	-4.12	119.09	123.34
2	2	966	2MG	C5-C6-N1	3.97	120.97	113.95
1	1	1939	5MU	O2-C2-N1	-3.86	117.66	122.79
1	1	1915	3TD	C4-N3-C2	-3.84	120.44	124.61
1	1	1835	2MG	C5-C6-N1	3.83	120.71	113.95
2	2	1407	5MC	C5-C6-N1	-3.82	119.41	123.34
55	5	20	H2U	N3-C2-N1	3.74	120.61	116.65
1	1	2251	OMG	C5-C6-N1	3.74	120.56	113.95
1	1	2445	2MG	CM2-N2-C2	-3.73	115.62	123.86
1	1	2457	PSU	C6-C5-C4	3.73	120.81	118.20
1	1	2445	2MG	C5-C6-N1	3.69	120.47	113.95
1	1	2503	2MA	C5-C6-N1	3.66	120.34	114.02
55	5	8	4SU	C5-C4-S4	-3.63	119.80	124.47
55	5	8	4SU	N3-C2-N1	3.60	119.67	114.89
55	5	54	5MU	C5M-C5-C6	-3.57	118.07	122.85
1	1	955	PSU	O2-C2-N1	-3.56	118.87	122.79
2	2	1516	2MG	C5-C6-N1	3.52	120.16	113.95
1	1	1939	5MU	C5M-C5-C6	-3.46	118.23	122.85
1	1	955	PSU	C6-N1-C2	-3.45	119.16	122.68
2	2	1207	2MG	C5-C6-N1	3.44	120.03	113.95
1	1	747	5MU	C6-C5-C4	3.43	120.90	118.03
1	1	2552	OMU	C5-C4-N3	3.40	119.93	114.84
1	1	745	1MG	CM1-N1-C6	3.39	122.19	117.55
1	1	2251	OMG	C2-N1-C6	-3.36	118.92	125.10
2	2	1516	2MG	CM2-N2-C2	-3.30	116.57	123.86
55	5	54	5MU	C5M-C5-C4	3.25	122.34	118.77
1	1	1939	5MU	C5M-C5-C4	3.20	122.29	118.77
2	2	516	PSU	C6-C5-C4	-3.20	115.96	118.20
2	2	516	PSU	C4-N3-C2	-3.18	121.76	126.34
1	1	747	5MU	O2-C2-N1	-3.12	118.64	122.79
55	5	8	4SU	C1'-N1-C2	3.12	123.22	117.57
1	1	2069	G7M	C2-N1-C6	-3.08	119.42	125.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1	2580	PSU	C6-N1-C2	-3.07	119.55	122.68
1	1	2552	OMU	O4-C4-C5	-3.06	119.78	125.16
1	1	2605	PSU	O2-C2-N1	-3.02	119.47	122.79
1	1	2498	OMC	O2-C2-N3	-2.99	117.46	122.33
2	2	1402	4OC	O2-C2-N3	-2.93	117.57	122.33
2	2	527	G7M	C2-N1-C6	-2.87	119.81	125.10
1	1	1835	2MG	CM2-N2-C2	-2.87	117.53	123.86
1	1	2445	2MG	O6-C6-C5	-2.83	118.85	124.37
1	1	2457	PSU	C6-N1-C2	-2.78	119.84	122.68
2	2	527	G7M	O6-C6-N1	-2.76	117.39	120.65
2	2	516	PSU	O3'-C3'-C4'	2.74	118.97	111.05
2	2	1207	2MG	CM2-N2-C2	-2.73	117.83	123.86
2	2	967	5MC	C5-C6-N1	-2.73	120.53	123.34
1	1	745	1MG	C8-N7-C5	2.73	108.19	102.99
55	5	20	H2U	C5-C4-N3	2.71	119.69	116.65
55	5	20	H2U	C5-C6-N1	2.69	120.46	111.61
1	1	1835	2MG	O6-C6-C5	-2.67	119.17	124.37
1	1	2580	PSU	O2-C2-N1	-2.64	119.89	122.79
2	2	1402	4OC	CM4-N4-C4	-2.64	117.30	122.45
1	1	2503	2MA	C8-N7-C5	2.62	107.98	102.99
44	q	89	0TD	OD1-CG-CB	-2.62	116.95	122.44
1	1	2251	OMG	O6-C6-C5	-2.62	119.26	124.37
2	2	516	PSU	O2-C2-N1	-2.61	119.92	122.79
55	5	55	PSU	O2-C2-N1	-2.60	119.93	122.79
1	1	1939	5MU	O4-C4-N3	-2.60	115.14	120.12
2	2	966	2MG	O6-C6-C5	-2.59	119.31	124.37
1	1	746	PSU	O2-C2-N1	-2.59	119.94	122.79
1	1	2445	2MG	C8-N7-C5	2.58	107.90	102.99
1	1	1917	PSU	C6-N1-C2	-2.57	120.06	122.68
1	1	1835	2MG	C8-N7-C5	2.56	107.87	102.99
2	2	1498	UR3	C1'-N1-C2	2.54	121.28	116.99
1	1	1911	PSU	O2-C2-N1	-2.54	120.00	122.79
1	1	2251	OMG	C8-N7-C5	2.54	107.82	102.99
2	2	966	2MG	C8-N7-C5	2.52	107.80	102.99
2	2	1207	2MG	O6-C6-C5	-2.51	119.47	124.37
55	5	54	5MU	O2-C2-N1	-2.50	119.47	122.79
1	1	2605	PSU	C6-N1-C2	-2.47	120.16	122.68
1	1	745	1MG	O6-C6-C5	-2.47	119.82	124.19
2	2	516	PSU	O3'-C3'-C2'	2.46	119.79	111.82
2	2	1207	2MG	C8-N7-C5	2.43	107.62	102.99
2	2	1516	2MG	O6-C6-C5	-2.41	119.66	124.37
1	1	1911	PSU	C6-N1-C2	-2.39	120.24	122.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
55	5	32	4OC	C6-C5-C4	2.35	119.84	116.96
2	2	1516	2MG	C8-N7-C5	2.33	107.43	102.99
1	1	747	5MU	C1'-N1-C2	2.33	121.79	117.57
1	1	746	PSU	C6-C5-C4	2.31	119.81	118.20
2	2	1518	MA6	C4-C5-N7	-2.30	107.01	109.40
1	1	2552	OMU	O2-C2-N1	-2.29	119.74	122.79
1	1	747	5MU	O4-C4-N3	-2.18	115.94	120.12
55	5	54	5MU	O4-C4-N3	-2.15	116.00	120.12
1	1	2498	OMC	C1'-N1-C2	2.12	123.14	118.42
1	1	745	1MG	CM1-N1-C2	-2.10	118.54	120.72
55	5	55	PSU	C6-N1-C2	-2.09	120.54	122.68
2	2	1402	4OC	C6-C5-C4	2.08	119.51	116.96
1	1	1962	5MC	CM5-C5-C6	-2.07	120.08	122.85
1	1	2457	PSU	O4'-C1'-C2'	2.07	108.06	105.14
1	1	745	1MG	C2-N1-C6	-2.07	119.27	120.95
55	5	20	H2U	O2-C2-N1	-2.06	120.52	123.11
1	1	747	5MU	C1'-N1-C6	-2.02	117.76	121.12

There are no chirality outliers.

All (42) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1	746	PSU	C2'-C1'-C5-C4
1	1	1618	6MZ	N1-C6-N6-C9
1	1	1915	3TD	O4'-C1'-C5-C4
1	1	1915	3TD	O4'-C1'-C5-C6
1	1	2445	2MG	C3'-C4'-C5'-O5'
2	2	516	PSU	O4'-C1'-C5-C4
2	2	516	PSU	O4'-C1'-C5-C6
2	2	966	2MG	C3'-C4'-C5'-O5'
2	2	1402	4OC	O4'-C4'-C5'-O5'
2	2	1519	MA6	O4'-C4'-C5'-O5'
2	2	1519	MA6	C3'-C4'-C5'-O5'
55	5	20	H2U	O4'-C1'-N1-C6
56	6	77	FME	O1-CN-N-CA
1	1	2030	6MZ	O4'-C4'-C5'-O5'
1	1	2030	6MZ	C3'-C4'-C5'-O5'
2	2	527	G7M	C3'-C4'-C5'-O5'
2	2	966	2MG	O4'-C4'-C5'-O5'
2	2	1402	4OC	C3'-C4'-C5'-O5'
1	1	2445	2MG	O4'-C4'-C5'-O5'
55	5	20	H2U	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
55	5	20	H2U	C3'-C4'-C5'-O5'
1	1	1835	2MG	C3'-C4'-C5'-O5'
56	6	77	FME	N-CA-CB-CG
1	1	1835	2MG	O4'-C4'-C5'-O5'
2	2	527	G7M	O4'-C4'-C5'-O5'
2	2	1519	MA6	C5-C6-N6-C10
55	5	8	4SU	O4'-C1'-N1-C6
56	6	77	FME	C-CA-CB-CG
55	5	8	4SU	O4'-C1'-N1-C2
44	q	89	0TD	CG-CB-SB-CSB
55	5	20	H2U	O4'-C1'-N1-C2
56	6	77	FME	CA-CB-CG-SD
2	2	516	PSU	C3'-C4'-C5'-O5'
2	2	527	G7M	C4'-C5'-O5'-P
2	2	1519	MA6	C4'-C5'-O5'-P
1	1	747	5MU	C4'-C5'-O5'-P
1	1	2504	PSU	O4'-C4'-C5'-O5'
1	1	2069	G7M	O4'-C4'-C5'-O5'
1	1	746	PSU	O4'-C1'-C5-C6
1	1	2498	OMC	O4'-C4'-C5'-O5'
1	1	2503	2MA	O4'-C4'-C5'-O5'
56	6	77	FME	CB-CA-N-CN

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 309 ligands modelled in this entry, 309 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)

There are no chain breaks in this entry.

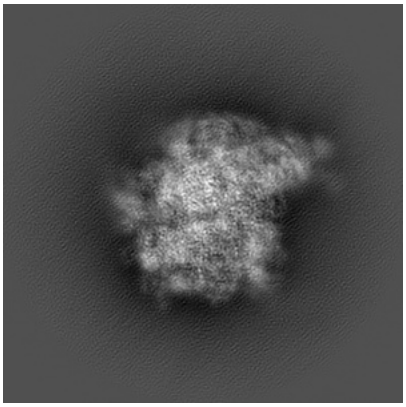
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-20184. These allow visual inspection of the internal detail of the map and identification of artifacts.

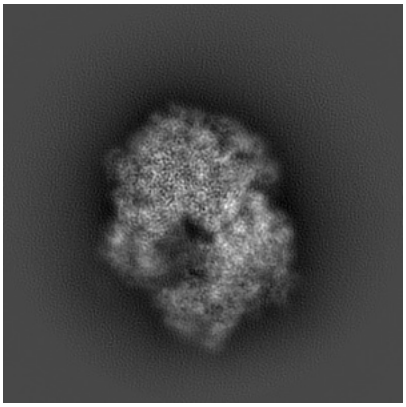
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

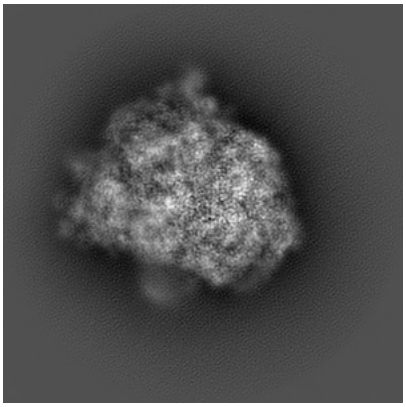
6.1.1 Primary map



X



Y

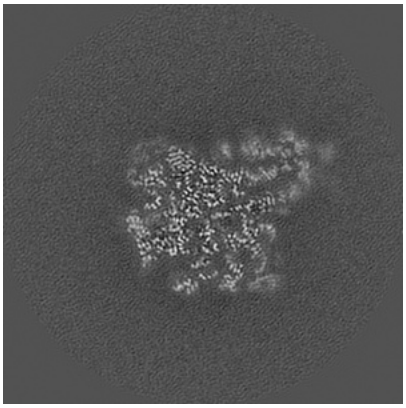


Z

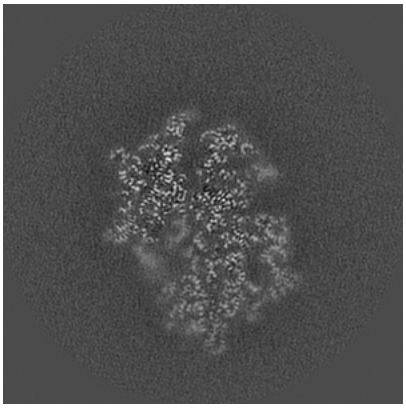
The images above show the map projected in three orthogonal directions.

6.2 Central slices

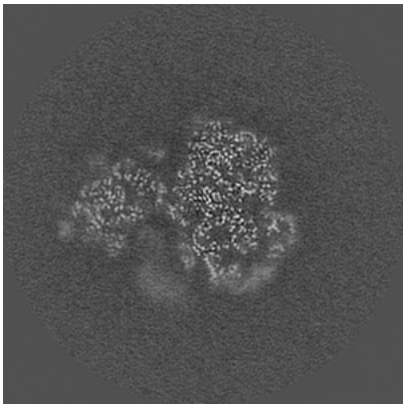
6.2.1 Primary map



X Index: 128



Y Index: 128

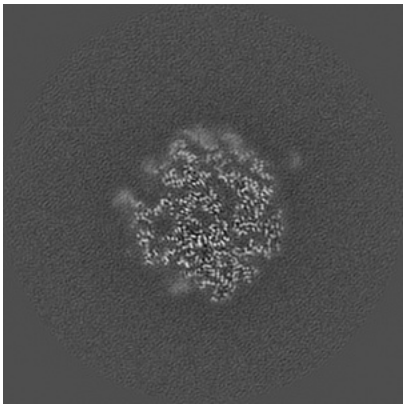


Z Index: 128

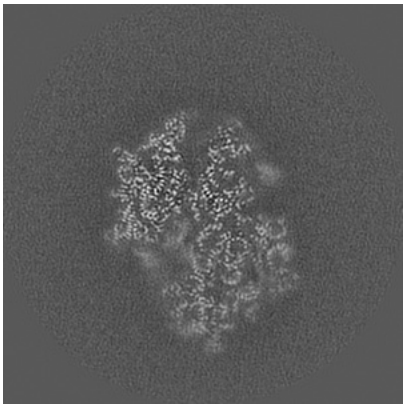
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

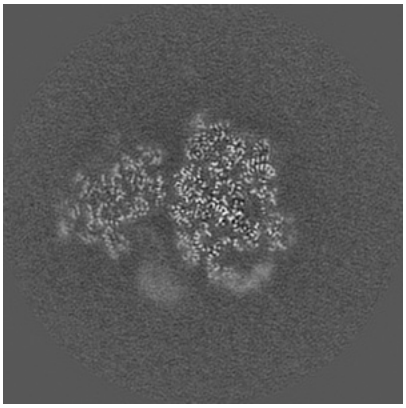
6.3.1 Primary map



X Index: 148



Y Index: 126



Z Index: 130

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

X

Y

Z

The images above show the 3D surface view of the map at the recommended contour level 0.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

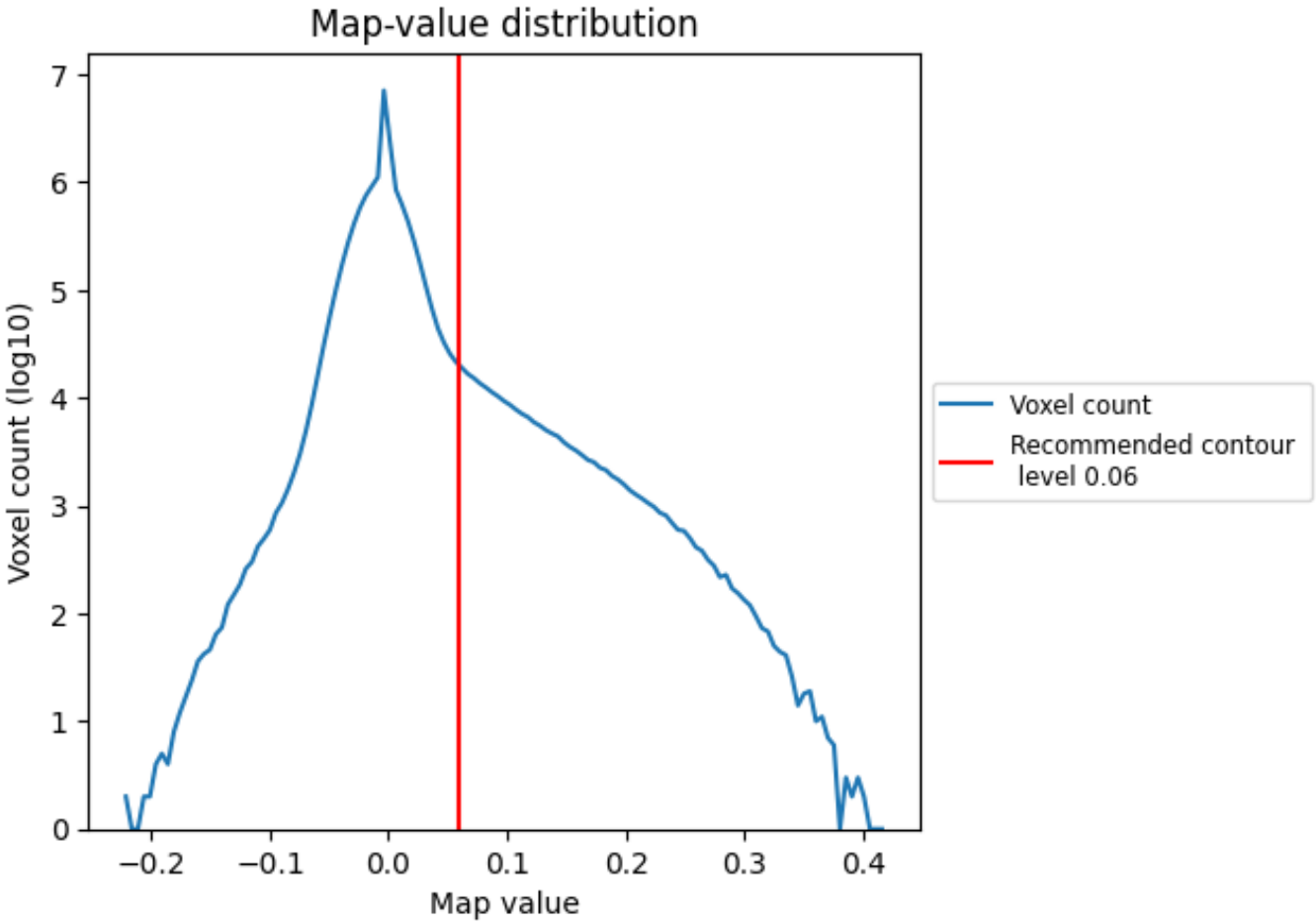
6.5 Mask visualisation (i)

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

7 Map analysis

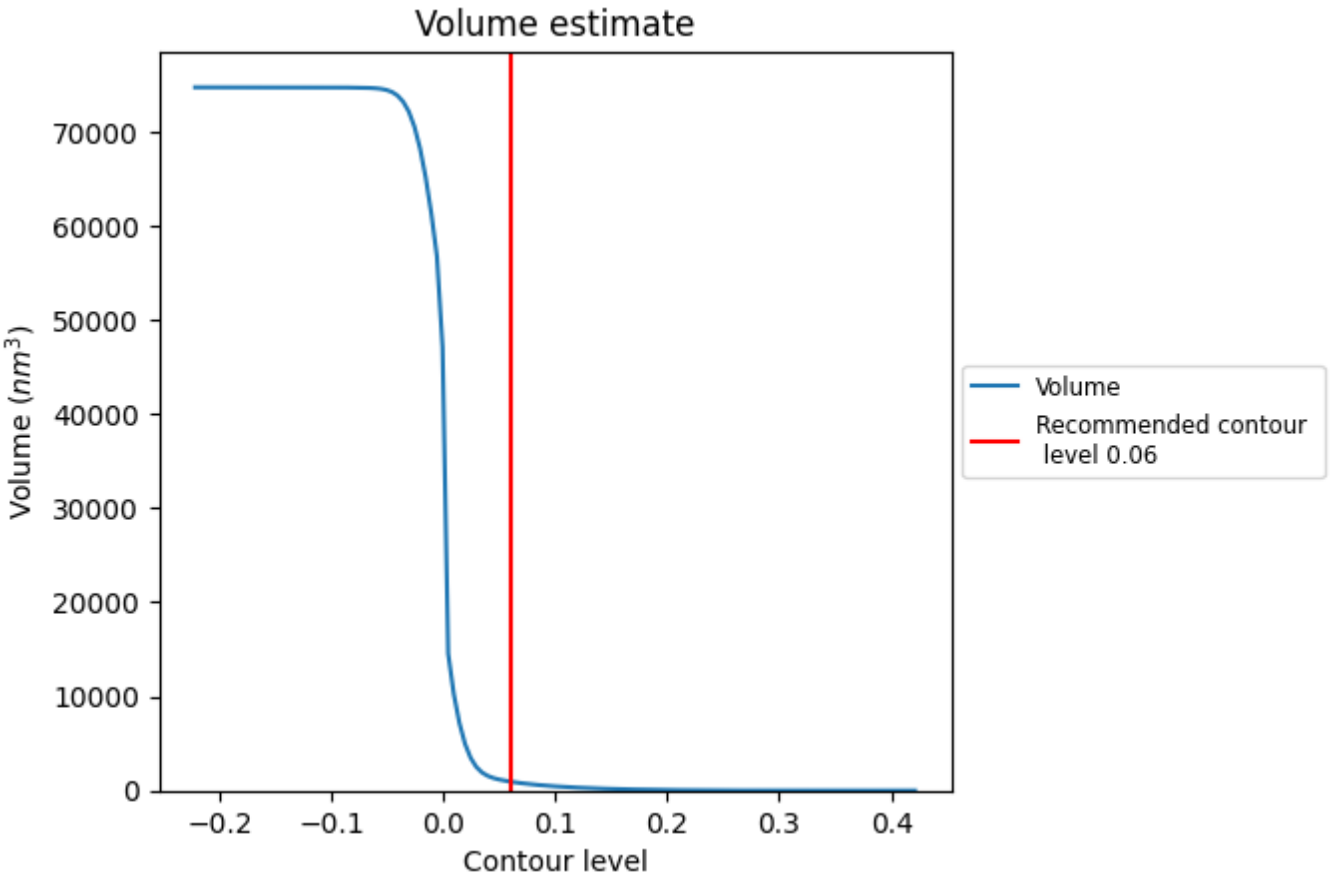
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

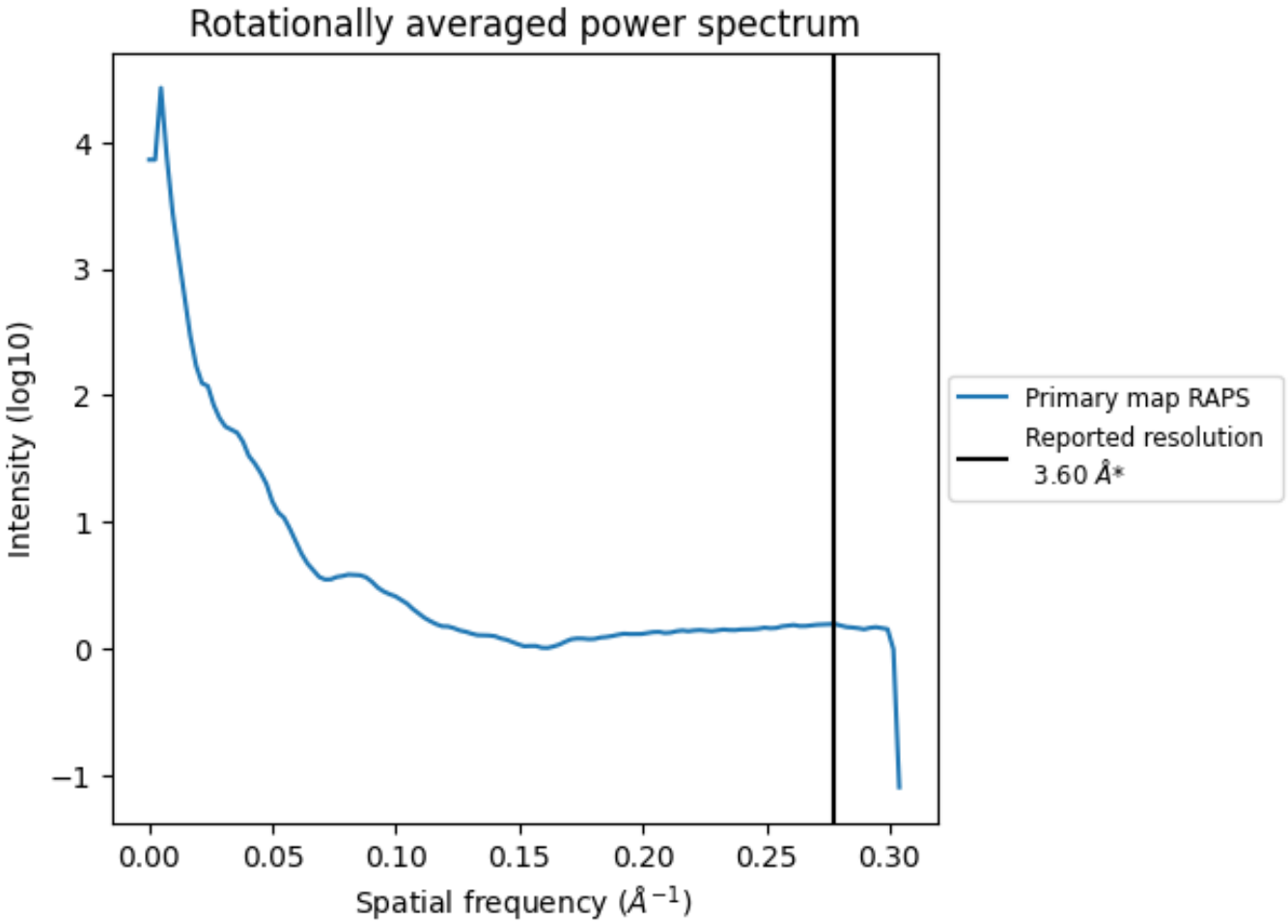
7.2 Volume estimate



The volume at the recommended contour level is 945 nm^3; this corresponds to an approximate mass of 854 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 0.278 Å^{-1}

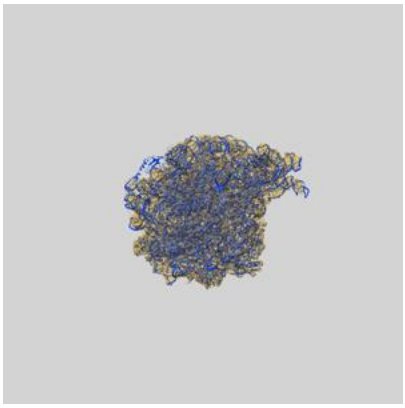
8 Fourier-Shell correlation (i)

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

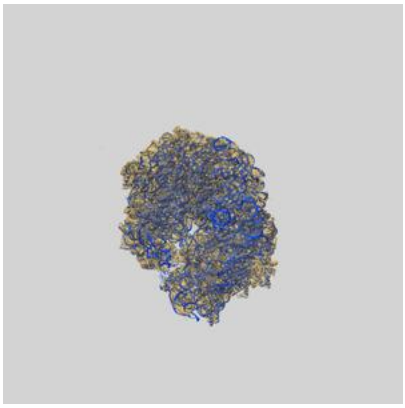
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-20184 and PDB model 6OSK. Per-residue inclusion information can be found in section 3 on page 14.

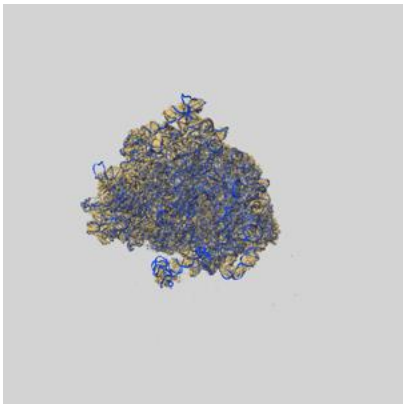
9.1 Map-model overlay



X



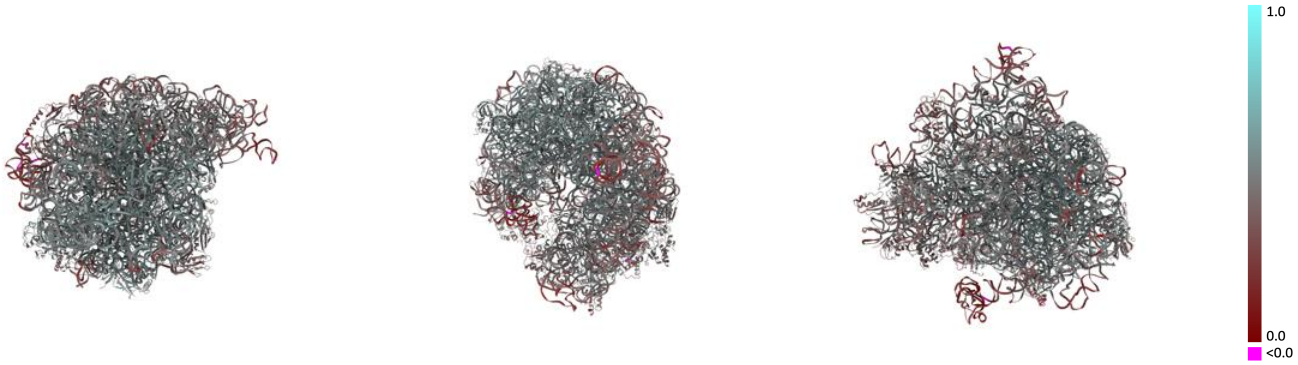
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.06 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.

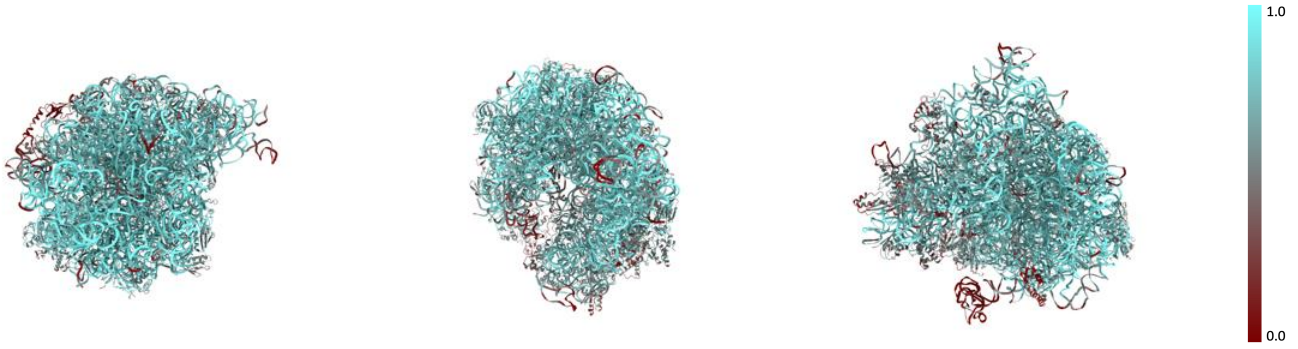
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

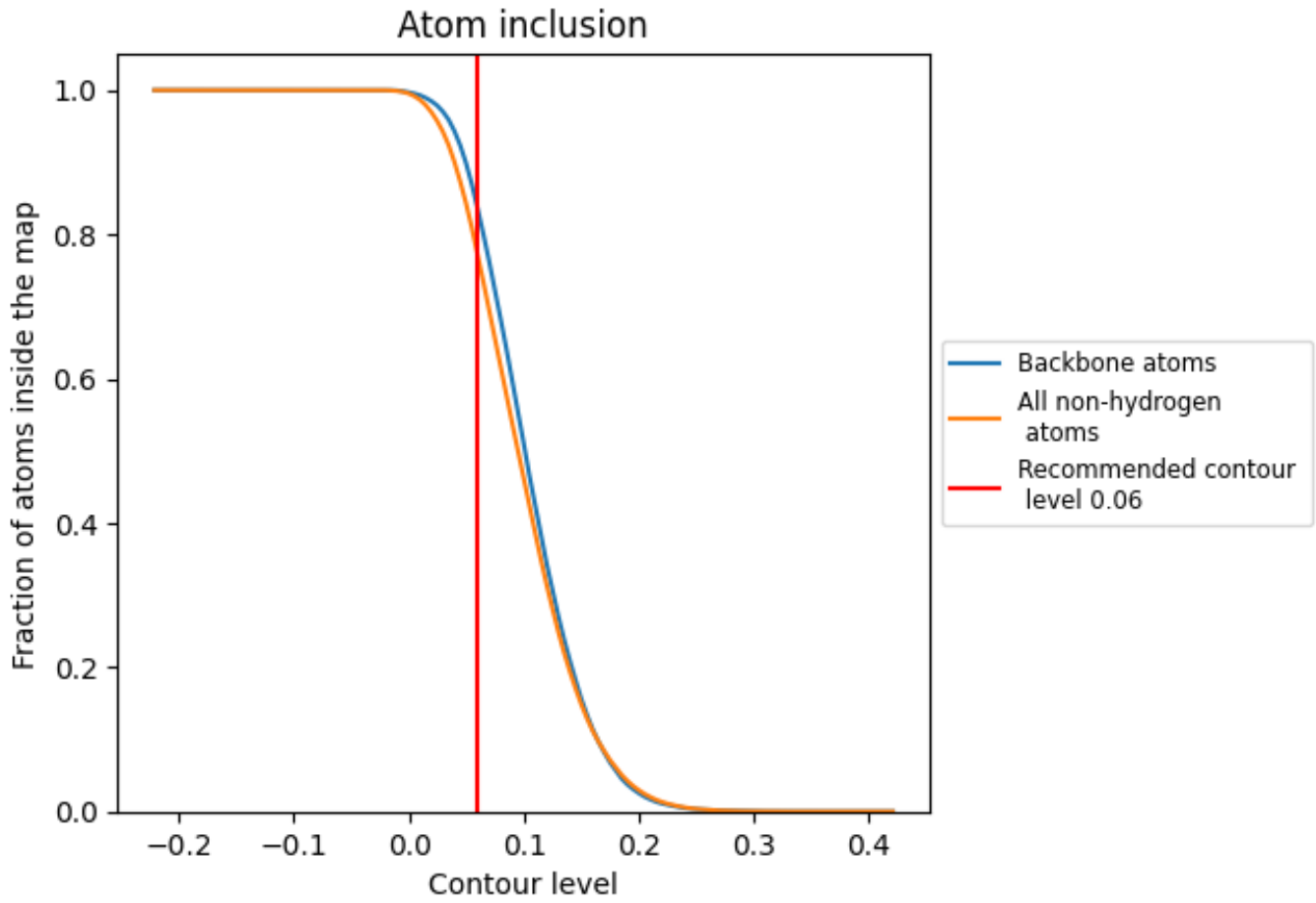
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.06).

9.4 Atom inclusion (i)



At the recommended contour level, 83% of all backbone atoms, 77% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7710	0.4670
1	0.8551	0.4830
2	0.8332	0.4470
3	0.8300	0.4240
4	0.7772	0.5030
5	0.6323	0.3710
6	0.4375	0.4210
A	0.4732	0.4330
B	0.7564	0.5360
C	0.7674	0.5280
D	0.7138	0.5080
E	0.4603	0.3880
F	0.5859	0.4280
G	0.1962	0.3400
J	0.7755	0.5330
K	0.6840	0.5190
L	0.7275	0.5180
M	0.6900	0.5080
N	0.8160	0.5370
O	0.6141	0.4280
P	0.6959	0.5160
Q	0.7896	0.5270
R	0.7616	0.5270
S	0.7428	0.5330
T	0.6658	0.4940
U	0.6302	0.4720
V	0.6057	0.4440
W	0.7332	0.5200
X	0.7205	0.5010
Y	0.6687	0.4600
Z	0.7500	0.5200
a	0.0000	0.1790
b	0.7669	0.5150
c	0.6699	0.5070
d	0.7915	0.5390

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Chain	Atom inclusion	Q-score
e	0.7373	0.5360
f	0.7143	0.5170
g	0.5414	0.4240
h	0.5824	0.4570
i	0.4155	0.3750
j	0.6841	0.4930
k	0.6106	0.4380
l	0.4510	0.4100
m	0.6573	0.4760
n	0.5485	0.4110
o	0.4719	0.4160
p	0.6249	0.4500
q	0.6284	0.4920
r	0.5196	0.4180
s	0.6034	0.4560
t	0.6348	0.4650
u	0.6045	0.4620
v	0.5443	0.4340
w	0.5335	0.4300
x	0.5162	0.4090
y	0.5566	0.4350
z	0.4615	0.3950