



## Full wwPDB EM Validation Report ⓘ

Dec 11, 2025 – 05:11 PM EST

PDB ID : 9YQ1 / pdb\_00009yq1  
EMDB ID : EMD-73317  
Title : Vacant ribosome with P-site tRNA, substate 3, Structure Ic  
Authors : Susorov, D.; Korostelev, A.A.  
Deposited on : 2025-10-14  
Resolution : 2.90 Å(reported)  
Based on initial model : 5LZS

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

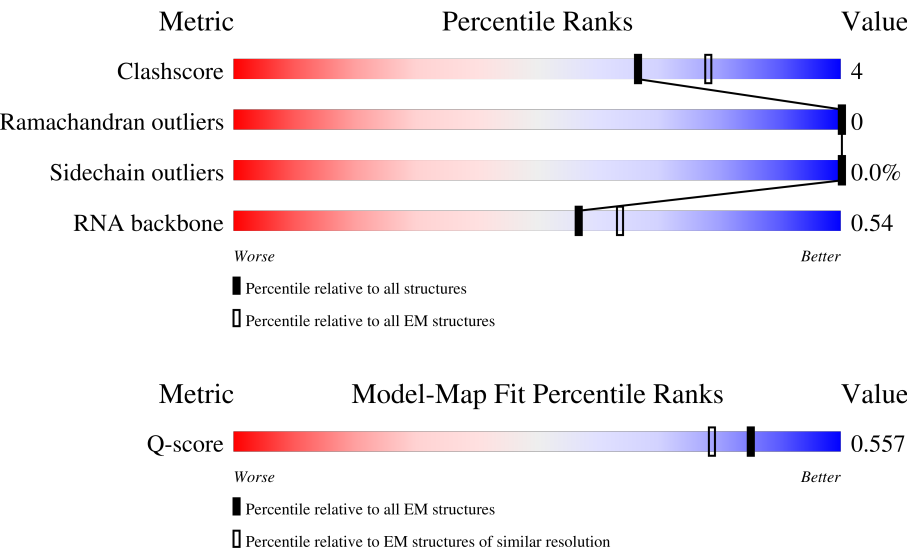
EMDB validation analysis : 0.0.1.dev129  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.47

# 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 2.90 Å.

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




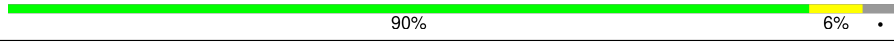
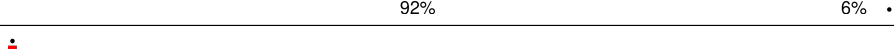
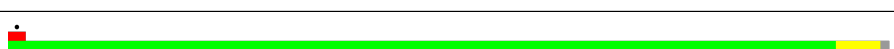


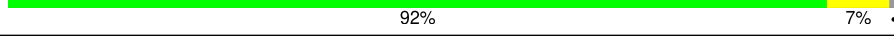
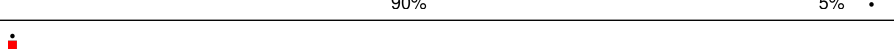

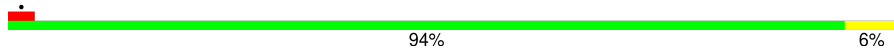

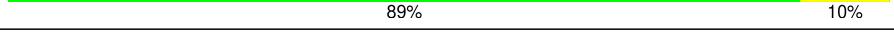
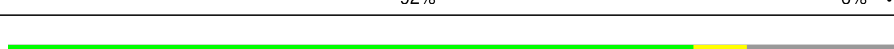
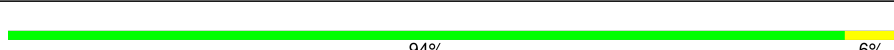

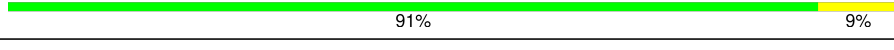
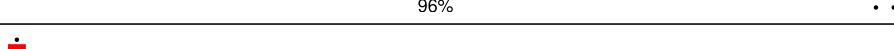







Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
RNA backbone	6643	2191	-
Q-score	-	25397	13054 ( 2.40 - 3.40 )

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	5	3601	<div> <div style="width: 67%;"></div> <div style="width: 27%;"></div> <div style="width: 5%;"></div> </div>
2	7	120	<div> <div style="width: 88%;"></div> <div style="width: 11%;"></div> </div>
3	8	156	<div> <div style="width: 74%;"></div> <div style="width: 17%;"></div> <div style="width: 6%;"></div> </div>

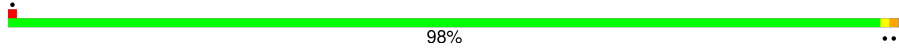
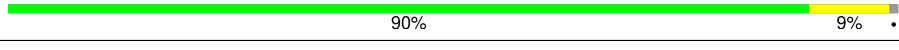
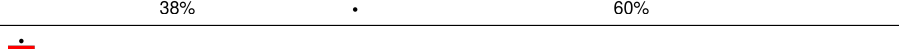
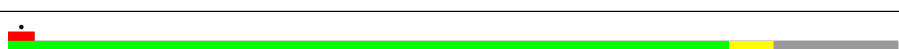

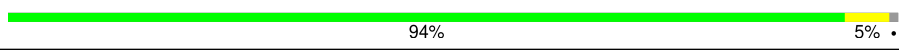
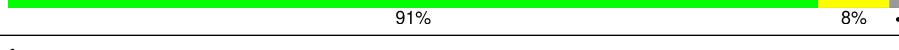
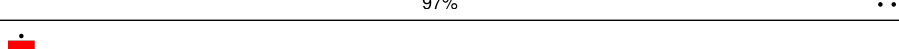
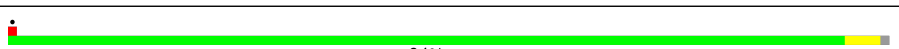


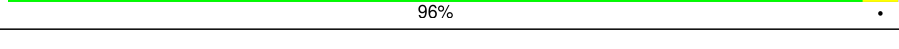

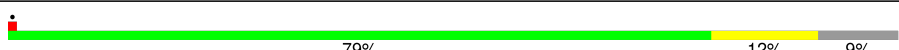


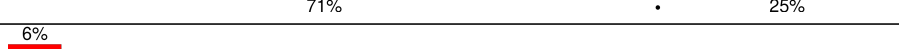







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Mol	Chain	Length	Quality of chain
4	9	1869	
5	A	257	
6	B	403	
7	C	425	
8	D	297	
9	E	291	
10	G	319	
11	H	192	
12	I	214	
13	J	178	
14	K	247	
15	L	211	
16	M	218	
17	N	204	
18	O	203	
19	P	184	
20	Q	188	
21	R	196	
22	S	176	
23	T	160	
24	U	128	
25	V	140	
26	W	157	
27	X	156	
28	Y	145	

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Mol	Chain	Length	Quality of chain
29	Z	136	
30	a	148	
31	b	245	
32	c	115	
33	d	125	
34	e	135	
35	f	110	
36	g	116	
37	h	123	
38	i	105	
39	k	70	
40	l	51	
41	m	102	
42	n	25	
43	o	106	
44	p	92	
45	r	137	
46	AA	295	
47	BB	264	
48	CC	293	
49	DD	243	
50	EE	263	
51	FF	204	
52	GG	249	
53	HH	194	

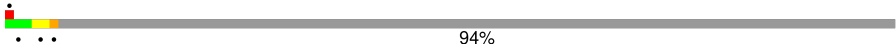
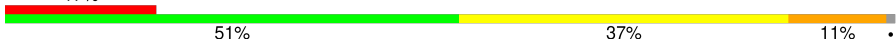
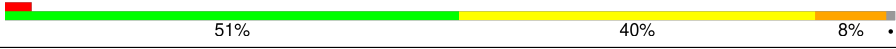

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Mol	Chain	Length	Quality of chain
54	II	208	
55	JJ	194	
56	KK	165	
57	LL	158	
58	MM	132	
59	NN	151	
60	OO	168	
61	PP	145	
62	QQ	146	
63	RR	135	
64	SS	152	
65	TT	145	
66	UU	119	
67	VV	83	
68	WW	130	
69	XX	143	
70	YY	130	
71	ZZ	125	
72	aa	115	
73	bb	84	
74	cc	69	
75	dd	56	
76	ee	133	
77	ff	156	
78	gg	317	

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Mol	Chain	Length	Quality of chain
79	10	185	 <div>94%</div>
80	11	75	 <div>17% 51% 37% 11%</div>
80	13	75	 <div>51% 40% 8%</div>
81	j	97	 <div>80% 8% 11%</div>

## 2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 213916 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 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	3601	Total	C	N	O	P	0	0
			77221	34390	14143	25087	3601		

There are 59 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5	1	C	N	conflict	GB 5LZS_5
5	3948	C	-	insertion	GB 5LZS_5
5	3949	A	-	insertion	GB 5LZS_5
5	3950	U	-	insertion	GB 5LZS_5
5	3951	G	-	insertion	GB 5LZS_5
5	3952	A	-	insertion	GB 5LZS_5
5	3953	G	-	insertion	GB 5LZS_5
5	3954	A	-	insertion	GB 5LZS_5
5	3955	G	-	insertion	GB 5LZS_5
5	3956	G	-	insertion	GB 5LZS_5
5	3957	U	-	insertion	GB 5LZS_5
5	3958	G	-	insertion	GB 5LZS_5
5	3959	U	-	insertion	GB 5LZS_5
5	3960	A	-	insertion	GB 5LZS_5
5	3961	G	-	insertion	GB 5LZS_5
5	3962	A	-	insertion	GB 5LZS_5
5	3963	A	-	insertion	GB 5LZS_5
5	3964	U	-	insertion	GB 5LZS_5
5	3965	A	-	insertion	GB 5LZS_5
5	3966	A	-	insertion	GB 5LZS_5
5	3967	G	-	insertion	GB 5LZS_5
5	3968	U	-	insertion	GB 5LZS_5
5	3969	G	-	insertion	GB 5LZS_5
5	3970	G	-	insertion	GB 5LZS_5
5	3971	G	-	insertion	GB 5LZS_5
5	3972	A	-	insertion	GB 5LZS_5
5	3973	G	-	insertion	GB 5LZS_5
5	3974	G	-	insertion	GB 5LZS_5

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Chain	Residue	Modelled	Actual	Comment	Reference
5	3975	C	-	insertion	GB 5LZS_5
5	3976	C	-	insertion	GB 5LZS_5
5	4035	G	-	insertion	GB 5LZS_5
5	4036	G	-	insertion	GB 5LZS_5
5	4037	C	-	insertion	GB 5LZS_5
5	4038	C	-	insertion	GB 5LZS_5
5	4039	G	-	insertion	GB 5LZS_5
5	4040	C	-	insertion	GB 5LZS_5
5	4041	C	-	insertion	GB 5LZS_5
5	4042	G	-	insertion	GB 5LZS_5
5	4043	G	-	insertion	GB 5LZS_5
5	4044	U	-	insertion	GB 5LZS_5
5	4045	G	-	insertion	GB 5LZS_5
5	4046	A	-	insertion	GB 5LZS_5
5	4047	A	-	insertion	GB 5LZS_5
5	4048	A	-	insertion	GB 5LZS_5
5	4049	U	-	insertion	GB 5LZS_5
5	4050	A	-	insertion	GB 5LZS_5
5	4051	C	-	insertion	GB 5LZS_5
5	4052	C	-	insertion	GB 5LZS_5
5	4053	A	-	insertion	GB 5LZS_5
5	4054	C	-	insertion	GB 5LZS_5
5	4055	U	-	insertion	GB 5LZS_5
5	4056	A	-	insertion	GB 5LZS_5
5	4057	C	-	insertion	GB 5LZS_5
5	4058	U	-	insertion	GB 5LZS_5
5	4059	C	-	insertion	GB 5LZS_5
5	4060	U	-	insertion	GB 5LZS_5
5	4061	G	-	insertion	GB 5LZS_5
5	4062	A	-	insertion	GB 5LZS_5
5	4063	U	-	insertion	GB 5LZS_5

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
7	2	U	N	conflict	GB X06789.1

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Chain	Residue	Modelled	Actual	Comment	Reference
7	36	C	N	conflict	GB X06789.1
7	102	U	N	conflict	GB X06789.1
7	112	U	N	conflict	GB X06789.1
7	114	U	N	conflict	GB X06789.1
7	119	U	C	conflict	GB X06789.1
7	120	U	N	conflict	GB X06789.1

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 4 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	9	1697	Total	C	N	O	P	0	0
			36229	16171	6507	11855	1696		

- Molecule 5 is a protein called Ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 6 is a protein called Ribosomal protein L3.

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

- Molecule 7 is a protein called 60S ribosomal protein L4.

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

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	378	LYS	-	insertion	UNP G1SVW5

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Chain	Residue	Modelled	Actual	Comment	Reference
C	379	VAL	-	insertion	UNP G1SVW5
C	380	LYS	-	insertion	UNP G1SVW5
C	381	LYS	-	insertion	UNP G1SVW5
C	382	PRO	-	insertion	UNP G1SVW5
C	383	ARG	-	insertion	UNP G1SVW5
C	384	ALA	-	insertion	UNP G1SVW5
C	385	VAL	-	insertion	UNP G1SVW5
C	386	GLY	-	insertion	UNP G1SVW5
C	387	ILE	-	insertion	UNP G1SVW5
C	388	LYS	-	insertion	UNP G1SVW5
C	389	GLN	-	insertion	UNP G1SVW5

- Molecule 8 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 9 is a protein called 60S ribosomal protein L6.

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

- Molecule 10 is a protein called 60S ribosomal protein L7a.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	244	GLY	CYS	conflict	UNP G1STW0

- Molecule 11 is a protein called 60S ribosomal protein L9.

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

- Molecule 12 is a protein called 60S ribosomal protein L10.

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

- Molecule 13 is a protein called Ribosomal protein L11.

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

- Molecule 14 is a protein called 60S ribosomal protein L7.

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

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	61	ARG	GLY	conflict	UNP G1TUB1
K	93	ARG	GLY	conflict	UNP G1TUB1
K	131	MET	VAL	conflict	UNP G1TUB1
K	153	ILE	VAL	conflict	UNP G1TUB1

- Molecule 15 is a protein called 60S ribosomal protein L13.

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

There are 9 discrepancies between the modelled and reference sequences:

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

- Molecule 16 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 17 is a protein called Ribosomal protein L15.

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

- Molecule 18 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	O	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 19 is a protein called Large ribosomal subunit protein uL22.

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

- Molecule 20 is a protein called Ribosomal protein L18.

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

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	4	ASP	ASN	conflict	UNP G1TFE0
Q	14	ARG	TRP	conflict	UNP G1TFE0
Q	53	MET	LEU	conflict	UNP G1TFE0
Q	58	ARG	TRP	conflict	UNP G1TFE0
Q	75	ARG	GLN	conflict	UNP G1TFE0
Q	80	ALA	PRO	conflict	UNP G1TFE0
Q	86	VAL	ILE	conflict	UNP G1TFE0
Q	104	ARG	HIS	conflict	UNP G1TFE0
Q	110	ARG	CYS	conflict	UNP G1TFE0
Q	137	VAL	GLY	conflict	UNP G1TFE0
Q	157	GLY	ARG	conflict	UNP G1TFE0

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	181	ARG	TRP	conflict	UNP G1TFE0

- Molecule 21 is a protein called Ribosomal protein L19.

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

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	38	ARG	CYS	conflict	UNP G1TJR3
R	64	ARG	GLN	conflict	UNP G1TJR3
R	94	THR	LYS	conflict	UNP G1TJR3

- Molecule 22 is a protein called 60S ribosomal protein L18a.

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

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	1	MET	THR	conflict	UNP G1TTY7
S	18	PRO	-	insertion	UNP G1TTY7
S	19	THR	-	insertion	UNP G1TTY7
S	20	PRO	SER	conflict	UNP G1TTY7
S	22	CYS	SER	conflict	UNP G1TTY7
S	23	ARG	PRO	conflict	UNP G1TTY7
S	24	THR	ALA	conflict	UNP G1TTY7
S	49	SER	LEU	conflict	UNP G1TTY7
S	50	GLN	GLU	conflict	UNP G1TTY7
S	95	ARG	HIS	conflict	UNP G1TTY7
S	101	THR	ILE	conflict	UNP G1TTY7
S	102	THR	MET	conflict	UNP G1TTY7
S	104	GLY	SER	conflict	UNP G1TTY7
S	126	ILE	VAL	conflict	UNP G1TTY7
S	132	ILE	MET	conflict	UNP G1TTY7
S	135	SER	ALA	conflict	UNP G1TTY7
S	136	LYS	ARG	conflict	UNP G1TTY7
S	138	ARG	PRO	conflict	UNP G1TTY7

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Chain	Residue	Modelled	Actual	Comment	Reference
S	149	LYS	ARG	conflict	UNP G1TTY7
S	151	LYS	ARG	conflict	UNP G1TTY7
S	168	THR	TYR	conflict	UNP G1TTY7
S	169	THR	ALA	conflict	UNP G1TTY7
S	176	PHE	-	insertion	UNP G1TTY7

- Molecule 23 is a protein called eL21.

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

- Molecule 24 is a protein called eL22.

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

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	18	LEU	VAL	conflict	UNP G1TSG1
U	32	GLY	ARG	conflict	UNP G1TSG1
U	36	ALA	GLU	conflict	UNP G1TSG1
U	39	PHE	SER	conflict	UNP G1TSG1
U	54	GLY	ARG	conflict	UNP G1TSG1
U	60	VAL	ALA	conflict	UNP G1TSG1
U	62	SER	THR	conflict	UNP G1TSG1
U	63	LEU	ILE	conflict	UNP G1TSG1
U	97	ARG	HIS	conflict	UNP G1TSG1
U	106	THR	SER	conflict	UNP G1TSG1
U	126	GLU	ASP	conflict	UNP G1TSG1

- Molecule 25 is a protein called Ribosomal protein L23.

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

- Molecule 26 is a protein called eL24.

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

- Molecule 27 is a protein called eL23.

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

- Molecule 28 is a protein called uL24.

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

- Molecule 29 is a protein called 60S ribosomal protein L27.

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

- Molecule 30 is a protein called 60S ribosomal protein L27a.

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

- Molecule 31 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	b	98	Total	C	N	O	S	0	0
			806	498	182	123	3		

- Molecule 32 is a protein called eL30.

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

- Molecule 33 is a protein called eL31.

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

- Molecule 34 is a protein called Ribosomal protein L32.

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

- Molecule 35 is a protein called eL33.

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

- Molecule 36 is a protein called Large ribosomal subunit protein eL34.

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

- Molecule 37 is a protein called eL35.

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

- Molecule 38 is a protein called 60S ribosomal protein L36.

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

- Molecule 39 is a protein called eL38.

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

There are 4 discrepancies between the modelled and reference sequences:



Chain	Residue	Modelled	Actual	Comment	Reference
k	3	ARG	GLN	conflict	UNP G1U3J0
k	38	CYS	TYR	conflict	UNP G1U3J0
k	48	THR	MET	conflict	UNP G1U3J0
k	66	VAL	MET	conflict	UNP G1U3J0

- Molecule 40 is a protein called eL39.

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

- Molecule 41 is a protein called Ubiquitin A-52 residue ribosomal protein fusion product 1.

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

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
m	1	MET	-	initiating methionine	UNP A0A2K5PSA0
m	2	GLY	-	expression tag	UNP A0A2K5PSA0
m	3	ASP	-	expression tag	UNP A0A2K5PSA0
m	4	PRO	-	expression tag	UNP A0A2K5PSA0
m	5	GLU	-	expression tag	UNP A0A2K5PSA0
m	6	SER	-	expression tag	UNP A0A2K5PSA0
m	7	GLY	-	expression tag	UNP A0A2K5PSA0
m	8	GLY	-	expression tag	UNP A0A2K5PSA0
m	9	CYS	-	expression tag	UNP A0A2K5PSA0

- Molecule 42 is a protein called eL41.

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

- Molecule 43 is a protein called Large ribosomal subunit protein eL42.

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

- Molecule 44 is a protein called eL43.

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

- Molecule 45 is a protein called eL28.

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

- Molecule 46 is a protein called uS2 (SA).

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AA	114	THR	ALA	conflict	UNP G1TLT8

- Molecule 47 is a protein called 40S ribosomal protein S3a.

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

- Molecule 48 is a protein called Small ribosomal subunit protein uS5.

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

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CC	13	ASP	GLY	conflict	UNP O18789
CC	19	ILE	MET	conflict	UNP O18789

- Molecule 49 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	DD	224	Total	C	N	O	S	0	0
			1739	1108	313	311	7		

- Molecule 50 is a protein called eS4 (S4 X isoform).

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

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EE	25	GLY	SER	conflict	UNP G1TK17
EE	51	ARG	LYS	conflict	UNP G1TK17
EE	78	THR	ALA	conflict	UNP G1TK17
EE	156	VAL	MET	conflict	UNP G1TK17

- Molecule 51 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	FF	184	Total	C	N	O	S	0	0
			1460	915	273	265	7		

- Molecule 52 is a protein called 40S ribosomal protein S6.

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

- Molecule 53 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	HH	185	Total	C	N	O	S	0	0
			1489	952	271	265	1		

- Molecule 54 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	II	198	Total	C	N	O	S	0	0
			1628	1021	322	280	5		

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 55 is a protein called Ribosomal protein S9 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
55	JJ	181	Total	C	N	O	S	0	0
			1508	960	302	244	2		

- Molecule 56 is a protein called S10\_ plectin domain-containing protein.

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

- Molecule 57 is a protein called Ribosomal protein S11.

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

- Molecule 58 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	MM	112	Total	C	N	O	S	0	0
			871	551	155	158	7		

- Molecule 59 is a protein called Ribosomal protein S13.

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

- Molecule 60 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 61 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	PP	129	Total	C	N	O	S	0	0
			1058	670	201	180	7		

- Molecule 62 is a protein called uS9.

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

- Molecule 63 is a protein called eS17.

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

- Molecule 64 is a protein called uS13.

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

- Molecule 65 is a protein called eS19.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
TT	119	GLY	TRP	conflict	UNP G1TN62

- Molecule 66 is a protein called uS10.

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

- Molecule 67 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	VV	83	Total	C	N	O	S	0	0
			637	393	117	122	5		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
VV	3	ASN	SER	conflict	UNP G1TM82
VV	4	ASP	ASN	conflict	UNP G1TM82
VV	33	GLN	PRO	conflict	UNP G1TM82
VV	50	PHE	SER	conflict	UNP G1TM82
VV	75	ALA	SER	conflict	UNP G1TM82
VV	76	ASP	HIS	conflict	UNP G1TM82
VV	81	LYS	GLN	conflict	UNP G1TM82

- Molecule 68 is a protein called Ribosomal protein S15a.

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

- Molecule 69 is a protein called uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	XX	140	Total	C	N	O	S	0	0
			1087	687	215	182	3		

- Molecule 70 is a protein called 40S ribosomal protein S24.

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

- Molecule 71 is a protein called eS25.

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

- Molecule 72 is a protein called 40S ribosomal protein S26.

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

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
aa	28	ARG	CYS	conflict	UNP G1TFE8
aa	56	ALA	VAL	conflict	UNP G1TFE8
aa	109	ARG	PRO	conflict	UNP G1TFE8

- Molecule 73 is a protein called 40S ribosomal protein S27.

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

- Molecule 74 is a protein called Ribosomal protein S28.

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

- Molecule 75 is a protein called eS29.

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

- Molecule 76 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	ee	55	Total	C	N	O	S	0	0
			443	274	97	71	1		

- Molecule 77 is a protein called Ribosomal protein S27a.

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

- Molecule 78 is a protein called RACK1.

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

- Molecule 79 is a RNA chain called MF mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	10	11	Total	C	N	O	P	0	0
			234	105	41	77	11		

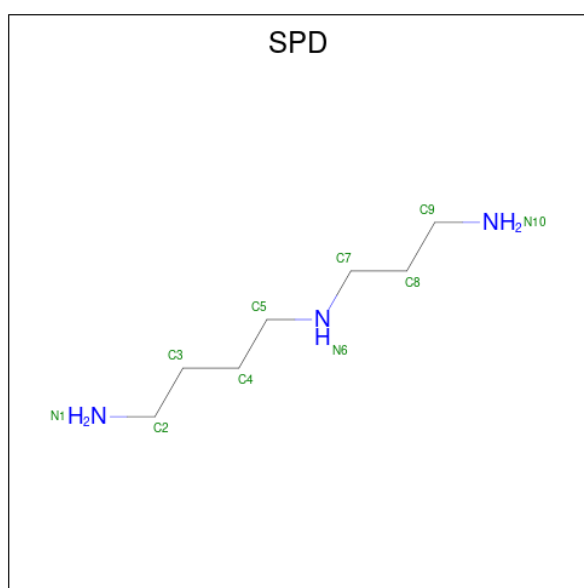
- Molecule 80 is a RNA chain called Met-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	13	74	Total	C	N	O	P	0	0
			1585	707	293	511	74		
80	11	74	Total	C	N	O	P	0	0
			1585	707	293	511	74		

- Molecule 81 is a protein called Ribosomal protein L37.

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

- Molecule 82 is SPERMIDINE (CCD ID: SPD) (formula: C<sub>7</sub>H<sub>19</sub>N<sub>3</sub>).



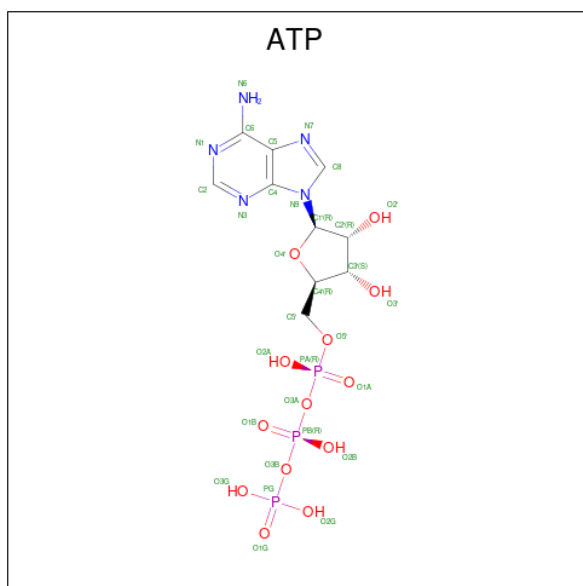


Mol	Chain	Residues	Atoms			AltConf
82	5	1	Total	C	N	0
			10	7	3	

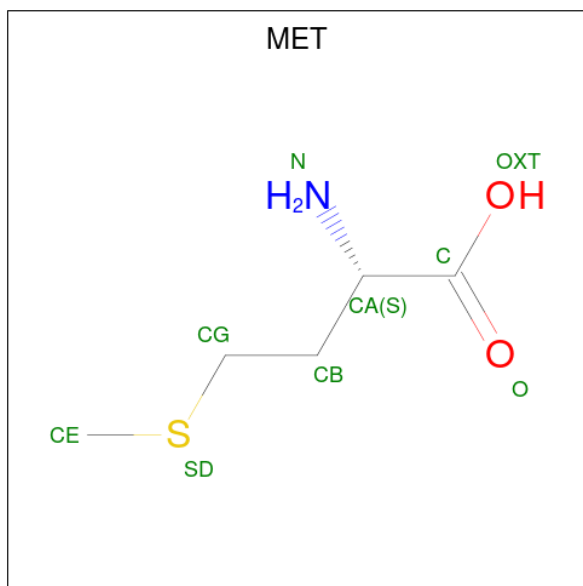
- Molecule 83 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
83	g	1	Total	Zn	0
			1	1	
83	m	1	Total	Zn	0
			1	1	
83	o	1	Total	Zn	0
			1	1	
83	p	1	Total	Zn	0
			1	1	
83	dd	1	Total	Zn	0
			1	1	
83	j	1	Total	Zn	0
			1	1	

- Molecule 84 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>13</sub>P<sub>3</sub>).



- Molecule 85 is METHIONINE (CCD ID: MET) (formula:  $C_5H_{11}NO_2S$ ).

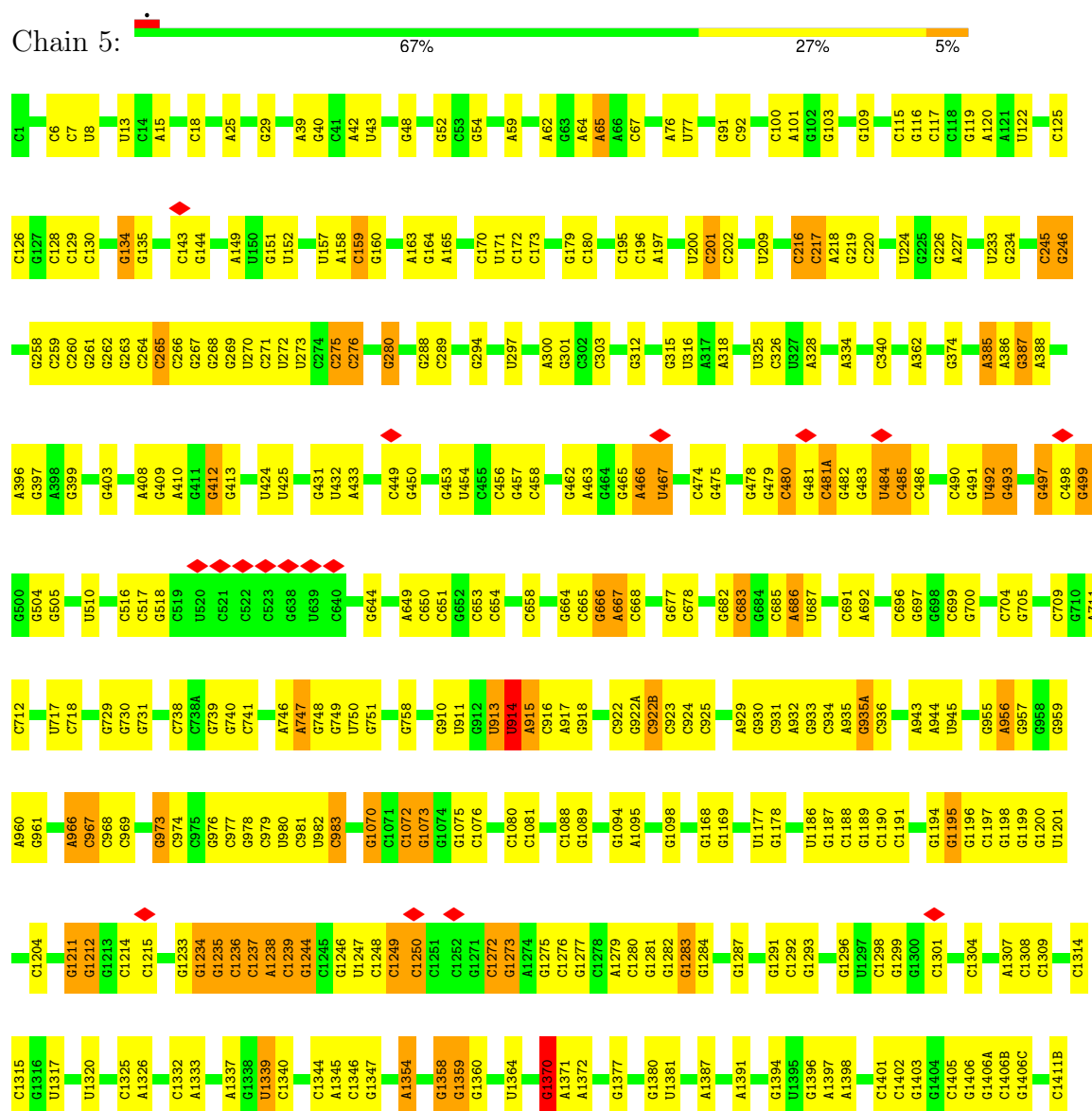


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
85	13	1	8	5	1	1	1	0

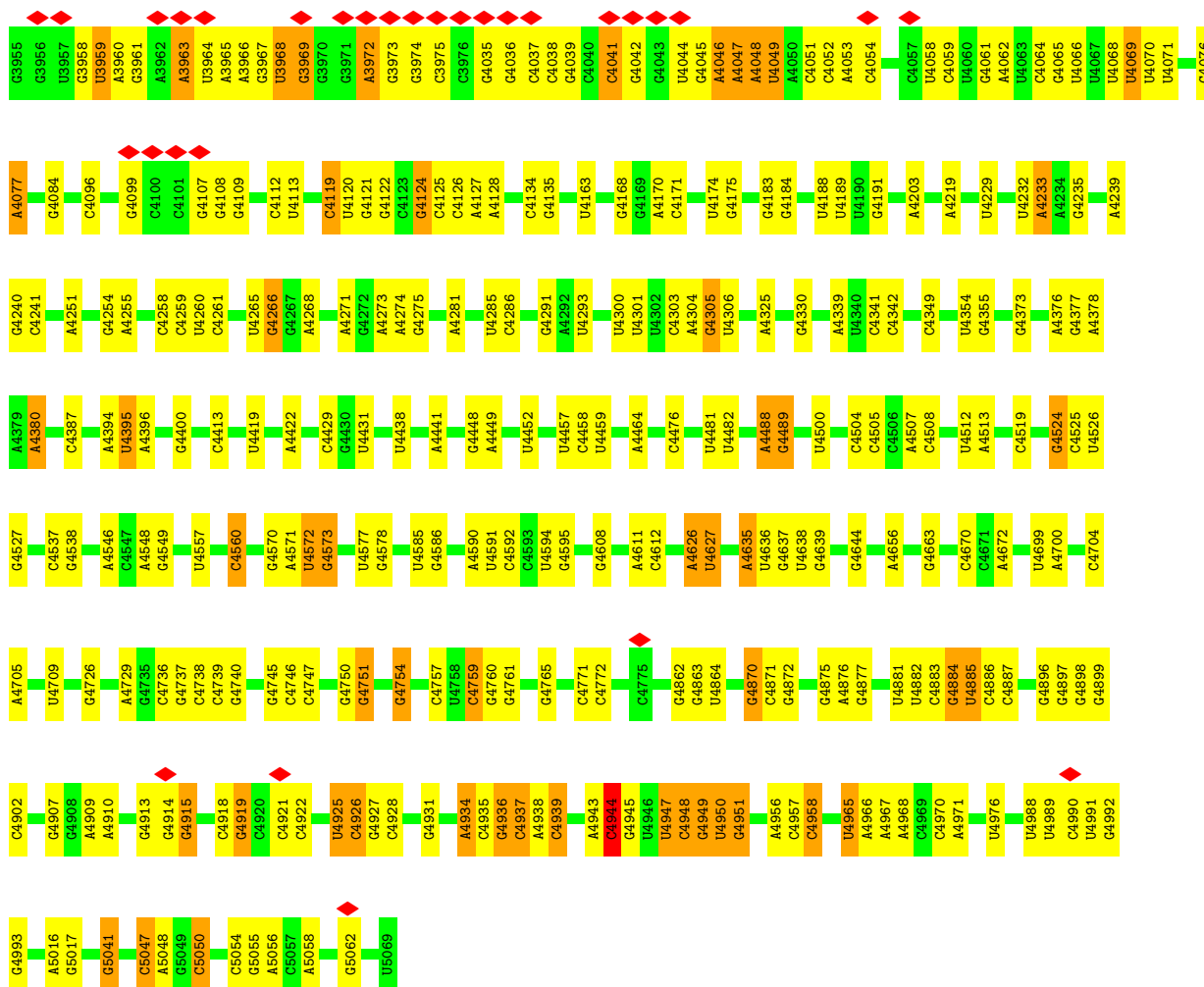
### 3 Residue-property plots [i](#)

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: 28S ribosomal RNA



A3860	A3861	A3862	U2874	G2724	C2571	G2471	C2317	G2079	G1973	U1677	G1529	C1411C
A3867	A3868	A3869	A2894	A2725	C2572	G2474	G2318	G2080	U1974	U1683	A1533	G1416
A3870	A3871	A3872	A2895	G2726	A2573	G2475	G2319	U2080	G1975	U1684	A1534	C1417
A3873	A3874	A3875	C2899	C2727	C2583	G2476	G2320	U2083	G1976	G1733	A1554	G1421
A3876	A3877	A3878	U2900	C2728	A2587	G2477	A2332	A2088	C1977	G1734	G1555	G1426
A3879	A3880	A3881	G3600	C2729	C2588	G2478	G2333	G2089	C1978	G1741	A1558	C1437
A3882	A3883	A3884	C3601	C2730	A2601	G2479	G2334	U2090	U1979	A1742	G1559	U1438
A3885	A3886	A3887	G3602	C2731	C2616	G2480	G2335	G2091	U1980	G1750	A1564	U1440
A3888	A3889	A3889	A3603	A2743	C2617	C2488	G2336	G2092	G1981	U1754	A1565	U1441
A3890	A3891	A3892	G3604	A2744	C2618	C2489	C2340	G2093	A1983	C1755	C1566	C1442
A3893	A3894	A3895	C3605	A2745	G2622	U2490	G2345	C2094	G1982	U1756	U1567	A1443
A3896	A3897	A3898	U3606	G2758	A2627	C2491	G2346	A2097	A1984	U1757	C1568	A1444
A3900	A3901	A3902	A3610	G2759	C2628	C2492	G2347	G2098	C1987	U1761	G1577	U1445
A3903	A3904	A3905	A3611	C2760	U2628	A2502	C2351	G2099	G1988	C1762	U1578	C1446
A3908	A3909	A3910	G3614	U2761	U2632	C2503	G2352	G2100	U1989	C1763	C1447	G1448
A3912	A3913	A3914	G3615	C2762	U2633	C2504	G2353	A2101	A1990	C1764	C1450	C1449
A3915	A3916	A3917	A3624	U2763	C2634	C2505	G2354	G2102	A1991	U1591	U1596	C1451
A3918	A3919	A3920	A3625	A2764	U2635	G2506	A2381	A2103	U1992	G1765	G1455	G1456
A3923	A3924	A3925	G3626	A2765	U2636	A2507	A2382	A2104	C1993	A1766	C1457	C1458
A3928	A3929	A3930	A3627	G2771	C2637	A2511	A2383	G2106	C1996	C1767	G1459	C1461
A3932	A3933	A3934	A3628	C2772	U2638	A2512	A2384	A2107	U1997	C1768	G1602	C1462
A3937	A3938	A3939	U3644	G2773	G2640	A2513	G2387	G2108	G2000	U1770	C1603	C1463
A3942	A3943	A3944	A3645	A2783	A2641	G2516	A2404	G2110	G2001	A1771	G1612	C1472
A3947	A3948	A3949	A3646	C2787	C2647	A2517	G2407	G2259	A2002	U1772	A1613	U1473
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A3953	A3954	A3955	U3648	A2789	C2664	G2521	U2409	G2261	U2004	C1774	G1617	C1476
A3958	A3959	A3960	A3649	U2790	G2665	G2522	G2412	G2262	G2005	A1775	C1628	C1477
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A3968	A3969	A3970	A3651	A2795	A2676	C2539	G2414	A2268	C2007	U1779	G1625	C1479
A3973	A3974	A3975	U3657	A2806	G2686	A2543	U2415	C2269	G2008	A1780	C1629	C1482
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A3988	A3989	A3990	G3672	U2826	A2695	G2546	C2422	G2277	A2012	A1788	G1633	C1485
A3993	A3994	A3995	C3674	G2827	A2696	G2547	A2428	G2278	A2013	C1789	A1634	C1486
A3998	A3999	A4000	U3688	U2828	A2697	A2553	A2431	G2283	C2014	A1802	G1641	U1494
A4003	A4004	A4005	A3692	U2829	G2703	U2554	U2440	G2287	U2015	G1803	G1654	G1495
A4008	A4009	A4010	C3696	C2837	C2705	G2555	C2441	G2288	C2016	A1804	G1655	C1496
A4013	A4014	A4015	U3695	G2855	G2706	G2556	G2455	C2289	A2017	A1805	C1661	G1498
A4018	A4019	A4020	C3697	G2856	U2707	G2557	G2456	U1959	C2018	C1807	C1662	C1502
A4023	A4024	A4025	A3928	C2862	U2708	C2558	G2457	A1961	A2025	C1808	C1663	U1513
A4028	A4029	A4030	G3707	G2863	C2709	G2559	G2458	A1962	A2026	G1818	G1670	U1514
A4033	A4034	A4035	C3708	U2864	C2710	C2563	G2459	A1963	C2020	U1819	U1673	C1674
A4038	A4039	A4040	U3709	G2865	G2711	G2564	G2461	A1964	A2030	U1820	C1675	A1523
A4043	A4044	A4045	G3710	U2866	C2712	A2565	C2462	A1965	C2031	U1821	C1676	C1677
A4048	A4049	A4050	A3711	G2867	C2713	A2566	C2463	C2302	A2042	U1822	C1677	C1678
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A4093	A4094	A4095	G2720	G2721	G2722	G2575	C2472	G2320	U2051	C1686	C1686	C1687
A4098	A4099	A4100	G2721	G2722	G2723	G2576	C2473	G2321	U2052	C1687	C1687	C1688
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A4153	A4154	A4155	G2732	G2733	G2734	G2587	C2484	G2332	U2063	C1698	C1698	C1699
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A4203	A4204	A4205	G2742	G2743	G2744	G2597	C2494	G2342	U2073	C1708	C1708	C1709
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A4228	A4229	A4230	G2747	G2748	G2749	G2602	C2499	G2347	U2078	C1713	C1713	C1714
A4233	A4234	A4235	G2748	G2749	G2750	G2603	C2500	G2348	U2079	C1714	C1714	C1715
A4238	A4239	A4240	G2749	G2750	G2751	G2604	C2501	G2349	U2080	C1715	C1715	C1716
A4243	A4244	A4245	G2750	G2751	G2752	G2605	C2502	G2350	U2081	C1716	C1716	C1717
A4248	A4249	A4250	G2751	G2752	G2753	G2606	C2503	G2351	U2082	C1717	C1717	C1718
A4253	A4254	A4255	G2752	G2753	G2754	G2607	C2504	G2352	U2083	C1718	C1718	C1719
A4258	A4259	A4260	G2753	G2754	G2755	G2608	C2505	G2353	U2084	C1719	C1719	C1720
A4263	A4264	A4265	G2754	G2755	G2756	G2609	C2506	G2354	U2085	C1720	C1720	C1721
A4268	A4269	A4270	G2755	G2756	G2757	G2610	C2507	G2355	U2086	C1721	C1721	C1722
A4273	A4274	A4275	G2756	G2757	G2758	G2611	C2508	G2356	U2087	C1722	C1722	C1723
A4278	A4279	A4280	G2757	G2758	G2759	G2612	C2509	G2357	U2088	C1723	C1723	C1724
A4283	A4284	A4285	G2758	G2759	G2760	G2613	C2510	G2358	U2089	C1724	C1724	C1725
A4288	A4289	A4290	G2759	G2760	G2761	G2614	C2511	G2359	U2090	C1725	C1725	C1726
A4293	A4294	A4295	G2760	G2761	G2762	G2615	C2512	G2360	U2091	C1726	C1726	C1727
A4298	A4299	A4300	G2761	G2762	G2763	G2616	C2513	G2361	U2092	C1727	C1727	C1728
A4303	A4304	A4305	G2762	G2763	G2764	G2617	C2514	G2362	U2093	C1728	C1728	C1729
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A4318	A4319	A4320	G2765	G2766	G2767	G2620	C2517	G2365	U2096	C1731	C1731	C1732
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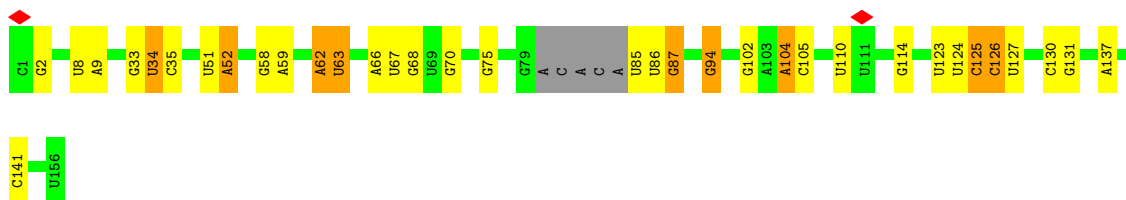
• Molecule 2: 5S ribosomal RNA

Chain 7: 88% 11%



• Molecule 3: 5.8S ribosomal RNA

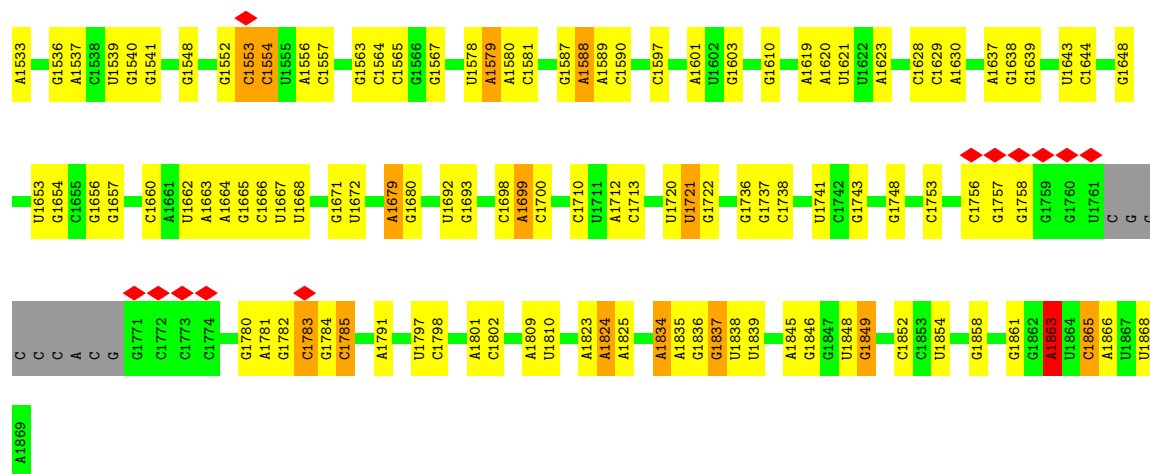
Chain 8: 74% 17% 6%



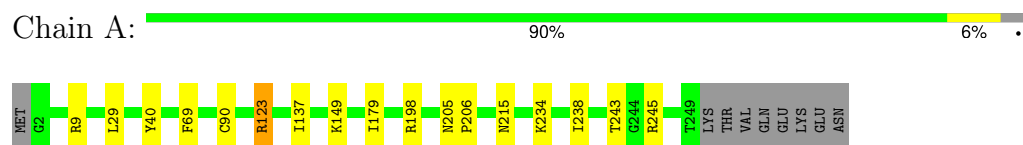
• Molecule 4: 18S ribosomal RNA

Chain 9: 61% 25% 9%

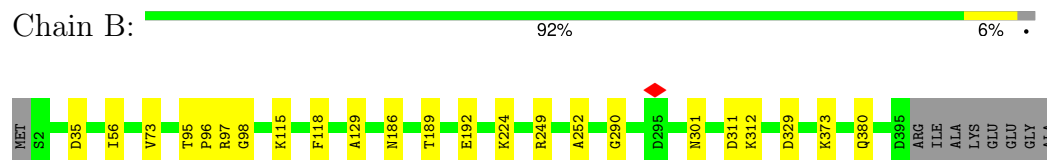




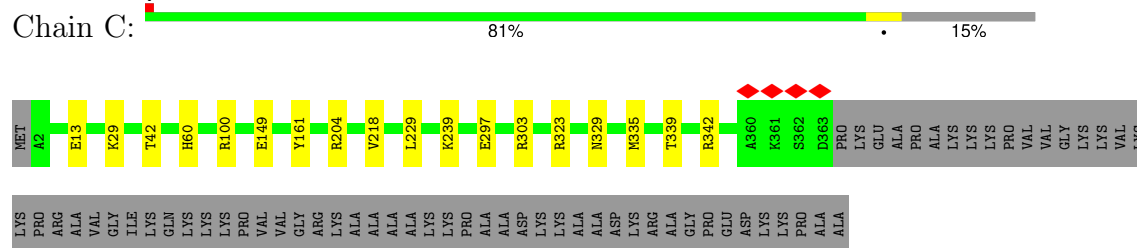
- Molecule 5: Ribosomal protein L8



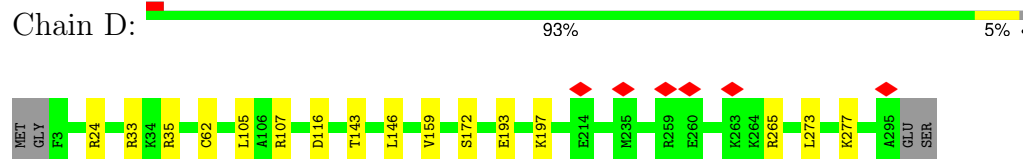
- Molecule 6: Ribosomal protein L3



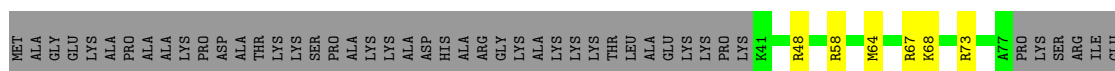
- Molecule 7: 60S ribosomal protein L4



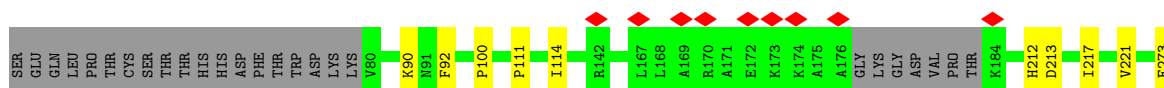
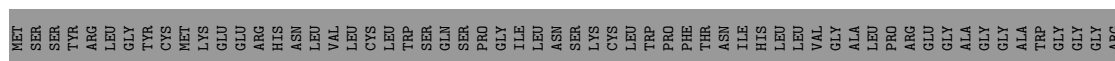
- Molecule 8: Large ribosomal subunit protein uL18



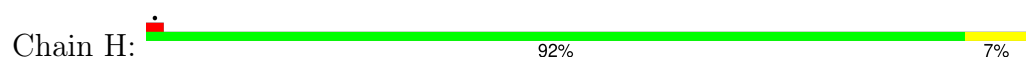
- Molecule 9: 60S ribosomal protein L6



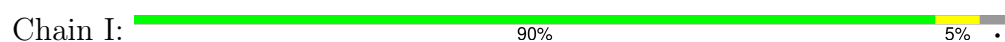
- Molecule 10: 60S ribosomal protein L7a



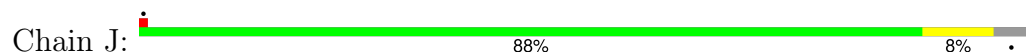
- Molecule 11: 60S ribosomal protein L9



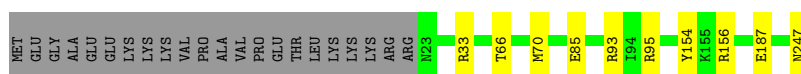
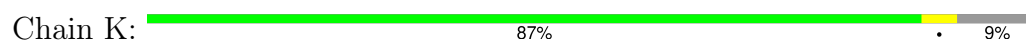
- Molecule 12: 60S ribosomal protein L10



- Molecule 13: Ribosomal protein L11



- Molecule 14: 60S ribosomal protein L7



- Molecule 15: 60S ribosomal protein L13



Number of genes

Category	Number of genes
MET	10
A2	15
G7	20
R36	25
P62	30
T63	35
R71	40
R74	45
R101	50
R116	55
R121	60
F127	65
K136	70
M155	75
K165	80
Q205	85
E208	90
K209	95
K210	100
K211	100

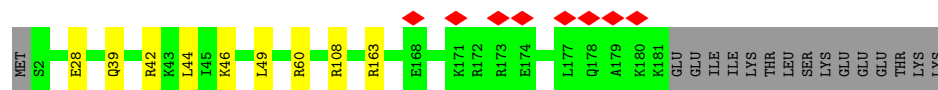
- [illegible]

- | MET  |
|------|
| G2   |
| A3   |
| Y4   |
| K14  |
| L33  |
| R38  |
| A39  |
| P40  |
| R49  |
| R65  |
| R68  |
| R73  |
| R108 |
| L113 |
| F138 |
| V155 |
| M161 |
| R162 |
| H178 |
| H181 |
| R189 |
| W192 |
| R202 |
| P203 |
| P204 |

- | MET  | ALA  | GLU  | GLY  |
|------|------|------|------|
| Q5   | D10  | R37  | R49  |
| R61  | I79  | T83  | P110 |
| Q173 | R176 | A181 | V185 |
| T193 | H199 | V203 |      |

- | MET  |
|------|
| V2   |
| R30  |
| E31  |
| G38  |
| N39  |
| K54  |
| W63  |
| P84  |
| K85  |
| E89  |
| I114 |
| R127 |
| R135 |
| E154 |
| GLN  |
| ILE  |
| VAL  |
| PRO  |
| LYS  |
| PRQ  |
| PRQ  |
| GIU  |
| GIU  |
| GIU  |
| VAL  |
| ALA  |
| ALA  |
| GLN  |
| LYS  |
| LYS  |
| LYS  |
| I LE |
| SER  |
| GLN  |
| LYS  |
| LYS  |
| LEU  |
| LYS  |
| LYS  |
| GLN  |
| LYS  |
| LEU  |
| MET  |
| ALA  |
| ARG  |
| GIU  |

- 
- | Amino Acid | Color  |
|------------|--------|
| MET        | Grey   |
| G2         | Green  |
| R14        | Yellow |
| R15        | Yellow |
| K16        | Yellow |
| R33        | Yellow |
| N40        | Yellow |
| D89        | Yellow |
| R108       | Yellow |
| L128       | Yellow |
| F152       | Yellow |
| G153       | Green  |
| K154       | Yellow |
| T158       | Yellow |
| R181       | Yellow |
| N188       | Green  |



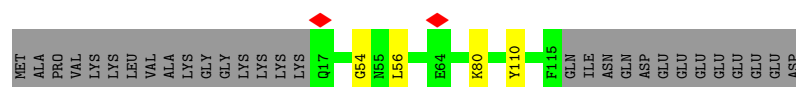
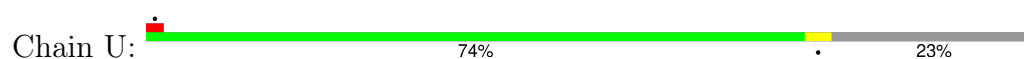
- Molecule 22: 60S ribosomal protein L18a



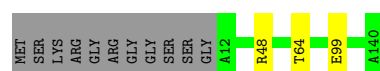
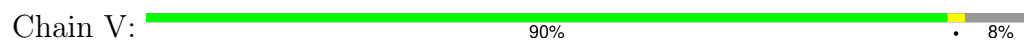
- Molecule 23: eL21



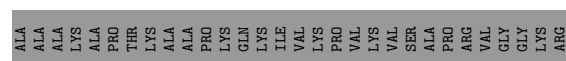
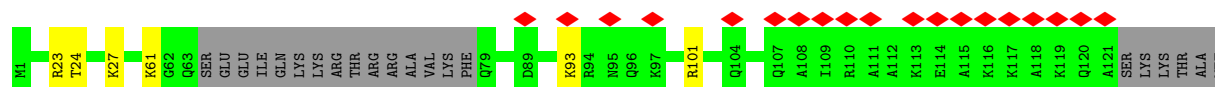
- Molecule 24: eL22



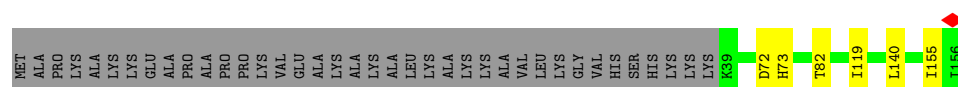
- Molecule 25: Ribosomal protein L23




- Molecule 26: eL24



- Molecule 27: eL23



- Molecule 34: Ribosomal protein L32

Chain e:  88% 7% 5%



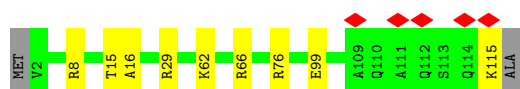
- Molecule 35: eL33

Chain f:  94% 5%



- Molecule 36: Large ribosomal subunit protein eL34

Chain g:  91% 8%



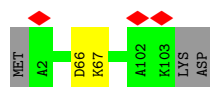
- Molecule 37: eL35

Chain h:  97%



- Molecule 38: 60S ribosomal protein L36

Chain i:  95%




- Molecule 39: eL38

Chain k:  94%

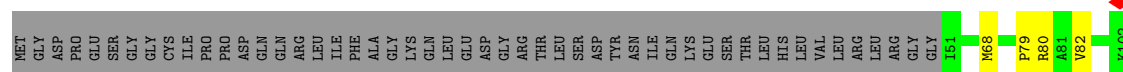


- Molecule 40: eL39

Chain l:  82% 16%



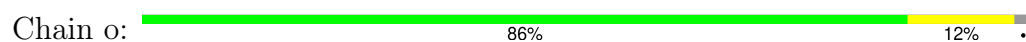
- Molecule 41: Ubiquitin A-52 residue ribosomal protein fusion product 1



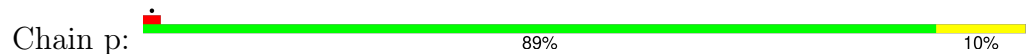
- Molecule 42: eL41



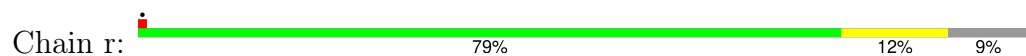
- Molecule 43: Large ribosomal subunit protein eL42



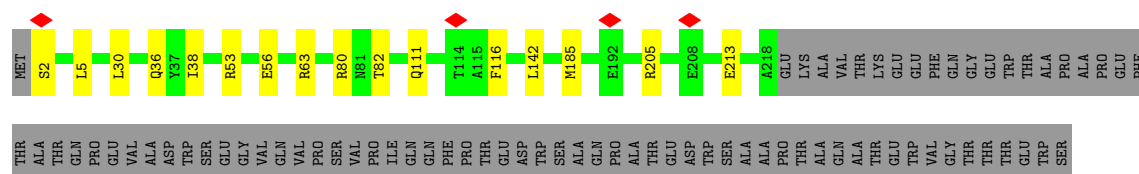
- Molecule 44: eL43



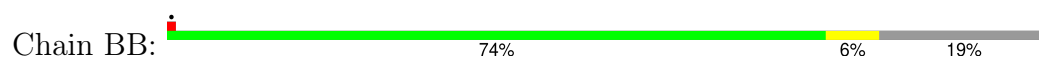
- Molecule 45: eL28

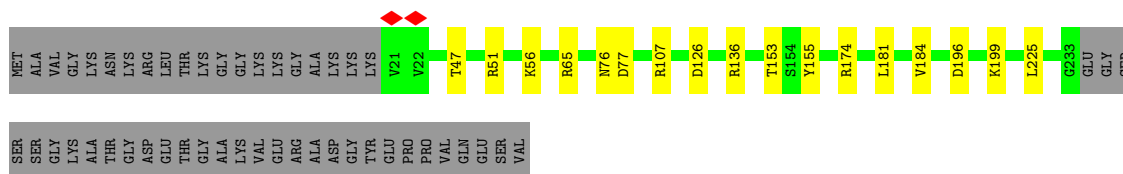


- Molecule 46: uS2 (SA)

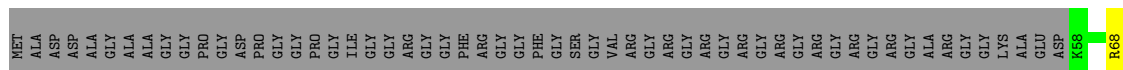


- Molecule 47: 40S ribosomal protein S3a

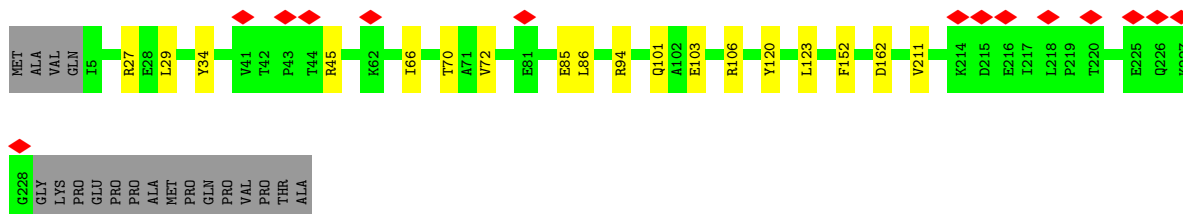
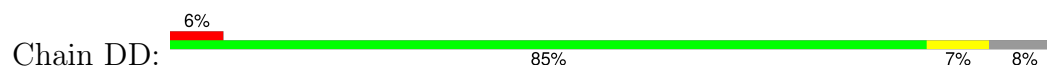




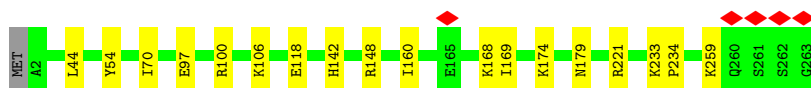
- Molecule 48: Small ribosomal subunit protein uS5



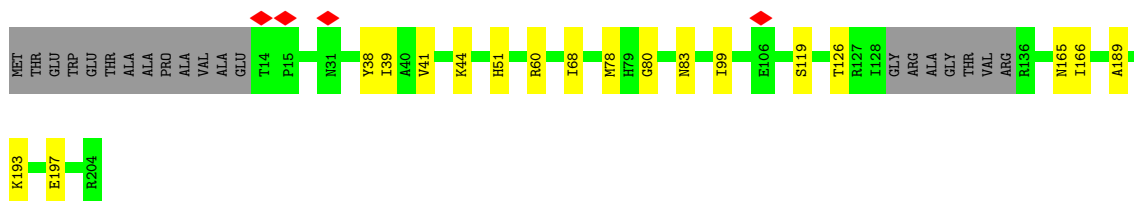
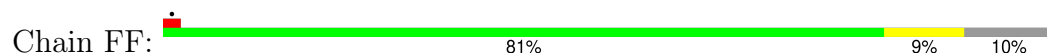
- Molecule 49: Ribosomal protein S3



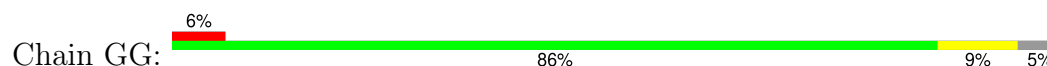
- Molecule 50: eS4 (S4 X isoform)

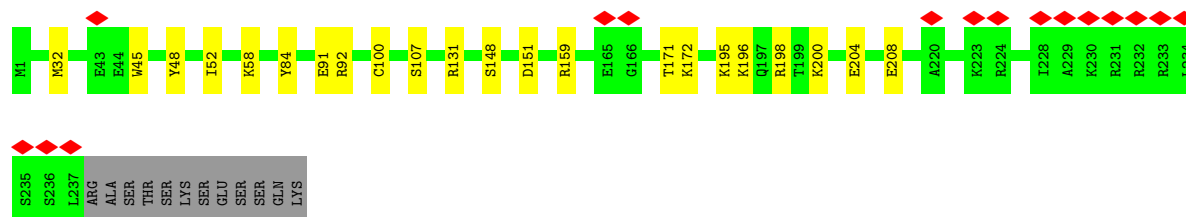


- Molecule 51: Ribosomal protein S5

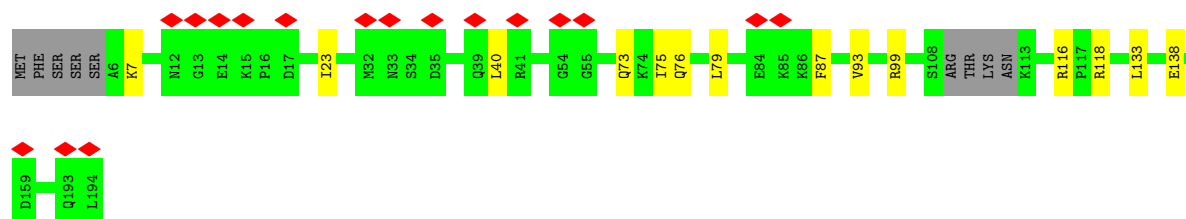
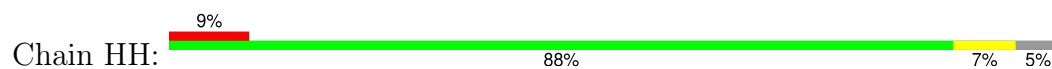


- Molecule 52: 40S ribosomal protein S6

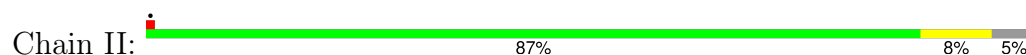




- Molecule 53: 40S ribosomal protein S7



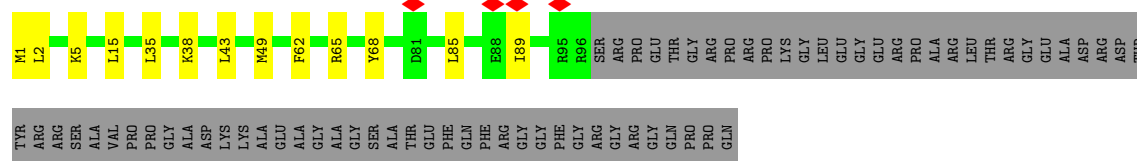
- Molecule 54: 40S ribosomal protein S8



- Molecule 55: Ribosomal protein S9 (Predicted)



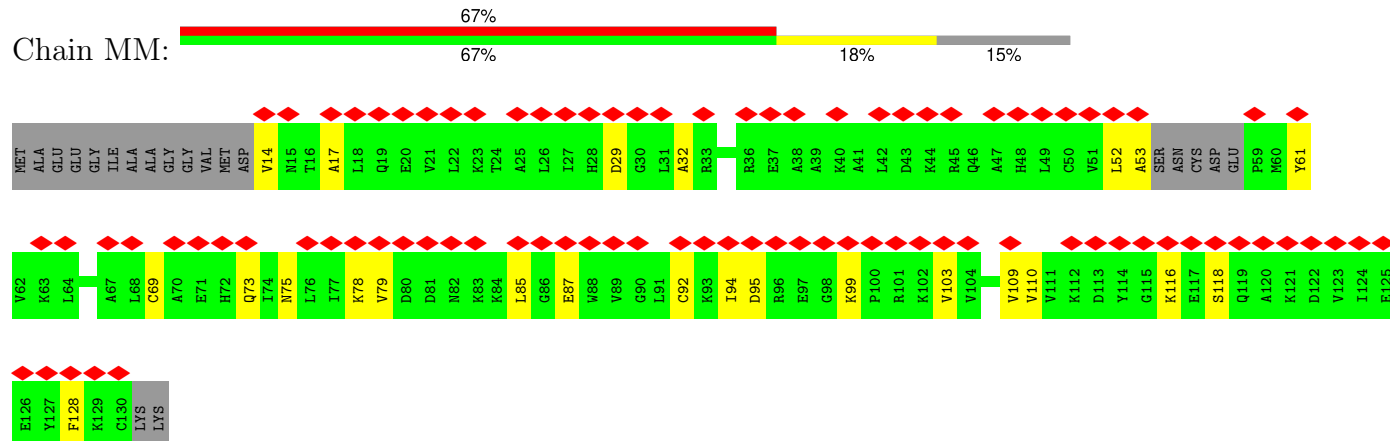
- Molecule 56: S10\_ plectin domain-containing protein



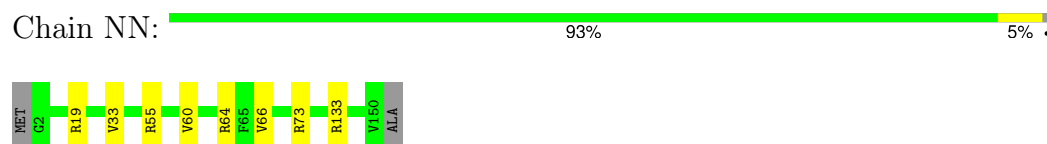
- Molecule 57: Ribosomal protein S11



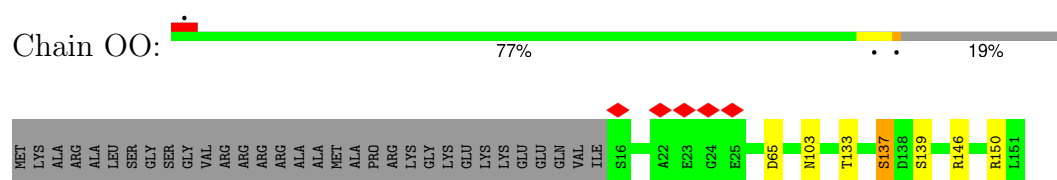
- Molecule 58: 40S ribosomal protein S12



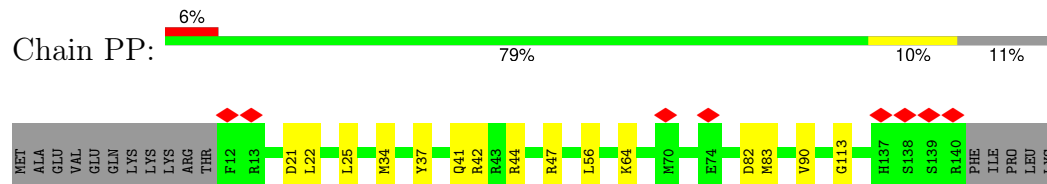
- Molecule 59: Ribosomal protein S13



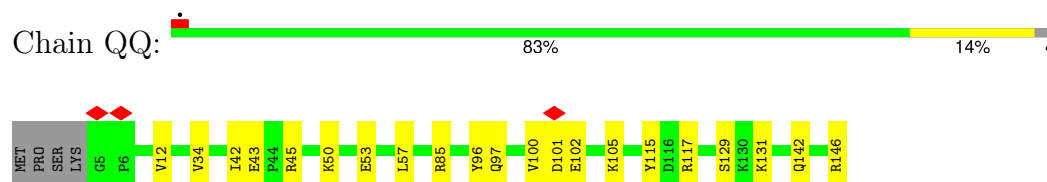
- Molecule 60: Small ribosomal subunit protein uS11



- Molecule 61: uS19



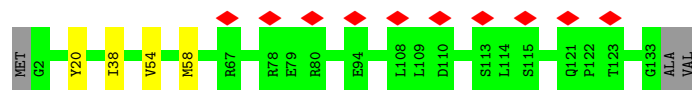
- Molecule 62: uS9



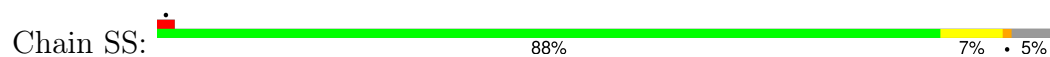
- Molecule 63: eS17



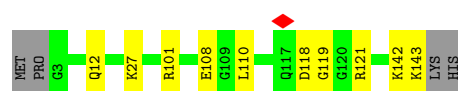




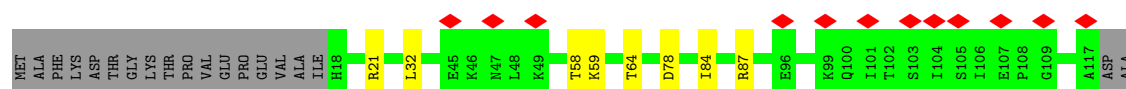
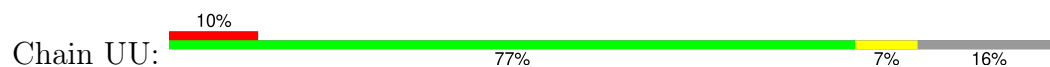
- Molecule 64: uS13



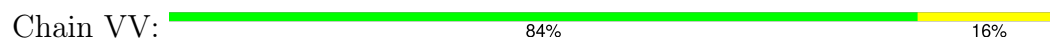
- Molecule 65: eS19



- Molecule 66: uS10



- Molecule 67: eS21



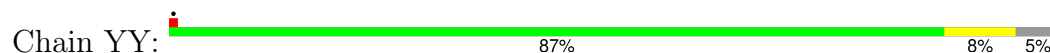
- Molecule 68: Ribosomal protein S15a

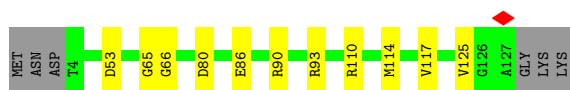


- Molecule 69: uS12

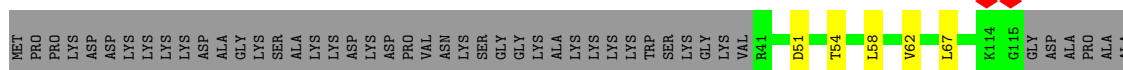


- Molecule 70: 40S ribosomal protein S24

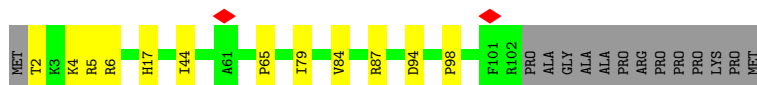
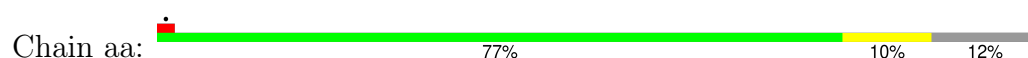




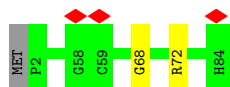
• Molecule 71: eS25



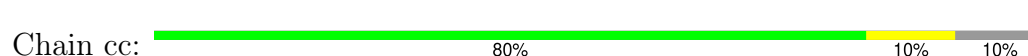
• Molecule 72: 40S ribosomal protein S26



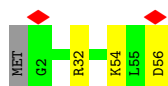
• Molecule 73: 40S ribosomal protein S27



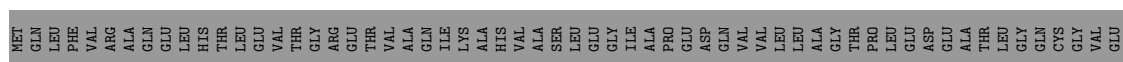
• Molecule 74: Ribosomal protein S28



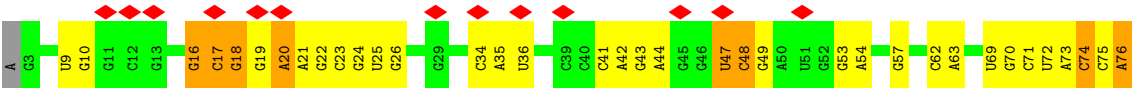
• Molecule 75: eS29



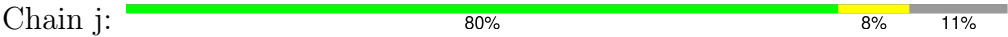
• Molecule 76: 40S ribosomal protein S30







● Molecule 81: Ribosomal protein L37



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	11317	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	30.0165	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.111	Depositor
Minimum map value	-0.031	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	464.8, 464.8, 464.8	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.162, 1.162, 1.162	Depositor

## 5 Model quality

### 5.1 Standard geometry

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

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	5	0.46	0/86380	0.68	14/134721 (0.0%)
2	7	0.45	0/2836	0.63	0/4421
3	8	0.44	0/3581	0.63	0/5577
4	9	0.43	0/40509	0.66	5/63128 (0.0%)
5	A	0.35	0/1936	0.53	0/2596
6	B	0.34	0/3240	0.53	0/4339
7	C	0.34	0/2937	0.52	0/3946
8	D	0.30	0/2437	0.48	0/3264
9	E	0.30	0/1762	0.53	0/2362
10	G	0.30	0/1910	0.55	0/2569
11	H	0.32	0/1535	0.51	0/2063
12	I	0.32	0/1702	0.51	0/2272
13	J	0.28	0/1385	0.51	0/1852
14	K	0.36	0/1911	0.53	0/2549
15	L	0.32	0/1733	0.49	0/2316
16	M	0.32	0/1158	0.48	0/1547
17	N	0.38	0/1746	0.54	0/2338
18	O	0.36	0/1662	0.55	1/2222 (0.0%)
19	P	0.34	0/1268	0.51	0/1700
20	Q	0.37	0/1539	0.55	0/2054
21	R	0.33	0/1524	0.52	0/2013
22	S	0.36	0/1501	0.45	0/2012
23	T	0.34	0/1326	0.53	0/1770
24	U	0.28	0/823	0.56	0/1104
25	V	0.33	0/983	0.50	0/1319
26	W	0.29	0/873	0.51	0/1158
27	X	0.31	0/984	0.53	0/1323
28	Y	0.32	0/1132	0.52	0/1504
29	Z	0.32	0/1130	0.46	0/1507
30	a	0.35	0/1191	0.53	0/1590
31	b	0.30	0/819	0.54	0/1081
32	c	0.33	0/771	0.49	0/1034

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	d	0.35	0/903	0.57	0/1216
34	e	0.37	0/1071	0.55	0/1429
35	f	0.37	0/895	0.49	0/1198
36	g	0.34	0/916	0.57	0/1220
37	h	0.30	0/1021	0.52	0/1348
38	i	0.29	0/841	0.52	0/1112
39	k	0.27	0/575	0.51	0/761
40	l	0.36	0/459	0.55	0/608
41	m	0.32	0/435	0.49	0/575
42	n	0.38	0/241	0.66	0/305
43	o	0.32	0/864	0.51	0/1140
44	p	0.37	0/718	0.60	0/953
45	r	0.34	0/1010	0.54	0/1354
46	AA	0.30	0/1747	0.49	0/2374
47	BB	0.30	0/1756	0.54	0/2350
48	CC	0.32	0/1753	0.51	0/2369
49	DD	0.25	0/1767	0.47	0/2378
50	EE	0.31	0/2118	0.50	0/2849
51	FF	0.28	0/1481	0.51	0/1991
52	GG	0.24	0/1946	0.51	0/2590
53	HH	0.24	0/1511	0.50	0/2022
54	II	0.31	0/1655	0.51	0/2205
55	JJ	0.32	0/1533	0.53	0/2047
56	KK	0.25	0/834	0.46	0/1125
57	LL	0.34	0/1195	0.50	0/1597
58	MM	0.19	0/880	0.55	0/1179
59	NN	0.32	0/1226	0.53	0/1649
60	OO	0.32	0/1029	0.54	0/1380
61	PP	0.24	0/1079	0.56	0/1441
62	QQ	0.29	0/1146	0.53	0/1534
63	RR	0.25	0/1082	0.47	0/1452
64	SS	0.27	0/1208	0.53	0/1618
65	TT	0.26	0/1115	0.54	0/1493
66	UU	0.25	0/805	0.48	0/1081
67	VV	0.31	0/644	0.47	0/860
68	WW	0.35	0/1051	0.48	0/1406
69	XX	0.32	0/1105	0.54	0/1476
70	YY	0.26	0/1028	0.49	0/1366
71	ZZ	0.24	0/604	0.48	0/810
72	aa	0.32	0/828	0.54	0/1109
73	bb	0.28	0/665	0.51	0/891
74	cc	0.27	0/490	0.39	0/656
75	dd	0.30	0/470	0.53	0/623

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
76	ee	0.28	0/447	0.60	0/587
77	ff	0.18	0/567	0.51	0/753
78	gg	0.21	0/2493	0.48	0/3394
79	10	0.39	0/261	0.63	0/404
80	11	0.27	0/1773	0.67	0/2763
80	13	0.33	0/1773	0.64	0/2763
81	j	0.36	0/720	0.57	0/952
All	All	0.40	0/229958	0.62	20/338007 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	5	0	1
5	A	0	1
7	C	0	1
8	D	0	3
9	E	0	1
11	H	0	1
12	I	0	1
15	L	0	1
17	N	0	1
18	O	0	2
22	S	0	1
23	T	0	1
25	V	0	1
28	Y	0	1
29	Z	0	1
35	f	0	1
36	g	0	1
41	m	0	1
47	BB	0	1
50	EE	0	2
54	II	0	3
55	JJ	0	1
59	NN	0	1
60	OO	0	1
64	SS	0	1
70	YY	0	1
All	All	0	32



There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	1440	U	C2'-C3'-O3'	6.64	119.47	109.50
4	9	889	U	N1-C1'-C2'	6.18	121.28	112.00
1	5	4944	C	C1'-O4'-C4'	-6.16	103.74	109.90
1	5	275	C	C2'-C3'-O3'	5.92	122.58	113.70
4	9	1863	A	C1'-O4'-C4'	-5.79	103.91	109.70
4	9	543	C	C1'-O4'-C4'	-5.66	104.04	109.70
1	5	914	U	C2'-C3'-O3'	5.64	117.96	109.50
4	9	1396	A	C2'-C3'-O3'	5.52	117.78	109.50
1	5	2089	G	C2'-C3'-O3'	5.46	117.69	109.50
1	5	2007	G	N9-C1'-C2'	5.43	120.14	112.00
1	5	4119	C	C2'-C3'-O3'	5.43	117.65	109.50
1	5	3876	A	C2'-C3'-O3'	5.43	117.64	109.50
18	O	110	PRO	N-CA-C	5.43	117.32	110.70
1	5	3710	G	O4'-C1'-N9	5.42	116.33	108.20
4	9	180	G	N9-C1'-C2'	5.42	120.13	112.00
1	5	1236	C	C4'-C3'-O3'	5.38	121.08	113.00
1	5	1370	G	C4'-C3'-O3'	5.30	117.36	109.40
1	5	1916	G	N9-C1'-C2'	5.30	119.95	112.00
1	5	1891	A	N9-C1'-C2'	5.20	119.80	112.00
1	5	1818	G	C2'-C3'-O3'	5.17	117.26	109.50

There are no chirality outliers.

All (32) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	5	216	C	Sidechain
5	A	123	ARG	Sidechain
47	BB	51	ARG	Sidechain
7	C	204	ARG	Sidechain
8	D	24	ARG	Sidechain
8	D	265	ARG	Sidechain
8	D	33	ARG	Sidechain
9	E	144	ARG	Sidechain
50	EE	148	ARG	Sidechain
50	EE	221	ARG	Sidechain
11	H	173	ARG	Sidechain
12	I	128	ARG	Sidechain
54	II	5	ARG	Sidechain
54	II	56	ARG	Sidechain
54	II	74	ARG	Sidechain

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Mol	Chain	Res	Type	Group
55	JJ	38	ARG	Sidechain
15	L	121	ARG	Sidechain
17	N	73	ARG	Sidechain
59	NN	55	ARG	Sidechain
18	O	49	ARG	Sidechain
18	O	61	ARG	Sidechain
60	OO	137	SER	Peptide
22	S	95	ARG	Sidechain
64	SS	132	ARG	Sidechain
23	T	136	ARG	Sidechain
25	V	48	ARG	Sidechain
28	Y	115	ARG	Sidechain
70	YY	65	GLY	Peptide
29	Z	65	ARG	Sidechain
35	f	100	ARG	Sidechain
36	g	8	ARG	Sidechain
41	m	80	ARG	Sidechain

## 5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	5	77221	0	39013	592	0
2	7	2538	0	1286	6	0
3	8	3208	0	1629	21	0
4	9	36229	0	18300	297	0
5	A	1898	0	1993	12	0
6	B	3172	0	3310	16	0
7	C	2883	0	3053	17	0
8	D	2391	0	2424	7	0
9	E	1729	0	1887	14	0
10	G	1879	0	2027	8	0
11	H	1516	0	1597	7	0
12	I	1664	0	1712	11	0
13	J	1362	0	1399	10	0
14	K	1875	0	1995	7	0
15	L	1702	0	1820	9	0
16	M	1137	0	1211	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	N	1701	0	1749	16	0
18	O	1630	0	1778	7	0
19	P	1242	0	1274	7	0
20	Q	1515	0	1634	9	0
21	R	1508	0	1664	8	0
22	S	1462	0	1508	7	0
23	T	1298	0	1366	8	0
24	U	809	0	833	2	0
25	V	969	0	1031	2	0
26	W	860	0	903	4	0
27	X	967	0	1040	3	0
28	Y	1115	0	1205	6	0
29	Z	1107	0	1182	2	0
30	a	1162	0	1209	13	0
31	b	806	0	866	4	0
32	c	761	0	794	1	0
33	d	888	0	930	3	0
34	e	1053	0	1147	6	0
35	f	876	0	912	5	0
36	g	906	0	998	8	0
37	h	1013	0	1147	3	0
38	i	830	0	916	1	0
39	k	569	0	637	2	0
40	l	447	0	480	8	0
41	m	429	0	465	2	0
42	n	240	0	289	1	0
43	o	851	0	920	9	0
44	p	708	0	756	9	0
45	r	994	0	1051	12	0
46	AA	1710	0	1708	11	0
47	BB	1729	0	1803	10	0
48	CC	1716	0	1806	8	0
49	DD	1739	0	1832	14	0
50	EE	2076	0	2177	9	0
51	FF	1460	0	1509	15	0
52	GG	1923	0	2089	16	0
53	HH	1489	0	1582	9	0
54	II	1628	0	1706	12	0
55	JJ	1508	0	1626	8	0
56	KK	810	0	836	8	0
57	LL	1175	0	1249	6	0
58	MM	871	0	913	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	NN	1202	0	1289	6	0
60	OO	1016	0	1039	6	0
61	PP	1058	0	1104	11	0
62	QQ	1128	0	1195	19	0
63	RR	1068	0	1121	3	0
64	SS	1190	0	1249	8	0
65	TT	1097	0	1132	7	0
66	UU	795	0	862	9	0
67	VV	637	0	637	10	0
68	WW	1034	0	1080	2	0
69	XX	1087	0	1154	11	0
70	YY	1011	0	1083	9	0
71	ZZ	598	0	656	3	0
72	aa	814	0	867	11	0
73	bb	651	0	672	2	0
74	cc	488	0	514	5	0
75	dd	459	0	448	3	0
76	ee	443	0	492	6	0
77	ff	555	0	567	9	0
78	gg	2436	0	2393	16	0
79	10	234	0	118	4	0
80	11	1585	0	804	28	0
80	13	1585	0	803	29	0
81	j	705	0	737	8	0
82	5	10	0	19	1	0
83	dd	1	0	0	0	0
83	g	1	0	0	0	0
83	j	1	0	0	0	0
83	m	1	0	0	0	0
83	o	1	0	0	0	0
83	p	1	0	0	0	0
84	11	31	0	11	1	0
84	13	31	0	11	2	0
85	13	8	0	8	0	0
All	All	213916	0	158241	1320	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (1320) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:980:U:H3	1:5:1275:G:H1	1.09	0.99
1:5:2638:G:N2	1:5:2697:A:N1	2.12	0.98
1:5:4039:G:N7	1:5:4041:C:N4	2.27	0.82
74:cc:44:ARG:NH2	74:cc:60:GLU:O	2.12	0.82
4:9:1272:C:O2'	4:9:1274:G:N2	2.11	0.82
4:9:1308:U:H2'	4:9:1309:C:C6	2.15	0.81
1:5:973:G:N2	1:5:1282:G:N7	2.29	0.80
1:5:3692:A:H62	1:5:3823:G:H21	1.28	0.80
1:5:2262:G:OP2	45:r:98:ARG:NH2	2.14	0.80
4:9:925:G:H1	4:9:1017:U:H3	1.30	0.79
1:5:2395:A:O2'	1:5:2806:A:H1'	1.85	0.77
53:HH:7:LYS:NZ	53:HH:40:LEU:O	2.17	0.77
1:5:2457:G:H21	1:5:3672:G:H21	1.33	0.77
4:9:562:U:OP1	55:JJ:134:HIS:NE2	2.17	0.76
1:5:980:U:OP2	9:E:68:LYS:NZ	2.18	0.76
4:9:952:G:OP1	47:BB:56:LYS:NZ	2.17	0.76
79:10:13:A:H61	80:11:34:C:N4	1.84	0.75
1:5:982:U:H3	1:5:1273:G:H1	1.34	0.75
1:5:2313:A:O2'	1:5:2314:G:OP1	2.03	0.75
1:5:4751:G:H1	1:5:4948:C:H5	1.33	0.75
4:9:1296:U:O2	4:9:1303:C:N4	2.20	0.75
1:5:3751:G:H21	1:5:3775:A:H8	1.34	0.75
1:5:1764:G:H8	1:5:1767:A:H62	1.34	0.75
65:TT:142:LYS:HE3	65:TT:143:LYS:HE3	1.69	0.75
1:5:691:C:H2'	1:5:692:A:C8	2.22	0.75
1:5:4305:G:H22	23:T:87:LYS:NZ	1.85	0.75
46:AA:36:GLN:O	46:AA:53:ARG:NH1	2.20	0.75
1:5:976:G:H21	7:C:323:ARG:HE	1.33	0.74
4:9:730:C:H2'	4:9:731:G:C8	2.23	0.74
1:5:4431:U:OP2	12:I:3:ARG:NH2	2.20	0.74
53:HH:138:GLU:OE2	59:NN:19:ARG:NH1	2.22	0.73
4:9:168:C:OP1	52:GG:131:ARG:NH1	2.19	0.73
1:5:2647:A:H62	1:5:2686:G:H8	1.37	0.73
4:9:1192:U:OP2	69:XX:119:ARG:NH2	2.21	0.72
1:5:2837:U:OP1	6:B:249:ARG:NH1	2.21	0.72
80:11:16:G:OP2	80:11:17:C:N4	2.22	0.72
54:II:139:LYS:O	54:II:141:ARG:NH1	2.23	0.72
1:5:1555:G:O6	44:p:4:ARG:NH2	2.23	0.72
4:9:1305:C:OP2	77:ff:93:HIS:ND1	2.21	0.71
25:V:99:GLU:HB3	26:W:24:THR:HG23	1.71	0.71
13:J:114:ASP:OD2	64:SS:14:ARG:NH1	2.23	0.71
8:D:107:ARG:NH2	8:D:116:ASP:OD1	2.23	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J:151:ILE:HD11	13:J:156:ARG:HG2	1.73	0.70
4:9:536:A:H61	4:9:547:G:H1	1.36	0.70
1:5:456:C:H2'	1:5:457:G:H8	1.56	0.70
68:WW:6:VAL:HG12	68:WW:34:ILE:HD11	1.74	0.70
1:5:262:G:H2'	1:5:263:G:H8	1.57	0.70
1:5:4635:A:H8	1:5:5048:A:H61	1.40	0.70
1:5:2457:G:H21	1:5:3672:G:N2	1.90	0.69
1:5:1441:C:H2'	1:5:1442:C:C6	2.28	0.69
61:PP:44:ARG:HH12	61:PP:82:ASP:HB2	1.57	0.69
1:5:4925:U:H4'	1:5:4926:C:H5'	1.75	0.68
1:5:1177:U:H2'	1:5:1178:G:C8	2.28	0.68
4:9:1664:A:O2'	4:9:1666:C:N4	2.23	0.68
1:5:3717:A:H2'	1:5:3718:A:C8	2.28	0.68
1:5:3860:A:H61	1:5:4560:C:H5	1.41	0.68
4:9:1228:A:H2'	4:9:1229:G:C8	2.28	0.68
4:9:730:C:H2'	4:9:731:G:H8	1.57	0.68
1:5:260:C:H2'	1:5:261:G:H8	1.59	0.68
4:9:1854:U:OP1	60:OO:150:ARG:NH2	2.26	0.68
9:E:157:THR:HG23	9:E:158:GLY:H	1.59	0.67
1:5:2489:C:O2'	1:5:2491:C:N4	2.27	0.67
1:5:1577:G:OP1	44:p:17:ARG:NH1	2.27	0.67
1:5:1502:G:H22	30:a:77:LYS:HD3	1.60	0.67
28:Y:54:GLU:OE1	28:Y:108:ARG:NH1	2.25	0.67
70:YY:117:VAL:HG21	70:YY:125:VAL:HG21	1.75	0.67
1:5:2553:A:H2	1:5:2765:A:H62	1.42	0.67
62:QQ:146:ARG:NH2	80:13:33:C:OP2	2.27	0.66
80:11:43:G:H2'	80:11:44:A:C8	2.30	0.66
1:5:270:U:H2'	1:5:271:C:C6	2.30	0.66
4:9:857:U:H2'	4:9:858:A:C8	2.30	0.66
80:13:63:A:H2'	80:13:64:U:C6	2.31	0.66
1:5:62:A:N3	1:5:77:U:O2'	2.25	0.66
1:5:2407:G:O6	40:l:2:SER:N	2.28	0.66
5:A:234:LYS:HG2	5:A:238:ILE:HD12	1.77	0.66
1:5:2478:C:H2'	1:5:2479:G:C8	2.31	0.66
4:9:555:A:H61	4:9:589:G:H21	1.43	0.65
79:10:22:U:O4	79:10:23:A:N6	2.30	0.65
4:9:1834:A:H2	4:9:1837:G:H1	1.42	0.65
1:5:456:C:H2'	1:5:457:G:C8	2.30	0.65
1:5:1198:G:H2'	1:5:1199:G:C8	2.32	0.65
1:5:1370:G:O6	7:C:239:LYS:NZ	2.27	0.65
4:9:1667:U:H2'	4:9:1668:U:C6	2.32	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:2431:A:OP1	40:l:41:ARG:NH1	2.28	0.65
49:DD:123:LEU:HD11	49:DD:152:PHE:HB3	1.77	0.65
69:XX:63:ASN:ND2	69:XX:114:ASP:OD1	2.27	0.65
49:DD:70:THR:HG22	49:DD:86:LEU:HD13	1.77	0.65
1:5:978:G:H22	1:5:1277:G:H1	1.45	0.65
1:5:4096:C:H5''	36:g:115:LYS:HE3	1.79	0.65
1:5:1405:C:H2'	1:5:1406:G:H8	1.60	0.65
4:9:1438:A:H2'	4:9:1439:A:C8	2.31	0.65
9:E:185:ASN:ND2	9:E:274:LEU:O	2.30	0.64
65:TT:142:LYS:HG3	65:TT:143:LYS:HG3	1.77	0.64
58:MM:52:LEU:HD23	58:MM:78:LYS:HE2	1.78	0.64
1:5:4635:A:H2	1:5:4663:G:H21	1.44	0.64
16:M:119:ARG:NH1	18:O:193:THR:OG1	2.29	0.64
1:5:4126:C:OP1	10:G:90:LYS:NZ	2.29	0.64
78:gg:254:PRO:HA	78:gg:285:GLN:HA	1.78	0.64
1:5:2477:A:H2'	1:5:2478:C:C6	2.32	0.64
1:5:4300:U:OP1	23:T:87:LYS:NZ	2.30	0.64
2:7:40:U:O2	13:J:75:ARG:NH1	2.30	0.64
1:5:3641:U:H5	1:5:3646:A:N7	1.95	0.64
12:I:14:ASN:O	12:I:128:ARG:NH2	2.31	0.64
1:5:1554:A:OP2	44:p:4:ARG:NH1	2.31	0.64
1:5:978:G:N2	1:5:1277:G:H1	1.97	0.63
4:9:1309:C:OP2	77:ff:118:ARG:NH1	2.30	0.63
50:EE:174:LYS:O	50:EE:179:ASN:ND2	2.30	0.63
1:5:956:A:H8	1:5:957:G:C8	2.17	0.63
4:9:560:A:OP2	55:JJ:177:ASN:ND2	2.27	0.63
1:5:260:C:H2'	1:5:261:G:C8	2.33	0.63
1:5:4413:C:H5	1:5:4429:C:H42	1.46	0.63
78:gg:83:TRP:HA	78:gg:107:ASP:HB2	1.80	0.63
1:5:1976:G:H1	1:5:1990:A:H61	1.44	0.63
1:5:4035:G:H2'	1:5:4036:G:C8	2.33	0.63
56:KK:5:LYS:NZ	58:MM:29:ASP:OD2	2.30	0.63
1:5:4772:C:N4	1:5:4864:U:O2	2.31	0.63
1:5:978:G:N2	1:5:1277:G:H22	1.96	0.63
64:SS:86:ARG:NH2	64:SS:89:ASP:OD1	2.23	0.63
4:9:115:U:H2'	4:9:116:U:C6	2.34	0.63
4:9:981:A:H2'	4:9:982:G:C8	2.33	0.63
1:5:2601:A:N6	1:5:2744:A:OP2	2.31	0.62
4:9:555:A:H61	4:9:589:G:N2	1.96	0.62
1:5:1405:C:H2'	1:5:1406:G:C8	2.34	0.62
1:5:294:G:O2'	30:a:59:ARG:NH2	2.33	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:2017:A:OP2	1:5:2018:C:N4	2.27	0.62
1:5:4039:G:H4'	1:5:4049:U:H2'	1.80	0.62
12:I:38:ARG:NH2	12:I:45:GLU:OE1	2.31	0.62
1:5:1339:U:H2'	1:5:1340:C:C6	2.34	0.62
1:5:1982:G:N3	1:5:2009:A:O2'	2.32	0.62
1:5:4305:G:H22	23:T:87:LYS:HZ3	1.44	0.62
80:11:23:C:H2'	80:11:24:G:H8	1.64	0.62
4:9:126:G:OP1	52:GG:198:ARG:NH1	2.28	0.62
4:9:640:A:H2'	4:9:641:A:C8	2.35	0.62
4:9:1693:G:H21	4:9:1834:A:H8	1.48	0.62
1:5:3910:C:H2'	1:5:3911:C:C6	2.35	0.62
4:9:179:C:H2'	4:9:180:G:C8	2.35	0.62
4:9:1741:U:OP1	54:II:42:ARG:NH2	2.33	0.61
1:5:2474:G:N2	1:5:2502:A:H2'	2.15	0.61
1:5:2478:C:H2'	1:5:2479:G:H8	1.65	0.61
26:W:93:LYS:O	26:W:101:ARG:NH2	2.30	0.61
50:EE:54:TYR:OH	50:EE:97:GLU:OE1	2.17	0.61
62:QQ:102:GLU:HA	62:QQ:105:LYS:HE3	1.81	0.61
1:5:1444:G:H21	1:5:2110:G:H1	1.47	0.61
1:5:4992:G:H2'	1:5:4993:G:C8	2.36	0.61
49:DD:45:ARG:NH2	49:DD:85:GLU:OE2	2.22	0.61
1:5:134:G:C8	1:5:134:G:H5'	2.36	0.61
4:9:1118:C:H2'	4:9:1119:A:C8	2.35	0.61
80:11:23:C:H2'	80:11:24:G:C8	2.36	0.60
4:9:1619:A:OP2	61:PP:47:ARG:NH1	2.34	0.60
10:G:111:PRO:HD2	10:G:114:ILE:HD12	1.83	0.60
1:5:1756:U:H2'	1:5:1757:U:C6	2.35	0.60
1:5:3760:A:N6	4:9:1824:A:H2'	2.17	0.60
1:5:1970:A:H1'	1:5:2017:A:H61	1.66	0.60
1:5:4927:G:H3'	1:5:4928:C:O2	2.01	0.60
3:8:67:U:H2'	3:8:68:G:H8	1.67	0.60
4:9:367:U:H4'	4:9:371:A:C8	2.36	0.60
4:9:688:U:OP1	53:HH:116:ARG:NH2	2.33	0.60
48:CC:146:GLU:OE1	49:DD:120:TYR:OH	2.18	0.60
62:QQ:53:GLU:OE1	62:QQ:85:ARG:NH1	2.32	0.60
4:9:878:G:H22	4:9:908:A:H2	1.49	0.60
13:J:95:ARG:NH1	13:J:176:PRO:O	2.31	0.60
4:9:909:G:H2'	4:9:910:G:H8	1.66	0.60
4:9:1738:C:OP1	52:GG:92:ARG:NH2	2.24	0.60
4:9:1305:C:H2'	4:9:1306:U:H6	1.66	0.60
53:HH:93:VAL:HG21	53:HH:133:LEU:HD12	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:4570:G:H2'	1:5:4571:A:H8	1.67	0.60
4:9:909:G:H2'	4:9:910:G:C8	2.37	0.60
1:5:1596:U:O2'	19:P:135:ARG:NH2	2.35	0.59
4:9:448:A:N6	54:II:29:LEU:HD13	2.16	0.59
1:5:1354:A:OP1	20:Q:108:ARG:NH2	2.35	0.59
14:K:93:ARG:NH1	14:K:95:ARG:O	2.32	0.59
4:9:176:U:H2'	4:9:177:G:C8	2.37	0.59
4:9:824:C:C2	55:JJ:144:ILE:HD13	2.37	0.59
1:5:271:C:H2'	1:5:272:U:C6	2.37	0.59
1:5:2520:C:O2	1:5:2640:G:N2	2.35	0.59
1:5:4944:C:H4'	1:5:4944:C:OP1	2.02	0.59
4:9:396:U:OP2	57:LL:79:LYS:NZ	2.35	0.59
4:9:1317:C:H2'	4:9:1318:G:H8	1.67	0.59
1:5:910:G:H2'	1:5:911:U:H6	1.67	0.59
4:9:1228:A:H2'	4:9:1229:G:H8	1.67	0.59
4:9:1285:G:O2'	4:9:1286:G:OP1	2.16	0.58
81:j:20:ARG:NH2	81:j:39:TYR:OH	2.36	0.58
51:FF:38:TYR:OH	74:cc:54:ASP:OD1	2.15	0.58
80:11:53:G:H2'	80:11:54:A:H8	1.68	0.58
1:5:976:G:H1	1:5:1279:A:H2	1.51	0.58
1:5:3827:G:O2'	1:5:3829:G:OP2	2.19	0.58
4:9:184:G:H2'	4:9:185:G:H8	1.68	0.58
4:9:74:G:N1	4:9:78:C:OP2	2.20	0.58
4:9:303:C:O2	54:II:184:ARG:NH2	2.36	0.58
4:9:1482:C:OP1	75:dd:54:LYS:NZ	2.30	0.58
10:G:314:LEU:HA	10:G:317:LYS:HB2	1.85	0.58
34:e:67:LYS:O	34:e:75:ARG:NH1	2.37	0.58
4:9:455:A:H2'	4:9:456:C:C6	2.38	0.58
1:5:1075:G:H22	1:5:1235:G:N2	2.00	0.58
4:9:1284:A:H5''	4:9:1285:G:H2'	1.85	0.58
72:aa:87:ARG:NH2	72:aa:94:ASP:O	2.26	0.58
1:5:1197:C:H2'	1:5:1198:G:C8	2.39	0.58
1:5:1234:G:HO2'	1:5:1235:G:H8	1.52	0.57
1:5:1970:A:H4'	1:5:2000:G:C8	2.39	0.57
1:5:1976:G:H1	1:5:1990:A:N6	2.02	0.57
4:9:1286:G:OP1	77:ff:99:LYS:NZ	2.25	0.57
46:AA:205:ARG:NH2	46:AA:213:GLU:OE1	2.35	0.57
1:5:1450:C:O2'	1:5:2104:A:H1'	2.04	0.57
1:5:1177:U:H2'	1:5:1178:G:H8	1.65	0.57
1:5:3938:G:N2	1:5:4171:C:OP2	2.31	0.57
79:10:13:A:H61	80:11:34:C:H42	1.51	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:9:928:G:H21	73:bb:68:GLY:HA2	1.69	0.57
64:SS:63:GLU:HG2	64:SS:66:ARG:HH21	1.69	0.57
1:5:490:C:H2'	1:5:491:G:C8	2.39	0.57
4:9:792:C:H2'	4:9:793:G:H8	1.68	0.57
4:9:1253:A:OP2	4:9:1526:G:N2	2.36	0.57
40:l:23:ILE:HD11	40:l:28:TRP:NE1	2.19	0.57
78:gg:145:GLU:O	78:gg:175:LYS:NZ	2.35	0.57
80:11:71:C:H2'	80:11:72:U:H6	1.69	0.57
5:A:29:LEU:O	5:A:123:ARG:NH1	2.38	0.57
80:11:71:C:H2'	80:11:72:U:C6	2.39	0.57
1:5:462:G:H2'	1:5:463:A:C8	2.40	0.57
4:9:5:U:H2'	4:9:6:G:H8	1.70	0.57
62:QQ:96:TYR:O	62:QQ:105:LYS:HE2	2.05	0.57
1:5:910:G:H2'	1:5:911:U:C6	2.39	0.57
4:9:792:C:H2'	4:9:793:G:C8	2.39	0.57
80:11:69:U:H2'	80:11:70:G:H8	1.68	0.57
1:5:1358:G:O2'	1:5:1359:G:O5'	2.21	0.56
1:5:2504:C:O2'	1:5:2505:C:O2	2.13	0.56
1:5:2899:C:P	21:R:108:ARG:HH22	2.28	0.56
1:5:4260:U:H2'	1:5:4261:C:C6	2.40	0.56
1:5:4274:A:H2'	1:5:4275:G:C8	2.40	0.56
4:9:126:G:OP2	52:GG:195:LYS:NZ	2.36	0.56
5:A:137:ILE:HD11	5:A:149:LYS:HB2	1.86	0.56
4:9:1693:G:N2	4:9:1834:A:H8	2.02	0.56
46:AA:5:LEU:HD21	67:VV:41:LYS:HA	1.86	0.56
1:5:914:U:O2'	1:5:915:A:OP2	2.19	0.56
4:9:1407:U:H2'	4:9:1408:U:C6	2.40	0.56
43:o:64:LYS:NZ	84:11:101:ATP:O2B	2.38	0.56
48:CC:102:LEU:HD21	48:CC:130:ILE:HD12	1.87	0.56
1:5:2546:G:O2'	1:5:2547:G:OP1	2.22	0.56
20:Q:16:LYS:O	20:Q:33:ARG:NH2	2.38	0.56
4:9:919:A:OP2	59:NN:64:ARG:NH2	2.33	0.56
4:9:1101:U:H2'	4:9:1102:G:C8	2.40	0.56
18:O:79:ILE:O	18:O:83:THR:HG23	2.04	0.56
1:5:976:G:N2	7:C:323:ARG:HH21	2.04	0.56
1:5:2639:U:O2'	1:5:2694:G:N1	2.32	0.56
1:5:4053:A:H2'	1:5:4054:C:C6	2.41	0.56
1:5:966:A:H5'	1:5:967:C:H2'	1.86	0.56
1:5:983:C:C5	9:E:73:ARG:HD3	2.40	0.56
1:5:2566:G:H2'	1:5:2567:G:H8	1.71	0.56
4:9:5:U:H2'	4:9:6:G:C8	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:9:804:U:H2'	4:9:805:U:C6	2.41	0.56
4:9:1232:U:H2'	4:9:1233:G:H8	1.70	0.56
4:9:1863:A:OP2	72:aa:4:LYS:NZ	2.34	0.56
80:13:18:G:H21	80:13:57:G:H2'	1.70	0.56
1:5:280:G:H5''	17:N:14:LYS:HE2	1.87	0.56
4:9:903:A:H2'	4:9:904:A:C8	2.41	0.56
4:9:1710:C:H42	4:9:1823:A:N6	2.03	0.56
1:5:982:U:O2	1:5:1273:G:N2	2.34	0.56
1:5:92:C:OP1	82:5:5101:SPD:N10	2.39	0.55
3:8:94:G:OP2	81:j:72:ARG:NH1	2.39	0.55
4:9:903:A:H2'	4:9:904:A:H8	1.71	0.55
1:5:3688:U:OP2	5:A:198:ARG:NH1	2.40	0.55
1:5:3736:A:H2'	1:5:3737:A:C8	2.40	0.55
74:cc:10:LYS:NZ	74:cc:36:ASP:OD2	2.26	0.55
1:5:76:A:OP2	15:L:74:ARG:NH1	2.38	0.55
1:5:1317:U:OP1	30:a:21:ARG:NH2	2.37	0.55
1:5:3663:A:N6	1:5:4168:G:O2'	2.39	0.55
1:5:4585:U:H2'	1:5:4586:G:H8	1.70	0.55
1:5:387:G:O2'	1:5:412:G:O6	2.19	0.55
4:9:1523:C:H2'	4:9:1524:G:H8	1.72	0.55
11:H:92:MET:HE2	11:H:179:ILE:HG22	1.89	0.55
61:PP:64:LYS:NZ	61:PP:90:VAL:O	2.21	0.55
62:QQ:97:GLN:HA	62:QQ:105:LYS:HD3	1.88	0.55
4:9:942:G:H2'	4:9:943:U:C6	2.41	0.55
1:5:2412:A:H2'	1:5:2413:U:C6	2.41	0.55
1:5:4925:U:H4'	1:5:4926:C:C5'	2.36	0.55
3:8:58:G:N7	81:j:63:ARG:NH2	2.54	0.55
4:9:64:A:H2	4:9:83:A:H62	1.53	0.55
4:9:1839:U:H1'	4:9:1863:A:H2	1.72	0.55
7:C:335:MET:O	7:C:339:THR:HG23	2.07	0.55
13:J:28:GLU:OE2	13:J:32:ARG:NH1	2.30	0.55
4:9:561:A:H2'	4:9:562:U:C6	2.42	0.55
43:o:63:THR:O	43:o:87:ARG:NH1	2.40	0.55
43:o:68:LEU:HD11	43:o:85:ILE:HD11	1.89	0.55
1:5:325:U:H2'	1:5:326:C:C6	2.42	0.54
3:8:8:U:H2'	3:8:9:A:C8	2.42	0.54
4:9:547:G:N3	4:9:548:C:H5	2.05	0.54
67:VV:20:SER:HB3	67:VV:59:ILE:HD11	1.89	0.54
1:5:2478:C:N4	1:5:2479:G:O6	2.41	0.54
4:9:1279:C:H2'	4:9:1280:G:H8	1.72	0.54
15:L:127:PHE:O	37:h:117:ARG:NH2	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:11:43:G:H2'	80:11:44:A:H8	1.71	0.54
1:5:1188:C:H2'	1:5:1189:G:H8	1.73	0.54
1:5:1846:G:H2'	1:5:1847:C:C6	2.42	0.54
1:5:3610:A:O2'	54:II:89:GLU:OE2	2.19	0.54
1:5:4037:C:H2'	1:5:4038:C:C6	2.42	0.54
4:9:429:C:O2'	4:9:811:A:N1	2.38	0.54
16:M:6:PHE:O	16:M:11:ARG:NE	2.40	0.54
62:QQ:129:SER:O	62:QQ:131:LYS:HE3	2.06	0.54
1:5:3911:C:H2'	1:5:3912:U:H6	1.72	0.54
1:5:4058:U:H2'	1:5:4059:C:C6	2.42	0.54
47:BB:107:ARG:NH1	60:OO:133:THR:O	2.35	0.54
1:5:65:A:OP2	15:L:101:ARG:NH1	2.40	0.54
1:5:4188:U:H2'	1:5:4189:U:C6	2.42	0.54
1:5:4944:C:N4	35:f:58:VAL:O	2.38	0.54
4:9:1305:C:H2'	4:9:1306:U:C6	2.42	0.54
4:9:1845:A:H2'	4:9:1846:G:C8	2.42	0.54
1:5:424:U:H2'	1:5:425:U:C6	2.42	0.54
1:5:2755:A:P	29:Z:65:ARG:HH22	2.30	0.54
4:9:1240:A:H8	4:9:1267:C:O2'	1.90	0.54
1:5:1094:G:H2'	1:5:1095:A:H8	1.72	0.54
4:9:539:C:O2	4:9:544:G:N1	2.35	0.54
78:gg:23:THR:HG22	78:gg:31:ILE:HD12	1.89	0.54
80:11:35:A:H2'	80:11:36:U:C6	2.42	0.54
81:j:63:ARG:HG2	81:j:63:ARG:HH11	1.73	0.54
4:9:178:C:H2'	4:9:179:C:C6	2.43	0.54
4:9:1597:C:H4'	4:9:1603:G:O6	2.07	0.54
80:13:62:C:H2'	80:13:63:A:C8	2.42	0.54
1:5:2404:A:H61	1:5:2787:A:N6	2.05	0.54
1:5:4926:C:H5'	1:5:4926:C:O2	2.08	0.54
61:PP:21:ASP:OD1	61:PP:22:LEU:N	2.41	0.54
1:5:2638:G:H22	1:5:2697:A:N6	2.06	0.54
4:9:107:A:H2'	4:9:108:G:C8	2.43	0.54
4:9:1227:G:C2	4:9:1228:A:C8	2.96	0.54
4:9:1710:C:H42	4:9:1823:A:H61	1.56	0.54
1:5:2001:G:N2	1:5:2017:A:H1'	2.23	0.53
4:9:369:C:O2'	4:9:370:G:OP1	2.23	0.53
4:9:1462:U:O2	4:9:1464:C:N4	2.41	0.53
21:R:39:GLN:OE1	21:R:42:ARG:NH1	2.39	0.53
1:5:4174:U:H2'	1:5:4175:G:H8	1.73	0.53
1:5:4759:C:H2'	1:5:4760:G:C8	2.43	0.53
1:5:4950:U:O2'	1:5:4951:G:OP1	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:9:1834:A:H2	4:9:1837:G:N1	2.05	0.53
80:11:41:C:H2'	80:11:42:A:H8	1.73	0.53
1:5:516:C:H2'	1:5:517:C:C6	2.43	0.53
4:9:847:A:H3'	4:9:848:U:O2	2.07	0.53
1:5:1075:G:H22	1:5:1235:G:H22	1.56	0.53
1:5:3877:A:O2'	1:5:4400:G:N2	2.40	0.53
1:5:3974:G:OP2	1:5:3975:C:N4	2.37	0.53
4:9:1797:U:H2'	4:9:1798:C:C6	2.43	0.53
1:5:4572:U:H2'	1:5:4573:G:H8	1.72	0.53
1:5:1558:A:H2'	1:5:1559:G:H8	1.74	0.53
1:5:1867:A:OP1	12:I:13:LYS:HE2	2.09	0.53
1:5:4293:U:O2'	43:o:81:ARG:NH2	2.41	0.53
1:5:4458:C:H2'	1:5:4459:U:C6	2.43	0.53
1:5:4537:C:H2'	1:5:4538:G:C8	2.44	0.53
58:MM:53:ALA:HA	58:MM:79:VAL:O	2.09	0.53
1:5:2083:C:OP2	20:Q:14:ARG:NH2	2.26	0.53
1:5:2088:A:H5''	1:5:2089:G:H3'	1.91	0.53
1:5:2899:C:H2'	1:5:2900:U:C6	2.44	0.53
1:5:3953:G:H2'	1:5:3954:A:C8	2.44	0.53
1:5:4099:G:H1	1:5:4109:G:H1	1.55	0.53
4:9:1395:C:O2'	4:9:1396:A:OP1	2.19	0.53
1:5:3760:A:C6	4:9:1824:A:H2'	2.44	0.53
1:5:3770:U:OP1	80:13:24:G:O2'	2.22	0.53
4:9:1248:U:H2'	4:9:1249:C:C6	2.44	0.53
1:5:1237:C:H4'	1:5:1238:A:O5'	2.09	0.53
1:5:2567:G:H2'	1:5:2568:C:H6	1.74	0.53
3:8:125:C:H1'	3:8:126:C:H3'	1.91	0.53
6:B:95:THR:HG22	6:B:97:ARG:H	1.74	0.53
80:11:69:U:H2'	80:11:70:G:C8	2.44	0.53
1:5:1186:U:H2'	1:5:1187:G:N3	2.24	0.52
1:5:4301:U:H4'	23:T:54:HIS:CD2	2.45	0.52
1:5:4626:A:OP2	6:B:224:LYS:NZ	2.20	0.52
4:9:1671:G:H2'	4:9:1672:U:C6	2.44	0.52
11:H:23:ARG:NH1	11:H:39:ASN:O	2.42	0.52
57:LL:150:GLY:O	59:NN:133:ARG:NH1	2.42	0.52
1:5:922:C:H2'	1:5:922(A):G:H8	1.73	0.52
1:5:1772:C:H2'	1:5:1773:U:O4'	2.09	0.52
4:9:552:G:H2'	4:9:553:U:C6	2.44	0.52
21:R:44:LEU:HD22	21:R:49:LEU:HD12	1.91	0.52
1:5:966:A:H5''	1:5:967:C:C6	2.44	0.52
4:9:60:A:N3	4:9:316:G:O2'	2.37	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:11:47:U:H3'	80:11:48:C:H5'	1.90	0.52
1:5:40:G:N2	1:5:4380:A:H62	2.07	0.52
1:5:264:C:H5''	1:5:265:C:OP2	2.09	0.52
1:5:1272:C:OP2	14:K:33:ARG:NH1	2.43	0.52
1:5:2382:A:N1	1:5:2829:U:O2'	2.37	0.52
1:5:4967:A:H2'	1:5:4968:A:H8	1.74	0.52
4:9:554:A:H5''	4:9:555:A:OP1	2.09	0.52
56:KK:85:LEU:HB3	56:KK:89:ILE:HD11	1.92	0.52
1:5:3904:G:O2'	1:5:3905:A:OP1	2.24	0.52
1:5:4594:U:H2'	1:5:4595:G:H8	1.73	0.52
4:9:1653:U:H3	4:9:1671:G:H1	1.57	0.52
78:gg:174:VAL:HB	78:gg:188:HIS:HB2	1.91	0.52
1:5:3707:U:H2'	1:5:3708:C:C6	2.44	0.52
1:5:4274:A:H2'	1:5:4275:G:H8	1.73	0.52
30:a:72:THR:HG22	30:a:110:LYS:HB3	1.91	0.52
80:13:12:C:H2'	80:13:13:G:C8	2.45	0.52
1:5:956:A:N6	1:5:1283:G:O2'	2.37	0.52
1:5:1298:C:H2'	1:5:1299:G:H8	1.75	0.52
1:5:1992:U:O2'	1:5:2002:A:OP1	2.25	0.52
4:9:791:C:H2'	4:9:792:C:C6	2.45	0.52
4:9:1203:G:H2'	4:9:1204:A:C8	2.45	0.52
4:9:1279:C:H2'	4:9:1280:G:C8	2.44	0.52
1:5:4546:A:N7	5:A:215:ASN:ND2	2.57	0.52
1:5:1802:A:H5''	1:5:1803:G:H5'	1.92	0.52
4:9:1310:U:H5''	77:ff:130:VAL:HG13	1.91	0.52
7:C:13:GLU:OE1	7:C:161:TYR:OH	2.24	0.52
10:G:217:ILE:O	10:G:221:VAL:HG13	2.10	0.51
1:5:2455:G:H1'	1:5:2471:G:C2	2.45	0.51
4:9:1253:A:H4'	4:9:1254:C:H5''	1.92	0.51
69:XX:63:ASN:HD22	69:XX:114:ASP:CG	2.17	0.51
1:5:1957:U:HO2'	1:5:1958:A:H8	1.58	0.51
1:5:2008:U:H1'	1:5:2011:C:H5	1.74	0.51
3:8:130:C:H2'	3:8:131:G:H8	1.75	0.51
4:9:380:G:P	54:II:56:ARG:HH22	2.33	0.51
4:9:416:U:O2'	4:9:652:U:O2'	2.22	0.51
4:9:686:U:O2	53:HH:118:ARG:NH2	2.35	0.51
4:9:913:A:OP1	53:HH:99:ARG:NE	2.39	0.51
28:Y:62:TYR:CG	28:Y:85:VAL:HG13	2.45	0.51
59:NN:33:VAL:HG21	59:NN:66:VAL:HG11	1.91	0.51
62:QQ:34:VAL:HB	62:QQ:42:ILE:HD11	1.93	0.51
1:5:1198:G:H2'	1:5:1199:G:H8	1.71	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:2899:C:OP1	21:R:108:ARG:NH2	2.40	0.51
1:5:3948:C:H5''	1:5:3949:A:OP2	2.10	0.51
1:5:4395:U:H6	1:5:4395:U:H5'	1.76	0.51
1:5:4739:C:H2'	1:5:4740:G:C8	2.45	0.51
1:5:4967:A:H2'	1:5:4968:A:C8	2.46	0.51
65:TT:108:GLU:OE2	65:TT:121:ARG:NH1	2.42	0.51
1:5:48:G:H5'	17:N:192:TRP:NE1	2.26	0.51
1:5:2318:G:N2	1:5:2321:G:OP2	2.31	0.51
22:S:173:ASN:ND2	22:S:175:PHE:O	2.43	0.51
55:JJ:60:LEU:HD22	55:JJ:70:ARG:HA	1.92	0.51
1:5:1391:A:P	20:Q:181:ARG:HH22	2.33	0.51
1:5:2567:G:H2'	1:5:2568:C:C6	2.46	0.51
1:5:3965:A:N1	1:5:4047:A:H2'	2.25	0.51
4:9:846:G:OP1	50:EE:106:LYS:NZ	2.41	0.51
1:5:268:G:H2'	1:5:269:G:H8	1.75	0.51
1:5:4934:A:H2'	1:5:4935:C:C6	2.45	0.51
4:9:1630:A:H5''	64:SS:37:GLY:H	1.76	0.51
1:5:1200:G:H2'	1:5:1201:U:C6	2.45	0.51
1:5:2001:G:O5'	1:5:2001:G:C8	2.63	0.51
1:5:3953:G:H2'	1:5:3954:A:H8	1.76	0.51
1:5:300:A:H2'	1:5:301:G:H8	1.76	0.51
1:5:3823:G:O5'	1:5:3823:G:H8	1.94	0.51
4:9:695:C:H2'	4:9:696:G:C8	2.45	0.51
12:I:30:LYS:HD3	12:I:63:GLU:HA	1.93	0.51
23:T:121:GLU:OE2	23:T:122:LYS:NZ	2.31	0.51
77:ff:126:CYS:HB3	77:ff:130:VAL:HB	1.93	0.51
1:5:2303:C:OP1	34:e:107:ASN:ND2	2.40	0.51
1:5:4870:G:H2'	16:M:91:TRP:CZ2	2.46	0.51
4:9:693:A:H2'	4:9:694:G:H8	1.76	0.51
23:T:63:ARG:NH2	31:b:30:GLU:OE1	2.44	0.51
53:HH:75:ILE:HG22	53:HH:79:LEU:HB2	1.91	0.51
57:LL:42:LEU:HD13	57:LL:72:ILE:HD11	1.93	0.51
72:aa:44:ILE:HD12	72:aa:65:PRO:HG2	1.93	0.51
1:5:691:C:H2'	1:5:692:A:H8	1.76	0.50
4:9:186:C:H2'	4:9:187:G:H8	1.77	0.50
4:9:1113:A:H2'	4:9:1114:U:C6	2.47	0.50
80:13:51:U:H2'	80:13:52:G:C8	2.46	0.50
1:5:1075:G:N2	1:5:1235:G:H22	2.10	0.50
1:5:1075:G:H1	1:5:1235:G:N2	2.10	0.50
1:5:4726:G:O2'	6:B:129:ALA:O	2.13	0.50
24:U:80:LYS:HG2	24:U:110:TYR:CE2	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:OO:103:ASN:HB3	60:OO:139:SER:OG	2.11	0.50
1:5:433:A:C2	1:5:3867:A:H4'	2.47	0.50
1:5:1942:A:H2'	1:5:1943:A:C8	2.47	0.50
1:5:3770:U:H2'	1:5:3771:C:C6	2.46	0.50
4:9:179:C:H2'	4:9:180:G:H8	1.76	0.50
80:11:18:G:H21	80:11:57:G:H2'	1.75	0.50
1:5:129:C:H2'	1:5:130:C:C6	2.46	0.50
1:5:976:G:H21	7:C:323:ARG:NE	2.06	0.50
1:5:1502:G:C8	1:5:1502:G:H5''	2.46	0.50
4:9:65:C:H4'	52:GG:172:LYS:HE2	1.94	0.50
4:9:1285:G:O4'	58:MM:61:TYR:OH	2.28	0.50
49:DD:29:LEU:HB2	49:DD:34:TYR:HB2	1.92	0.50
77:ff:100:LEU:HG	77:ff:103:LEU:HD13	1.92	0.50
1:5:653:C:H2'	1:5:654:C:C6	2.45	0.50
1:5:1402:C:H2'	1:5:1403:G:H8	1.77	0.50
1:5:2583:C:OP2	36:g:76:ARG:NH1	2.32	0.50
1:5:3692:A:H62	1:5:3823:G:N2	2.05	0.50
4:9:184:G:H2'	4:9:185:G:C8	2.45	0.50
4:9:575:A:P	70:YY:93:ARG:HH21	2.34	0.50
80:13:16:G:O2'	80:13:17:C:OP1	2.28	0.50
1:5:67:C:OP2	1:5:312:G:N2	2.45	0.50
4:9:1507:G:N2	77:ff:87:THR:O	2.32	0.50
17:N:155:VAL:O	17:N:162:ARG:NH2	2.45	0.50
41:m:68:MET:HG2	41:m:79:PRO:HA	1.93	0.50
1:5:490:C:H2'	1:5:491:G:H8	1.77	0.50
1:5:2706:G:O6	21:R:46:LYS:NZ	2.37	0.50
4:9:1597:C:H4'	4:9:1603:G:C6	2.47	0.50
4:9:1858:G:OP2	60:OO:146:ARG:NH2	2.45	0.50
14:K:156:ARG:NH1	14:K:247:ASN:OXT	2.43	0.50
58:MM:75:ASN:HB3	58:MM:128:PHE:CZ	2.47	0.50
1:5:52:G:H4'	1:5:1529:G:H4'	1.94	0.50
1:5:1416:G:H2'	1:5:1417:C:C6	2.47	0.50
1:5:2638:G:H22	1:5:2697:A:H61	1.58	0.50
4:9:1845:A:H2'	4:9:1846:G:H8	1.77	0.50
49:DD:66:ILE:O	49:DD:70:THR:HG23	2.11	0.50
63:RR:54:VAL:O	63:RR:58:MET:HG2	2.11	0.50
78:gg:40:ILE:HB	78:gg:59:LEU:HB2	1.93	0.50
1:5:4585:U:H2'	1:5:4586:G:C8	2.47	0.50
4:9:1292:C:O2	77:ff:138:ARG:NH1	2.44	0.50
4:9:1303:C:H2'	4:9:1304:U:H6	1.77	0.50
9:E:64:MET:HG3	9:E:68:LYS:HE2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:e:84:GLU:CD	45:r:20:ARG:HH22	2.20	0.50
14:K:85:GLU:OE2	23:T:136:ARG:NH1	2.45	0.49
1:5:179:G:H2'	1:5:180:C:C6	2.47	0.49
1:5:1788:A:H2'	12:I:22:PHE:CZ	2.46	0.49
1:5:2313:A:HO2'	1:5:2314:G:P	2.32	0.49
4:9:1462:U:H2'	4:9:1464:C:C4	2.48	0.49
4:9:1692:U:H2'	4:9:1693:G:C8	2.46	0.49
9:E:144:ARG:NH1	35:f:110:ILE:OXT	2.45	0.49
12:I:30:LYS:HD2	12:I:63:GLU:HG3	1.93	0.49
56:KK:35:LEU:O	56:KK:38:LYS:N	2.41	0.49
1:5:1346:C:H2'	1:5:1347:G:H8	1.76	0.49
1:5:2431:A:P	40:l:41:ARG:HH12	2.35	0.49
4:9:1199:A:H2'	4:9:1200:A:C8	2.47	0.49
4:9:1736:G:H2'	4:9:1737:G:H8	1.77	0.49
18:O:173:GLN:OE1	18:O:176:ARG:NH1	2.42	0.49
37:h:87:LYS:NZ	81:j:80:GLU:OE2	2.45	0.49
1:5:158:A:H5''	1:5:159:C:H2'	1.94	0.49
1:5:3942:A:H2'	1:5:3943:A:H8	1.77	0.49
4:9:379:C:H5'	54:II:33:ALA:HA	1.94	0.49
4:9:1736:G:H2'	4:9:1737:G:C8	2.47	0.49
17:N:108:ARG:HB2	17:N:161:MET:HE1	1.93	0.49
1:5:1075:G:H1	1:5:1235:G:H22	1.60	0.49
1:5:2557:G:H1	1:5:2570:U:H3	1.59	0.49
1:5:4303:C:H2'	1:5:4305:G:C8	2.48	0.49
1:5:4638:U:H2'	1:5:4639:G:N3	2.28	0.49
4:9:1698:C:O2'	4:9:1699:A:OP1	2.28	0.49
1:5:3635:A:N6	44:p:17:ARG:O	2.39	0.49
1:5:4481:U:H2'	1:5:4482:U:C6	2.47	0.49
2:7:92:C:H2'	2:7:93:G:H8	1.78	0.49
15:L:116:ARG:NH2	15:L:155:MET:O	2.33	0.49
1:5:1072:C:O2'	1:5:1073:G:O5'	2.26	0.49
7:C:329:ASN:ND2	14:K:187:GLU:OE2	2.45	0.49
1:5:4038:C:H2'	1:5:4039:G:C8	2.48	0.49
1:5:4525:C:H2'	1:5:4526:U:C6	2.48	0.49
4:9:1848:U:H2'	4:9:1849:G:H5'	1.93	0.49
61:PP:41:GLN:NE2	61:PP:113:GLY:O	2.46	0.49
1:5:465:G:H2'	1:5:466:A:C8	2.47	0.49
3:8:141:C:OP1	17:N:38:ARG:NH1	2.46	0.49
10:G:317:LYS:HG2	47:BB:225:LEU:HD23	1.95	0.49
14:K:154:TYR:OH	14:K:187:GLU:OE2	2.30	0.49
80:13:12:C:H2'	80:13:13:G:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:13:69:U:H2'	80:13:70:G:H8	1.78	0.49
1:5:2543:A:H2	1:5:2773:G:H22	1.61	0.49
2:7:3:C:H2'	2:7:4:U:H6	1.77	0.49
7:C:339:THR:HG22	7:C:342:ARG:HH22	1.78	0.49
1:5:935(A):G:OP1	16:M:23:LYS:NZ	2.46	0.48
1:5:978:G:H22	1:5:1277:G:H22	1.61	0.48
1:5:4935:C:H2'	1:5:4936:G:C8	2.48	0.48
4:9:1303:C:H2'	4:9:1304:U:C6	2.48	0.48
4:9:1309:C:H2'	4:9:1310:U:H6	1.78	0.48
4:9:1404:U:OP1	66:UU:21:ARG:NH2	2.43	0.48
46:AA:2:SER:HB3	67:VV:80:SER:HB2	1.94	0.48
50:EE:233:LYS:HD3	50:EE:234:PRO:HD2	1.95	0.48
69:XX:28:LYS:HE2	69:XX:32:LEU:HD22	1.95	0.48
70:YY:110:ARG:NH1	70:YY:114:MET:SD	2.86	0.48
1:5:2758:G:O2'	1:5:2765:A:N3	2.36	0.48
1:5:4325:A:C2	8:D:35:ARG:HB2	2.48	0.48
4:9:1780:G:H2'	4:9:1781:A:C8	2.47	0.48
10:G:273:GLU:CD	10:G:276:ARG:HH12	2.21	0.48
29:Z:84:ARG:NH1	36:g:99:GLU:OE1	2.43	0.48
1:5:152:U:P	17:N:49:ARG:HH12	2.35	0.48
1:5:164:G:H2'	1:5:165:A:C8	2.48	0.48
1:5:746:A:H2'	1:5:913:U:O4	2.13	0.48
1:5:1558:A:H2'	1:5:1559:G:C8	2.48	0.48
4:9:816:A:N1	4:9:848:U:H5	2.11	0.48
4:9:1401:A:H2'	4:9:1402:A:C8	2.49	0.48
51:FF:39:ILE:HG23	51:FF:68:ILE:HG21	1.94	0.48
57:LL:120:VAL:HG22	57:LL:145:VAL:HG11	1.94	0.48
1:5:976:G:H22	7:C:323:ARG:HH21	1.60	0.48
1:5:2465:C:H1'	1:5:3672:G:H22	1.78	0.48
1:5:4918:C:H2'	1:5:4919:G:O4'	2.12	0.48
4:9:1389:C:O2'	49:DD:162:ASP:HB3	2.13	0.48
34:e:113:GLU:OE2	34:e:117:GLN:NE2	2.32	0.48
69:XX:68:LYS:HE2	76:ee:82:VAL:HG22	1.96	0.48
1:5:2570:U:H2'	1:5:2571:C:C6	2.48	0.48
1:5:3961:G:H4'	1:5:4044:U:H1'	1.96	0.48
1:5:4957:C:H3'	1:5:4958:C:H5''	1.95	0.48
4:9:1317:C:H2'	4:9:1318:G:C8	2.46	0.48
4:9:1447:G:P	66:UU:87:ARG:HH22	2.36	0.48
46:AA:80:ARG:NH2	46:AA:82:THR:OG1	2.46	0.48
61:PP:44:ARG:NH1	61:PP:82:ASP:O	2.46	0.48
79:10:21:C:H2'	79:10:22:U:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:1779:U:H2'	1:5:1780:A:C8	2.49	0.48
1:5:2422:C:P	19:P:127:ARG:HH22	2.37	0.48
1:5:4457:U:H1'	6:B:252:ALA:HB3	1.96	0.48
4:9:1397:U:H2'	4:9:1397:U:O2	2.13	0.48
45:r:97:ILE:HD13	45:r:107:ARG:HA	1.94	0.48
1:5:2730:U:H2'	1:5:2731:C:C6	2.47	0.48
1:5:3799:A:OP1	25:V:64:THR:HG21	2.14	0.48
1:5:4936:G:O2'	1:5:4937:C:OP1	2.24	0.48
4:9:1101:U:H2'	4:9:1102:G:H8	1.79	0.48
8:D:273:LEU:HD11	8:D:277:LYS:HE2	1.96	0.48
1:5:478:G:H2'	1:5:479:G:H8	1.79	0.48
1:5:1298:C:H2'	1:5:1299:G:C8	2.49	0.48
1:5:3942:A:H2'	1:5:3943:A:C8	2.48	0.48
4:9:852:G:H3'	4:9:853:C:O2	2.14	0.48
4:9:1010:G:H2'	4:9:1011:A:C8	2.49	0.48
1:5:1372:A:OP1	17:N:202:ARG:NH2	2.41	0.48
1:5:1502:G:O6	20:Q:89:ASP:HA	2.13	0.48
1:5:3932:U:H2'	1:5:3933:G:H8	1.78	0.48
4:9:1232:U:H2'	4:9:1233:G:C8	2.47	0.48
6:B:95:THR:HB	6:B:98:GLY:O	2.14	0.48
80:11:41:C:H2'	80:11:42:A:C8	2.49	0.48
1:5:217:C:H2'	1:5:217:C:O2	2.14	0.48
1:5:424:U:H2'	1:5:425:U:H6	1.79	0.48
2:7:92:C:H2'	2:7:93:G:C8	2.49	0.48
4:9:1536:G:H2'	4:9:1537:A:C8	2.49	0.48
1:5:1238:A:O2'	1:5:1239:C:OP1	2.27	0.47
4:9:1565:C:OP2	65:TT:101:ARG:NH1	2.45	0.47
1:5:303:C:OP2	17:N:68:ARG:NH2	2.47	0.47
1:5:699:C:H2'	1:5:700:G:H8	1.79	0.47
1:5:709:C:OP1	35:f:89:ARG:NH2	2.36	0.47
1:5:1308:C:H2'	1:5:1309:C:C6	2.49	0.47
1:5:4525:C:H2'	1:5:4526:U:H6	1.79	0.47
4:9:1348:G:OP2	4:9:1348:G:N2	2.46	0.47
4:9:1784:G:C6	4:9:1785:C:C4	3.01	0.47
17:N:178:HIS:HA	17:N:181:HIS:NE2	2.29	0.47
48:CC:166:ARG:NH1	67:VV:10:ASP:OD2	2.47	0.47
66:UU:32:LEU:HD21	66:UU:87:ARG:HD3	1.94	0.47
1:5:115:C:O2'	1:5:276:C:OP1	2.31	0.47
1:5:2412:A:H2'	1:5:2413:U:H6	1.79	0.47
61:PP:44:ARG:NH2	61:PP:82:ASP:OD2	2.34	0.47
1:5:699:C:H2'	1:5:700:G:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:9:1286:G:OP2	77:ff:99:LYS:HD3	2.14	0.47
4:9:1588:A:H2'	4:9:1589:A:C8	2.49	0.47
6:B:35:ASP:HB3	6:B:186:ASN:CG	2.40	0.47
40:l:12:PHE:CD1	40:l:51:LEU:HD11	2.50	0.47
1:5:1804:A:H5''	1:5:1805:A:H2'	1.96	0.47
1:5:3873:G:H2'	1:5:3874:G:C8	2.48	0.47
3:8:130:C:H2'	3:8:131:G:C8	2.49	0.47
4:9:570:C:H3'	4:9:571:U:O2	2.14	0.47
4:9:1374:C:H2'	4:9:1375:G:O4'	2.14	0.47
7:C:218:VAL:HA	7:C:229:LEU:CD1	2.44	0.47
30:a:103:VAL:CG1	30:a:108:TYR:HB2	2.44	0.47
61:PP:56:LEU:HD23	61:PP:83:MET:HG3	1.97	0.47
1:5:1461:C:H2'	1:5:1462:A:C8	2.50	0.47
1:5:4305:G:N2	23:T:87:LYS:HZ3	2.11	0.47
4:9:118:C:H1'	4:9:445:A:C5	2.49	0.47
4:9:526:A:OP1	76:ee:108:ARG:NH1	2.45	0.47
4:9:1539:U:H2'	4:9:1540:G:H8	1.79	0.47
4:9:1610:G:OP2	64:SS:132:ARG:NH1	2.47	0.47
58:MM:94:ILE:HG22	58:MM:95:ASP:O	2.15	0.47
1:5:100:C:H2'	1:5:101:A:H8	1.79	0.47
1:5:499:G:H2'	1:5:499:G:N3	2.29	0.47
1:5:1401:C:H2'	1:5:1402:C:C6	2.50	0.47
1:5:1475:G:H2'	1:5:1476:C:C6	2.50	0.47
1:5:1982:G:H5'	1:5:1982:G:H8	1.79	0.47
1:5:2517:A:N3	1:5:2539:C:O2'	2.43	0.47
1:5:4239:A:H2'	1:5:4240:G:C8	2.50	0.47
1:5:4627:U:H4'	6:B:373:LYS:HD2	1.96	0.47
1:5:4899:G:H3'	1:5:4902:C:OP2	2.14	0.47
3:8:52:A:H62	40:l:27:ILE:HD13	1.80	0.47
4:9:533:A:H2'	4:9:534:G:C8	2.50	0.47
4:9:1314:U:H3'	4:9:1315:U:O2	2.14	0.47
4:9:1498:A:P	49:DD:27:ARG:HH22	2.37	0.47
4:9:1693:G:N2	4:9:1834:A:C8	2.83	0.47
17:N:33:LEU:O	17:N:65:ARG:NH2	2.47	0.47
54:II:114:GLU:CD	54:II:123:ARG:HH21	2.23	0.47
78:gg:124:SER:H	78:gg:151:VAL:HB	1.80	0.47
80:13:63:A:H2'	80:13:64:U:H6	1.77	0.47
1:5:717:U:H2'	1:5:718:C:C6	2.49	0.47
1:5:1662:C:H2'	1:5:1663:C:C6	2.50	0.47
1:5:2007:G:C2	1:5:2013:A:N6	2.83	0.47
1:5:4124:G:H3'	5:A:69:PHE:CE1	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:4431:U:P	12:I:3:ARG:HH22	2.37	0.47
4:9:945:U:H2'	4:9:946:U:C6	2.50	0.47
4:9:1147:C:OP1	72:aa:6:ARG:NH1	2.44	0.47
34:e:40:GLY:O	34:e:46:ARG:NH1	2.48	0.47
80:13:65:C:H2'	80:13:66:C:C6	2.50	0.47
1:5:1244:G:O5'	1:5:1244:G:H8	1.98	0.47
1:5:1279:A:O2'	7:C:323:ARG:NH2	2.44	0.47
1:5:1903:G:OP1	35:f:87:LYS:NZ	2.39	0.47
1:5:2569:G:H2'	1:5:2570:U:C6	2.50	0.47
4:9:1553:C:H2'	4:9:1554:C:C6	2.50	0.47
4:9:1720:U:H5''	4:9:1721:U:OP2	2.15	0.47
38:i:66:ASP:OD1	38:i:67:LYS:N	2.48	0.47
1:5:2276:A:H2'	1:5:2277:C:O4'	2.15	0.47
1:5:4285:U:H2'	1:5:4286:C:C6	2.50	0.47
1:5:5047:C:O2'	1:5:5050:C:OP2	2.22	0.47
3:8:62:A:H4'	3:8:63:U:O5'	2.15	0.47
3:8:102:G:OP2	3:8:104:A:O2'	2.29	0.47
4:9:1523:C:H2'	4:9:1524:G:C8	2.50	0.47
13:J:109:ILE:HD11	13:J:128:LEU:HD13	1.97	0.47
80:13:35:A:H2'	80:13:36:U:C6	2.50	0.47
1:5:1807:C:H2'	1:5:1808:C:C6	2.50	0.46
1:5:1932:A:OP2	18:O:49:ARG:NH2	2.41	0.46
1:5:3911:C:H2'	1:5:3912:U:C6	2.50	0.46
4:9:104:A:H62	4:9:356:C:H5	1.61	0.46
4:9:633:C:H1'	76:ee:89:THR:HG21	1.98	0.46
4:9:1809:A:H2'	4:9:1810:U:C6	2.50	0.46
33:d:19:GLU:OE1	33:d:92:ARG:NH1	2.47	0.46
78:gg:129:ILE:HB	78:gg:142:VAL:HB	1.97	0.46
1:5:682:G:H5'	1:5:683:C:OP2	2.16	0.46
1:5:977:C:N4	1:5:978:G:O6	2.48	0.46
1:5:3657:U:OP1	5:A:245:ARG:NH1	2.48	0.46
1:5:4746:C:H2'	1:5:4747:C:C6	2.51	0.46
4:9:1679:A:C2	51:FF:60:ARG:HA	2.50	0.46
1:5:115:C:OP1	17:N:2:GLY:N	2.48	0.46
1:5:151:G:OP2	17:N:4:TYR:OH	2.27	0.46
1:5:3961:G:C6	1:5:3963:A:H2'	2.50	0.46
1:5:4259:C:O4'	13:J:23:ASN:ND2	2.49	0.46
1:5:4572:U:H2'	1:5:4573:G:C8	2.50	0.46
54:II:22:HIS:ND1	54:II:23:LYS:O	2.40	0.46
63:RR:20:TYR:CD2	63:RR:38:ILE:HD12	2.50	0.46
65:TT:27:LYS:HG3	65:TT:110:LEU:HD21	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:1513:U:H2'	1:5:1514:U:O4'	2.16	0.46
1:5:2440:U:O2'	1:5:2441:C:OP1	2.31	0.46
1:5:4304:A:C2	30:a:43:ILE:HG23	2.50	0.46
4:9:692:G:H2'	4:9:693:A:H8	1.80	0.46
22:S:78:PHE:CE1	22:S:102:THR:HG22	2.50	0.46
45:r:38:PHE:O	45:r:45:HIS:HE1	1.98	0.46
1:5:54:G:OP1	81:j:43:ARG:NH1	2.49	0.46
1:5:466:A:H4'	1:5:467:U:OP1	2.14	0.46
1:5:2287:G:O6	30:a:10:LYS:HE2	2.15	0.46
1:5:4481:U:H2'	1:5:4482:U:H6	1.81	0.46
1:5:4507:A:H2'	1:5:4508:C:C6	2.51	0.46
3:8:8:U:H2'	3:8:9:A:H8	1.79	0.46
3:8:75:G:OP2	28:Y:74:TYR:OH	2.23	0.46
4:9:1010:G:H2'	4:9:1011:A:H8	1.79	0.46
4:9:1404:U:P	66:UU:21:ARG:HH22	2.37	0.46
11:H:120:GLU:OE1	11:H:124:ARG:NH2	2.38	0.46
18:O:181:ALA:O	18:O:185:VAL:HG22	2.16	0.46
22:S:28:TYR:CE1	22:S:52:LYS:HE3	2.50	0.46
80:13:53:G:H2'	80:13:54:A:H8	1.79	0.46
1:5:1402:C:H2'	1:5:1403:G:C8	2.51	0.46
1:5:1406(B):C:H2'	1:5:1406(C):G:C8	2.50	0.46
1:5:1890:G:H22	1:5:1939:A:H61	1.64	0.46
1:5:4635:A:H8	1:5:5048:A:N6	2.11	0.46
4:9:344:U:H2'	4:9:345:U:C6	2.51	0.46
4:9:1375:G:H2'	4:9:1376:A:C8	2.50	0.46
51:FF:99:ILE:HG23	71:ZZ:67:LEU:HD22	1.98	0.46
1:5:272:U:H2'	1:5:273:U:C6	2.51	0.46
1:5:1088:C:H2'	1:5:1089:G:H8	1.81	0.46
1:5:4537:C:H2'	1:5:4538:G:H8	1.81	0.46
4:9:789:G:H2'	4:9:790:C:C6	2.50	0.46
4:9:1858:G:OP1	72:aa:17:HIS:HE1	1.99	0.46
49:DD:120:TYR:HA	49:DD:123:LEU:HD12	1.97	0.46
55:JJ:35:TYR:CD2	55:JJ:106:LEU:HD23	2.50	0.46
80:13:3:G:C8	84:13:101:ATP:H2'	2.51	0.46
80:11:18:G:H1'	80:11:57:G:N2	2.30	0.46
1:5:8:U:H5''	17:N:40:PRO:HG3	1.98	0.46
1:5:1189:G:C6	1:5:1190:C:C4	3.03	0.46
1:5:1883:G:O6	1:5:1896:A:H2	1.99	0.46
1:5:4935:C:H2'	1:5:4936:G:H8	1.81	0.46
4:9:533:A:H2'	4:9:534:G:H8	1.80	0.46
4:9:986:G:C8	60:OO:137:SER:O	2.69	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:9:1060:A:O2'	4:9:1062:A:N7	2.39	0.46
4:9:1589:A:H2'	4:9:1590:C:C6	2.51	0.46
78:gg:244:ASN:ND2	78:gg:294:ASP:O	2.48	0.46
1:5:163:A:H2'	1:5:164:G:C8	2.50	0.46
1:5:1975:G:N2	1:5:1983:A:OP1	2.40	0.46
1:5:2566:G:H2'	1:5:2567:G:C8	2.50	0.46
1:5:3642:A:C4	81:j:3:LYS:HB3	2.51	0.46
1:5:4045:G:H2'	1:5:4046:A:H3'	1.98	0.46
1:5:4897:G:H2'	1:5:4898:G:C8	2.50	0.46
1:5:4937:C:H2'	1:5:4939:C:C5	2.51	0.46
6:B:56:ILE:O	6:B:73:VAL:HA	2.16	0.46
22:S:81:TRP:HB3	22:S:127:MET:HE3	1.98	0.46
62:QQ:97:GLN:HA	62:QQ:105:LYS:CE	2.45	0.46
1:5:664:G:H2'	1:5:665:C:C6	2.51	0.46
1:5:3732:A:H2'	1:5:3733:A:C8	2.51	0.46
1:5:3968:U:O2'	1:5:3969:G:OP1	2.26	0.46
4:9:398:A:H5'	4:9:398:A:C8	2.51	0.46
4:9:789:G:H2'	4:9:790:C:H6	1.82	0.46
47:BB:153:THR:HB	47:BB:155:TYR:CD2	2.51	0.46
1:5:374:G:OP2	81:j:56:ARG:NH2	2.42	0.45
1:5:665:C:H5''	1:5:666:G:O5'	2.16	0.45
1:5:1190:C:H2'	1:5:1191:C:C6	2.51	0.45
1:5:1771:U:H2'	1:5:1772:C:C6	2.51	0.45
1:5:4754:G:OP1	35:f:4:ARG:NH1	2.49	0.45
4:9:940:U:H2'	4:9:941:C:C6	2.52	0.45
11:H:41:ILE:HG21	11:H:73:ILE:HD11	1.96	0.45
80:13:74:C:O2'	80:13:75:C:OP1	2.25	0.45
4:9:200:G:H2'	4:9:201:C:C6	2.52	0.45
4:9:1310:U:H2'	4:9:1311:C:C6	2.52	0.45
19:P:54:LYS:HA	19:P:83:TRP:CD1	2.51	0.45
19:P:85:LYS:NZ	19:P:89:GLU:OE2	2.42	0.45
58:MM:75:ASN:HB3	58:MM:128:PHE:CE2	2.52	0.45
1:5:2079:G:H2'	1:5:2080:U:C6	2.52	0.45
4:9:958:G:H2'	4:9:959:G:C8	2.51	0.45
15:L:62:PRO:O	15:L:63:THR:HB	2.17	0.45
40:l:23:ILE:HD11	40:l:28:TRP:HE1	1.82	0.45
51:FF:165:ASN:OD1	51:FF:166:ILE:N	2.49	0.45
58:MM:92:CYS:SG	58:MM:103:VAL:HG13	2.57	0.45
62:QQ:102:GLU:HA	62:QQ:105:LYS:CE	2.47	0.45
1:5:2016:C:H2'	1:5:2017:A:H8	1.82	0.45
1:5:2809:G:O2'	1:5:4644:G:OP1	2.26	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:3625:G:O2'	1:5:3626:G:OP1	2.34	0.45
1:5:4342:C:O3'	43:o:37:GLY:HA3	2.17	0.45
1:5:4611:A:H2'	1:5:4612:C:C6	2.51	0.45
1:5:4704:C:H2'	1:5:4705:A:H8	1.82	0.45
4:9:1527:C:OP1	62:QQ:142:GLN:NE2	2.38	0.45
4:9:1539:U:H2'	4:9:1540:G:C8	2.52	0.45
50:EE:168:LYS:NZ	52:GG:208:GLU:OE2	2.45	0.45
1:5:516:C:H2'	1:5:517:C:H6	1.81	0.45
1:5:3917:A:H2'	1:5:3918:G:H8	1.81	0.45
19:P:39:MET:O	19:P:114:ILE:HG22	2.17	0.45
46:AA:111:GLN:HA	46:AA:116:PHE:CD1	2.52	0.45
54:II:119:LEU:HD11	54:II:153:LYS:HG2	1.99	0.45
67:VV:20:SER:C	67:VV:22:ARG:H	2.25	0.45
80:11:35:A:H2'	80:11:36:U:H6	1.81	0.45
1:5:492:U:H4'	1:5:493:G:OP2	2.17	0.45
1:5:686:A:N3	1:5:686:A:H2'	2.32	0.45
1:5:746:A:O2'	1:5:747:A:H8	2.00	0.45
1:5:3611:A:H2	1:5:5016:A:H8	1.63	0.45
1:5:4051:C:H2'	1:5:4052:C:C6	2.51	0.45
1:5:4233:A:C4	1:5:4235:G:N7	2.85	0.45
3:8:141:C:H5'	17:N:113:LEU:HD11	1.99	0.45
4:9:1337:C:H2'	4:9:1338:G:C8	2.51	0.45
4:9:1643:U:H2'	4:9:1644:C:C6	2.51	0.45
80:13:69:U:H2'	80:13:70:G:C8	2.52	0.45
80:11:9:U:H1'	80:11:48:C:H1'	1.99	0.45
80:11:62:C:H2'	80:11:63:A:C8	2.52	0.45
1:5:6:C:H2'	1:5:7:C:C6	2.52	0.45
1:5:1982:G:H5'	1:5:1982:G:C8	2.52	0.45
1:5:4896:G:N2	1:5:4927:G:O6	2.44	0.45
4:9:693:A:H2'	4:9:694:G:C8	2.52	0.45
4:9:1017:U:H2'	4:9:1018:U:C6	2.51	0.45
4:9:1520:G:H2'	4:9:1520:G:N3	2.32	0.45
4:9:1553:C:H2'	4:9:1554:C:C5	2.52	0.45
7:C:60:HIS:NE2	7:C:100:ARG:HD3	2.32	0.45
9:E:96:THR:HG22	9:E:109:VAL:HG22	1.98	0.45
27:X:82:THR:HG22	27:X:155:ILE:HG23	1.98	0.45
52:GG:84:TYR:OH	52:GG:91:GLU:OE1	2.33	0.45
66:UU:64:THR:HA	66:UU:78:ASP:O	2.16	0.45
1:5:677:G:H2'	1:5:678:C:C6	2.51	0.45
1:5:4047:A:O2'	1:5:4048:A:OP1	2.28	0.45
50:EE:44:LEU:HD11	50:EE:70:ILE:HG21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:PP:22:LEU:HA	61:PP:25:LEU:HD12	1.99	0.45
70:YY:53:ASP:OD1	70:YY:53:ASP:N	2.49	0.45
1:5:2345:G:N7	30:a:9:ARG:NH2	2.64	0.45
1:5:3923:A:H2'	1:5:3924:C:C6	2.52	0.45
1:5:4174:U:H2'	1:5:4175:G:C8	2.51	0.45
4:9:581:U:H4'	70:YY:66:GLY:CA	2.47	0.45
4:9:928:G:H2'	4:9:929:G:C8	2.52	0.45
7:C:303:ARG:NH1	20:Q:40:ASN:OD1	2.49	0.45
1:5:457:G:H2'	1:5:458:C:C6	2.52	0.44
1:5:711:A:H2'	1:5:712:C:C6	2.52	0.44
1:5:2894:A:H2'	1:5:2895:A:C8	2.51	0.44
3:8:70:G:H5''	28:Y:27:ARG:CZ	2.47	0.44
4:9:642:U:OP2	76:ee:107:ARG:NH2	2.50	0.44
4:9:916:A:C5	59:NN:73:ARG:HD3	2.51	0.44
49:DD:123:LEU:HD11	49:DD:152:PHE:CB	2.45	0.44
78:gg:191:HIS:CG	78:gg:195:LEU:HD21	2.52	0.44
80:11:73:A:HO2'	80:11:74:C:P	2.39	0.44
1:5:1670:G:N2	1:5:1854:G:H2'	2.33	0.44
1:5:2266:C:O2'	45:r:39:ARG:NH1	2.50	0.44
3:8:67:U:H2'	3:8:68:G:C8	2.49	0.44
50:EE:100:ARG:HH21	50:EE:118:GLU:HB3	1.82	0.44
51:FF:193:LYS:HE2	51:FF:197:GLU:OE2	2.18	0.44
52:GG:58:LYS:HA	52:GG:107:SER:HB2	1.99	0.44
1:5:1070:G:OP2	9:E:67:ARG:NH2	2.50	0.44
1:5:1364:U:OP2	15:L:36:ARG:NH2	2.39	0.44
1:5:1617:G:H1'	1:5:2513:A:N6	2.32	0.44
1:5:1890:G:N2	1:5:1939:A:H61	2.14	0.44
1:5:4458:C:H2'	1:5:4459:U:H6	1.82	0.44
4:9:1260:A:C2	4:9:1620:A:C8	3.05	0.44
6:B:189:THR:HG23	6:B:192:GLU:H	1.82	0.44
13:J:99:PHE:CD2	13:J:105:PHE:HB3	2.52	0.44
1:5:262:G:H2'	1:5:263:G:C8	2.46	0.44
1:5:474:C:H2'	1:5:475:G:C8	2.53	0.44
1:5:1461:C:H2'	1:5:1462:A:H8	1.83	0.44
1:5:2317:C:OP1	34:e:14:LYS:NZ	2.42	0.44
1:5:2335:C:H2'	1:5:2336:G:H8	1.82	0.44
1:5:2479:G:H2'	1:5:2480:G:H8	1.83	0.44
1:5:2714:G:OP2	39:k:70:LYS:NZ	2.46	0.44
1:5:2872:C:H5''	42:n:25:LYS:HE2	2.00	0.44
1:5:3717:A:H2'	1:5:3718:A:H8	1.78	0.44
4:9:537:C:C2	4:9:538:U:C5	3.05	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:9:1671:G:H2'	4:9:1672:U:H6	1.81	0.44
4:9:1868:U:O4	72:aa:98:PRO:HG2	2.17	0.44
49:DD:103:GLU:OE1	49:DD:106:ARG:NH1	2.49	0.44
1:5:396:A:H2'	1:5:397:G:C8	2.52	0.44
1:5:1957:U:O2'	1:5:1958:A:H8	2.00	0.44
1:5:3635:A:H61	44:p:18:TYR:HA	1.81	0.44
1:5:4099:G:N2	1:5:4109:G:H22	2.15	0.44
1:5:4266:G:N3	1:5:4266:G:H2'	2.32	0.44
2:7:3:C:H2'	2:7:4:U:C6	2.51	0.44
33:d:36:VAL:HG21	33:d:44:ARG:HG2	1.99	0.44
62:QQ:102:GLU:HB2	78:gg:55:PRO:O	2.18	0.44
1:5:2275:G:H2'	1:5:2276:A:C8	2.53	0.44
4:9:349:A:H2'	4:9:350:C:C6	2.52	0.44
4:9:898:U:H2'	4:9:899:U:C6	2.52	0.44
4:9:1700:C:C2	4:9:1834:A:N6	2.86	0.44
33:d:98:SER:HB2	33:d:99:PRO:CD	2.48	0.44
44:p:38:THR:HA	44:p:45:THR:HA	2.00	0.44
1:5:268:G:H2'	1:5:269:G:C8	2.53	0.44
1:5:484:U:O2'	1:5:485:C:OP1	2.28	0.44
1:5:4068:U:H2'	1:5:4069:U:O4'	2.18	0.44
1:5:4341:C:N3	80:11:76:A:O2'	2.34	0.44
1:5:4504:C:H2'	1:5:4505:C:C6	2.53	0.44
4:9:128:U:OP2	4:9:129:C:N4	2.44	0.44
4:9:575:A:OP2	70:YY:93:ARG:NH2	2.46	0.44
4:9:1083:A:H4'	4:9:1085:C:C4	2.52	0.44
4:9:1446:A:OP1	66:UU:58:THR:HG22	2.18	0.44
4:9:1679:A:P	51:FF:60:ARG:HE	2.40	0.44
43:o:24:THR:HG23	43:o:69:ARG:HB3	2.00	0.44
43:o:72:CYS:O	43:o:78:ARG:HA	2.18	0.44
56:KK:1:MET:HE1	56:KK:43:LEU:HG	1.99	0.44
1:5:497:G:H5'	1:5:497:G:C8	2.53	0.44
1:5:956:A:C8	1:5:957:G:C8	3.03	0.44
1:5:1411(B):C:H2'	1:5:1411(C):C:C6	2.53	0.44
1:5:4594:U:H2'	1:5:4595:G:C8	2.52	0.44
13:J:99:PHE:O	13:J:159:LYS:NZ	2.45	0.44
52:GG:200:LYS:NZ	52:GG:204:GLU:OE2	2.46	0.44
1:5:116:G:H2'	1:5:117:C:C6	2.53	0.44
1:5:510:U:H5'	30:a:86:THR:HG22	2.00	0.44
1:5:1098:G:C8	1:5:1198:G:N2	2.86	0.44
1:5:1195:G:H2'	1:5:1196:G:C8	2.52	0.44
1:5:4591:U:H2'	1:5:4592:C:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:4886:C:H2'	1:5:4887:C:C6	2.52	0.44
3:8:86:U:O2'	3:8:87:G:OP1	2.31	0.44
4:9:963:A:H2'	4:9:964:A:C8	2.53	0.44
45:r:103:HIS:ND1	45:r:105:ASP:OD1	2.50	0.44
1:5:481(A):C:H5'	1:5:484:U:OP2	2.18	0.43
1:5:967:C:H3'	1:5:968:C:C5	2.53	0.43
1:5:1396:G:N7	30:a:110:LYS:NZ	2.56	0.43
1:5:1406:G:H2'	1:5:1406(A):G:H8	1.82	0.43
1:5:1568:C:OP2	44:p:3:LYS:HE3	2.18	0.43
1:5:2415:U:H2'	1:5:2416:G:C8	2.53	0.43
1:5:2894:A:H2'	1:5:2895:A:H8	1.83	0.43
1:5:3726:A:H2'	1:5:3727:A:C8	2.53	0.43
1:5:3890:A:N6	1:5:4570:G:O2'	2.50	0.43
3:8:85:U:O4	28:Y:50:ARG:NH2	2.39	0.43
4:9:1479:G:O2'	62:QQ:131:LYS:HE2	2.18	0.43
4:9:1865:C:OP1	72:aa:87:ARG:NH1	2.40	0.43
9:E:191:ARG:NH1	9:E:217:ASP:OD1	2.46	0.43
59:NN:60:VAL:HG13	59:NN:66:VAL:HG21	2.00	0.43
61:PP:34:MET:O	61:PP:42:ARG:HG2	2.17	0.43
1:5:1984:A:C8	1:5:2011:C:OP1	2.70	0.43
1:5:2522:G:P	36:g:29:ARG:HH21	2.41	0.43
1:5:3652:A:H2'	1:5:3653:A:C5	2.52	0.43
1:5:4233:A:C8	1:5:4235:G:C8	3.06	0.43
1:5:5055:G:H2'	1:5:5056:A:C8	2.53	0.43
4:9:186:C:H2'	4:9:187:G:C8	2.53	0.43
78:gg:87:LEU:HB2	78:gg:101:PHE:CD1	2.54	0.43
1:5:474:C:H2'	1:5:475:G:H8	1.81	0.43
1:5:1080:C:H2'	1:5:1081:C:C6	2.53	0.43
1:5:1194:G:C2	1:5:1195:G:H1'	2.53	0.43
1:5:1233:G:O2'	1:5:1234:G:OP2	2.32	0.43
1:5:1249:C:H4'	1:5:1250:C:OP2	2.18	0.43
1:5:2862:G:N3	1:5:3624:A:H2'	2.32	0.43
1:5:3727:A:H2'	1:5:3728:A:C8	2.53	0.43
4:9:1293:A:H62	4:9:1306:U:H3	1.66	0.43
4:9:1660:C:OP2	75:dd:32:ARG:NH2	2.43	0.43
7:C:149:GLU:OE2	45:r:71:ARG:NE	2.47	0.43
47:BB:199:LYS:HE3	47:BB:199:LYS:HB3	1.89	0.43
80:13:72:U:H3	84:13:101:ATP:HN62	1.65	0.43
1:5:288:G:H2'	1:5:289:C:C6	2.53	0.43
1:5:922(A):G:H2'	1:5:922(B):C:C6	2.54	0.43
1:5:2520:C:H2'	1:5:2521:G:H8	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:2864:A:H2'	1:5:2865:U:C6	2.53	0.43
1:5:4524:G:C2	6:B:252:ALA:HB1	2.53	0.43
1:5:4897:G:H2'	1:5:4898:G:H8	1.81	0.43
4:9:190:G:O2'	4:9:209:A:N6	2.51	0.43
4:9:830:A:OP2	4:9:846:G:N2	2.52	0.43
4:9:1115:U:O2'	4:9:1116:C:P	2.77	0.43
19:P:38:GLY:H	19:P:114:ILE:HG23	1.83	0.43
22:S:86:SER:N	22:S:89:GLY:O	2.51	0.43
36:g:15:THR:HG22	36:g:16:ALA:H	1.83	0.43
47:BB:174:ARG:NH2	47:BB:196:ASP:OD2	2.46	0.43
1:5:1195:G:C6	1:5:1196:G:C6	3.07	0.43
1:5:2621:A:H2'	1:5:2622:G:C8	2.54	0.43
1:5:4862:G:H2'	1:5:4863:G:C8	2.53	0.43
4:9:866:U:H2'	4:9:867:G:C8	2.54	0.43
4:9:1531:A:H2'	4:9:1532:C:C6	2.54	0.43
27:X:72:ASP:OD1	27:X:73:HIS:N	2.49	0.43
57:LL:101:ARG:NH1	69:XX:5:ARG:O	2.51	0.43
58:MM:14:VAL:HG12	58:MM:17:ALA:H	1.84	0.43
80:11:9:U:H5'	80:11:49:G:H5'	2.01	0.43
80:11:73:A:O2'	80:11:74:C:O5'	2.36	0.43
1:5:163:A:H2'	1:5:164:G:H8	1.82	0.43
1:5:918:G:H5'	16:M:72:TYR:CZ	2.54	0.43
4:9:126:G:O2'	4:9:127:C:OP1	2.35	0.43
4:9:873:G:N2	21:R:163:ARG:HH11	2.17	0.43
4:9:1347:U:H2'	4:9:1348:G:N3	2.33	0.43
21:R:28:GLU:HG3	21:R:49:LEU:HD22	2.01	0.43
66:UU:59:LYS:HD2	66:UU:84:ILE:HD11	1.99	0.43
80:13:23:C:H2'	80:13:24:G:C8	2.53	0.43
1:5:1683:U:H2'	1:5:1684:A:C8	2.54	0.43
4:9:1177:U:H2'	4:9:1178:U:C6	2.54	0.43
51:FF:51:HIS:O	62:QQ:50:LYS:HE3	2.18	0.43
1:5:29:G:OP2	17:N:189:ARG:NH1	2.49	0.43
1:5:1472:C:H2'	1:5:1473:U:C6	2.53	0.43
1:5:2520:C:H2'	1:5:2521:G:C8	2.54	0.43
1:5:2616:C:OP1	21:R:60:ARG:NH1	2.52	0.43
1:5:2663:G:H2'	1:5:2664:G:H8	1.84	0.43
1:5:2694:G:H5'	1:5:2696:A:N7	2.34	0.43
1:5:4704:C:H2'	1:5:4705:A:C8	2.53	0.43
1:5:4949:G:N3	1:5:4949:G:H5'	2.33	0.43
4:9:74:G:O6	52:GG:159:ARG:NH1	2.48	0.43
4:9:494:C:N4	4:9:509:G:H21	2.16	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:9:495:U:H2'	4:9:496:C:O4'	2.18	0.43
4:9:521:A:OP1	55:JJ:45:ARG:NH1	2.49	0.43
4:9:543:C:O2'	4:9:544:G:OP1	2.36	0.43
4:9:1475:G:P	62:QQ:117:ARG:HH22	2.41	0.43
19:P:30:ARG:NH1	19:P:31:GLU:OE1	2.51	0.43
20:Q:154:LYS:HE2	20:Q:158:THR:HG21	2.00	0.43
46:AA:142:LEU:O	67:VV:60:ARG:NH2	2.51	0.43
69:XX:60:LYS:HD2	69:XX:116:PRO:HB3	2.00	0.43
1:5:172:C:O2	37:h:112:ARG:NH1	2.40	0.43
1:5:974:C:H41	1:5:1281:G:N2	2.17	0.43
69:XX:88:ASP:OD1	76:ee:83:GLY:HA2	2.18	0.43
1:5:201:C:H2'	1:5:202:C:C6	2.54	0.43
4:9:1863:A:H1'	72:aa:79:ILE:HD13	2.01	0.43
40:l:24:PRO:HD2	40:l:27:ILE:HD12	2.01	0.43
67:VV:2:GLN:HA	67:VV:7:GLU:O	2.18	0.43
1:5:3968:U:HO2'	1:5:3969:G:P	2.41	0.42
4:9:1114:U:H5''	4:9:1115:U:OP2	2.19	0.42
9:E:176:LEU:O	9:E:192:THR:N	2.49	0.42
31:b:108:ALA:O	31:b:112:ILE:HG12	2.19	0.42
45:r:46:ARG:HA	45:r:70:GLN:NE2	2.34	0.42
1:5:5041:G:OP2	26:W:61:LYS:NZ	2.43	0.42
4:9:1656:G:C2	4:9:1657:G:C8	3.07	0.42
8:D:193:GLU:O	8:D:197:LYS:HG2	2.19	0.42
11:H:54:ARG:HG2	11:H:54:ARG:HH11	1.84	0.42
16:M:10:GLY:HA2	16:M:64:PHE:CZ	2.54	0.42
78:gg:199:THR:HG23	78:gg:241:PHE:CE2	2.54	0.42
1:5:318:A:O2'	1:5:3727:A:H1'	2.20	0.42
1:5:1307:A:H2'	1:5:1308:C:C6	2.54	0.42
1:5:1847:C:H4'	20:Q:152:PHE:CE2	2.54	0.42
1:5:1957:U:O2'	1:5:1958:A:O5'	2.37	0.42
1:5:2517:A:O2'	36:g:66:ARG:NH2	2.52	0.42
1:5:2640:G:H2'	1:5:2641:A:C8	2.54	0.42
1:5:2703:G:C6	1:5:2714:G:C6	3.08	0.42
1:5:3867:A:H2'	1:5:3868:G:C8	2.54	0.42
1:5:3972:A:O5'	1:5:3972:A:C8	2.72	0.42
1:5:4070:U:H2'	1:5:4071:U:C6	2.54	0.42
1:5:4134:C:H2'	1:5:4135:G:C8	2.54	0.42
3:8:33:G:H4'	3:8:34:U:C5	2.55	0.42
4:9:1222:G:H5''	51:FF:78:MET:HE3	2.02	0.42
4:9:1423:C:H2'	4:9:1424:G:O4'	2.20	0.42
4:9:1743:G:H21	4:9:1791:A:H62	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:92:PHE:CD1	10:G:100:PRO:HD3	2.54	0.42
70:YY:80:ASP:OD1	70:YY:80:ASP:N	2.53	0.42
80:13:51:U:H2'	80:13:52:G:H8	1.83	0.42
1:5:2299:G:H5''	1:5:2300:A:OP2	2.19	0.42
1:5:2771:G:H2'	1:5:2772:C:O4'	2.18	0.42
4:9:529:A:H2'	4:9:530:U:H6	1.83	0.42
4:9:634:A:H2'	4:9:635:G:H8	1.85	0.42
4:9:1088:U:H4'	4:9:1089:G:OP2	2.19	0.42
4:9:1117:C:O2'	4:9:1118:C:O4'	2.37	0.42
4:9:1479:G:N2	75:dd:56:ASP:OD2	2.52	0.42
4:9:1522:A:P	64:SS:144:ARG:HH21	2.41	0.42
43:o:77:CYS:SG	43:o:78:ARG:N	2.93	0.42
48:CC:169:TYR:CG	48:CC:173:LYS:HA	2.54	0.42
49:DD:72:VAL:CG1	56:KK:68:TYR:HD2	2.32	0.42
51:FF:39:ILE:HG22	51:FF:41:VAL:HG23	2.01	0.42
51:FF:119:SER:OG	51:FF:189:ALA:HB1	2.19	0.42
58:MM:69:CYS:O	58:MM:73:GLN:N	2.52	0.42
1:5:981:C:OP2	9:E:48:ARG:NH2	2.51	0.42
1:5:4737:G:H2'	1:5:4738:C:C6	2.55	0.42
4:9:51:U:H2'	4:9:52:G:C8	2.54	0.42
4:9:96:C:H2'	4:9:97:U:C6	2.55	0.42
4:9:1120:U:H5''	73:bb:72:ARG:NH2	2.35	0.42
4:9:1315:U:H4'	56:KK:2:LEU:HG	2.02	0.42
4:9:1698:C:HO2'	4:9:1699:A:P	2.41	0.42
9:E:118:TYR:CE1	45:r:119:ARG:HD2	2.55	0.42
11:H:59:LYS:HE2	11:H:66:GLU:HB3	2.01	0.42
47:BB:76:ASN:ND2	47:BB:77:ASP:OD2	2.52	0.42
1:5:2083:C:H5''	1:5:2084:U:OP2	2.19	0.42
1:5:2543:A:H4'	3:8:126:C:O2	2.18	0.42
1:5:2634:C:H2'	1:5:2635:U:C6	2.54	0.42
4:9:608:C:H5'	4:9:608:C:C6	2.54	0.42
4:9:1865:C:OP2	72:aa:5:ARG:NH1	2.53	0.42
4:9:1866:A:N6	72:aa:84:VAL:HB	2.35	0.42
6:B:95:THR:HG23	6:B:96:PRO:HD2	2.02	0.42
8:D:62:CYS:HB3	8:D:105:LEU:HD22	2.01	0.42
36:g:15:THR:HG22	36:g:16:ALA:N	2.35	0.42
52:GG:52:ILE:HG23	52:GG:52:ILE:O	2.19	0.42
58:MM:32:ALA:N	58:MM:110:VAL:O	2.52	0.42
62:QQ:97:GLN:HA	62:QQ:105:LYS:CD	2.50	0.42
62:QQ:100:VAL:HG12	62:QQ:101:ASP:N	2.34	0.42
67:VV:1:MET:O	67:VV:9:VAL:HG22	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:XX:68:LYS:HG2	76:ee:82:VAL:HG22	2.02	0.42
80:13:65:C:H2'	80:13:66:C:H6	1.85	0.42
1:5:746:A:HO2'	1:5:747:A:H8	1.66	0.42
1:5:4577:U:H2'	1:5:4578:G:H8	1.85	0.42
46:AA:63:ARG:HG3	46:AA:185:MET:HE1	2.00	0.42
70:YY:86:GLU:OE2	70:YY:90:ARG:HD2	2.18	0.42
1:5:195:C:H2'	1:5:196:C:C6	2.54	0.42
1:5:1211:G:O2'	1:5:1212:G:OP1	2.32	0.42
1:5:1344:C:H2'	1:5:1345:A:C8	2.54	0.42
4:9:182:C:H4'	4:9:183:G:O5'	2.20	0.42
4:9:1662:U:O4	4:9:1663:A:N6	2.51	0.42
9:E:48:ARG:C	9:E:64:MET:HE1	2.45	0.42
9:E:58:ARG:O	9:E:58:ARG:NH1	2.39	0.42
18:O:10:ASP:OD1	18:O:37:ARG:HD3	2.19	0.42
58:MM:85:LEU:HD21	58:MM:109:VAL:HG23	2.01	0.42
68:WW:121:THR:HG22	68:WW:122:GLY:O	2.19	0.42
1:5:750:U:H2'	1:5:751:G:O4'	2.20	0.42
1:5:1246:G:H2'	1:5:1247:U:C6	2.54	0.42
1:5:1320:U:O2'	1:5:1891:A:N1	2.34	0.42
1:5:1358:G:H2'	1:5:1360:G:O6	2.19	0.42
1:5:1920:C:H3'	1:5:1921:C:H5''	2.01	0.42
1:5:2004:U:O2	1:5:2016:C:H1'	2.20	0.42
1:5:2491:C:H2'	1:5:2492:C:C6	2.54	0.42
1:5:3695:U:H2'	1:5:3696:C:O4'	2.20	0.42
1:5:4884:G:H2'	1:5:4885:U:O4'	2.20	0.42
4:9:368:U:O2'	4:9:369:C:OP1	2.36	0.42
4:9:626:G:N3	4:9:626:G:H2'	2.34	0.42
4:9:1578:U:H5'	4:9:1579:A:N3	2.33	0.42
8:D:146:LEU:HD21	8:D:159:VAL:HG12	2.01	0.42
28:Y:111:LEU:HB3	28:Y:116:LYS:HE3	2.02	0.42
50:EE:160:ILE:HD12	50:EE:169:ILE:HG12	2.01	0.42
55:JJ:136:ARG:NH1	55:JJ:159:PHE:O	2.45	0.42
1:5:667:A:C2	7:C:29:LYS:HE3	2.55	0.42
1:5:4099:G:N2	1:5:4109:G:N2	2.68	0.42
1:5:4112:C:H2'	1:5:4113:U:C6	2.55	0.42
4:9:383:G:H21	57:LL:133:PRO:HG2	1.85	0.42
26:W:23:ARG:NH2	26:W:27:LYS:HD3	2.34	0.42
46:AA:30:LEU:HD13	46:AA:38:ILE:CD1	2.50	0.42
56:KK:62:PHE:CZ	56:KK:65:ARG:HA	2.55	0.42
1:5:128:C:H2'	1:5:129:C:C6	2.55	0.41
1:5:1564:A:H2'	1:5:1565:A:C8	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:4099:G:H22	1:5:4109:G:N2	2.17	0.41
1:5:4927:G:OP2	1:5:4927:G:N2	2.37	0.41
4:9:1204:A:H2'	4:9:1205:C:O4'	2.20	0.41
4:9:1337:C:H2'	4:9:1338:G:H8	1.85	0.41
14:K:66:THR:O	14:K:70:MET:HG2	2.20	0.41
15:L:7:GLY:O	30:a:49:HIS:NE2	2.51	0.41
22:S:41:LYS:HG2	22:S:61:ILE:HD13	2.02	0.41
24:U:54:GLY:C	24:U:56:LEU:H	2.27	0.41
46:AA:2:SER:CB	67:VV:80:SER:HB2	2.50	0.41
47:BB:181:LEU:HA	47:BB:184:VAL:HG22	2.01	0.41
51:FF:80:GLY:HA2	51:FF:83:ASN:ND2	2.35	0.41
58:MM:95:ASP:HB2	58:MM:99:LYS:HG2	2.02	0.41
71:ZZ:51:ASP:O	71:ZZ:54:THR:OG1	2.32	0.41
80:11:62:C:H2'	80:11:63:A:H8	1.85	0.41
1:5:1628:C:OP2	5:A:9:ARG:NH1	2.47	0.41
1:5:3653:A:H4'	5:A:179:ILE:O	2.20	0.41
1:5:3789:C:OP2	1:5:3790:U:O2'	2.36	0.41
1:5:3947:A:H2'	1:5:3948:C:C6	2.56	0.41
4:9:1653:U:H2'	4:9:1654:G:C8	2.55	0.41
32:c:29:LEU:HD11	32:c:87:LYS:HE3	2.01	0.41
1:5:103:G:P	15:L:71:ARG:HD3	2.60	0.41
1:5:245:C:O2'	1:5:246:G:OP2	2.29	0.41
1:5:388:A:H1'	1:5:403:G:N2	2.36	0.41
1:5:650:C:H2'	1:5:651:C:C6	2.54	0.41
1:5:1761:G:N2	1:5:1772:C:C2	2.88	0.41
1:5:1786:A:H2'	1:5:1789:C:C5	2.55	0.41
1:5:2568:C:H2'	1:5:2569:G:H8	1.85	0.41
1:5:2874:U:O2	44:p:19:GLY:HA2	2.20	0.41
1:5:2899:C:H2'	1:5:2900:U:H6	1.84	0.41
1:5:3672:G:O5'	1:5:3672:G:C8	2.73	0.41
1:5:3773:U:H1'	1:5:3775:A:H2	1.85	0.41
1:5:3932:U:H2'	1:5:3933:G:C8	2.55	0.41
1:5:4524:G:H4'	1:5:4524:G:OP2	2.20	0.41
4:9:107:A:H2'	4:9:108:G:H8	1.86	0.41
4:9:1481:G:H2'	4:9:1482:C:O4'	2.21	0.41
7:C:297:GLU:HG2	20:Q:128:LEU:O	2.20	0.41
8:D:143:THR:HA	8:D:172:SER:O	2.20	0.41
22:S:99:ASP:OD2	22:S:108:GLN:NE2	2.47	0.41
30:a:127:LYS:NZ	30:a:148:ALA:O	2.50	0.41
47:BB:126:ASP:OD1	47:BB:136:ARG:HD3	2.21	0.41
50:EE:259:LYS:HE2	50:EE:259:LYS:HB2	1.92	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:FF:39:ILE:HG23	51:FF:68:ILE:HD13	2.02	0.41
51:FF:126:THR:HG21	74:cc:27:CYS:SG	2.59	0.41
58:MM:87:GLU:HA	58:MM:92:CYS:SG	2.60	0.41
61:PP:37:TYR:HB3	61:PP:41:GLN:HB2	2.01	0.41
1:5:1094:G:H2'	1:5:1095:A:C8	2.52	0.41
1:5:2030:A:H2'	1:5:2031:C:O4'	2.19	0.41
1:5:2559:G:C6	1:5:2569:G:C6	3.08	0.41
1:5:3934:G:H2'	1:5:3935:C:C6	2.55	0.41
2:7:105:C:OP2	12:I:203:ARG:NH1	2.34	0.41
4:9:30:C:O2'	4:9:596:U:OP1	2.28	0.41
4:9:674:C:H2'	4:9:675:U:C6	2.56	0.41
4:9:872:A:H2'	4:9:872:A:N3	2.35	0.41
4:9:1113:A:C6	4:9:1121:G:C6	3.08	0.41
4:9:1712:A:H2'	4:9:1713:C:C6	2.55	0.41
6:B:312:LYS:HE2	6:B:380:GLN:HB3	2.01	0.41
10:G:212:HIS:CE1	10:G:213:ASP:HB3	2.55	0.41
52:GG:32:MET:HB3	52:GG:100:CYS:HB2	2.02	0.41
69:XX:87:ASN:HB2	69:XX:90:CYS:SG	2.59	0.41
80:13:18:G:N2	80:13:57:G:H2'	2.35	0.41
1:5:510:U:C5'	30:a:86:THR:HG22	2.51	0.41
1:5:1440:U:H2'	1:5:1441:C:C6	2.56	0.41
1:5:1444:G:H2'	1:5:1445:U:C5	2.54	0.41
1:5:1961:G:O2'	1:5:2025:A:N6	2.54	0.41
1:5:2340:C:H5'	7:C:42:THR:HG21	2.03	0.41
1:5:4259:C:C4'	13:J:23:ASN:HD22	2.33	0.41
1:5:4441:A:H5''	12:I:114:GLY:HA2	2.01	0.41
1:5:4947:U:O2'	1:5:4948:C:OP1	2.33	0.41
3:8:66:A:H2'	3:8:67:U:C6	2.56	0.41
4:9:4:C:H4'	48:CC:207:ALA:HB2	2.03	0.41
4:9:1397:U:O4	62:QQ:12:VAL:HA	2.20	0.41
15:L:165:LYS:HB3	15:L:165:LYS:HE2	1.86	0.41
55:JJ:22:LYS:NZ	55:JJ:26:ASP:OD1	2.52	0.41
62:QQ:57:LEU:HD21	62:QQ:115:TYR:CD1	2.55	0.41
74:cc:7:GLN:N	74:cc:7:GLN:OE1	2.53	0.41
80:13:35:A:H2'	80:13:36:U:H6	1.85	0.41
80:11:20:A:O2'	80:11:21:A:OP2	2.35	0.41
1:5:1494:U:H2'	1:5:1495:G:C8	2.56	0.41
1:5:1673:U:H2'	1:5:1674:C:C6	2.55	0.41
1:5:1851:G:H4'	1:5:2283:G:H5'	2.02	0.41
1:5:2726:G:H2'	1:5:2727:C:C6	2.56	0.41
1:5:4729:A:H5''	1:5:4965:U:H1'	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:9:448:A:H62	54:II:29:LEU:HD13	1.83	0.41
4:9:581:U:H4'	70:YY:66:GLY:HA2	2.03	0.41
4:9:663:C:H2'	4:9:664:A:O4'	2.21	0.41
4:9:906:U:H2'	4:9:907:G:C8	2.55	0.41
4:9:1117:C:O2'	4:9:1118:C:C2	2.73	0.41
4:9:1199:A:OP1	72:aa:2:THR:N	2.54	0.41
6:B:115:LYS:HA	6:B:118:PHE:CD2	2.55	0.41
16:M:89:THR:HG22	16:M:91:TRP:H	1.85	0.41
51:FF:44:LYS:HB3	51:FF:44:LYS:HE2	1.92	0.41
52:GG:45:TRP:HA	52:GG:48:TYR:CD1	2.56	0.41
80:13:57:G:H2'	80:13:58:A:H5''	2.01	0.41
1:5:300:A:H2'	1:5:301:G:C8	2.55	0.41
1:5:2378:G:N2	1:5:2381:A:OP2	2.52	0.41
1:5:2516:G:O2'	36:g:62:LYS:NZ	2.53	0.41
1:5:2566:G:C2	1:5:2567:G:C5	3.08	0.41
1:5:4065:G:H2'	1:5:4066:U:C6	2.56	0.41
1:5:4077:A:N1	1:5:4171:C:N4	2.67	0.41
5:A:205:ASN:HB3	5:A:206:PRO:HD2	2.03	0.41
53:HH:23:ILE:HD13	53:HH:87:PHE:CZ	2.56	0.41
66:UU:59:LYS:HB2	66:UU:84:ILE:HG12	2.01	0.41
80:13:16:G:OP2	80:13:17:C:N4	2.54	0.41
1:5:263:G:C5	1:5:264:C:C4	3.09	0.41
1:5:2461:G:H2'	1:5:2462:C:C6	2.56	0.41
4:9:35:C:H5''	4:9:579:C:H5''	2.01	0.41
4:9:71:G:C6	4:9:79:A:C8	3.09	0.41
4:9:111:A:H2'	4:9:112:U:H5'	2.02	0.41
4:9:1541:G:N3	65:TT:12:GLN:NE2	2.69	0.41
49:DD:94:ARG:O	49:DD:101:GLN:NE2	2.54	0.41
56:KK:15:LEU:HD22	56:KK:49:MET:HE1	2.02	0.41
60:OO:65:ASP:OD1	60:OO:65:ASP:N	2.52	0.41
78:gg:105:THR:N	78:gg:126:ASP:OD2	2.46	0.41
1:5:480:C:P	45:r:67:ARG:HH21	2.44	0.41
1:5:978:G:H22	1:5:1277:G:N2	2.17	0.41
1:5:1276:C:H2'	1:5:1277:G:O4'	2.21	0.41
1:5:1314:C:C2	1:5:1315:C:C5	3.09	0.41
1:5:1332:C:H2'	1:5:1333:A:H8	1.86	0.41
1:5:1468:C:H2'	1:5:1469:C:C6	2.56	0.41
1:5:1483:C:H5''	1:5:1483:C:O2	2.20	0.41
1:5:1775:A:H2'	1:5:1776:A:C8	2.56	0.41
1:5:1804:A:H4'	1:5:1805:A:O5'	2.20	0.41
1:5:1947:U:C4	41:m:82:VAL:HG21	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:2440:U:HO2'	1:5:2441:C:P	2.43	0.41
1:5:2478:C:N3	1:5:2479:G:C5	2.88	0.41
1:5:3600:G:C6	1:5:3601:C:C4	3.08	0.41
1:5:3605:C:H5'	1:5:3606:U:OP2	2.21	0.41
1:5:3861:A:H2'	1:5:3862:A:C8	2.55	0.41
1:5:4107:G:H2'	1:5:4108:G:H8	1.86	0.41
1:5:4240:G:H2'	1:5:4241:C:O4'	2.20	0.41
1:5:4934:A:H2'	1:5:4935:C:H6	1.84	0.41
4:9:29:G:H2'	4:9:30:C:C6	2.55	0.41
4:9:1139:C:H5	4:9:1149:A:H62	1.69	0.41
4:9:1563:G:H2'	4:9:1564:C:C6	2.55	0.41
16:M:108:ASP:HB3	18:O:199:HIS:CD2	2.55	0.41
27:X:119:ILE:HG21	27:X:140:LEU:HD22	2.03	0.41
46:AA:2:SER:N	46:AA:56:GLU:OE2	2.53	0.41
48:CC:196:ILE:HB	48:CC:223:TYR:HB2	2.03	0.41
53:HH:73:GLN:OE1	53:HH:76:GLN:NE2	2.53	0.41
64:SS:120:HIS:CE1	64:SS:124:ARG:HD2	2.56	0.41
80:13:58:A:H5'	80:13:58:A:C8	2.56	0.41
1:5:100:C:H2'	1:5:101:A:C8	2.56	0.41
1:5:1080:C:H2'	1:5:1081:C:H6	1.86	0.41
1:5:1234:G:O2'	1:5:1235:G:H8	2.03	0.41
1:5:1604:G:H2'	1:5:1605:G:C8	2.56	0.41
1:5:2632:U:H2'	1:5:2633:U:C6	2.56	0.41
1:5:4907:G:N2	1:5:4915:G:C4	2.89	0.41
1:5:4970:C:H2'	1:5:4971:A:H8	1.86	0.41
4:9:1447:G:O5'	66:UU:87:ARG:NH2	2.48	0.41
5:A:40:TYR:HA	5:A:90:CYS:O	2.21	0.41
6:B:301:ASN:ND2	6:B:311:ASP:OD1	2.44	0.41
58:MM:116:LYS:O	58:MM:118:SER:N	2.50	0.41
1:5:1168:G:H2'	1:5:1169:G:H8	1.86	0.40
1:5:1444:G:O5'	1:5:1444:G:H8	2.04	0.40
4:9:196:C:H2'	4:9:197:U:C6	2.56	0.40
4:9:1628:C:H2'	4:9:1629:C:C6	2.55	0.40
6:B:290:GLY:N	6:B:329:ASP:OD1	2.49	0.40
1:5:258:G:H2'	1:5:259:C:C6	2.56	0.40
1:5:740:G:H2'	1:5:741:C:C6	2.55	0.40
1:5:1872:G:O2'	1:5:4219:A:N3	2.45	0.40
1:5:2573:A:N7	1:5:2761:U:O4	2.54	0.40
1:5:4064:C:H2'	1:5:4065:G:O4'	2.21	0.40
4:9:547:G:C6	4:9:549:C:N4	2.89	0.40
4:9:649:U:H2'	4:9:650:A:H8	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:9:1309:C:H2'	4:9:1310:U:C6	2.55	0.40
11:H:40:HIS:ND1	11:H:41:ILE:HG13	2.36	0.40
12:I:38:ARG:HE	12:I:41:ALA:HB2	1.85	0.40
43:o:104:ILE:HG21	80:13:56:C:C4	2.56	0.40
44:p:8:VAL:O	44:p:11:VAL:HG22	2.21	0.40
47:BB:47:THR:OG1	47:BB:65:ARG:NH1	2.54	0.40
54:II:6:ASP:HB2	54:II:8:TRP:CD1	2.57	0.40
71:ZZ:58:LEU:HD12	71:ZZ:62:VAL:HG21	2.03	0.40
1:5:18:C:H4'	17:N:138:PHE:CD2	2.55	0.40
1:5:385:A:N3	1:5:387:G:H5''	2.36	0.40
1:5:518:G:C6	1:5:644:G:C6	3.08	0.40
1:5:1426:G:N2	1:5:1458:C:OP2	2.51	0.40
1:5:1882:U:C4	1:5:2279:A:C2	3.10	0.40
1:5:2409:U:H5	1:5:2783:A:N1	2.19	0.40
1:5:2627:C:C2	1:5:2628:U:C5	3.09	0.40
1:5:3748:A:H5''	5:A:243:THR:OG1	2.22	0.40
4:9:416:U:H2'	4:9:417:C:O4'	2.20	0.40
39:k:24:LYS:HA	39:k:67:LYS:O	2.20	0.40
45:r:90:LEU:HG	45:r:111:ILE:HG23	2.02	0.40
48:CC:68:ARG:HH21	48:CC:72:ASP:CG	2.27	0.40
48:CC:76:LYS:NZ	48:CC:80:GLU:OE2	2.38	0.40
52:GG:196:LYS:HB2	52:GG:196:LYS:HE3	1.87	0.40
78:gg:121:VAL:HG22	78:gg:131:LEU:HG	2.02	0.40
80:11:25:U:C2	80:11:26:G:C8	3.09	0.40
1:5:149:A:H8	1:5:149:A:H5'	1.87	0.40
1:5:1855:G:OP1	31:b:4:SER:HB2	2.21	0.40
4:9:1208:A:H2'	4:9:1209:A:C8	2.57	0.40
4:9:1782:G:H5''	4:9:1783:C:OP2	2.21	0.40
4:9:1801:A:H2'	4:9:1802:C:C6	2.56	0.40
45:r:46:ARG:HA	45:r:70:GLN:HE22	1.85	0.40
49:DD:211:VAL:O	63:RR:20:TYR:OH	2.34	0.40
52:GG:159:ARG:HB3	52:GG:171:THR:CG2	2.52	0.40
62:QQ:43:GLU:CD	62:QQ:45:ARG:HE	2.29	0.40
64:SS:130:ARG:HA	64:SS:130:ARG:HD3	1.94	0.40
69:XX:102:VAL:CG1	69:XX:120:PHE:HB3	2.51	0.40
78:gg:74:ASP:C	78:gg:76:GLN:H	2.30	0.40
1:5:746:A:O2'	1:5:747:A:C8	2.69	0.40
1:5:1970:A:H1'	1:5:2017:A:N6	2.33	0.40
1:5:2635:U:C4	1:5:2636:U:C4	3.10	0.40
1:5:3958:G:H2'	1:5:3959:U:C5	2.56	0.40
1:5:4061:G:H2'	1:5:4062:A:H8	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:4488:A:H4'	1:5:4489:G:H8	1.87	0.40
31:b:101:HIS:CD2	31:b:102:PRO:HD2	2.57	0.40
52:GG:148:SER:N	52:GG:151:ASP:OD2	2.41	0.40
65:TT:118:ASP:OD1	65:TT:119:GLY:N	2.53	0.40
67:VV:37:ALA:HB1	67:VV:46:PHE:CD1	2.57	0.40
80:13:17:C:H4'	80:13:60:A:H2	1.85	0.40
80:13:62:C:H2'	80:13:63:A:H8	1.85	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	A	246/257 (96%)	238 (97%)	8 (3%)	0	100	100
6	B	392/403 (97%)	377 (96%)	15 (4%)	0	100	100
7	C	360/425 (85%)	354 (98%)	6 (2%)	0	100	100
8	D	291/297 (98%)	284 (98%)	7 (2%)	0	100	100
9	E	208/291 (72%)	202 (97%)	6 (3%)	0	100	100
10	G	229/319 (72%)	221 (96%)	8 (4%)	0	100	100
11	H	188/192 (98%)	182 (97%)	6 (3%)	0	100	100
12	I	201/214 (94%)	196 (98%)	5 (2%)	0	100	100
13	J	168/178 (94%)	164 (98%)	4 (2%)	0	100	100
14	K	223/247 (90%)	217 (97%)	6 (3%)	0	100	100
15	L	208/211 (99%)	202 (97%)	6 (3%)	0	100	100
16	M	136/218 (62%)	133 (98%)	3 (2%)	0	100	100
17	N	201/204 (98%)	197 (98%)	4 (2%)	0	100	100
18	O	197/203 (97%)	193 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	P	151/184 (82%)	147 (97%)	4 (3%)	0	100	100
20	Q	185/188 (98%)	177 (96%)	8 (4%)	0	100	100
21	R	178/196 (91%)	176 (99%)	2 (1%)	0	100	100
22	S	174/176 (99%)	170 (98%)	4 (2%)	0	100	100
23	T	157/160 (98%)	154 (98%)	3 (2%)	0	100	100
24	U	97/128 (76%)	96 (99%)	1 (1%)	0	100	100
25	V	127/140 (91%)	126 (99%)	1 (1%)	0	100	100
26	W	102/157 (65%)	100 (98%)	2 (2%)	0	100	100
27	X	116/156 (74%)	113 (97%)	3 (3%)	0	100	100
28	Y	132/145 (91%)	131 (99%)	1 (1%)	0	100	100
29	Z	133/136 (98%)	129 (97%)	4 (3%)	0	100	100
30	a	145/148 (98%)	141 (97%)	4 (3%)	0	100	100
31	b	94/245 (38%)	92 (98%)	2 (2%)	0	100	100
32	c	96/115 (84%)	95 (99%)	1 (1%)	0	100	100
33	d	105/125 (84%)	98 (93%)	7 (7%)	0	100	100
34	e	126/135 (93%)	124 (98%)	2 (2%)	0	100	100
35	f	107/110 (97%)	106 (99%)	1 (1%)	0	100	100
36	g	112/116 (97%)	110 (98%)	2 (2%)	0	100	100
37	h	120/123 (98%)	120 (100%)	0	0	100	100
38	i	100/105 (95%)	97 (97%)	3 (3%)	0	100	100
39	k	67/70 (96%)	66 (98%)	1 (2%)	0	100	100
40	l	48/51 (94%)	48 (100%)	0	0	100	100
41	m	50/102 (49%)	49 (98%)	1 (2%)	0	100	100
42	n	23/25 (92%)	23 (100%)	0	0	100	100
43	o	102/106 (96%)	97 (95%)	5 (5%)	0	100	100
44	p	89/92 (97%)	87 (98%)	2 (2%)	0	100	100
45	r	122/137 (89%)	120 (98%)	2 (2%)	0	100	100
46	AA	215/295 (73%)	208 (97%)	7 (3%)	0	100	100
47	BB	211/264 (80%)	204 (97%)	7 (3%)	0	100	100
48	CC	219/293 (75%)	214 (98%)	5 (2%)	0	100	100
49	DD	222/243 (91%)	216 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	EE	260/263 (99%)	253 (97%)	7 (3%)	0	100	100
51	FF	180/204 (88%)	169 (94%)	11 (6%)	0	100	100
52	GG	235/249 (94%)	232 (99%)	3 (1%)	0	100	100
53	HH	181/194 (93%)	176 (97%)	5 (3%)	0	100	100
54	II	194/208 (93%)	188 (97%)	6 (3%)	0	100	100
55	JJ	179/194 (92%)	177 (99%)	2 (1%)	0	100	100
56	KK	94/165 (57%)	90 (96%)	4 (4%)	0	100	100
57	LL	139/158 (88%)	137 (99%)	2 (1%)	0	100	100
58	MM	108/132 (82%)	103 (95%)	5 (5%)	0	100	100
59	NN	147/151 (97%)	146 (99%)	1 (1%)	0	100	100
60	OO	134/168 (80%)	131 (98%)	3 (2%)	0	100	100
61	PP	127/145 (88%)	124 (98%)	3 (2%)	0	100	100
62	QQ	140/146 (96%)	137 (98%)	3 (2%)	0	100	100
63	RR	130/135 (96%)	128 (98%)	2 (2%)	0	100	100
64	SS	142/152 (93%)	136 (96%)	6 (4%)	0	100	100
65	TT	139/145 (96%)	135 (97%)	4 (3%)	0	100	100
66	UU	98/119 (82%)	96 (98%)	2 (2%)	0	100	100
67	VV	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
68	WW	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
69	XX	138/143 (96%)	132 (96%)	6 (4%)	0	100	100
70	YY	122/130 (94%)	118 (97%)	4 (3%)	0	100	100
71	ZZ	73/125 (58%)	71 (97%)	2 (3%)	0	100	100
72	aa	99/115 (86%)	98 (99%)	1 (1%)	0	100	100
73	bb	81/84 (96%)	80 (99%)	1 (1%)	0	100	100
74	cc	60/69 (87%)	59 (98%)	1 (2%)	0	100	100
75	dd	53/56 (95%)	50 (94%)	3 (6%)	0	100	100
76	ee	53/133 (40%)	50 (94%)	3 (6%)	0	100	100
77	ff	66/156 (42%)	62 (94%)	4 (6%)	0	100	100
78	gg	311/317 (98%)	296 (95%)	15 (5%)	0	100	100
81	j	84/97 (87%)	81 (96%)	3 (4%)	0	100	100
All	All	11148/12891 (86%)	10850 (97%)	298 (3%)	0	100	100



There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	A	190/199 (96%)	190 (100%)	0	100	100
6	B	342/348 (98%)	342 (100%)	0	100	100
7	C	302/347 (87%)	302 (100%)	0	100	100
8	D	247/250 (99%)	247 (100%)	0	100	100
9	E	190/251 (76%)	190 (100%)	0	100	100
10	G	200/272 (74%)	200 (100%)	0	100	100
11	H	169/171 (99%)	169 (100%)	0	100	100
12	I	175/181 (97%)	175 (100%)	0	100	100
13	J	143/149 (96%)	143 (100%)	0	100	100
14	K	196/215 (91%)	196 (100%)	0	100	100
15	L	175/176 (99%)	175 (100%)	0	100	100
16	M	117/161 (73%)	117 (100%)	0	100	100
17	N	171/172 (99%)	171 (100%)	0	100	100
18	O	171/173 (99%)	171 (100%)	0	100	100
19	P	134/163 (82%)	134 (100%)	0	100	100
20	Q	164/165 (99%)	164 (100%)	0	100	100
21	R	159/175 (91%)	159 (100%)	0	100	100
22	S	157/157 (100%)	157 (100%)	0	100	100
23	T	139/140 (99%)	139 (100%)	0	100	100
24	U	89/114 (78%)	89 (100%)	0	100	100
25	V	100/107 (94%)	100 (100%)	0	100	100
26	W	86/126 (68%)	86 (100%)	0	100	100
27	X	106/134 (79%)	106 (100%)	0	100	100
28	Y	124/135 (92%)	124 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	Z	117/118 (99%)	117 (100%)	0	100	100
30	a	119/120 (99%)	119 (100%)	0	100	100
31	b	80/184 (44%)	80 (100%)	0	100	100
32	c	84/98 (86%)	84 (100%)	0	100	100
33	d	98/110 (89%)	98 (100%)	0	100	100
34	e	114/121 (94%)	114 (100%)	0	100	100
35	f	88/89 (99%)	88 (100%)	0	100	100
36	g	98/99 (99%)	98 (100%)	0	100	100
37	h	109/110 (99%)	109 (100%)	0	100	100
38	i	86/89 (97%)	86 (100%)	0	100	100
39	k	64/65 (98%)	64 (100%)	0	100	100
40	l	47/48 (98%)	47 (100%)	0	100	100
41	m	48/90 (53%)	48 (100%)	0	100	100
42	n	24/24 (100%)	24 (100%)	0	100	100
43	o	92/94 (98%)	92 (100%)	0	100	100
44	p	74/75 (99%)	74 (100%)	0	100	100
45	r	108/121 (89%)	108 (100%)	0	100	100
46	AA	180/245 (74%)	180 (100%)	0	100	100
47	BB	194/231 (84%)	194 (100%)	0	100	100
48	CC	187/225 (83%)	187 (100%)	0	100	100
49	DD	187/202 (93%)	187 (100%)	0	100	100
50	EE	224/225 (100%)	223 (100%)	1 (0%)	89	97
51	FF	157/170 (92%)	157 (100%)	0	100	100
52	GG	207/218 (95%)	207 (100%)	0	100	100
53	HH	165/174 (95%)	165 (100%)	0	100	100
54	II	172/180 (96%)	172 (100%)	0	100	100
55	JJ	161/168 (96%)	161 (100%)	0	100	100
56	KK	87/136 (64%)	87 (100%)	0	100	100
57	LL	130/142 (92%)	130 (100%)	0	100	100
58	MM	94/108 (87%)	94 (100%)	0	100	100
59	NN	130/131 (99%)	130 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
60	OO	106/130 (82%)	106 (100%)	0	100	100
61	PP	115/130 (88%)	115 (100%)	0	100	100
62	QQ	117/121 (97%)	117 (100%)	0	100	100
63	RR	119/121 (98%)	119 (100%)	0	100	100
64	SS	125/132 (95%)	125 (100%)	0	100	100
65	TT	111/115 (96%)	111 (100%)	0	100	100
66	UU	92/107 (86%)	92 (100%)	0	100	100
67	VV	67/67 (100%)	67 (100%)	0	100	100
68	WW	112/113 (99%)	112 (100%)	0	100	100
69	XX	112/115 (97%)	112 (100%)	0	100	100
70	YY	107/112 (96%)	107 (100%)	0	100	100
71	ZZ	66/103 (64%)	66 (100%)	0	100	100
72	aa	88/98 (90%)	88 (100%)	0	100	100
73	bb	75/76 (99%)	75 (100%)	0	100	100
74	cc	55/62 (89%)	55 (100%)	0	100	100
75	dd	48/49 (98%)	48 (100%)	0	100	100
76	ee	46/106 (43%)	46 (100%)	0	100	100
77	ff	61/140 (44%)	61 (100%)	0	100	100
78	gg	272/275 (99%)	272 (100%)	0	100	100
81	j	73/80 (91%)	73 (100%)	0	100	100
All	All	9738/10943 (89%)	9737 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
50	EE	142	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (115) such sidechains are listed below:

Mol	Chain	Res	Type
5	A	8	GLN
5	A	194	ASN
5	A	216	HIS
6	B	68	ASN

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Mol	Chain	Res	Type
6	B	276	HIS
6	B	354	GLN
7	C	43	ASN
7	C	178	ASN
7	C	223	ASN
7	C	346	ASN
8	D	138	GLN
9	E	185	ASN
10	G	96	GLN
10	G	119	GLN
10	G	134	ASN
10	G	202	ASN
11	H	78	GLN
11	H	189	GLN
12	I	51	HIS
12	I	100	ASN
12	I	144	ASN
12	I	163	GLN
12	I	213	HIS
13	J	104	ASN
14	K	79	ASN
14	K	199	HIS
16	M	70	GLN
16	M	131	GLN
17	N	8	GLN
17	N	109	HIS
17	N	156	HIS
18	O	26	GLN
18	O	50	ASN
18	O	167	HIS
19	P	21	ASN
19	P	116	HIS
20	Q	7	HIS
20	Q	57	ASN
20	Q	188	ASN
22	S	37	HIS
24	U	17	GLN
24	U	44	GLN
26	W	17	HIS
26	W	107	GLN
27	X	93	ASN
28	Y	56	GLN

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Mol	Chain	Res	Type
30	a	19	HIS
30	a	28	HIS
30	a	60	HIS
31	b	27	GLN
31	b	60	ASN
31	b	101	HIS
33	d	100	ASN
34	e	52	GLN
37	h	68	ASN
39	k	31	ASN
40	l	33	ASN
43	o	105	GLN
44	p	72	ASN
45	r	45	HIS
45	r	70	GLN
46	AA	169	HIS
46	AA	193	HIS
46	AA	215	GLN
47	BB	40	ASN
47	BB	76	ASN
47	BB	95	ASN
47	BB	163	GLN
48	CC	115	GLN
48	CC	178	HIS
48	CC	272	HIS
49	DD	22	ASN
49	DD	159	HIS
50	EE	50	ASN
50	EE	188	ASN
52	GG	163	ASN
53	HH	12	ASN
53	HH	44	ASN
53	HH	76	GLN
53	HH	97	GLN
53	HH	157	HIS
53	HH	186	ASN
55	JJ	124	HIS
56	KK	28	HIS
56	KK	66	HIS
57	LL	94	HIS
57	LL	106	HIS
57	LL	112	HIS

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Mol	Chain	Res	Type
59	NN	105	ASN
60	OO	26	ASN
60	OO	32	HIS
60	OO	43	HIS
61	PP	103	ASN
61	PP	128	HIS
62	QQ	11	GLN
62	QQ	80	GLN
62	QQ	97	GLN
64	SS	11	HIS
65	TT	85	ASN
68	WW	56	HIS
69	XX	77	ASN
69	XX	87	ASN
70	YY	63	HIS
70	YY	124	ASN
71	ZZ	89	GLN
72	aa	17	HIS
74	cc	7	GLN
74	cc	29	GLN
76	ee	117	ASN
77	ff	139	HIS
78	gg	64	HIS
78	gg	117	ASN
81	j	57	ASN
81	j	66	HIS
81	j	76	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3578/3601 (99%)	566 (15%)	179 (5%)
2	7	118/120 (98%)	7 (5%)	0
3	8	149/156 (95%)	20 (13%)	3 (2%)
4	9	1685/1869 (90%)	232 (13%)	68 (4%)
79	10	10/185 (5%)	2 (20%)	0
80	11	73/75 (97%)	10 (13%)	5 (6%)
80	13	73/75 (97%)	11 (15%)	4 (5%)
All	All	5686/6081 (93%)	848 (14%)	259 (4%)

All (848) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	13	U
1	5	15	A
1	5	25	A
1	5	39	A
1	5	42	A
1	5	43	U
1	5	59	A
1	5	65	A
1	5	91	G
1	5	109	G
1	5	119	G
1	5	120	A
1	5	122	U
1	5	126	C
1	5	134	G
1	5	135	G
1	5	143	C
1	5	144	G
1	5	159	C
1	5	160	G
1	5	170	C
1	5	171	U
1	5	173	C
1	5	197	A
1	5	200	U
1	5	201	C
1	5	209	U
1	5	216	C
1	5	217	C
1	5	218	A
1	5	219	G
1	5	220	C
1	5	224	U
1	5	226	G
1	5	227	A
1	5	233	U
1	5	234	G
1	5	246	G
1	5	265	C
1	5	266	C
1	5	267	G
1	5	275	C
1	5	276	C

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Mol	Chain	Res	Type
1	5	280	G
1	5	297	U
1	5	315	G
1	5	316	U
1	5	328	A
1	5	334	A
1	5	340	C
1	5	362	A
1	5	386	A
1	5	387	G
1	5	399	G
1	5	408	A
1	5	409	G
1	5	410	A
1	5	412	G
1	5	413	G
1	5	431	G
1	5	432	U
1	5	449	C
1	5	450	G
1	5	453	G
1	5	454	U
1	5	467	U
1	5	480	C
1	5	481	G
1	5	481(A)	C
1	5	482	G
1	5	483	G
1	5	484	U
1	5	485	C
1	5	486	C
1	5	492	U
1	5	493	G
1	5	497	G
1	5	498	C
1	5	499	G
1	5	505	G
1	5	658	C
1	5	666	G
1	5	667	A
1	5	668	C
1	5	683	C

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Mol	Chain	Res	Type
1	5	685	C
1	5	686	A
1	5	687	U
1	5	696	C
1	5	697	G
1	5	704	C
1	5	705	G
1	5	730	G
1	5	731	G
1	5	738	C
1	5	739	G
1	5	747	A
1	5	748	G
1	5	749	G
1	5	758	G
1	5	913	U
1	5	914	U
1	5	915	A
1	5	916	C
1	5	917	A
1	5	923	C
1	5	924	C
1	5	925	C
1	5	929	A
1	5	931	C
1	5	932	A
1	5	933	G
1	5	934	C
1	5	935	A
1	5	935(A)	G
1	5	936	C
1	5	943	A
1	5	944	A
1	5	945	U
1	5	955	G
1	5	956	A
1	5	959	G
1	5	960	A
1	5	961	G
1	5	967	C
1	5	969	C
1	5	973	G

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Mol	Chain	Res	Type
1	5	979	C
1	5	983	C
1	5	1070	G
1	5	1072	C
1	5	1073	G
1	5	1076	C
1	5	1195	G
1	5	1204	C
1	5	1211	G
1	5	1212	G
1	5	1214	C
1	5	1215	C
1	5	1234	G
1	5	1235	G
1	5	1236	C
1	5	1237	C
1	5	1238	A
1	5	1239	C
1	5	1244	G
1	5	1248	C
1	5	1249	C
1	5	1250	C
1	5	1272	C
1	5	1273	G
1	5	1280	C
1	5	1283	G
1	5	1284	G
1	5	1287	G
1	5	1292	C
1	5	1293	G
1	5	1296	G
1	5	1301	C
1	5	1304	C
1	5	1326	A
1	5	1337	A
1	5	1339	U
1	5	1354	A
1	5	1358	G
1	5	1359	G
1	5	1370	G
1	5	1371	A
1	5	1377	G

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Mol	Chain	Res	Type
1	5	1380	G
1	5	1381	U
1	5	1387	A
1	5	1394	G
1	5	1397	A
1	5	1398	A
1	5	1421	G
1	5	1437	C
1	5	1438	U
1	5	1441	C
1	5	1445	U
1	5	1446	C
1	5	1448	G
1	5	1449	C
1	5	1455	G
1	5	1456	C
1	5	1458	C
1	5	1478	C
1	5	1482	G
1	5	1483	C
1	5	1484	G
1	5	1485	C
1	5	1486	C
1	5	1498	G
1	5	1502	G
1	5	1523	A
1	5	1534	A
1	5	1566	C
1	5	1578	U
1	5	1591	U
1	5	1596	U
1	5	1602	U
1	5	1612	G
1	5	1613	A
1	5	1614	C
1	5	1624	G
1	5	1625	G
1	5	1631	A
1	5	1633	G
1	5	1634	A
1	5	1641	G
1	5	1654	G

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Mol	Chain	Res	Type
1	5	1661	C
1	5	1676	C
1	5	1677	U
1	5	1733	G
1	5	1734	G
1	5	1741	G
1	5	1742	A
1	5	1750	G
1	5	1754	U
1	5	1755	C
1	5	1756	U
1	5	1761	G
1	5	1764	G
1	5	1766	A
1	5	1768	C
1	5	1769	G
1	5	1773	U
1	5	1787	A
1	5	1804	A
1	5	1805	A
1	5	1819	G
1	5	1821	G
1	5	1822	U
1	5	1836	G
1	5	1837	A
1	5	1842	G
1	5	1855	G
1	5	1869	G
1	5	1897	A
1	5	1918	U
1	5	1919	G
1	5	1921	C
1	5	1922	G
1	5	1931	C
1	5	1940	G
1	5	1948	G
1	5	1958	A
1	5	1959	U
1	5	1962	A
1	5	1964	A
1	5	1978	C
1	5	1980	U

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Mol	Chain	Res	Type
1	5	1981	G
1	5	1982	G
1	5	1983	A
1	5	1984	A
1	5	1987	C
1	5	1991	A
1	5	1992	U
1	5	1993	C
1	5	2001	G
1	5	2002	A
1	5	2004	U
1	5	2005	G
1	5	2007	G
1	5	2008	U
1	5	2011	C
1	5	2026	A
1	5	2042	A
1	5	2043	A
1	5	2044	U
1	5	2048	U
1	5	2055	G
1	5	2056	G
1	5	2069	A
1	5	2084	U
1	5	2089	G
1	5	2090	U
1	5	2092	G
1	5	2093	G
1	5	2094	C
1	5	2097	A
1	5	2098	G
1	5	2100	G
1	5	2101	A
1	5	2102	G
1	5	2104	A
1	5	2106	G
1	5	2107	A
1	5	2108	G
1	5	2259	G
1	5	2260	C
1	5	2266	C
1	5	2267	U

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Mol	Chain	Res	Type
1	5	2268	A
1	5	2269	C
1	5	2279	A
1	5	2289	C
1	5	2300	A
1	5	2301	G
1	5	2313	A
1	5	2314	G
1	5	2332	A
1	5	2333	G
1	5	2348	G
1	5	2351	C
1	5	2395	A
1	5	2396	A
1	5	2397	G
1	5	2422	C
1	5	2441	C
1	5	2471	G
1	5	2475	G
1	5	2488	C
1	5	2489	C
1	5	2490	U
1	5	2491	C
1	5	2502	A
1	5	2503	G
1	5	2504	C
1	5	2505	C
1	5	2506	G
1	5	2507	A
1	5	2511	A
1	5	2513	A
1	5	2520	C
1	5	2546	G
1	5	2547	G
1	5	2553	A
1	5	2554	U
1	5	2555	G
1	5	2587	A
1	5	2588	C
1	5	2601	A
1	5	2627	C
1	5	2669	C

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Mol	Chain	Res	Type
1	5	2676	A
1	5	2686	G
1	5	2687	U
1	5	2695	A
1	5	2696	A
1	5	2705	G
1	5	2707	U
1	5	2708	U
1	5	2709	C
1	5	2710	C
1	5	2711	G
1	5	2712	G
1	5	2724	G
1	5	2725	A
1	5	2726	G
1	5	2740	U
1	5	2743	A
1	5	2760	G
1	5	2761	U
1	5	2762	G
1	5	2763	U
1	5	2764	A
1	5	2772	C
1	5	2787	A
1	5	2788	U
1	5	2790	U
1	5	2794	C
1	5	2795	A
1	5	2814	C
1	5	2826	U
1	5	2827	G
1	5	2828	U
1	5	2855	G
1	5	3604	A
1	5	3605	C
1	5	3606	U
1	5	3614	G
1	5	3615	G
1	5	3625	G
1	5	3626	G
1	5	3635	A
1	5	3644	U

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Mol	Chain	Res	Type
1	5	3653	A
1	5	3662	A
1	5	3672	G
1	5	3673	C
1	5	3674	G
1	5	3711	A
1	5	3712	A
1	5	3748	A
1	5	3753	G
1	5	3759	A
1	5	3760	A
1	5	3761	C
1	5	3776	G
1	5	3777	G
1	5	3783	A
1	5	3784	A
1	5	3811	G
1	5	3814	U
1	5	3817	A
1	5	3819	G
1	5	3838	U
1	5	3839	G
1	5	3840	U
1	5	3877	A
1	5	3878	C
1	5	3879	G
1	5	3888	G
1	5	3889	G
1	5	3897	G
1	5	3901	A
1	5	3905	A
1	5	3906	A
1	5	3907	G
1	5	3908	A
1	5	3915	U
1	5	3939	G
1	5	3949	A
1	5	3950	U
1	5	3960	A
1	5	3963	A
1	5	3964	U
1	5	3966	A

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Mol	Chain	Res	Type
1	5	3967	G
1	5	3969	G
1	5	3972	A
1	5	3973	G
1	5	4041	C
1	5	4042	G
1	5	4046	A
1	5	4047	A
1	5	4048	A
1	5	4049	U
1	5	4069	U
1	5	4076	G
1	5	4077	A
1	5	4084	G
1	5	4119	C
1	5	4120	U
1	5	4121	G
1	5	4122	G
1	5	4124	G
1	5	4125	C
1	5	4127	A
1	5	4128	A
1	5	4163	U
1	5	4170	A
1	5	4183	G
1	5	4184	G
1	5	4191	G
1	5	4203	A
1	5	4229	U
1	5	4233	A
1	5	4251	A
1	5	4255	A
1	5	4258	C
1	5	4266	G
1	5	4268	A
1	5	4271	A
1	5	4273	A
1	5	4281	A
1	5	4291	G
1	5	4305	G
1	5	4306	U
1	5	4330	G

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Mol	Chain	Res	Type
1	5	4339	A
1	5	4349	C
1	5	4354	U
1	5	4355	G
1	5	4373	G
1	5	4376	A
1	5	4377	G
1	5	4378	A
1	5	4380	A
1	5	4387	C
1	5	4394	A
1	5	4395	U
1	5	4396	A
1	5	4419	U
1	5	4422	A
1	5	4438	U
1	5	4448	G
1	5	4449	A
1	5	4452	U
1	5	4464	A
1	5	4476	C
1	5	4488	A
1	5	4489	G
1	5	4500	U
1	5	4512	U
1	5	4513	A
1	5	4519	C
1	5	4524	G
1	5	4548	A
1	5	4549	G
1	5	4557	U
1	5	4560	C
1	5	4572	U
1	5	4573	G
1	5	4590	A
1	5	4608	G
1	5	4627	U
1	5	4635	A
1	5	4636	U
1	5	4637	G
1	5	4656	A
1	5	4670	C

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Mol	Chain	Res	Type
1	5	4672	A
1	5	4700	A
1	5	4709	U
1	5	4736	C
1	5	4745	G
1	5	4750	G
1	5	4751	G
1	5	4754	G
1	5	4757	C
1	5	4759	C
1	5	4761	G
1	5	4765	G
1	5	4771	C
1	5	4870	G
1	5	4871	C
1	5	4872	G
1	5	4875	G
1	5	4876	A
1	5	4877	G
1	5	4881	U
1	5	4882	U
1	5	4883	C
1	5	4885	U
1	5	4909	A
1	5	4910	A
1	5	4913	G
1	5	4914	G
1	5	4915	G
1	5	4919	G
1	5	4921	C
1	5	4922	C
1	5	4925	U
1	5	4926	C
1	5	4931	G
1	5	4934	A
1	5	4937	C
1	5	4938	A
1	5	4939	C
1	5	4943	A
1	5	4944	C
1	5	4945	G
1	5	4948	C

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Mol	Chain	Res	Type
1	5	4949	G
1	5	4950	U
1	5	4951	G
1	5	4956	A
1	5	4958	C
1	5	4965	U
1	5	4966	A
1	5	4976	U
1	5	4988	U
1	5	4989	U
1	5	4990	C
1	5	4991	U
1	5	5017	G
1	5	5041	G
1	5	5047	C
1	5	5050	C
1	5	5054	C
1	5	5058	A
1	5	5062	G
2	7	7	G
2	7	41	G
2	7	42	A
2	7	53	U
2	7	64	G
2	7	100	A
2	7	110	G
3	8	2	G
3	8	34	U
3	8	35	C
3	8	51	U
3	8	52	A
3	8	59	A
3	8	62	A
3	8	63	U
3	8	87	G
3	8	94	G
3	8	104	A
3	8	105	C
3	8	110	U
3	8	114	G
3	8	123	U
3	8	124	U

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Mol	Chain	Res	Type
3	8	125	C
3	8	126	C
3	8	127	U
3	8	137	A
4	9	4	C
4	9	17	C
4	9	25	A
4	9	26	U
4	9	33	G
4	9	41	G
4	9	42	A
4	9	46	A
4	9	56	G
4	9	58	C
4	9	59	U
4	9	65	C
4	9	67	C
4	9	68	A
4	9	73	C
4	9	74	G
4	9	75	G
4	9	76	U
4	9	79	A
4	9	103	A
4	9	111	A
4	9	112	U
4	9	113	G
4	9	115	U
4	9	126	G
4	9	127	C
4	9	130	G
4	9	143	U
4	9	147	A
4	9	155	G
4	9	161	U
4	9	162	C
4	9	182	C
4	9	183	G
4	9	184	G
4	9	192	C
4	9	215	G
4	9	294	U

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Mol	Chain	Res	Type
4	9	302	A
4	9	309	G
4	9	312	G
4	9	319	C
4	9	347	G
4	9	362	C
4	9	364	A
4	9	369	C
4	9	370	G
4	9	385	G
4	9	386	C
4	9	400	C
4	9	401	A
4	9	407	G
4	9	408	A
4	9	409	C
4	9	418	A
4	9	428	U
4	9	448	A
4	9	449	A
4	9	450	C
4	9	466	G
4	9	472	C
4	9	474	G
4	9	482	G
4	9	487	U
4	9	492	C
4	9	496	C
4	9	516	A
4	9	517	C
4	9	531	A
4	9	532	C
4	9	533	A
4	9	544	G
4	9	550	C
4	9	551	U
4	9	554	A
4	9	555	A
4	9	556	U
4	9	557	U
4	9	559	G
4	9	562	U

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Mol	Chain	Res	Type
4	9	564	A
4	9	587	A
4	9	588	G
4	9	591	U
4	9	593	C
4	9	594	A
4	9	606	G
4	9	607	U
4	9	608	C
4	9	614	C
4	9	620	G
4	9	621	C
4	9	628	A
4	9	643	A
4	9	644	G
4	9	668	A
4	9	669	A
4	9	671	A
4	9	672	A
4	9	673	G
4	9	752	G
4	9	753	C
4	9	754	G
4	9	799	U
4	9	811	A
4	9	821	G
4	9	822	U
4	9	830	A
4	9	844	U
4	9	847	A
4	9	859	G
4	9	867	G
4	9	868	G
4	9	870	A
4	9	872	A
4	9	873	G
4	9	874	G
4	9	875	A
4	9	887	U
4	9	888	U
4	9	889	U
4	9	912	C

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Mol	Chain	Res	Type
4	9	913	A
4	9	914	U
4	9	919	A
4	9	920	A
4	9	922	A
4	9	933	G
4	9	943	U
4	9	990	A
4	9	992	A
4	9	999	G
4	9	1016	U
4	9	1017	U
4	9	1023	A
4	9	1062	A
4	9	1082	A
4	9	1083	A
4	9	1085	C
4	9	1115	U
4	9	1116	C
4	9	1117	C
4	9	1118	C
4	9	1133	A
4	9	1139	C
4	9	1153	C
4	9	1154	U
4	9	1195	A
4	9	1207	G
4	9	1208	A
4	9	1215	C
4	9	1216	C
4	9	1242	U
4	9	1251	A
4	9	1253	A
4	9	1254	C
4	9	1256	G
4	9	1257	G
4	9	1259	A
4	9	1274	G
4	9	1275	G
4	9	1286	G
4	9	1289	U
4	9	1290	G

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Mol	Chain	Res	Type
4	9	1300	U
4	9	1301	A
4	9	1302	G
4	9	1303	C
4	9	1309	C
4	9	1314	U
4	9	1371	U
4	9	1372	U
4	9	1378	A
4	9	1396	A
4	9	1397	U
4	9	1428	G
4	9	1454	A
4	9	1455	A
4	9	1462	U
4	9	1463	U
4	9	1476	A
4	9	1477	U
4	9	1490	G
4	9	1498	A
4	9	1508	A
4	9	1509	U
4	9	1520	G
4	9	1521	C
4	9	1533	A
4	9	1548	G
4	9	1552	G
4	9	1553	C
4	9	1554	C
4	9	1556	A
4	9	1557	C
4	9	1567	G
4	9	1579	A
4	9	1580	A
4	9	1581	C
4	9	1587	G
4	9	1588	A
4	9	1601	A
4	9	1621	U
4	9	1623	A
4	9	1637	A
4	9	1638	G

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Mol	Chain	Res	Type
4	9	1639	G
4	9	1648	G
4	9	1665	G
4	9	1680	G
4	9	1699	A
4	9	1721	U
4	9	1722	G
4	9	1748	G
4	9	1753	C
4	9	1756	C
4	9	1757	G
4	9	1758	G
4	9	1783	C
4	9	1785	C
4	9	1824	A
4	9	1825	A
4	9	1834	A
4	9	1835	A
4	9	1836	G
4	9	1837	G
4	9	1838	U
4	9	1849	G
4	9	1852	C
4	9	1861	G
4	9	1863	A
4	9	1865	C
79	10	19	U
79	10	23	A
80	13	17	C
80	13	18	G
80	13	20	A
80	13	22	G
80	13	47	U
80	13	48	C
80	13	58	A
80	13	59	A
80	13	74	C
80	13	75	C
80	13	76	A
80	11	10	G
80	11	17	C
80	11	18	G

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Mol	Chain	Res	Type
80	11	20	A
80	11	22	G
80	11	47	U
80	11	48	C
80	11	74	C
80	11	75	C
80	11	76	A

All (259) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	42	A
1	5	64	A
1	5	125	C
1	5	134	G
1	5	135	G
1	5	143	C
1	5	157	U
1	5	170	C
1	5	200	U
1	5	217	C
1	5	218	A
1	5	224	U
1	5	226	G
1	5	245	C
1	5	265	C
1	5	266	C
1	5	275	C
1	5	315	G
1	5	385	A
1	5	408	A
1	5	449	C
1	5	466	A
1	5	480	C
1	5	482	G
1	5	484	U
1	5	485	C
1	5	492	U
1	5	504	G
1	5	649	A
1	5	667	A
1	5	685	C

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Mol	Chain	Res	Type
1	5	696	C
1	5	729	G
1	5	747	A
1	5	749	G
1	5	913	U
1	5	914	U
1	5	916	C
1	5	922(B)	C
1	5	924	C
1	5	930	G
1	5	935(A)	G
1	5	955	G
1	5	959	G
1	5	960	A
1	5	966	A
1	5	1072	C
1	5	1211	G
1	5	1214	C
1	5	1236	C
1	5	1237	C
1	5	1238	A
1	5	1249	C
1	5	1283	G
1	5	1291	G
1	5	1304	C
1	5	1325	C
1	5	1358	G
1	5	1370	G
1	5	1377	G
1	5	1380	G
1	5	1387	A
1	5	1440	U
1	5	1445	U
1	5	1448	G
1	5	1455	G
1	5	1477	C
1	5	1483	C
1	5	1484	G
1	5	1485	C
1	5	1502	G
1	5	1533	A
1	5	1534	A

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Mol	Chain	Res	Type
1	5	1578	U
1	5	1590	C
1	5	1613	A
1	5	1625	G
1	5	1631	A
1	5	1633	G
1	5	1733	G
1	5	1741	G
1	5	1754	U
1	5	1773	U
1	5	1804	A
1	5	1818	G
1	5	1835	G
1	5	1918	U
1	5	1920	C
1	5	1921	C
1	5	1958	A
1	5	1979	A
1	5	1982	G
1	5	1992	U
1	5	2001	G
1	5	2007	G
1	5	2010	A
1	5	2017	A
1	5	2042	A
1	5	2088	A
1	5	2089	G
1	5	2093	G
1	5	2100	G
1	5	2106	G
1	5	2266	C
1	5	2267	U
1	5	2268	A
1	5	2278	G
1	5	2313	A
1	5	2396	A
1	5	2421	G
1	5	2428	A
1	5	2474	G
1	5	2502	A
1	5	2505	C
1	5	2506	G

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Mol	Chain	Res	Type
1	5	2529	A
1	5	2546	G
1	5	2553	A
1	5	2587	A
1	5	2696	A
1	5	2710	C
1	5	2711	G
1	5	2724	G
1	5	2725	A
1	5	2761	U
1	5	2763	U
1	5	2794	C
1	5	3603	G
1	5	3614	G
1	5	3625	G
1	5	3672	G
1	5	3673	C
1	5	3777	G
1	5	3810	C
1	5	3876	A
1	5	3878	C
1	5	3888	G
1	5	3904	G
1	5	3949	A
1	5	3959	U
1	5	3966	A
1	5	3968	U
1	5	3972	A
1	5	4041	C
1	5	4046	A
1	5	4047	A
1	5	4119	C
1	5	4121	G
1	5	4124	G
1	5	4127	A
1	5	4232	U
1	5	4233	A
1	5	4254	G
1	5	4265	U
1	5	4266	G
1	5	4291	G
1	5	4305	G

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Mol	Chain	Res	Type
1	5	4354	U
1	5	4395	U
1	5	4448	G
1	5	4488	A
1	5	4527	G
1	5	4572	U
1	5	4626	A
1	5	4635	A
1	5	4699	U
1	5	4876	A
1	5	4884	G
1	5	4909	A
1	5	4913	G
1	5	4921	C
1	5	4925	U
1	5	4936	G
1	5	4938	A
1	5	4947	U
1	5	4949	G
1	5	4965	U
1	5	4988	U
1	5	4990	C
3	8	51	U
3	8	94	G
3	8	124	U
4	9	24	C
4	9	41	G
4	9	58	C
4	9	72	C
4	9	110	U
4	9	112	U
4	9	126	G
4	9	160	U
4	9	182	C
4	9	312	G
4	9	369	C
4	9	400	C
4	9	407	G
4	9	465	A
4	9	516	A
4	9	532	C
4	9	543	C

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Mol	Chain	Res	Type
4	9	550	C
4	9	553	U
4	9	555	A
4	9	561	A
4	9	593	C
4	9	606	G
4	9	607	U
4	9	620	G
4	9	631	U
4	9	655	A
4	9	690	G
4	9	752	G
4	9	798	G
4	9	821	G
4	9	858	A
4	9	867	G
4	9	869	A
4	9	872	A
4	9	873	G
4	9	874	G
4	9	887	U
4	9	912	C
4	9	919	A
4	9	1016	U
4	9	1061	U
4	9	1115	U
4	9	1153	C
4	9	1165	G
4	9	1215	C
4	9	1253	A
4	9	1274	G
4	9	1289	U
4	9	1308	U
4	9	1313	A
4	9	1395	C
4	9	1396	A
4	9	1428	G
4	9	1454	A
4	9	1476	A
4	9	1489	A
4	9	1508	A
4	9	1519	U

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Mol	Chain	Res	Type
4	9	1520	G
4	9	1553	C
4	9	1580	A
4	9	1601	A
4	9	1637	A
4	9	1638	G
4	9	1679	A
4	9	1757	G
4	9	1837	G
80	13	16	G
80	13	19	G
80	13	58	A
80	13	74	C
80	11	10	G
80	11	16	G
80	11	19	G
80	11	47	U
80	11	74	C

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 6 are monoatomic - leaving 4 for Mogul analysis.

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



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
84	ATP	11	101	80	28,33,33	0.68	0	34,52,52	0.72	1 (2%)
82	SPD	5	5101	-	9,9,9	0.35	0	8,8,8	0.40	0
85	MET	13	102	80	6,7,8	0.49	0	2,7,9	0.16	0
84	ATP	13	101	80	28,33,33	0.63	0	34,52,52	0.76	1 (2%)

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
84	ATP	11	101	80	-	3/18/38/38	0/3/3/3
82	SPD	5	5101	-	-	1/7/7/7	-
85	MET	13	102	80	-	0/5/6/8	-
84	ATP	13	101	80	-	0/18/38/38	0/3/3/3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	11	101	ATP	C5-C6-N6	2.31	123.82	120.31
84	13	101	ATP	C5-C6-N6	2.30	123.81	120.31

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
84	11	101	ATP	PB-O3A-PA-O2A
82	5	5101	SPD	N6-C7-C8-C9
84	11	101	ATP	C3'-C4'-C5'-O5'
84	11	101	ATP	PB-O3A-PA-O1A

There are no ring outliers.

3 monomers are involved in 4 short contacts:

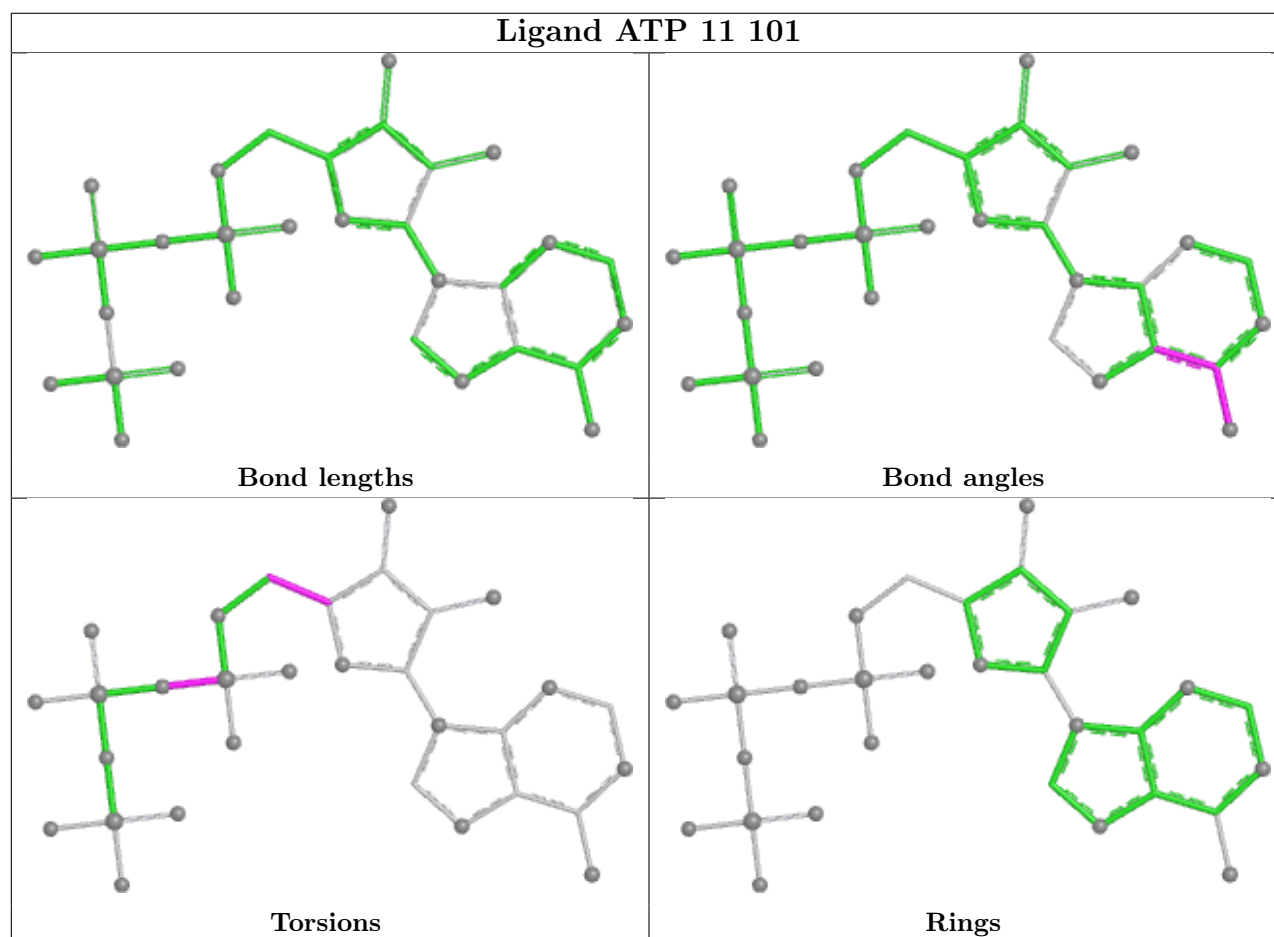
Mol	Chain	Res	Type	Clashes	Symm-Clashes
84	11	101	ATP	1	0

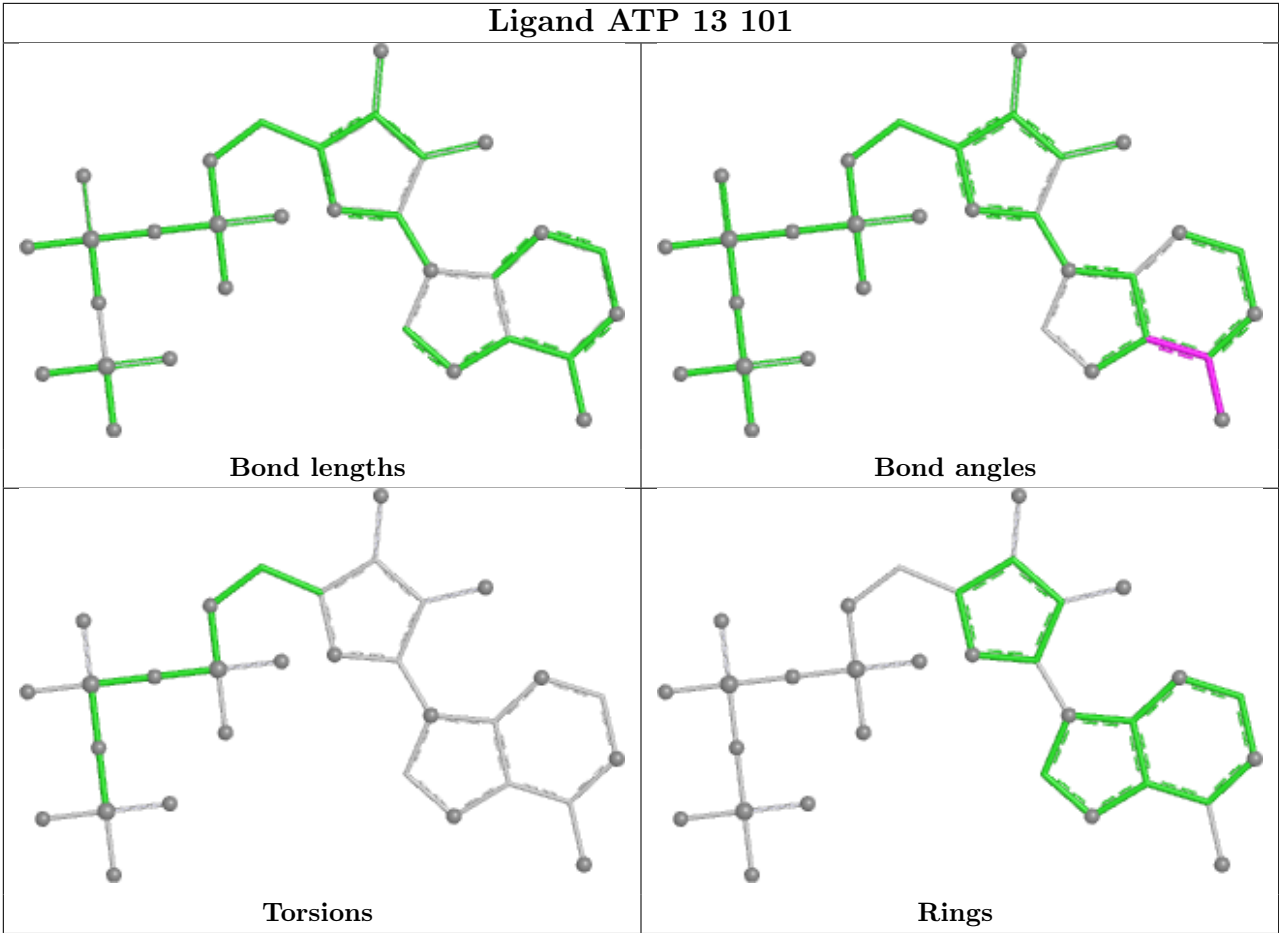
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
82	5	5101	SPD	1	0
84	13	101	ATP	2	0

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





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	5	23

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	2113:G	O3'	2258:C	P	41.66
1	5	1252:C	O3'	1271:G	P	36.31
1	5	1219:G	O3'	1233:G	P	20.36
1	5	523:C	O3'	638:G	P	18.21
1	5	4101:C	O3'	4107:G	P	18.02

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	3976:C	O3'	4035:G	P	17.99
1	5	1406(C):G	O3'	1411:C	P	17.73
1	5	4777:C	O3'	4859:C	P	16.25
1	5	990:C	O3'	1064:G	P	16.12
1	5	4138:C	O3'	4146:G	P	15.93
1	5	5022:U	O3'	5028:G	P	15.60
1	5	1364:U	O3'	1368:A	P	15.03
1	5	760:G	O3'	904:C	P	14.09
1	5	2901:G	O3'	3597:G	P	13.99
1	5	1696:C	O3'	1720:C	P	13.65
1	5	182:G	O3'	189:G	P	10.88
1	5	1180:C	O3'	1183:C	P	10.41
1	5	4729:A	O3'	4735:G	P	8.83
1	5	512:U	O3'	515:C	P	7.68
1	5	500:G	O3'	504:G	P	6.52
1	5	4740:G	O3'	4743:G	P	5.78
1	5	1100:U	O3'	1168:G	P	5.30
1	5	4899:G	O3'	4902:C	P	3.83

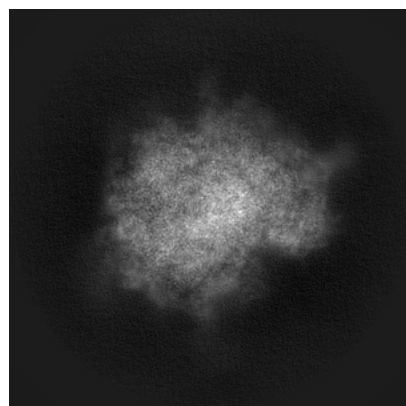
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-73317. These allow visual inspection of the internal detail of the map and identification of artifacts.

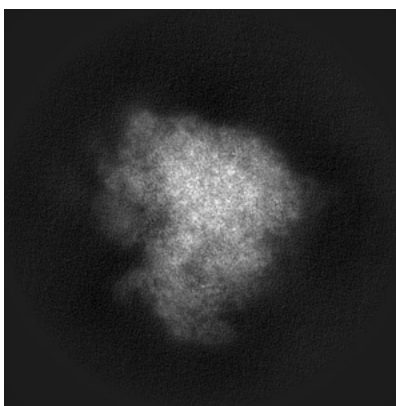
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

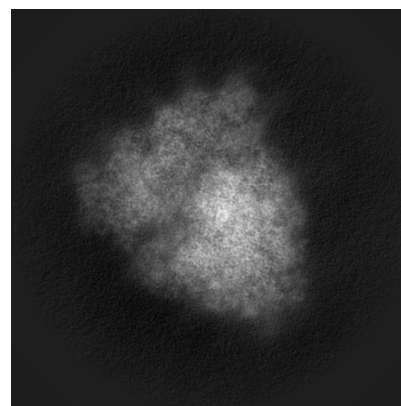
#### 6.1.1 Primary map



X

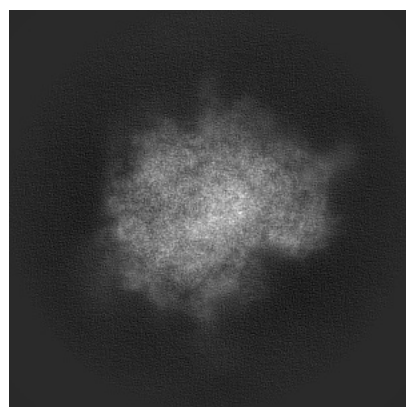


Y

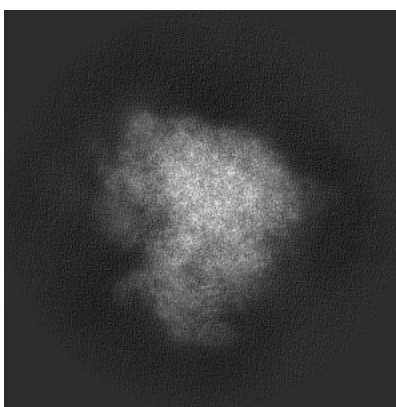


Z

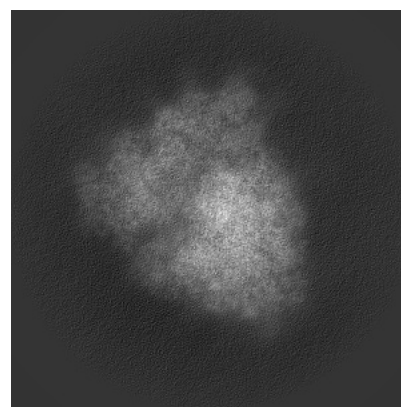
#### 6.1.2 Raw map



X



Y

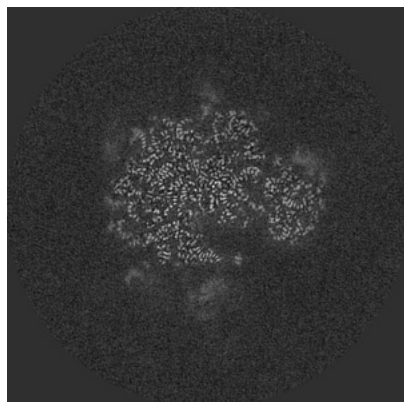


Z

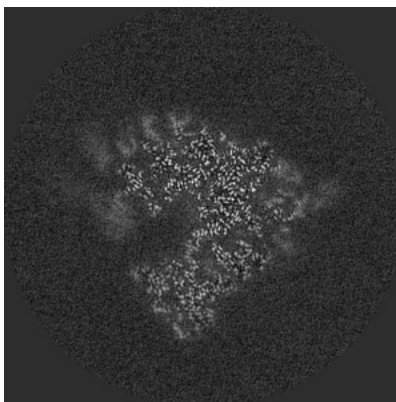
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

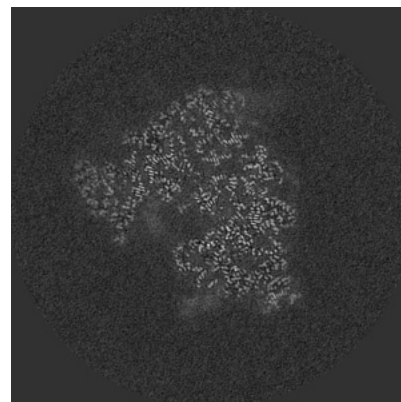
### 6.2.1 Primary map



X Index: 200

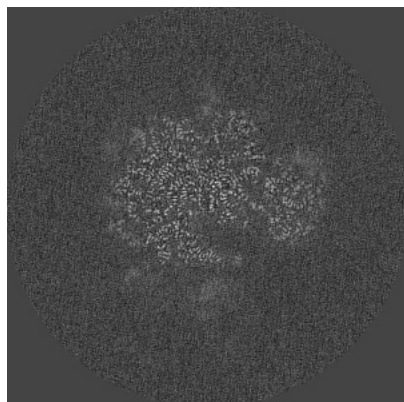


Y Index: 200

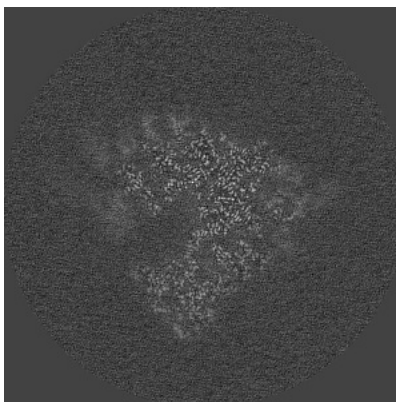


Z Index: 200

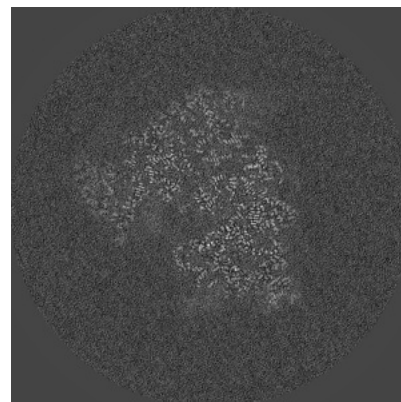
### 6.2.2 Raw map



X Index: 200



Y Index: 200



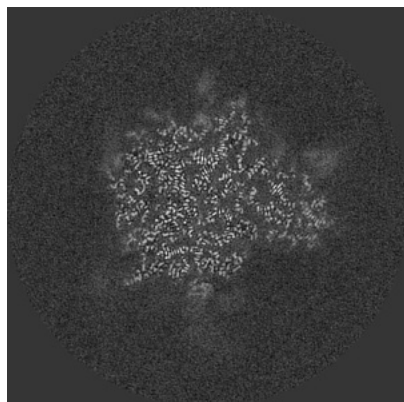
Z Index: 200

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

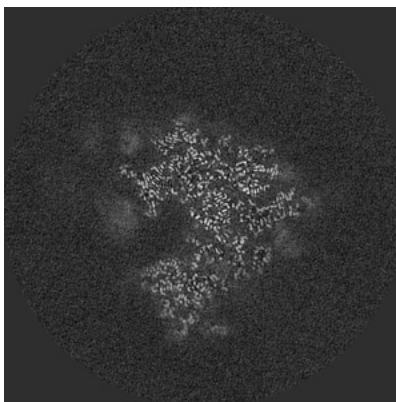


## 6.3 Largest variance slices [i](#)

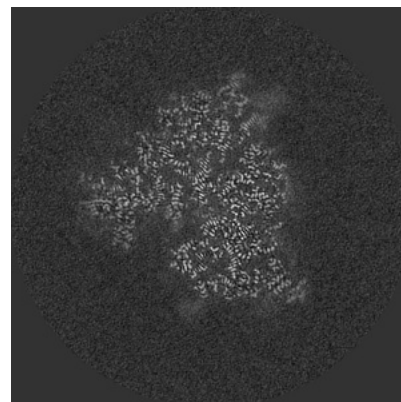
### 6.3.1 Primary map



X Index: 214

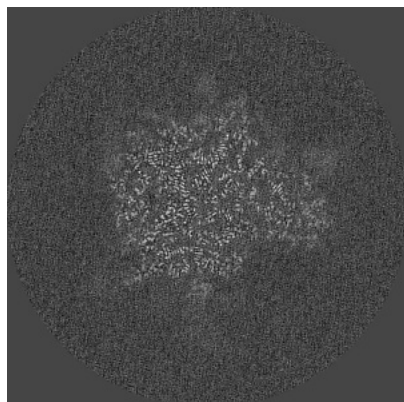


Y Index: 209

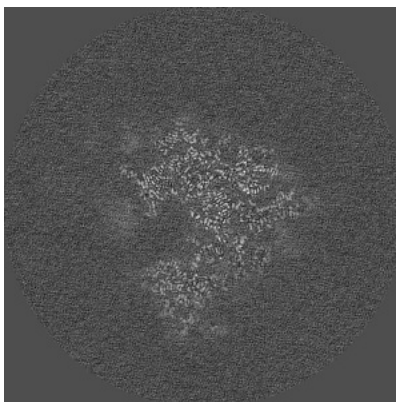


Z Index: 192

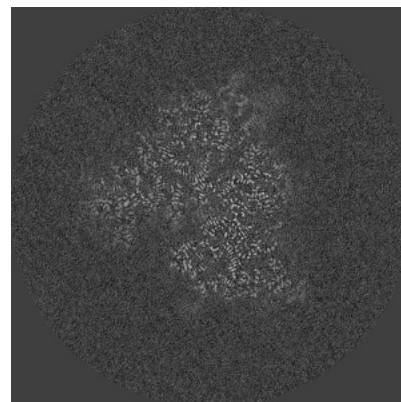
### 6.3.2 Raw map



X Index: 214



Y Index: 209

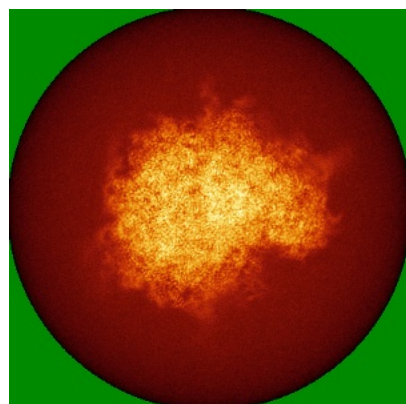


Z Index: 192

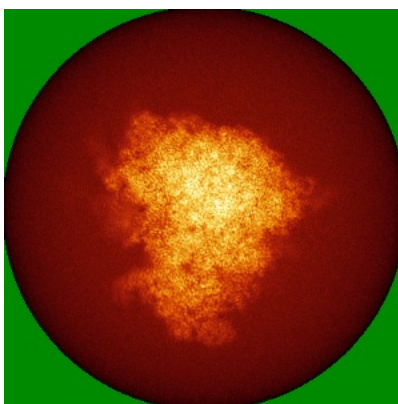
The images above show the largest variance slices of the map in three orthogonal directions.

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

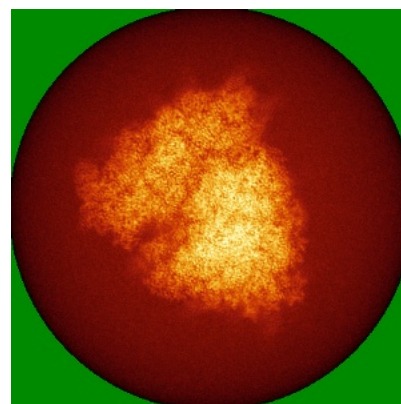
### 6.4.1 Primary map



X

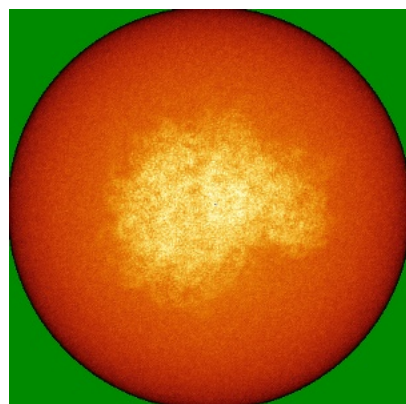


Y

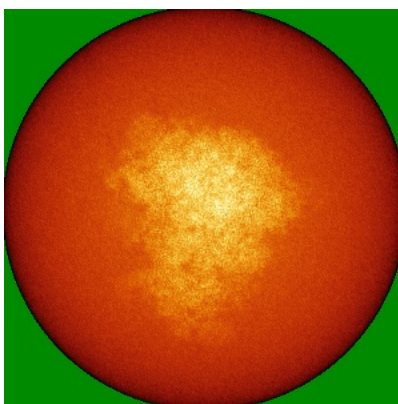


Z

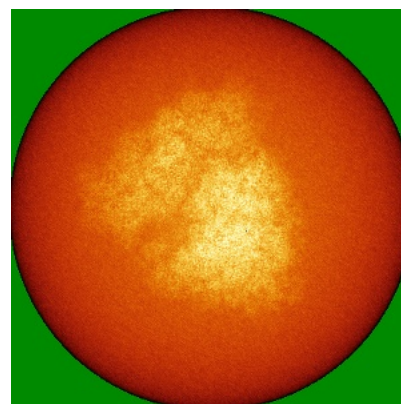
### 6.4.2 Raw map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.



## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



X



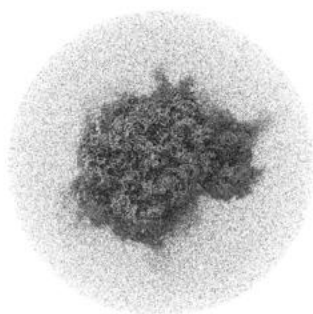
Y



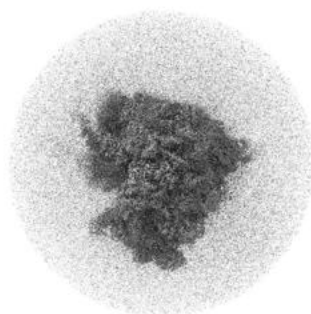
Z

The images above show the 3D surface view of the map at the recommended contour level 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

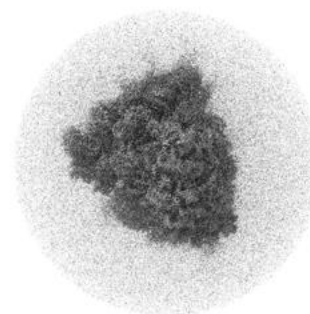
### 6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

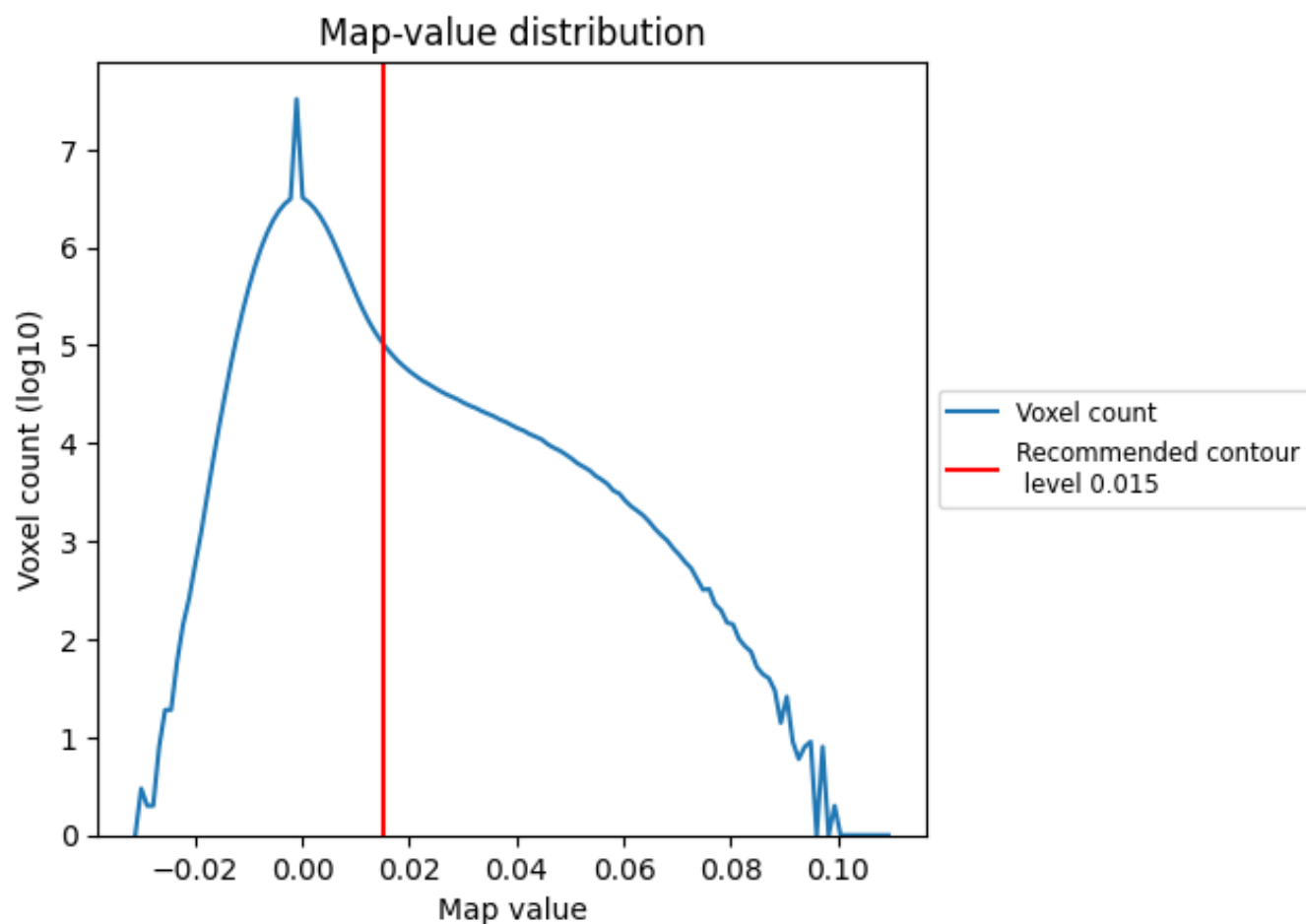
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

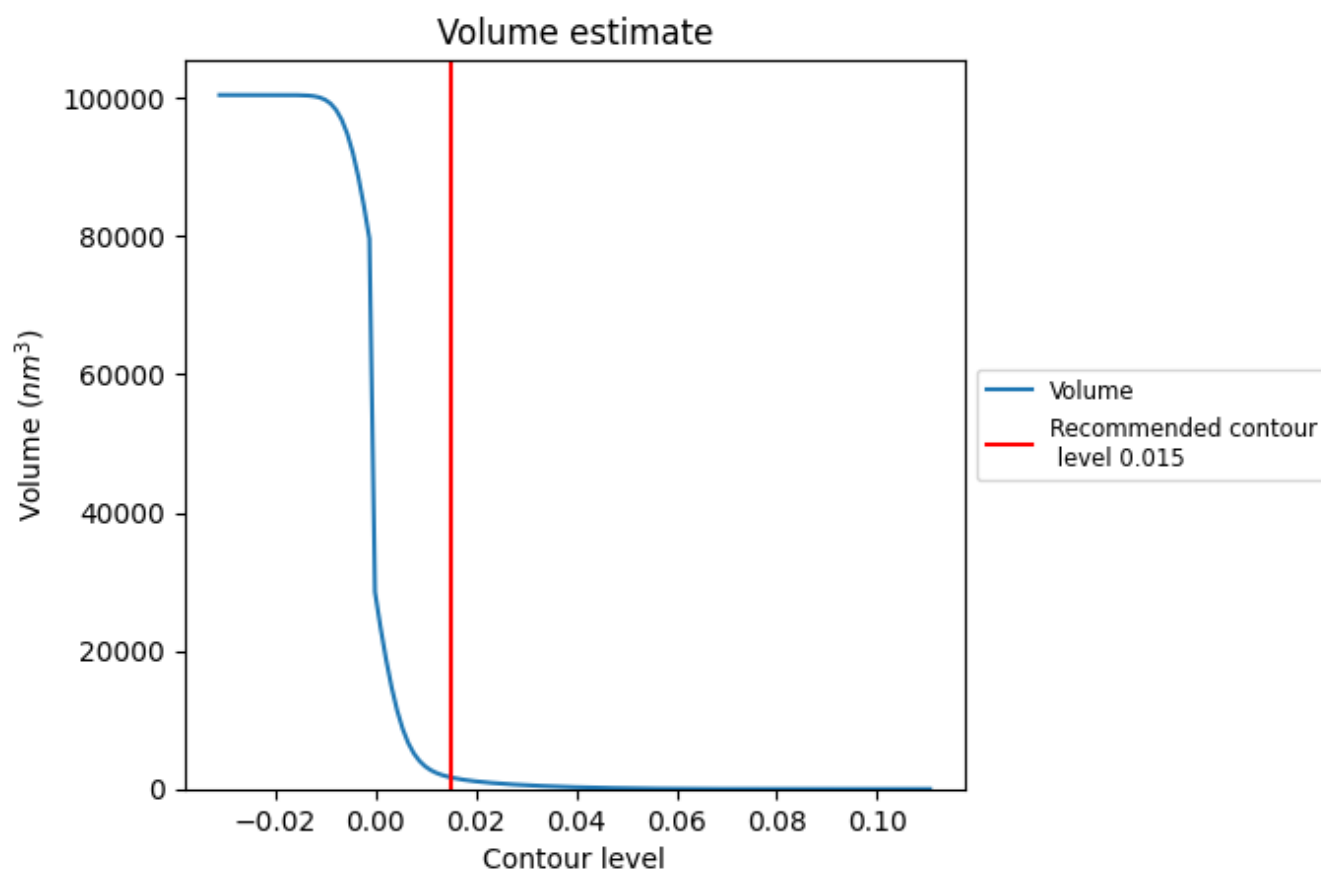
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

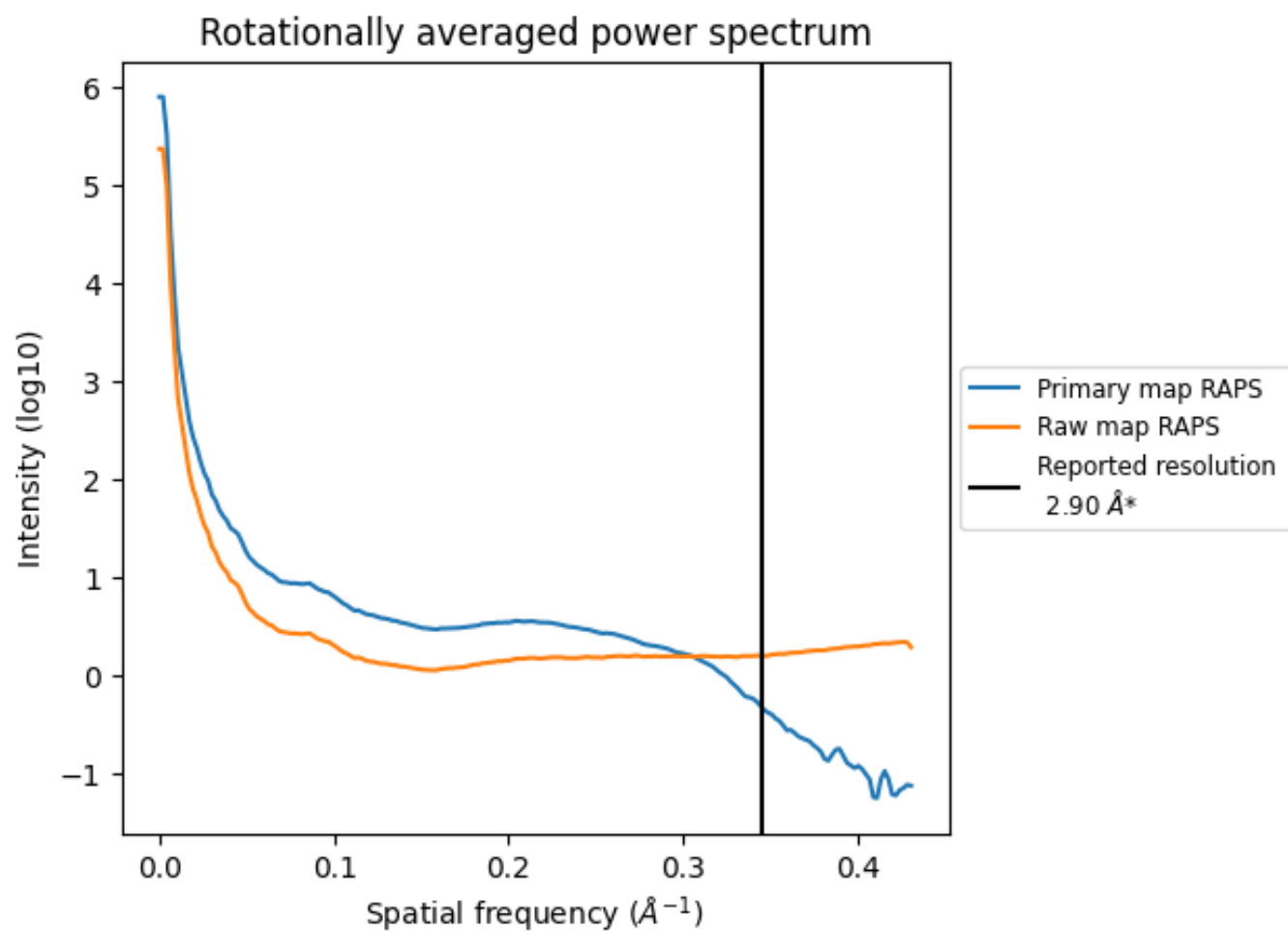
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1674  $\text{nm}^3$ ; this corresponds to an approximate mass of 1512 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum ⓘ

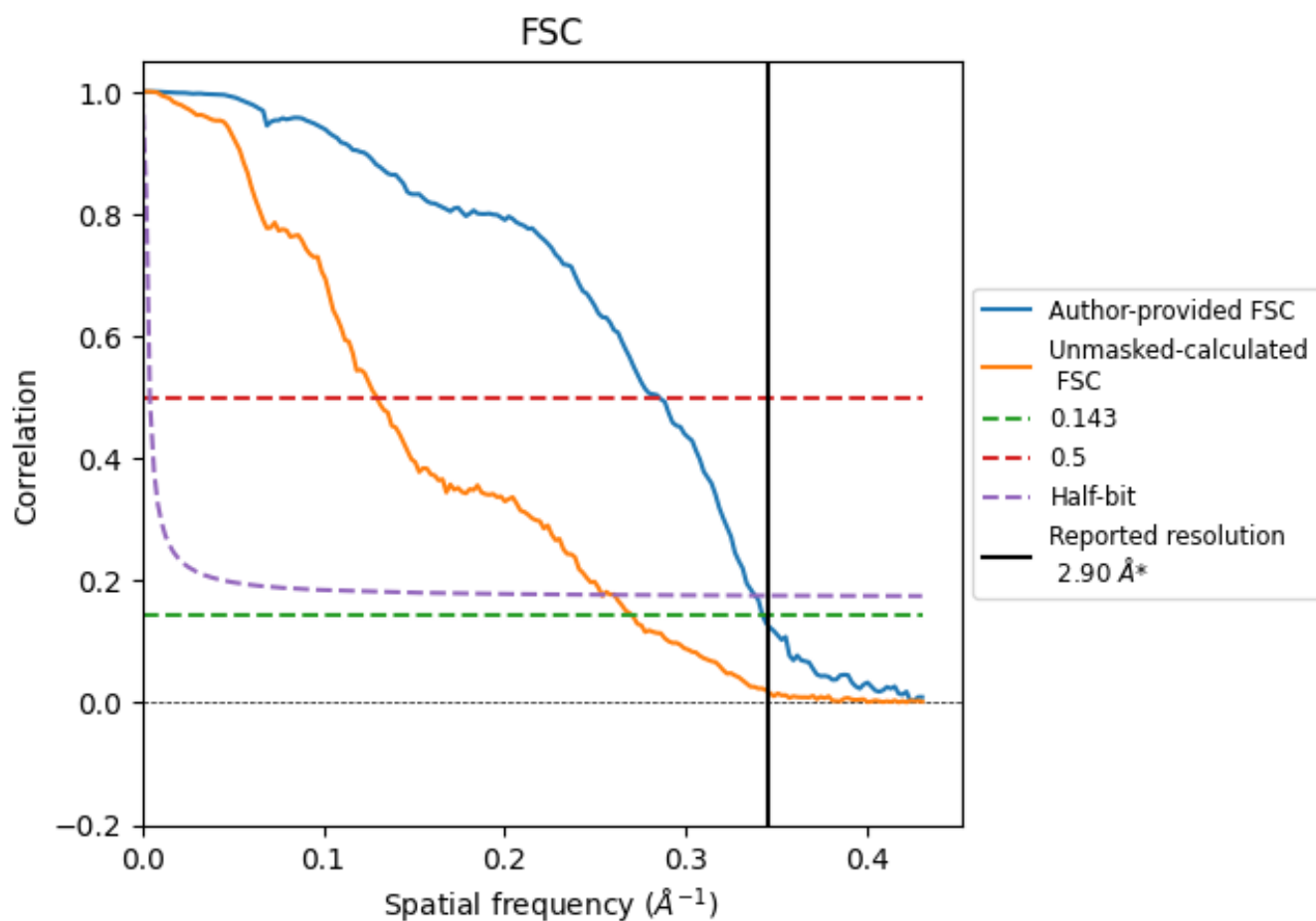


\*Reported resolution corresponds to spatial frequency of 0.345 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.345  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

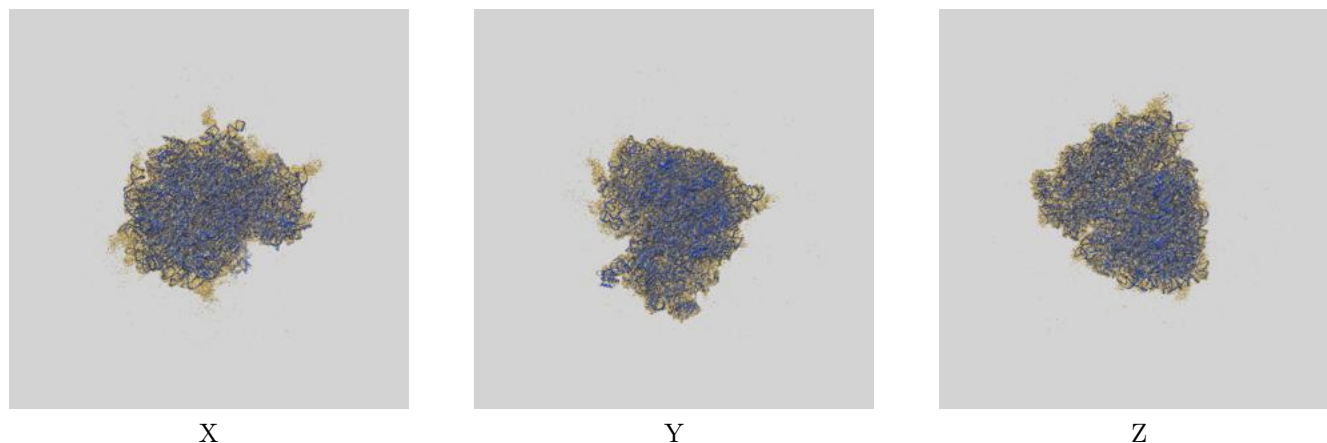
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.92	3.51	2.96
Unmasked-calculated*	3.70	7.73	3.94

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.70 differs from the reported value 2.9 by more than 10 %

## 9 Map-model fit [i](#)

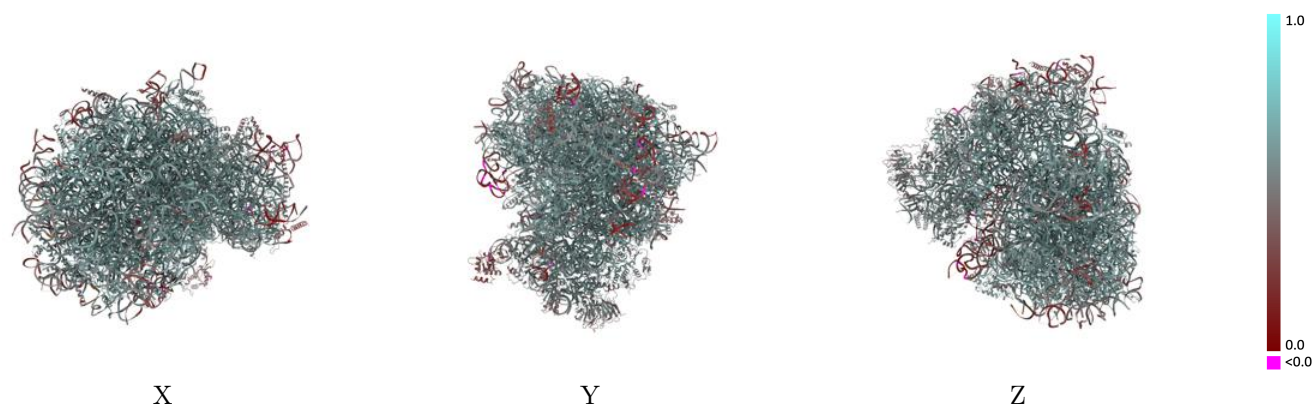
This section contains information regarding the fit between EMDB map EMD-73317 and PDB model 9YQ1. Per-residue inclusion information can be found in [section 3](#) on [page 27](#).

### 9.1 Map-model overlay [i](#)



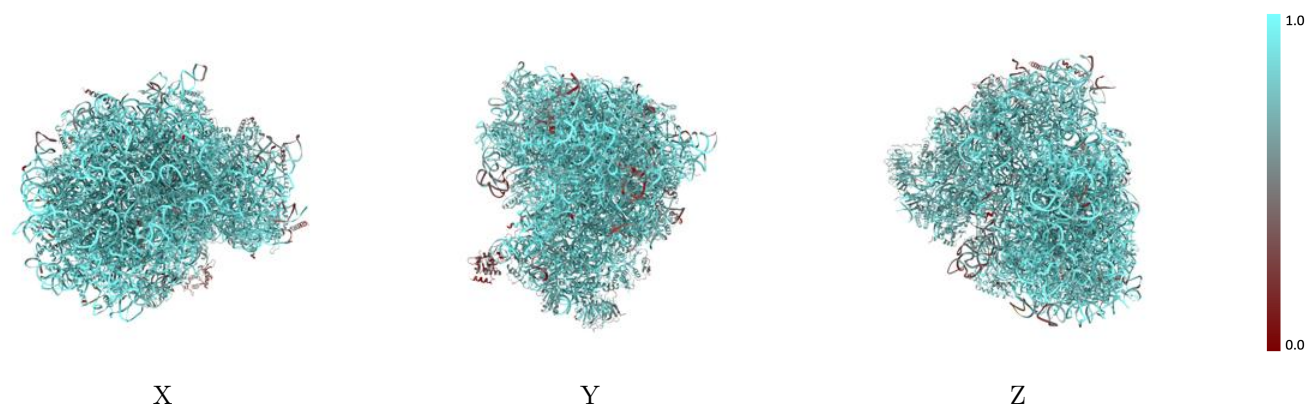
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



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

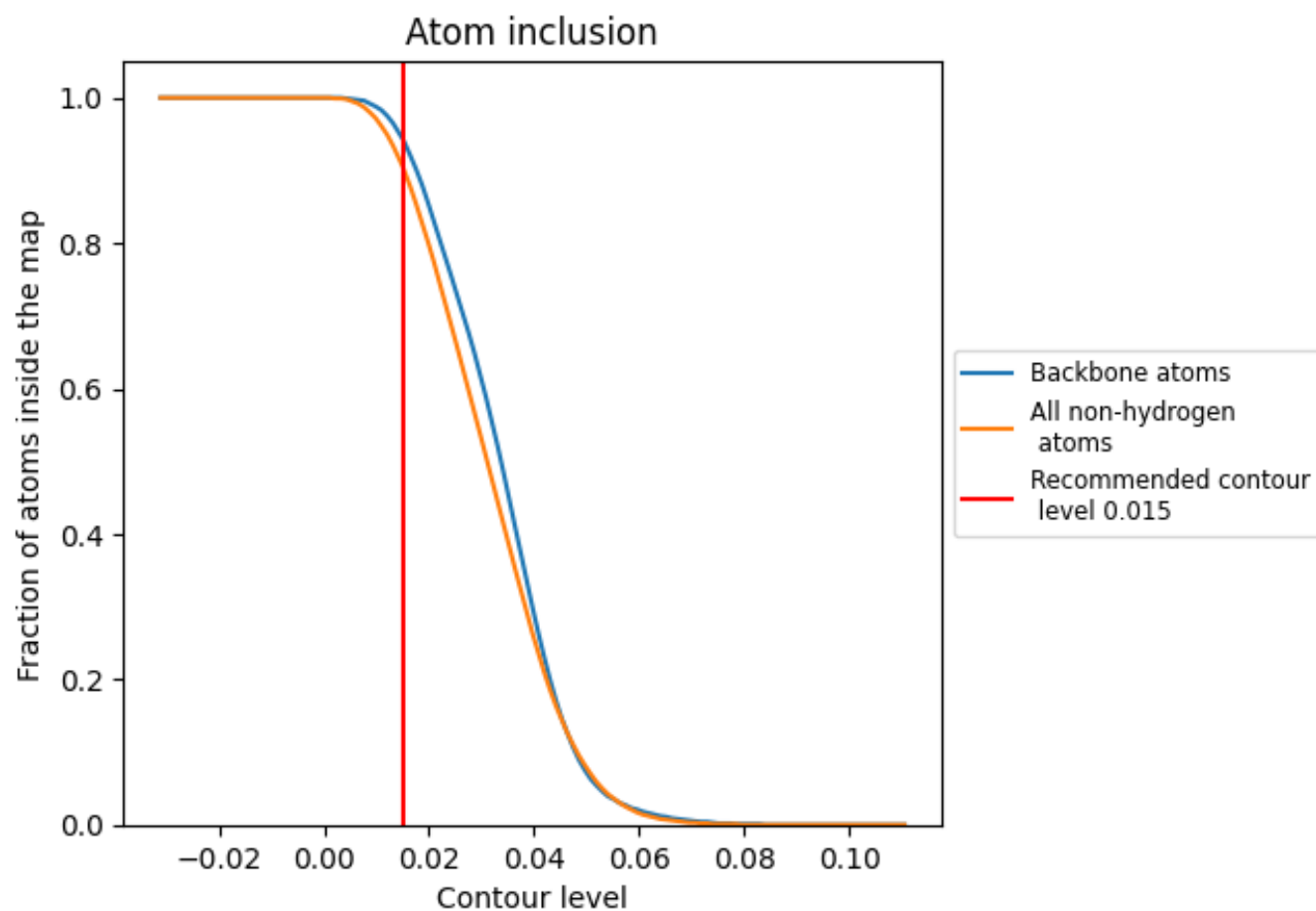
## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.015).









































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9050	 0.5570
10	 0.7730	 0.4470
11	 0.6300	 0.2780
13	 0.9170	 0.4890
5	 0.9390	 0.5570
7	 0.9970	 0.6070
8	 0.9700	 0.5810
9	 0.9410	 0.5540
A	 0.9610	 0.6160
AA	 0.8470	 0.5520
B	 0.9290	 0.6020
BB	 0.8590	 0.5630
C	 0.9290	 0.5980
CC	 0.8780	 0.5720
D	 0.8730	 0.5700
DD	 0.7740	 0.5090
E	 0.8840	 0.5640
EE	 0.8820	 0.5720
FF	 0.8380	 0.5430
G	 0.8190	 0.5480
GG	 0.7770	 0.5010
H	 0.8600	 0.5740
HH	 0.7050	 0.5020
I	 0.9080	 0.5950
II	 0.8870	 0.5630
J	 0.8500	 0.5510
JJ	 0.8590	 0.5600
K	 0.9370	 0.6010
KK	 0.7710	 0.4820
L	 0.8690	 0.5750
LL	 0.9020	 0.5850
M	 0.9070	 0.5720
MM	 0.2370	 0.2930
N	 0.9670	 0.6170
NN	 0.8930	 0.5660















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Chain	Atom inclusion	Q-score
O	 0.9460	 0.6000
OO	 0.8950	 0.5770
P	 0.9290	 0.6010
PP	 0.7540	 0.5010
Q	 0.9390	 0.6040
QQ	 0.8440	 0.5420
R	 0.8780	 0.5670
RR	 0.7600	 0.5060
S	 0.9370	 0.6020
SS	 0.8180	 0.5280
T	 0.8970	 0.5850
TT	 0.8490	 0.5260
U	 0.7990	 0.5280
UU	 0.7110	 0.4800
V	 0.9330	 0.6060
VV	 0.8360	 0.5530
W	 0.7530	 0.5000
WW	 0.9140	 0.5900
X	 0.8940	 0.5830
XX	 0.9080	 0.5840
Y	 0.8730	 0.5730
YY	 0.8400	 0.5400
Z	 0.8880	 0.5710
ZZ	 0.7740	 0.5190
a	 0.9450	 0.6110
aa	 0.9000	 0.5780
b	 0.8510	 0.5510
bb	 0.8090	 0.5430
c	 0.8630	 0.5700
cc	 0.8060	 0.5440
d	 0.8940	 0.5800
dd	 0.8730	 0.5540
e	 0.9430	 0.6110
ee	 0.7320	 0.5040
f	 0.9540	 0.6140
ff	 0.3020	 0.3340
g	 0.9060	 0.5890
gg	 0.6880	 0.4650
h	 0.8800	 0.5730
i	 0.8660	 0.5580
j	 0.9750	 0.6170
k	 0.7860	 0.5330

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Chain	Atom inclusion	Q-score
l	 0.9110	 0.5990
m	 0.8850	 0.5870
n	 0.9220	 0.5940
o	 0.9150	 0.6000
p	 0.9090	 0.6050
r	 0.9370	 0.5970