



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 12:14 PM UTC

PDB ID : 9YPZ / pdb_00009ypz
EMDB ID : EMD-73315
Title : Vacant ribosome with P-site tRNA, substate 1, Structure Ia
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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMD 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) : 2.49

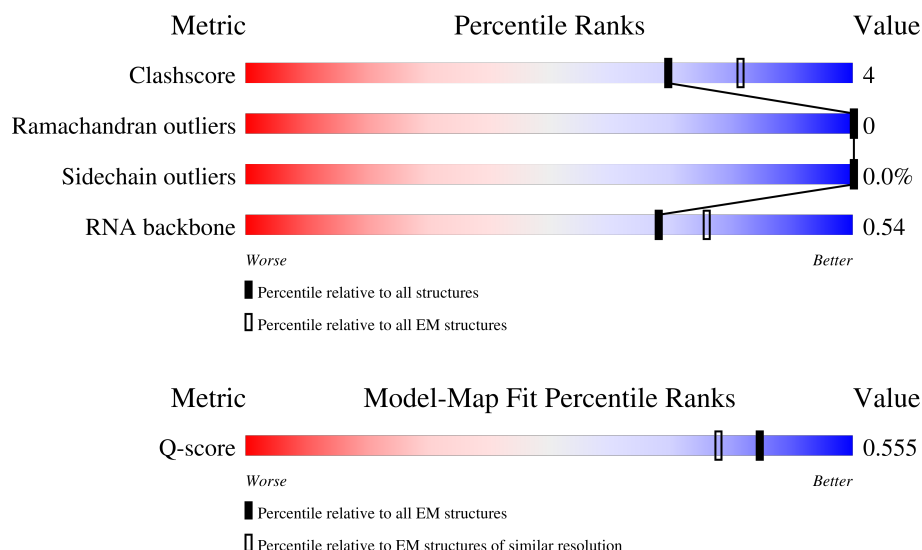
1 Overall quality at a glance i

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.



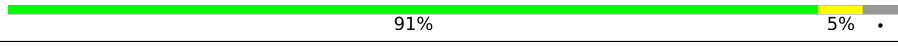
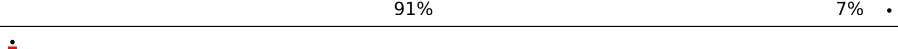
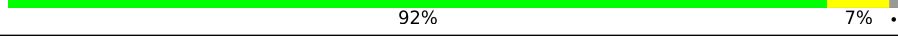
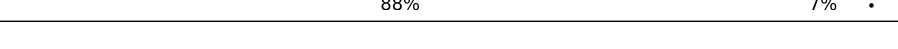
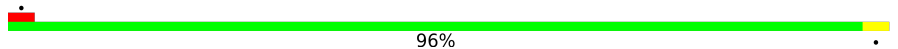
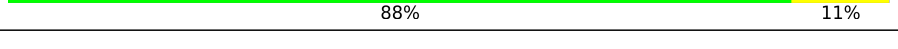
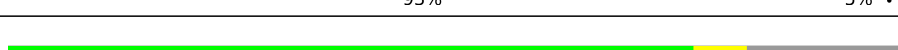
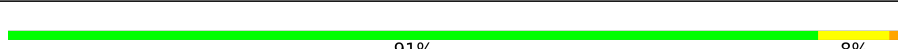
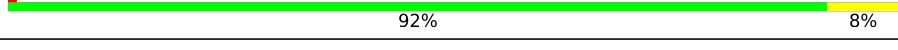
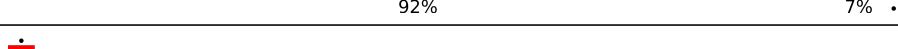
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13054 (2.40 - 3.40)

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 ≥ 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	
2	7	120	
3	8	156	

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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	

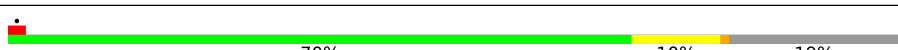
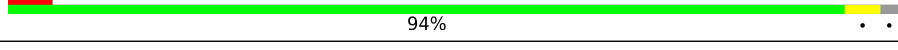
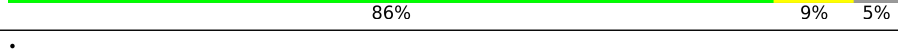
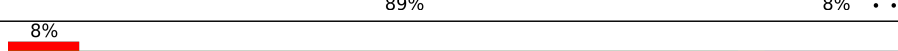
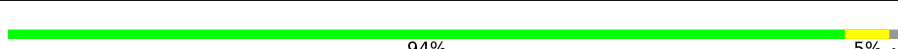
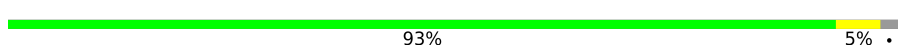
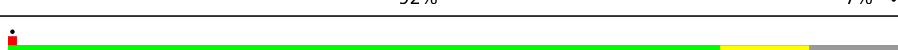
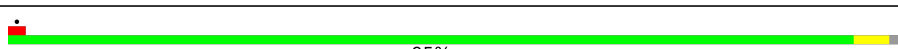
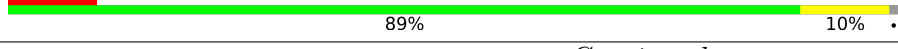
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Mol	Chain	Length	Quality of chain
29	Z	136	
30	a	148	
31	b	245	
32	c	115	
33	d	125	
34	e	135	
35	f	110	
36	g	116	
37	h	123	
38	i	105	
39	k	70	
40	l	51	
41	m	102	
42	n	25	
43	o	106	
44	p	92	
45	r	137	
46	AA	295	
47	BB	264	
48	CC	293	
49	DD	243	
50	EE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

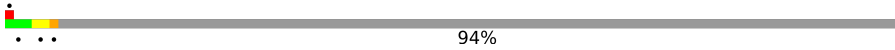
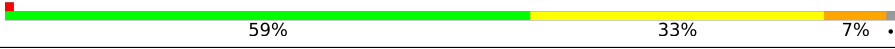
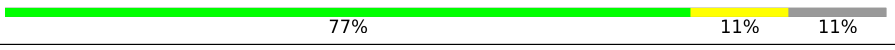
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Mol	Chain	Length	Quality of chain
54	II	208	
55	JJ	194	
56	KK	165	
57	LL	158	
58	MM	132	
59	NN	151	
60	OO	168	
61	PP	145	
62	QQ	146	
63	RR	135	
64	SS	152	
65	TT	145	
66	UU	119	
67	VV	83	
68	WW	130	
69	XX	143	
70	YY	130	
71	ZZ	125	
72	aa	115	
73	bb	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	 94% 8%
80	11	75	 44% 47% 8%
80	13	75	 59% 33% 7%
81	j	97	 77% 11% 11%

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		

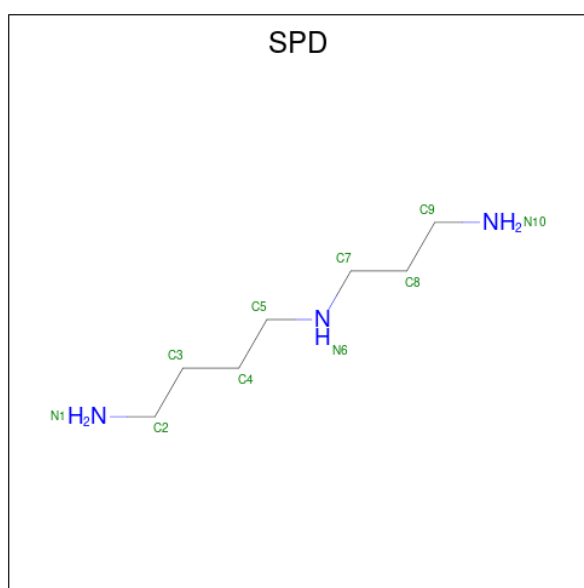
- Molecule 80 is a RNA chain called Met-tRNA.

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: C₇H₁₉N₃).

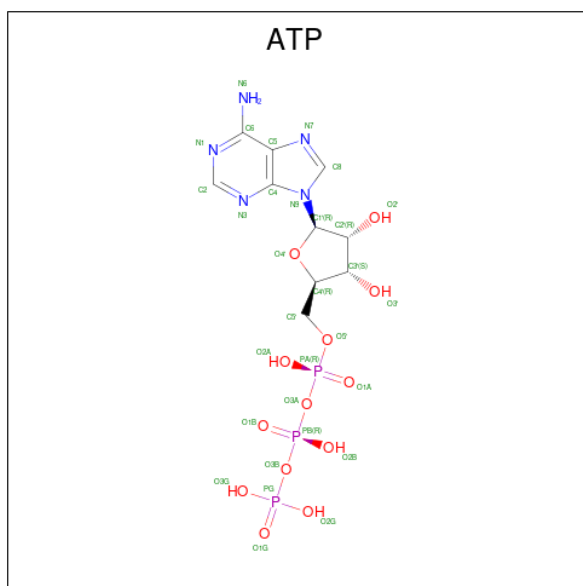


Mol	Chain	Residues	Atoms			AltConf
82	5	1	Total	C	N	0
			10	7	3	

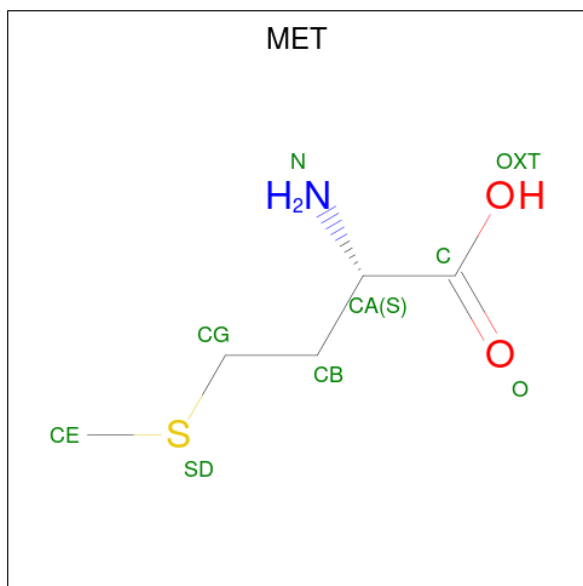
- Molecule 83 is ZINC ION (CCD ID: ZN) (formula: Zn).

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: C₁₀H₁₆N₅O₁₃P₃).



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

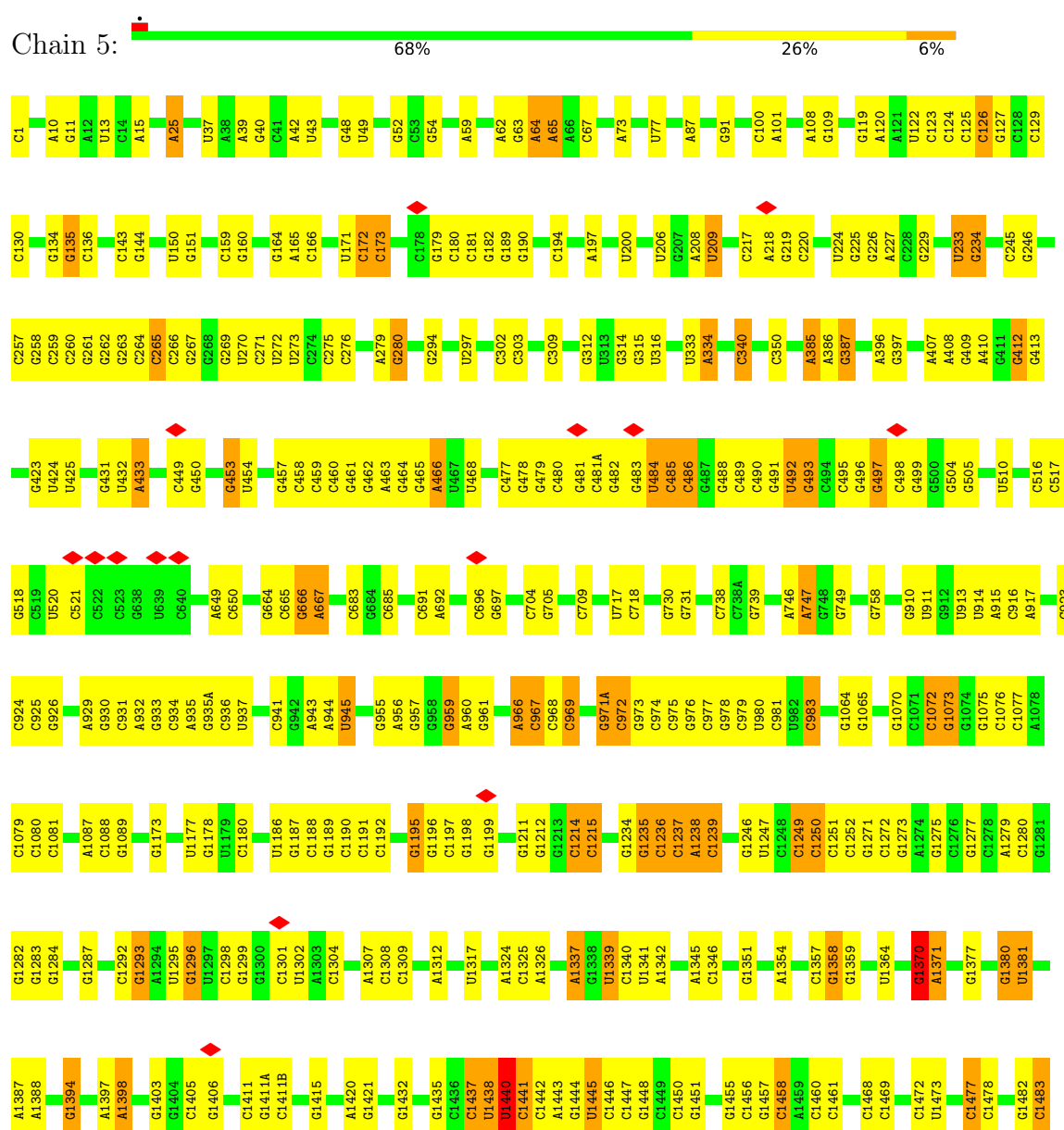


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
85	13	1	8	5	1	1	1	0

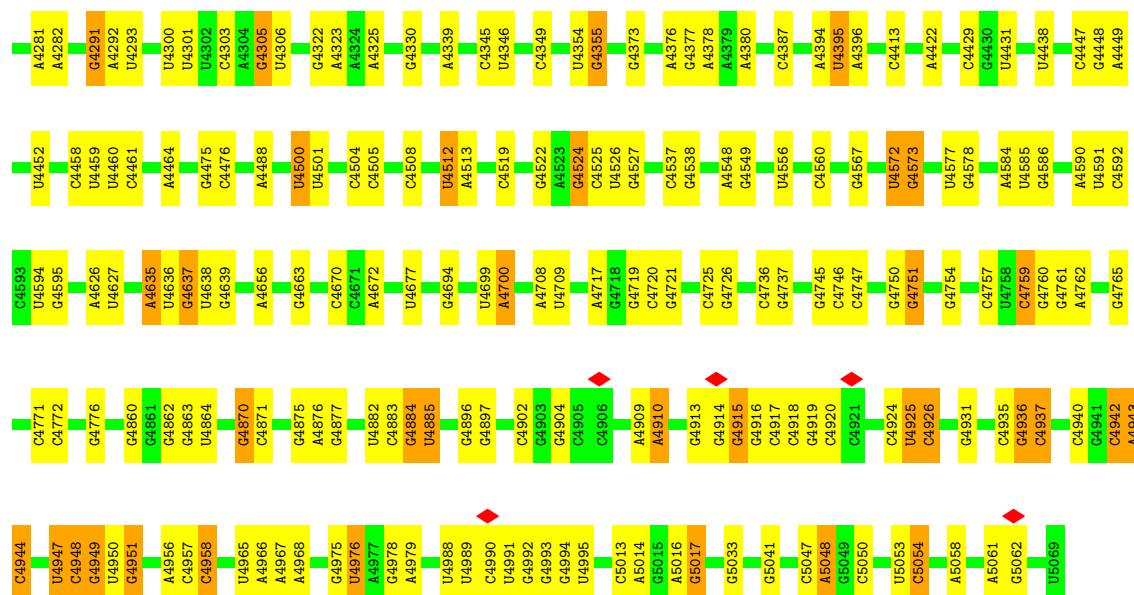
3 Residue-property plots

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



G1484	C1661	G1821	G2058	A2313	C2465	G2559	G2711	G2855	A3727	G3873	U3964	U4118
C1485	C1662	U1822	G2065	A2314	G2466	C2560	G2712	A2864	A3728	G3874	A3965	C4119
C1486	C1663	U1834	G2066	G2318	U2467	C2563	G2724	U2865	A3732	G3875	A3966	U4120
G1498	C1676	U1835	G2067	G2318	G2471	G2566	G2725	C2899	A3733	A3876	U3967	G4121
G1502	C1678	G1836	A2069	G2321	G2472	G2567	G2726	U2900	A3736	A3877	G3969	G4122
A1523	C1683	A1837	U2070	A2332	G2473	G2568	U2730	C3598	A3737	C3878	G3970	A4127
G1529	A1684	G1842	C2083	G2333	G2475	C2569	C2731	A3599	A3738	G3879	G3971	G4146
G1593	C1690	G1846	U2084	G2334	A2477	G2570	G2732	G3600	A3748	G3880	A3972	G4147
A1594	G1691	C1847	C2084	G2335	G2479	C2571	C2733	A3749	G3735	G3881	G3973	A4157
A1594	G1691	G1855	G2088	G2336	G2480	U2580	U2740	G3603	G3749	G3888	G3974	A4169
A1547	G1724	G1855	G2089	G2336	G2481	U2580	U2740	A3604	G3750	G3889	C3975	A4170
A1547	G1724	G1855	G2090	G2336	G2482	U2580	U2740	U3606	G3751	A3894	G3976	C4171
A1547	G1724	G1855	G2091	G2336	G2483	U2580	U2740	A3611	A3759	G3897	G4035	A4172
A1547	G1724	G1855	G2092	G2336	G2484	U2580	U2740	A3612	A3760	A3905	G4036	U4203
A1547	G1724	G1855	G2093	G2336	G2485	U2580	U2740	A3613	A3761	A3906	C4037	U4203
A1547	G1724	G1855	G2094	G2336	G2486	U2580	U2740	A3614	A3762	A3907	C4038	U4203
A1547	G1724	G1855	G2095	G2336	G2487	U2580	U2740	A3615	A3763	G3900	C4039	U4203
A1547	G1724	G1855	G2096	G2336	G2488	U2580	U2740	A3616	A3764	A3901	C4040	U4203
A1547	G1724	G1855	G2097	G2336	G2489	U2580	U2740	A3617	A3765	G3902	C4041	U4203
A1547	G1724	G1855	G2098	G2336	G2490	U2580	U2740	A3618	A3766	A3903	C4042	U4203
A1547	G1724	G1855	G2099	G2336	G2491	U2580	U2740	A3619	A3767	A3904	C4043	U4203
A1547	G1724	G1855	G2100	G2336	G2492	U2580	U2740	A3620	A3768	A3905	C4044	U4203
A1547	G1724	G1855	G2101	G2336	G2493	U2580	U2740	A3621	A3769	A3906	C4045	U4203
A1547	G1724	G1855	G2102	G2336	G2494	U2580	U2740	A3622	A3770	A3907	C4046	U4203
A1547	G1724	G1855	G2103	G2336	G2495	U2580	U2740	A3623	A3771	A3908	C4047	U4203
A1547	G1724	G1855	G2104	G2336	G2496	U2580	U2740	A3624	A3772	A3909	C4048	U4203
A1547	G1724	G1855	G2105	G2336	G2497	U2580	U2740	A3625	A3773	A3910	C4049	U4203
A1547	G1724	G1855	G2106	G2336	G2498	U2580	U2740	A3626	A3774	A3911	C4050	U4203
A1547	G1724	G1855	G2107	G2336	G2499	U2580	U2740	A3627	A3775	A3912	C4051	U4203
A1547	G1724	G1855	G2108	G2336	G2500	U2580	U2740	A3628	A3776	A3913	C4052	U4203
A1547	G1724	G1855	G2109	G2336	G2501	U2580	U2740	A3629	A3777	A3914	C4053	U4203
A1547	G1724	G1855	G2110	G2336	G2502	U2580	U2740	A3630	A3778	A3915	C4054	U4203
A1547	G1724	G1855	G2111	G2336	G2503	U2580	U2740	A3631	A3779	A3916	C4055	U4203
A1547	G1724	G1855	G2112	G2336	G2504	U2580	U2740	A3632	A3780	A3917	C4056	U4203
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A1547	G1724	G1855	G2116	G2336	G2508	U2580	U2740	A3636	A3784	A3921	C4060	U4203
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A1547	G1724	G1855	G2163	G2336	G2555	U2580	U2740	A3683	A3831	A3968	C4107	U4203
A1547	G1724	G1855	G2164	G2336	G2556	U2580	U2740	A3684	A3832	A3969	C4108	U4203
A1547	G1724	G1855	G2165	G2336	G2557	U2580	U2740	A3685	A3833	A3970	C4109	U4203
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A1547	G1724	G1855	G2167	G2336	G2559	U2580	U2740	A3687	A3835	A3972	C4111	U4203
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A1547	G1724	G1855	G2169	G2336	G2561	U2580	U2740	A3689	A3837	A3974	C4113	U4203
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A1547	G1724	G1855	G2174	G2336	G2566	U2580	U2740	A3694	A3842	A3979	C4118	U4203
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A1547	G1724	G1855	G2176	G2336	G2568	U2580	U2740	A3696	A3844	A3981	C4120	U4203
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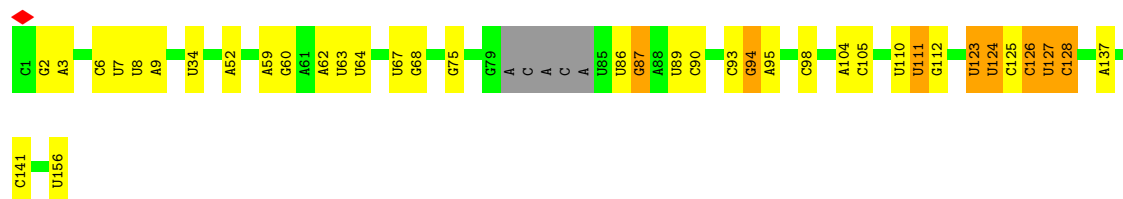
• Molecule 2: 5S ribosomal RNA

Chain 7: 83% 15% ..



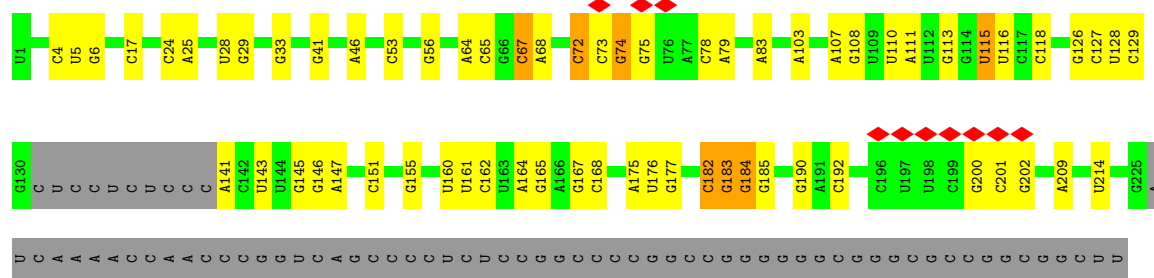
• Molecule 3: 5.8S ribosomal RNA

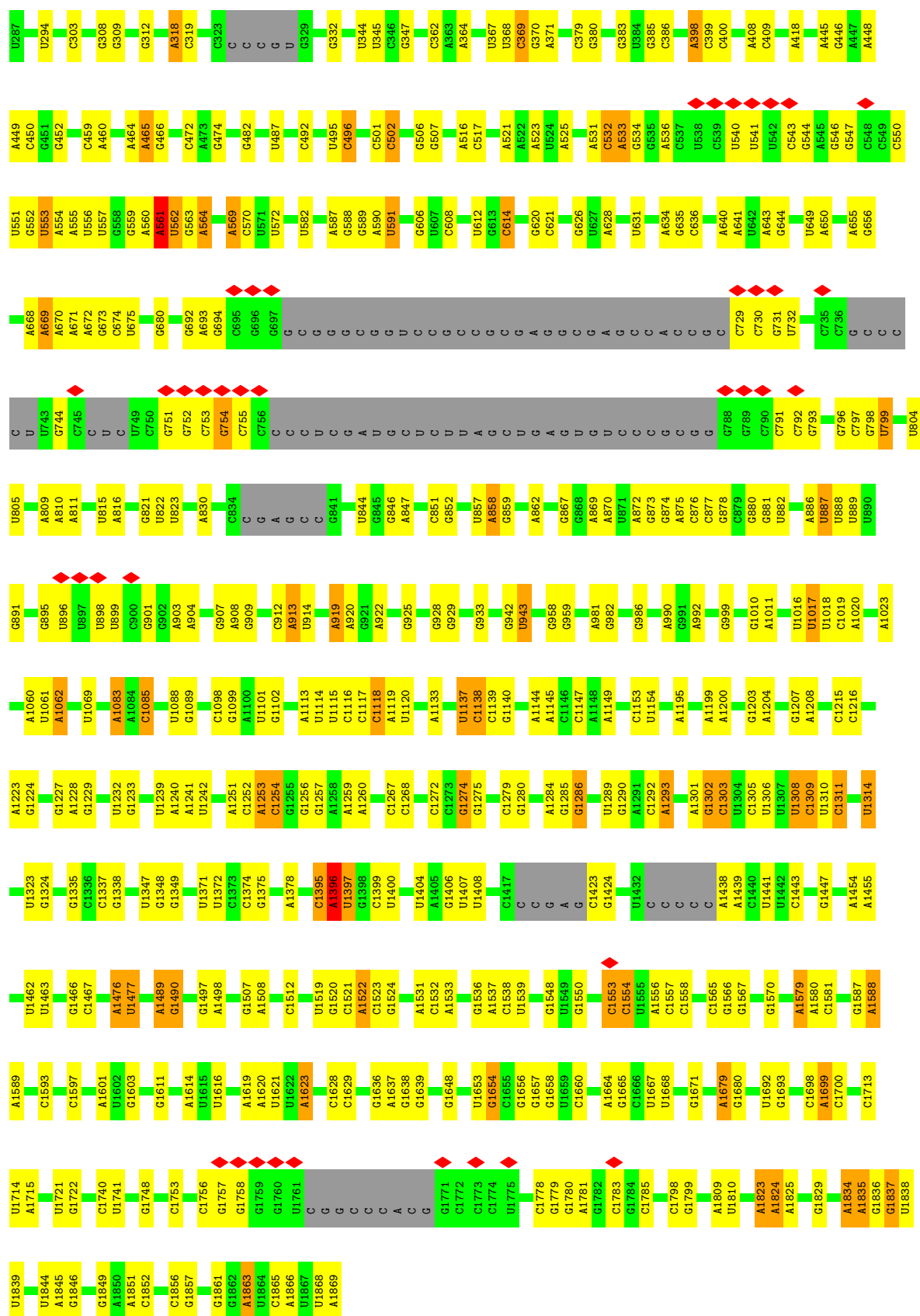
Chain 8: 72% 19% 5% .



• Molecule 4: 18S ribosomal RNA

Chain 9: 63% 24% 9%

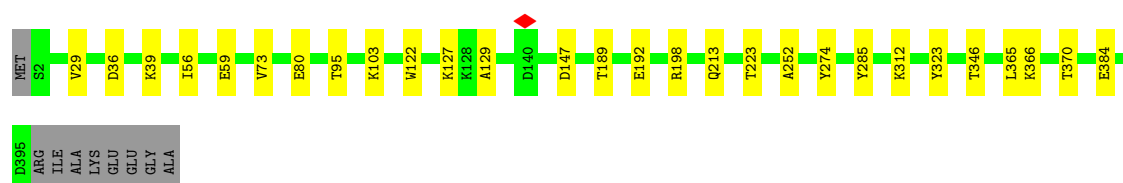


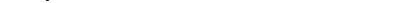


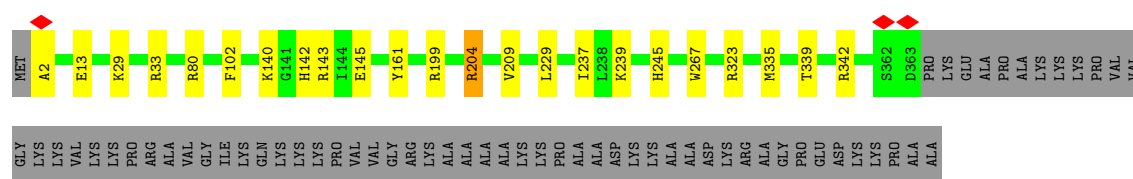
• Molecule 5: Ribosomal protein L8

MET
G2
R30
D33
K70
K71
R72
P108
E117
R123
G124
E142
T143
R198
R227
K234
I238
R247
G248
T249
LYS
THR
VAL
CIN
GLU
LYS
GIU
ASN

- Chain B:  91% 7%



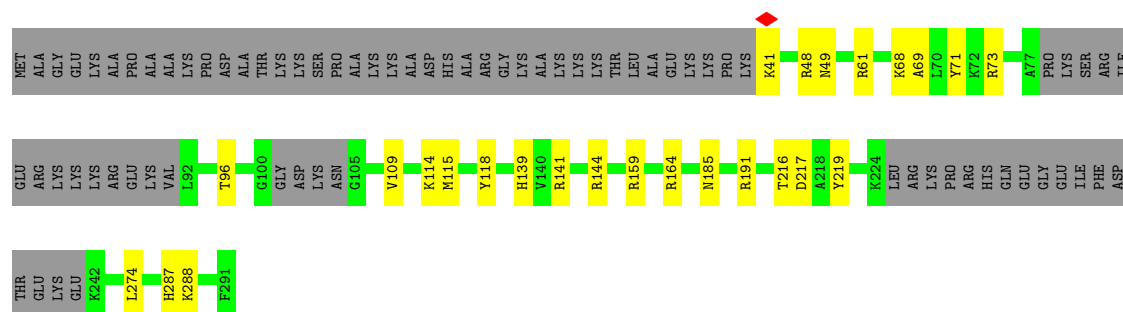
- Chain C:  80% 5% 15%

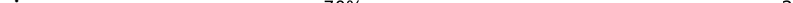


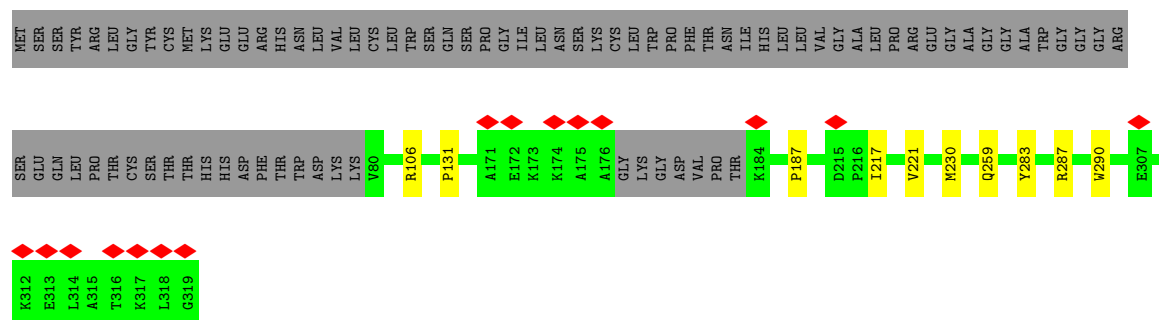
- Chain D:  94% . .



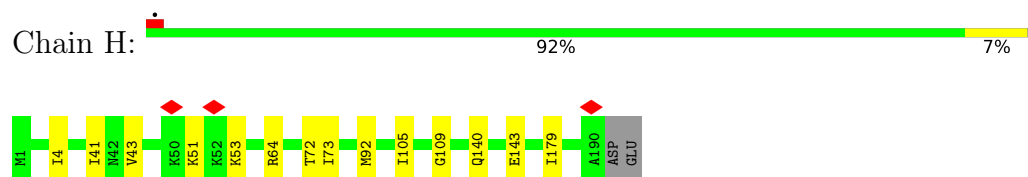
- Chain E: 65% 9% 26%



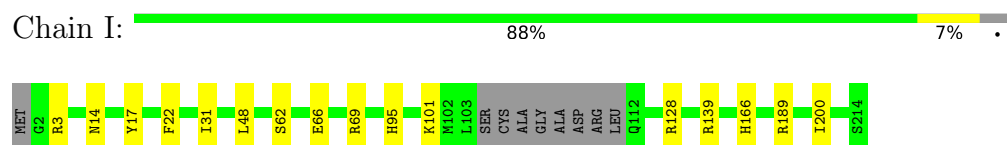
- Chain G:  5% 70% 27%



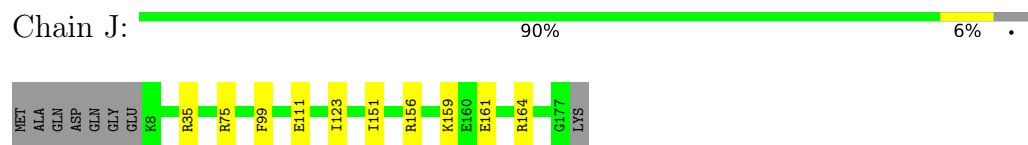
- Molecule 11: 60S ribosomal protein L9



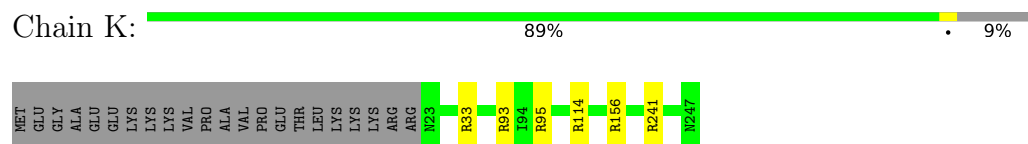
- Molecule 12: 60S ribosomal protein L10



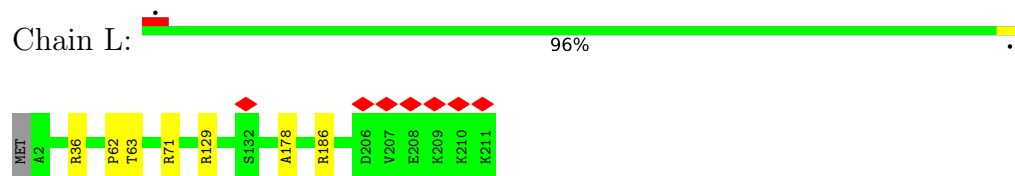
- Molecule 13: Ribosomal protein L11



- Molecule 14: 60S ribosomal protein L7

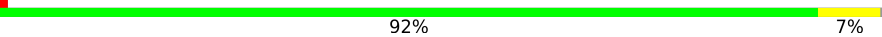


- Molecule 15: 60S ribosomal protein L13



- Molecule 16: 60S ribosomal protein L14

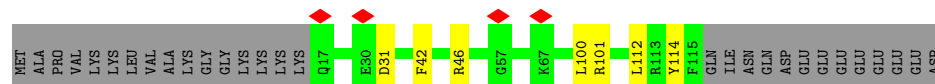


Chain T:  92% 7%



- Molecule 24: eL22

Chain U:  72% 5% 23%



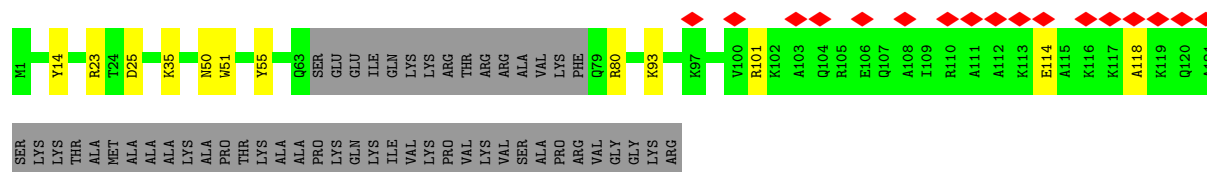
- Molecule 25: Ribosomal protein L23

Chain V:  88% 8%



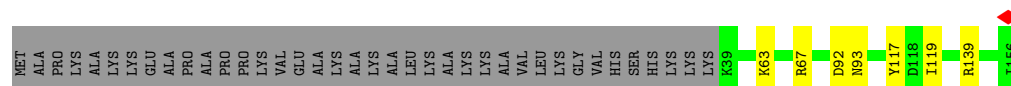
- Molecule 26: eL24

Chain W:  11% 60% 8% 32%



- Molecule 27: eL23

Chain X:  71% 24%



- Molecule 28: uL24

Chain Y:  86% 6% 8%



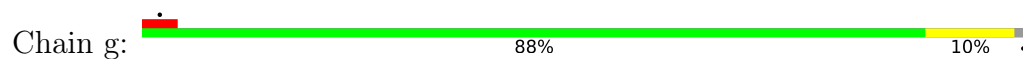
- Molecule 29: 60S ribosomal protein L27

Chain Z:  90% 8%





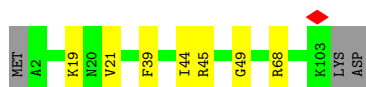
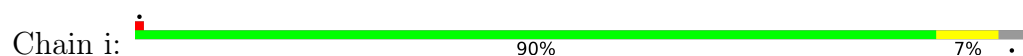
- Molecule 36: Large ribosomal subunit protein eL34



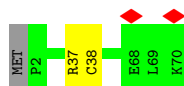
- Molecule 37: eL35



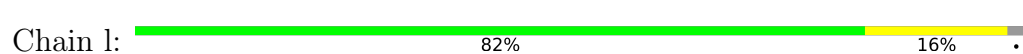
- Molecule 38: 60S ribosomal protein L36



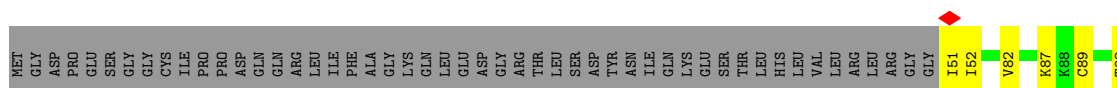
- Molecule 39: eL38



- Molecule 40: eL39



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



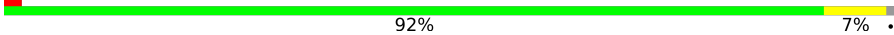
• Molecule 42: eL41

Chain n:  80% 20%

• Molecule 43: Large ribosomal subunit protein eL42

Chain o:  92% 6%

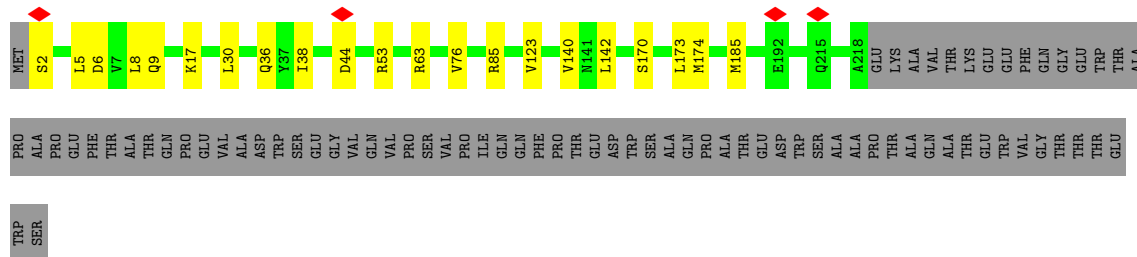
• Molecule 44: eL43

Chain p:  92% 7%

• Molecule 45: eL28

Chain r:  82% 9% 9%

• Molecule 46: uS2 (SA)

Chain AA:  66% 7% 26%

• Molecule 47: 40S ribosomal protein S3a

Chain BB:  77% 19%

GLY
ALA
LYS
VAL
GLU
ARG
ALA
ASP
GLY
TVR
GLU
PRO
PRO
VAL
GLN
GLU
SER
VAL

- Molecule 48: Small ribosomal subunit protein uS5

Chain CC:  71% 25%

MET
ALA
ASP
ASP
ALA
GLY
ALA
ALA
GLY
PRO
GLY
ASP
PRO
VAL
GLN
GLU
SER
VAL
TLE
GLY
ARG
GLY
PHE
ARG
GLY
GLN
PHE
GLY
SER
GLY
VAL
ARG
GLY
ARG
GLY
ARG
GLY
GLY
GLY
ARG
ALA
ARG
GLY
LYS
GLY
LYS
ALA
GLU
ASP
K58
I88

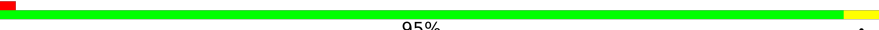
I94
V106
V128
E146
I162
I196
Y223
R227
D271
K275
T276
H277
T278
ARG
VAL
SER
VAL
GLN
THR
THR
GLN
ALA
PRO
ALA
VAL
ALA
ALA
THR
THR

- Molecule 49: Ribosomal protein S3

Chain DD:  87% 5% 8%

MET
ALA
VAL
GLN
I6
L29
Y34
T44
G63
R64
R65
I66
T70
R76
G82
L86
Y120
L177
L182
K185
D215
L218
Q226
K227
G228
GLY
LYS
PRO
GLU
PRO
PRO
PRO
ALA
MET
PRO
GLN
PRO
VAL
THR
ALA

- Molecule 50: eS4 (S4 X isoform)

Chain EE:  95%

MET
A2
Y54
E97
K106
C124
L139
Y140
T141
H142
D143
R148
Y149
P150
D212
A213
Q260
S261
S262
G263

- Molecule 51: Ribosomal protein S5

Chain FF:  83% 7% 10%

MET
THR
GLU
TRP
GLU
THR
ALA
ALA
ALA
VAL
ALA
ALA
GLU
T14
P15
D16
D27
I39
R60
I68
T73
M76
M77
M78
H79
G80
N83
T89
L102
S119
I128
GLY
ARG
ALA
GLY
THR
VAL
ARG
R136
D140
A189
R204

- Molecule 52: 40S ribosomal protein S6

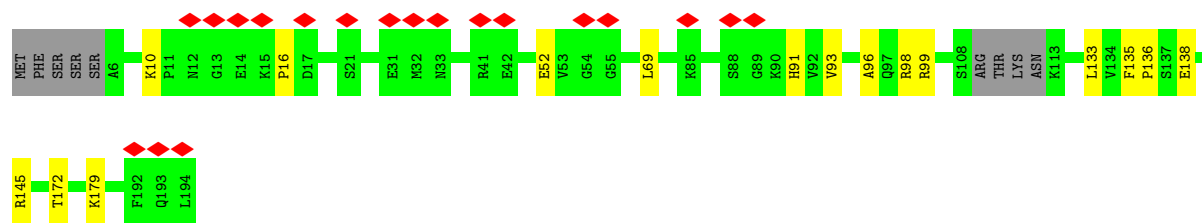
Chain GG:  7% 84% 11% 5%

M1
K2
F7
L24
G42
E43
E44
I52
D57
K58
V67
R68
G99
S107
V108
D120
I121
L124
T125
R131
R132
R142
D151
D152
V153
N163
K164
E165
Q186
R189
K201
N202
E219
A220
Q225
E226
Q227
I228
A229
K230
R231

R232
R233
L234
S235
S236
L237
ARG
ALA
SER
THR
SER
LYS
SER
GLU
SER
SER
GLN
LYS

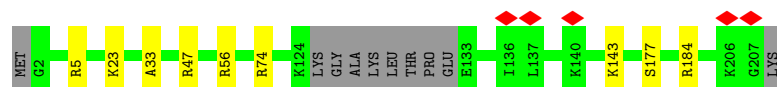
- Molecule 53: 40S ribosomal protein S7

Chain HH:  10% 87% 8% 5%



- Molecule 54: 40S ribosomal protein S8

Chain II: 91% 5%



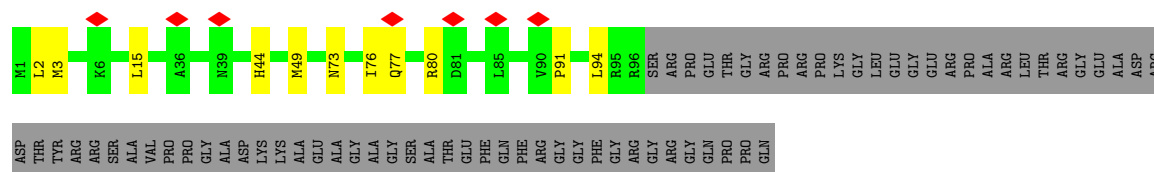
- Molecule 55: Ribosomal protein S9 (Predicted)

Chain JJ: 84% 10% 7%



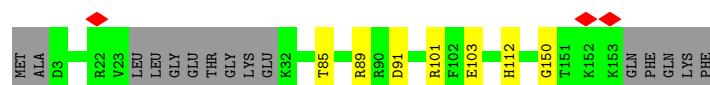
- Molecule 56: S10_pectin domain-containing protein

Chain KK: 52% 7% 42%



- Molecule 57: Ribosomal protein S11

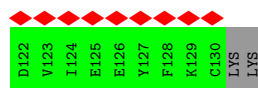
Chain LL: 86% 9%



- Molecule 58: 40S ribosomal protein S12

Chain MM: 72% 67% 17% 15%





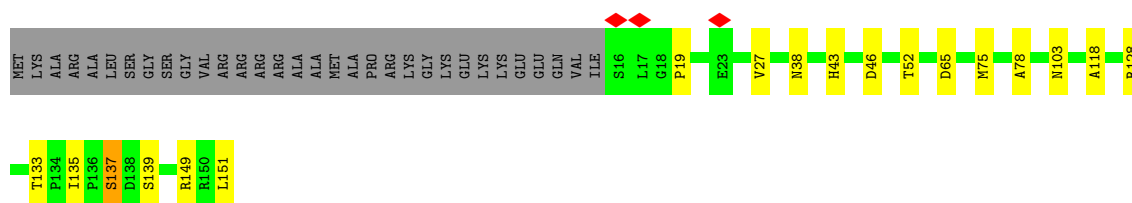
- Molecule 59: Ribosomal protein S13

Chain NN: 93% 5%



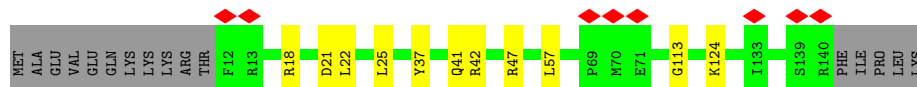
- Molecule 60: Small ribosomal subunit protein uS11

Chain OO: 70% 10% 19%



- Molecule 61: uS19

Chain PP: 6% 81% 8% 11%



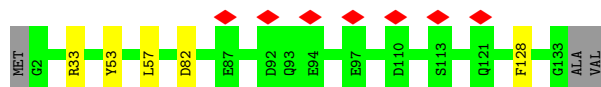
- Molecule 62: uS9

Chain QQ: 88% 10%



- Molecule 63: eS17

Chain RR: 5% 94% 1%



- Molecule 64: uS13

Chain SS: 86% 9% 5%



GLY
GLU
ASP
ALA

- Molecule 72: 40S ribosomal protein S26

Chain aa:  83% 12%

MET T2 R6 I79 V84 R87 D94 F101 R102 PRO ALA GLY ALA ALA PRO ARG PRO PRO LYS PRO MET

- Molecule 73: 40S ribosomal protein S27

Chain bb:  92% 7%

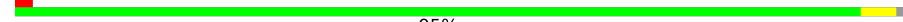
MET P2 M33 K42 S48 V57 G68 R72 H84

- Molecule 74: Ribosomal protein S28

Chain cc:  80% 10% 10%

MET ASP THR SER ARG VAL Q7 T21 Q24 Q25 Q26 R44 R51 E60 R67 L68 ARG

- Molecule 75: eS29

Chain dd:  95%

MET G2 Y7 R22 D86

- Molecule 76: 40S ribosomal protein S30

Chain ee:  39% 59%

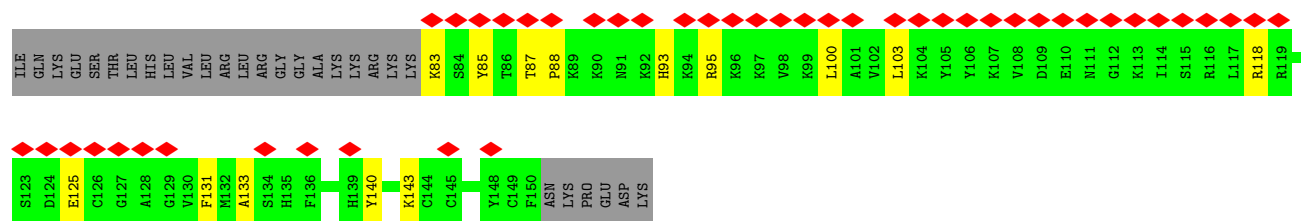
MET GLN LEU PHE THR VAL ARG ALA GLN GLU HIS THR LEU GLU VAL THR VAL ARG GLU THR VAL ALA GLN ILE LYS ALA HIS VAL ALA SER LEU LEU GLU GLY ILE ALA PRO GLU ASP GLN VAL LEU LEU LEU ALA GLY THR PRO LEU ASP GLU ALA THR LEU GLN CYS GLY VAL GLU

ALA LEU SER THR LEU VAL ALA GLY ARG MET LEU GLY VAL LYS VAL GLY S78 Q88 R101 Y111 V119 F120 T121 F122 S132

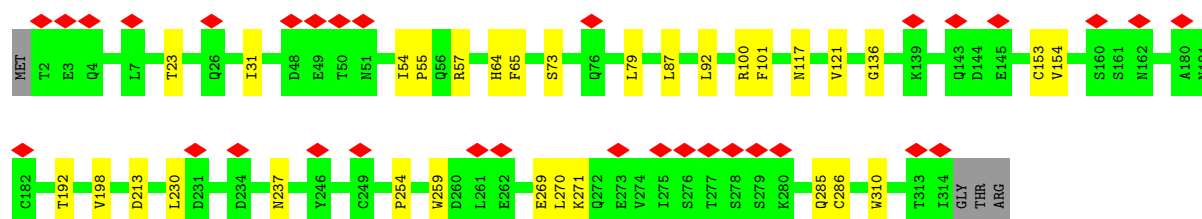
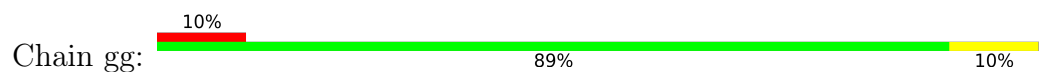
- Molecule 77: Ribosomal protein S27a

Chain ff:  29% 35% 9% 56%

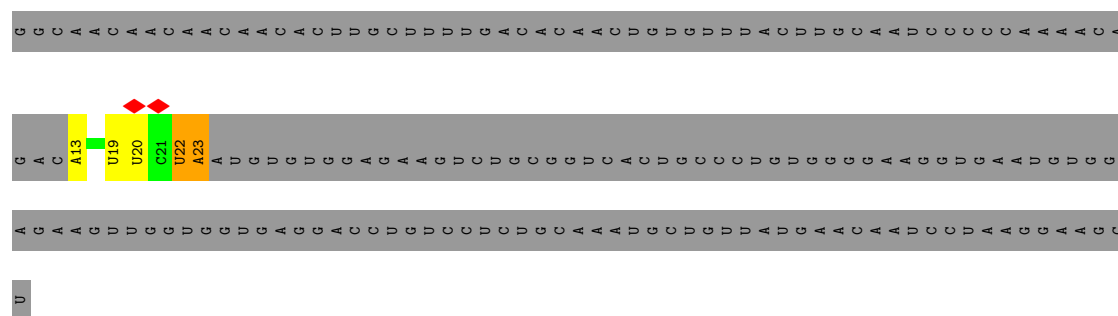
MET GLN ILE PHE VAL LYS THR LEU GLY LYS THR ILE THR LEU VAL HIS VAL PRO SER ASP THR ILE GLU ASN VAL LYS ALA LYS ILE GLN ASP LYS GLY ILE PRO PRO ASP GLN ARG ARG LEU PHE ALA GLY LYS LEU ASP GLY ARG THR LEU SER ASP TYR ASN



• Molecule 78: RACK1



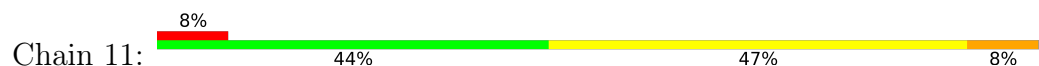
• Molecule 79: MF mRNA



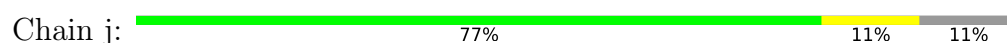
• Molecule 80: Met-tRNA



• Molecule 80: Met-tRNA



• Molecule 81: Ribosomal protein L37



MET	T2	K3	N13	K14	T16	R20	H28	L29	Q30	Y39	R43	R55	H76	T82	K87	ARG	ALA	ALA	ALA	VAL	ALA	ALA	SER	SER	SER	SER
-----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	10400	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	0.102	Depositor
Minimum map value	-0.029	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: SPD, ATP, 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	0.44	0/86380	0.68	21/134721 (0.0%)
2	7	0.43	0/2836	0.62	0/4421
3	8	0.43	0/3581	0.64	0/5577
4	9	0.41	0/40509	0.66	8/63128 (0.0%)
5	A	0.34	0/1936	0.54	0/2596
6	B	0.33	0/3240	0.52	0/4339
7	C	0.33	0/2937	0.55	0/3946
8	D	0.29	0/2437	0.50	0/3264
9	E	0.28	0/1762	0.55	0/2362
10	G	0.29	0/1910	0.56	0/2569
11	H	0.30	0/1535	0.47	0/2063
12	I	0.29	0/1702	0.49	0/2272
13	J	0.27	0/1385	0.50	0/1852
14	K	0.35	0/1911	0.53	0/2549
15	L	0.31	0/1733	0.51	0/2316
16	M	0.31	0/1158	0.53	0/1547
17	N	0.38	0/1746	0.57	0/2338
18	O	0.34	0/1662	0.57	1/2222 (0.0%)
19	P	0.34	0/1268	0.59	0/1700
20	Q	0.35	0/1539	0.54	0/2054
21	R	0.31	0/1524	0.54	0/2013
22	S	0.34	0/1501	0.50	0/2012
23	T	0.31	0/1326	0.50	0/1770
24	U	0.25	0/823	0.56	0/1104
25	V	0.33	0/983	0.51	0/1319
26	W	0.29	0/873	0.51	0/1158
27	X	0.30	0/984	0.48	0/1323
28	Y	0.30	0/1132	0.50	0/1504
29	Z	0.33	0/1130	0.51	0/1507
30	a	0.34	0/1191	0.59	0/1590
31	b	0.28	0/819	0.53	0/1081
32	c	0.34	0/771	0.53	0/1034

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	d	0.33	0/903	0.54	0/1216
34	e	0.35	0/1071	0.55	0/1429
35	f	0.37	0/895	0.49	0/1198
36	g	0.34	0/916	0.55	0/1220
37	h	0.30	0/1021	0.54	0/1348
38	i	0.28	0/841	0.58	0/1112
39	k	0.27	0/575	0.50	0/761
40	l	0.34	0/459	0.53	0/608
41	m	0.31	0/435	0.45	0/575
42	n	0.38	0/241	0.71	0/305
43	o	0.32	0/864	0.52	0/1140
44	p	0.35	0/718	0.58	0/953
45	r	0.33	0/1010	0.52	0/1354
46	AA	0.27	0/1747	0.47	0/2374
47	BB	0.29	0/1756	0.52	0/2350
48	CC	0.30	0/1753	0.51	0/2369
49	DD	0.24	0/1767	0.48	0/2378
50	EE	0.29	0/2118	0.50	0/2849
51	FF	0.25	0/1481	0.50	0/1991
52	GG	0.25	0/1946	0.50	0/2590
53	HH	0.24	0/1511	0.51	0/2022
54	II	0.29	0/1655	0.51	0/2205
55	JJ	0.30	0/1533	0.53	0/2047
56	KK	0.23	0/834	0.49	0/1125
57	LL	0.30	0/1195	0.49	0/1597
58	MM	0.18	0/880	0.50	0/1179
59	NN	0.30	0/1226	0.53	0/1649
60	OO	0.32	0/1029	0.60	0/1380
61	PP	0.22	0/1079	0.54	0/1441
62	QQ	0.26	0/1146	0.51	0/1534
63	RR	0.24	0/1082	0.49	0/1452
64	SS	0.26	0/1208	0.52	0/1618
65	TT	0.25	0/1115	0.53	0/1493
66	UU	0.24	0/805	0.48	0/1081
67	VV	0.28	0/644	0.52	0/860
68	WW	0.34	0/1051	0.47	0/1406
69	XX	0.30	0/1105	0.55	0/1476
70	YY	0.25	0/1028	0.47	0/1366
71	ZZ	0.23	0/604	0.53	0/810
72	aa	0.31	0/828	0.49	0/1109
73	bb	0.26	0/665	0.52	0/891
74	cc	0.25	0/490	0.46	0/656
75	dd	0.29	0/470	0.54	0/623

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
76	ee	0.25	0/447	0.57	0/587
77	ff	0.17	0/567	0.53	0/753
78	gg	0.21	0/2493	0.47	0/3394
79	10	0.30	0/261	0.63	0/404
80	11	0.26	0/1773	0.66	0/2763
80	13	0.31	0/1773	0.61	0/2763
81	j	0.35	0/720	0.58	0/952
All	All	0.38	0/229958	0.62	30/338007 (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	2
7	C	0	1
8	D	0	3
9	E	0	1
14	K	0	1
15	L	0	1
16	M	0	1
17	N	0	2
20	Q	0	3
22	S	0	1
25	V	0	1
28	Y	0	1
29	Z	0	1
34	e	0	1
36	g	0	1
41	m	0	1
44	p	0	1
47	BB	0	1
49	DD	0	1
54	II	0	2
55	JJ	0	1
60	OO	0	1
63	RR	0	1
64	SS	0	1
65	TT	0	1
66	UU	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
69	XX	0	1
72	aa	0	1
All	All	0	36

There are no bond length outliers.

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	9	1835	A	C2'-C3'-O3'	6.86	119.79	109.50
1	5	2709	C	C4'-C3'-O3'	6.49	119.14	109.40
1	5	4170	A	C4'-C3'-O3'	6.18	118.67	109.40
1	5	1440	U	C2'-C3'-O3'	6.17	118.75	109.50
1	5	4119	C	C2'-C3'-O3'	6.03	118.55	109.50
1	5	2553	A	C2'-C3'-O3'	6.00	118.50	109.50
4	9	1396	A	C2'-C3'-O3'	5.70	118.05	109.50
18	O	110	PRO	N-CA-C	5.69	117.64	110.70
1	5	3888	G	C2'-C3'-O3'	5.62	122.12	113.70
1	5	2395	A	C2'-C3'-O3'	5.59	117.88	109.50
1	5	2709	C	C5'-C4'-O4'	5.54	117.41	109.10
1	5	1236	C	C4'-C3'-O3'	5.52	121.28	113.00
1	5	4170	A	C2'-C3'-O3'	5.50	117.75	109.50
4	9	72	C	P-O3'-C3'	5.43	128.34	120.20
1	5	2709	C	O4'-C1'-C2'	-5.42	100.38	105.80
1	5	2007	G	N9-C1'-C2'	5.36	120.03	112.00
1	5	1370	G	C2'-C3'-O3'	5.29	117.44	109.50
4	9	561	A	C2'-C3'-O3'	5.26	121.60	113.70
1	5	2474	G	C4'-C3'-O3'	5.19	117.19	109.40
4	9	532	C	C5'-C4'-O4'	5.17	117.56	109.80
4	9	1311	C	N1-C1'-C2'	5.17	119.75	112.00
4	9	532	C	C2'-C3'-O3'	5.12	121.38	113.70
1	5	2709	C	O5'-C5'-C4'	-5.12	104.02	111.70
1	5	2526	C	N1-C1'-C2'	5.11	119.66	112.00
1	5	1477	C	C2'-C3'-O3'	5.09	121.33	113.70
1	5	2709	C	C1'-O4'-C4'	-5.09	104.61	109.70
4	9	1137	U	C2'-C3'-O3'	5.05	121.28	113.70
1	5	4947	U	C2'-C3'-O3'	5.04	121.26	113.70
1	5	2089	G	C2'-C3'-O3'	5.03	117.04	109.50
1	5	4121	G	C2'-C3'-O3'	5.02	117.03	109.50

There are no chirality outliers.

All (36) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	5	1962	A	Sidechain
5	A	123	ARG	Sidechain
5	A	227	ARG	Sidechain
47	BB	51	ARG	Sidechain
7	C	204	ARG	Sidechain
8	D	24	ARG	Sidechain
8	D	248	ARG	Sidechain
8	D	33	ARG	Sidechain
49	DD	76	ARG	Sidechain
9	E	144	ARG	Sidechain
54	II	5	ARG	Sidechain
54	II	74	ARG	Sidechain
55	JJ	38	ARG	Sidechain
14	K	156	ARG	Sidechain
15	L	71	ARG	Peptide
16	M	47	ARG	Sidechain
17	N	68	ARG	Sidechain
17	N	73	ARG	Sidechain
60	OO	137	SER	Peptide
20	Q	108	ARG	Sidechain
20	Q	14	ARG	Sidechain
20	Q	143	ARG	Sidechain
63	RR	33	ARG	Sidechain
22	S	95	ARG	Sidechain
64	SS	132	ARG	Sidechain
65	TT	102	ARG	Sidechain
66	UU	79	ARG	Sidechain
25	V	15	ARG	Sidechain
69	XX	107	ARG	Sidechain
28	Y	115	ARG	Sidechain
29	Z	65	ARG	Sidechain
72	aa	87	ARG	Sidechain
34	e	27	ARG	Sidechain
36	g	8	ARG	Sidechain
41	m	96	ARG	Sidechain
44	p	49	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	585	0
2	7	2538	0	1286	9	0
3	8	3208	0	1629	21	0
4	9	36229	0	18300	274	0
5	A	1898	0	1993	11	0
6	B	3172	0	3310	17	0
7	C	2883	0	3053	18	0
8	D	2391	0	2424	9	0
9	E	1729	0	1887	19	0
10	G	1879	0	2027	6	0
11	H	1516	0	1597	9	0
12	I	1664	0	1712	10	0
13	J	1362	0	1399	6	0
14	K	1875	0	1995	4	0
15	L	1702	0	1820	8	0
16	M	1137	0	1211	7	0
17	N	1701	0	1749	22	0
18	O	1630	0	1778	7	0
19	P	1242	0	1274	10	0
20	Q	1515	0	1634	10	0
21	R	1508	0	1664	11	0
22	S	1462	0	1508	8	0
23	T	1298	0	1366	12	0
24	U	809	0	833	4	0
25	V	969	0	1031	3	0
26	W	860	0	903	8	0
27	X	967	0	1040	5	0
28	Y	1115	0	1205	7	0
29	Z	1107	0	1182	14	0
30	a	1162	0	1209	13	0
31	b	806	0	866	5	0
32	c	761	0	794	5	0
33	d	888	0	930	0	0
34	e	1053	0	1147	8	0
35	f	876	0	912	2	0
36	g	906	0	998	8	0
37	h	1013	0	1147	2	0
38	i	830	0	916	5	0
39	k	569	0	637	1	0
40	l	447	0	480	8	0
41	m	429	0	465	5	0
42	n	240	0	289	3	0
43	o	851	0	920	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	p	708	0	756	7	0
45	r	994	0	1051	10	0
46	AA	1710	0	1708	16	0
47	BB	1729	0	1803	7	0
48	CC	1716	0	1806	10	0
49	DD	1739	0	1832	8	0
50	EE	2076	0	2177	7	0
51	FF	1460	0	1509	12	0
52	GG	1923	0	2089	22	0
53	HH	1489	0	1582	10	0
54	II	1628	0	1706	7	0
55	JJ	1508	0	1626	15	0
56	KK	810	0	836	6	0
57	LL	1175	0	1249	5	0
58	MM	871	0	913	14	0
59	NN	1202	0	1289	7	0
60	OO	1016	0	1039	12	0
61	PP	1058	0	1104	10	0
62	QQ	1128	0	1195	8	0
63	RR	1068	0	1121	3	0
64	SS	1190	0	1249	11	0
65	TT	1097	0	1132	8	0
66	UU	795	0	862	3	0
67	VV	637	0	637	7	0
68	WW	1034	0	1080	5	0
69	XX	1087	0	1154	5	0
70	YY	1011	0	1083	9	0
71	ZZ	598	0	656	3	0
72	aa	814	0	867	6	0
73	bb	651	0	672	4	0
74	cc	488	0	514	5	0
75	dd	459	0	448	2	0
76	ee	443	0	492	3	0
77	ff	555	0	567	13	0
78	gg	2436	0	2393	18	0
79	10	234	0	118	2	0
80	11	1585	0	804	30	0
80	13	1585	0	803	22	0
81	j	705	0	737	10	0
82	5	10	0	19	1	0
83	dd	1	0	0	0	0
83	g	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	0	0
84	13	31	0	11	3	0
85	13	8	0	8	0	0
All	All	213916	0	158241	1310	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 (1310) 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)
1:5:4099:G:H22	1:5:4109:G:H22	1.04	0.98
1:5:980:U:H3	1:5:1275:G:H1	1.10	0.94
1:5:2638:G:N2	1:5:2697:A:N1	2.16	0.92
1:5:978:G:N2	1:5:1277:G:H1	1.71	0.88
1:5:1075:G:H1	1:5:1235:G:H22	1.25	0.84
1:5:2553:A:H2	1:5:2765:A:H62	1.25	0.84
1:5:3692:A:H62	1:5:3823:G:H21	1.26	0.84
4:9:190:G:O2'	4:9:209:A:N6	2.10	0.84
4:9:925:G:H1	4:9:1017:U:H3	1.25	0.84
1:5:4039:G:N7	1:5:4041:C:N4	2.27	0.83
1:5:2361:G:N7	19:P:25:HIS:ND1	2.26	0.82
1:5:2639:U:HO2'	1:5:2694:G:H1	0.84	0.82
58:MM:89:VAL:HG11	58:MM:109:VAL:HG21	1.60	0.82
1:5:4099:G:H22	1:5:4109:G:N2	1.83	0.77
78:gg:73:SER:OG	78:gg:117:ASN:ND2	2.16	0.77
1:5:4751:G:H1	1:5:4948:C:H5	1.30	0.77
1:5:4635:A:H8	1:5:5048:A:H61	1.32	0.76
4:9:560:A:OP2	55:JJ:177:ASN:ND2	2.16	0.76
1:5:453:G:N2	1:5:1293:G:O6	2.16	0.75
1:5:1555:G:O6	44:p:4:ARG:NH2	2.19	0.75
1:5:2706:G:O6	21:R:46:LYS:NZ	2.20	0.75
29:Z:77:TYR:CZ	32:c:39:ARG:HG3	2.22	0.75
1:5:978:G:H22	1:5:1277:G:H1	1.35	0.74
74:cc:44:ARG:NH2	74:cc:60:GLU:O	2.20	0.74
1:5:976:G:H1	1:5:1279:A:H2	1.34	0.74
1:5:1975:G:N2	1:5:1983:A:OP1	2.19	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:9:540:U:O2'	4:9:543:C:N4	2.21	0.74
1:5:1075:G:H1	1:5:1235:G:N2	1.86	0.73
4:9:184:G:H2'	4:9:185:G:H8	1.54	0.73
4:9:959:G:N1	60:OO:65:ASP:OD2	2.18	0.73
4:9:318:A:H61	52:GG:186:GLN:HE22	1.37	0.72
64:SS:91:LYS:NZ	64:SS:109:GLU:OE1	2.21	0.72
1:5:4099:G:N2	1:5:4109:G:H22	1.84	0.72
4:9:692:G:H2'	4:9:693:A:H8	1.53	0.71
80:13:62:C:H2'	80:13:63:A:C8	2.25	0.71
1:5:1394:G:OP1	15:L:186:ARG:NH1	2.22	0.71
4:9:1693:G:H21	4:9:1834:A:H8	1.39	0.71
1:5:2465:C:H1'	1:5:3672:G:H22	1.55	0.70
4:9:1438:A:H2'	4:9:1439:A:C8	2.26	0.70
80:11:23:C:H2'	80:11:24:G:H8	1.56	0.70
1:5:4635:A:H2	1:5:4663:G:H21	1.39	0.70
1:5:1317:U:OP1	30:a:21:ARG:NH2	2.25	0.70
4:9:1834:A:H2	4:9:1837:G:H1	1.39	0.70
1:5:2395:A:O2'	1:5:2806:A:H1'	1.91	0.70
1:5:4413:C:H5	1:5:4429:C:H42	1.40	0.70
1:5:983:C:OP2	9:E:41:LYS:NZ	2.25	0.69
1:5:4146:G:C8	1:5:4146:G:H5'	2.26	0.69
1:5:2489:C:O2'	1:5:2491:C:N4	2.25	0.69
1:5:4725:C:OP1	6:B:103:LYS:NZ	2.25	0.69
64:SS:26:ILE:HD11	64:SS:52:LEU:HA	1.73	0.69
1:5:1364:U:OP2	15:L:36:ARG:NH2	2.23	0.69
43:o:67:VAL:HG11	43:o:82:MET:HE3	1.75	0.69
57:LL:150:GLY:O	59:NN:133:ARG:NH1	2.25	0.69
81:j:20:ARG:NH2	81:j:39:TYR:OH	2.26	0.69
9:E:115:MET:O	45:r:87:ARG:NH1	2.26	0.69
1:5:1198:G:H2'	1:5:1199:G:H8	1.58	0.68
1:5:2088:A:H5''	1:5:2089:G:H3'	1.75	0.68
1:5:189:G:H2'	1:5:190:G:H8	1.59	0.68
4:9:1616:U:H3	4:9:1620:A:H2	1.42	0.68
4:9:656:G:O2'	48:CC:227:ARG:NH1	2.28	0.67
52:GG:142:ARG:HE	52:GG:153:VAL:HG21	1.59	0.67
1:5:981:C:OP2	9:E:48:ARG:NH2	2.27	0.67
1:5:2899:C:H2'	1:5:2900:U:C6	2.30	0.67
52:GG:120:ASP:OD1	52:GG:125:THR:OG1	2.07	0.67
1:5:2457:G:H21	1:5:3672:G:N2	1.93	0.67
12:I:14:ASN:O	12:I:128:ARG:NH2	2.26	0.67
80:11:23:C:H2'	80:11:24:G:C8	2.30	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:3760:A:H61	4:9:1824:A:H1'	1.60	0.67
4:9:1308:U:H2'	4:9:1309:C:C6	2.30	0.66
1:5:976:G:H21	7:C:323:ARG:NE	1.92	0.66
1:5:980:U:OP2	9:E:68:LYS:NZ	2.24	0.66
6:B:147:ASP:OD1	6:B:198:ARG:NH2	2.25	0.66
18:O:173:GLN:OE1	18:O:176:ARG:NH1	2.29	0.66
1:5:126:C:H2'	1:5:127:G:H8	1.60	0.66
1:5:2533:C:OP1	27:X:139:ARG:NH1	2.29	0.66
4:9:1619:A:OP2	61:PP:47:ARG:NH1	2.28	0.66
48:CC:196:ILE:HB	48:CC:223:TYR:HB2	1.76	0.66
51:FF:102:LEU:HD11	71:ZZ:100:VAL:HG11	1.78	0.65
1:5:691:C:H2'	1:5:692:A:C8	2.32	0.65
1:5:2758:G:O2'	1:5:2765:A:N3	2.26	0.65
4:9:303:C:O2	54:II:184:ARG:NH2	2.28	0.65
4:9:1588:A:H2'	4:9:1589:A:C8	2.31	0.65
1:5:135:G:OP2	37:h:87:LYS:NZ	2.30	0.65
1:5:1198:G:H2'	1:5:1199:G:C8	2.32	0.65
4:9:582:U:OP1	55:JJ:162:ARG:NH1	2.30	0.65
1:5:2457:G:H21	1:5:3672:G:H21	1.43	0.65
64:SS:14:ARG:NH1	64:SS:19:ASN:OD1	2.30	0.65
1:5:2553:A:O2'	1:5:2554:U:OP2	2.14	0.64
68:WW:6:VAL:HG12	68:WW:34:ILE:HD11	1.78	0.64
1:5:3717:A:H2'	1:5:3718:A:C8	2.32	0.64
7:C:13:GLU:OE1	7:C:161:TYR:OH	2.13	0.64
1:5:2407:G:O6	40:l:2:SER:N	2.29	0.64
29:Z:5:MET:HE2	29:Z:77:TYR:CE2	2.32	0.64
46:AA:36:GLN:O	46:AA:53:ARG:NH1	2.30	0.64
62:QQ:132:PHE:O	62:QQ:140:ARG:NH2	2.31	0.64
1:5:2821:U:OP1	21:R:21:LYS:NZ	2.26	0.64
1:5:4303:C:H2'	1:5:4305:G:C8	2.33	0.64
4:9:64:A:H2	4:9:83:A:H62	1.45	0.64
80:11:62:C:H2'	80:11:63:A:H8	1.63	0.64
1:5:2477:A:H2'	1:5:2478:C:C6	2.33	0.64
1:5:1931:C:OP1	41:m:87:LYS:NZ	2.31	0.63
1:5:1577:G:OP1	44:p:17:ARG:NH1	2.32	0.63
1:5:4035:G:H2'	1:5:4036:G:C8	2.34	0.63
13:J:151:ILE:HD11	13:J:156:ARG:HG2	1.81	0.63
80:11:33:C:O2'	80:11:35:A:N7	2.29	0.63
1:5:1188:C:H2'	1:5:1189:G:H8	1.64	0.63
29:Z:5:MET:HG3	29:Z:77:TYR:HE2	1.64	0.63
1:5:3770:U:OP1	80:13:24:G:O2'	2.10	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:966:A:H5'	1:5:967:C:H2'	1.81	0.62
4:9:919:A:OP2	59:NN:64:ARG:NH2	2.29	0.62
1:5:4925:U:H4'	1:5:4926:C:H5'	1.80	0.62
4:9:1522:A:OP2	64:SS:144:ARG:NH1	2.29	0.62
26:W:93:LYS:O	26:W:101:ARG:NH2	2.33	0.62
4:9:1228:A:H2'	4:9:1229:G:C8	2.35	0.62
80:11:62:C:H2'	80:11:63:A:C8	2.34	0.62
1:5:10:A:H2'	1:5:11:G:C8	2.35	0.62
1:5:3751:G:H21	1:5:3775:A:H8	1.45	0.62
1:5:4572:U:H2'	1:5:4573:G:H8	1.65	0.62
4:9:903:A:H2'	4:9:904:A:C8	2.35	0.61
11:H:92:MET:HE2	11:H:179:ILE:HG22	1.81	0.61
80:11:25:U:H2'	80:11:26:G:H8	1.64	0.61
14:K:93:ARG:NH1	14:K:95:ARG:O	2.30	0.61
1:5:2638:G:H22	1:5:2697:A:H61	1.48	0.61
1:5:3611:A:H2	1:5:5016:A:H8	1.49	0.61
1:5:2546:G:O2'	1:5:2547:G:OP1	2.16	0.61
58:MM:89:VAL:HG23	58:MM:91:LEU:HG	1.82	0.61
3:8:8:U:H2'	3:8:9:A:C8	2.36	0.61
22:S:112:ASP:OD1	22:S:116:ARG:NH1	2.28	0.61
1:5:194:C:O2	28:Y:121:ARG:NH2	2.33	0.61
1:5:1441:C:H2'	1:5:1442:C:C6	2.36	0.61
57:LL:101:ARG:NH1	69:XX:5:ARG:O	2.33	0.61
1:5:3965:A:H61	1:5:4045:G:H21	1.49	0.61
80:13:3:G:H8	84:13:101:ATP:H3'	1.65	0.61
1:5:478:G:H2'	1:5:479:G:H8	1.66	0.60
1:5:1246:G:H2'	1:5:1247:U:C6	2.35	0.60
4:9:1395:C:O2'	4:9:1396:A:OP1	2.15	0.60
29:Z:5:MET:HG3	29:Z:77:TYR:CE2	2.36	0.60
4:9:1839:U:H1'	4:9:1863:A:H2	1.65	0.60
1:5:1764:G:H8	1:5:1767:A:H62	1.49	0.60
4:9:1138:C:O2'	67:VV:61:ARG:NH1	2.29	0.60
4:9:1823:A:H3'	4:9:1824:A:H5''	1.83	0.60
53:HH:138:GLU:OE2	59:NN:19:ARG:NH1	2.25	0.60
80:13:63:A:H2'	80:13:64:U:C6	2.37	0.60
1:5:3910:C:H2'	1:5:3911:C:C6	2.36	0.60
1:5:4772:C:N4	1:5:4864:U:O2	2.31	0.60
1:5:1339:U:H2'	1:5:1340:C:C6	2.37	0.60
1:5:1444:G:H21	1:5:2110:G:H1	1.48	0.60
4:9:640:A:H2'	4:9:641:A:C8	2.36	0.60
7:C:143:ARG:NH1	7:C:145:GLU:OE2	2.28	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:O:37:ARG:HD2	18:O:108:ILE:HD11	1.83	0.60
1:5:3961:G:C6	1:5:3963:A:H2'	2.36	0.60
12:I:66:GLU:OE1	12:I:69:ARG:NH1	2.35	0.60
64:SS:46:ARG:NH1	65:TT:50:GLU:OE1	2.34	0.60
4:9:546:G:H2'	4:9:547:G:C8	2.37	0.60
4:9:1566:G:O3'	4:9:1567:G:N2	2.34	0.60
1:5:2566:G:H2'	1:5:2567:G:C8	2.37	0.59
1:5:2647:A:H62	1:5:2686:G:H8	1.48	0.59
55:JJ:136:ARG:NH1	55:JJ:159:PHE:O	2.32	0.59
1:5:3904:G:O2'	1:5:3905:A:OP1	2.19	0.59
1:5:424:U:H2'	1:5:425:U:C6	2.38	0.59
1:5:1801:A:O3'	23:T:102:ARG:NH1	2.34	0.59
4:9:5:U:H2'	4:9:6:G:H8	1.67	0.59
4:9:614:C:H2'	4:9:626:G:C8	2.37	0.59
21:R:105:LEU:HD22	21:R:135:LYS:HG3	1.85	0.59
58:MM:53:ALA:HA	58:MM:79:VAL:O	2.02	0.59
1:5:2638:G:H22	1:5:2697:A:N6	2.01	0.59
53:HH:145:ARG:NH1	68:WW:51:GLU:OE1	2.31	0.59
1:5:4108:G:H2'	1:5:4109:G:C8	2.37	0.59
4:9:1290:G:N7	77:f:95:ARG:NH2	2.44	0.59
52:GG:67:VAL:HB	52:GG:99:GLY:HA2	1.83	0.59
69:XX:63:ASN:ND2	69:XX:114:ASP:OD1	2.26	0.59
16:M:89:THR:HG22	16:M:91:TRP:H	1.66	0.59
1:5:2580:U:H1'	29:Z:76:ASN:HB2	1.85	0.59
56:KK:15:LEU:HD22	56:KK:49:MET:HE1	1.85	0.59
1:5:181:C:N4	1:5:182:G:O6	2.36	0.58
1:5:1405:C:H2'	1:5:1406:G:H8	1.68	0.58
1:5:4944:C:N4	35:f:58:VAL:O	2.34	0.58
26:W:114:GLU:O	26:W:118:ALA:HB3	2.04	0.58
1:5:5016:A:H2	1:5:5033:G:H21	1.48	0.58
1:5:54:G:OP1	81:j:43:ARG:NH1	2.35	0.58
1:5:165:A:H2'	1:5:166:C:C6	2.39	0.58
1:5:956:A:H8	1:5:957:G:C8	2.21	0.58
1:5:4500:U:H2'	1:5:4501:U:C6	2.37	0.58
3:8:141:C:OP1	17:N:38:ARG:NH1	2.36	0.58
1:5:2583:C:OP2	36:g:76:ARG:NH1	2.32	0.58
1:5:3911:C:H2'	1:5:3912:U:H6	1.68	0.58
1:5:3736:A:H2'	1:5:3737:A:C8	2.38	0.58
1:5:1440:U:OP2	14:K:33:ARG:NH1	2.37	0.58
4:9:1404:U:OP1	66:UU:21:ARG:NH2	2.33	0.58
1:5:1186:U:H2'	1:5:1187:G:N3	2.19	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:9:903:A:H2'	4:9:904:A:H8	1.68	0.58
4:9:981:A:H2'	4:9:982:G:C8	2.39	0.58
8:D:107:ARG:NH2	8:D:116:ASP:OD1	2.37	0.58
1:5:87:A:OP2	20:Q:173:LYS:NZ	2.36	0.58
4:9:816:A:OP2	55:JJ:10:ARG:NH2	2.28	0.58
4:9:1407:U:H2'	4:9:1408:U:C6	2.39	0.58
4:9:1565:C:OP2	65:TT:101:ARG:NH1	2.37	0.57
11:H:41:ILE:HG21	11:H:73:ILE:HD11	1.86	0.57
50:EE:124:CYS:HB3	50:EE:141:THR:HB	1.85	0.57
1:5:2478:C:N4	1:5:2479:G:O6	2.38	0.57
4:9:908:A:OP1	21:R:172:ARG:NH2	2.29	0.57
1:5:3635:A:N6	44:p:17:ARG:O	2.32	0.57
4:9:1628:C:H2'	4:9:1629:C:C6	2.40	0.57
7:C:335:MET:O	7:C:339:THR:HG23	2.04	0.57
1:5:1502:G:O6	20:Q:89:ASP:HA	2.04	0.57
1:5:4936:G:O2'	1:5:4937:C:OP1	2.21	0.57
1:5:4992:G:H2'	1:5:4993:G:C8	2.39	0.57
1:5:2848:G:O2'	1:5:3838:U:O4	2.17	0.57
28:Y:115:ARG:HG3	28:Y:115:ARG:HH11	1.70	0.57
4:9:1119:A:H2'	4:9:1120:U:C6	2.39	0.57
4:9:1597:C:H4'	4:9:1603:G:C6	2.40	0.57
1:5:206:U:O2'	1:5:208:A:N7	2.33	0.57
1:5:1351:G:OP1	7:C:33:ARG:NH1	2.34	0.57
1:5:1739:G:N3	1:5:1742:A:N6	2.53	0.57
4:9:1512:C:O2'	75:dd:7:TYR:O	2.20	0.57
1:5:1942:A:H2'	1:5:1943:A:C8	2.40	0.57
1:5:462:G:H2'	1:5:463:A:C8	2.40	0.57
1:5:2515:G:OP1	36:g:37:LYS:NZ	2.29	0.57
4:9:928:G:H2'	4:9:929:G:C8	2.40	0.56
1:5:2478:C:H2'	1:5:2479:G:C8	2.40	0.56
1:5:1645:C:P	7:C:80:ARG:HH12	2.28	0.56
1:5:4099:G:H1	1:5:4109:G:H1	1.53	0.56
3:8:75:G:OP2	28:Y:74:TYR:OH	2.17	0.56
17:N:124:ASP:OD1	17:N:125:SER:N	2.37	0.56
1:5:40:G:N2	1:5:4380:A:H62	2.03	0.56
1:5:1890:G:N2	1:5:1939:A:H61	2.03	0.56
1:5:2415:U:H2'	1:5:2416:G:C8	2.41	0.56
1:5:4925:U:H4'	1:5:4926:C:C5'	2.35	0.56
4:9:692:G:H2'	4:9:693:A:C8	2.38	0.56
80:11:51:U:H2'	80:11:52:G:C8	2.41	0.56
4:9:958:G:H2'	4:9:959:G:C8	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:1180:C:OP2	8:D:289:ARG:NH1	2.38	0.56
1:5:4395:U:H6	1:5:4395:U:H5'	1.70	0.56
4:9:846:G:OP1	50:EE:106:LYS:NZ	2.38	0.56
6:B:384:GLU:OE2	26:W:14:TYR:OH	2.23	0.56
34:e:103:VAL:O	34:e:108:ARG:NH1	2.38	0.56
1:5:1405:C:H2'	1:5:1406:G:C8	2.41	0.56
1:5:1771:U:H2'	1:5:1772:C:C6	2.41	0.56
4:9:525:A:OP2	76:ee:101:ARG:NH1	2.36	0.56
4:9:1679:A:C2	51:FF:60:ARG:HA	2.41	0.56
4:9:1239:U:H5''	61:PP:124:LYS:HD3	1.88	0.56
18:O:80:PHE:O	18:O:83:THR:HG22	2.05	0.56
58:MM:52:LEU:HD21	58:MM:62:VAL:HG23	1.88	0.56
1:5:465:G:H2'	1:5:466:A:C8	2.41	0.55
1:5:495:C:H2'	1:5:496:G:H8	1.70	0.55
1:5:3799:A:OP1	25:V:64:THR:HG21	2.06	0.55
43:o:26:TYR:CD1	43:o:82:MET:HE1	2.40	0.55
1:5:2567:G:H2'	1:5:2568:C:C6	2.41	0.55
4:9:501:C:H2'	4:9:502:C:H5''	1.88	0.55
4:9:791:C:H2'	4:9:792:C:C6	2.42	0.55
1:5:1190:C:H2'	1:5:1191:C:C6	2.40	0.55
1:5:2474:G:O2'	1:5:2475:G:OP1	2.23	0.55
46:AA:5:LEU:HD21	67:VV:41:LYS:HA	1.88	0.55
70:YY:14:THR:HG22	70:YY:21:LYS:HG2	1.89	0.55
1:5:1450:C:O2'	1:5:2104:A:H1'	2.07	0.55
1:5:271:C:H2'	1:5:272:U:C6	2.42	0.55
1:5:1357:C:H2'	1:5:1358:G:H5''	1.89	0.55
4:9:1653:U:H2'	4:9:1654:G:C8	2.42	0.55
3:8:8:U:H2'	3:8:9:A:H8	1.71	0.55
4:9:5:U:H2'	4:9:6:G:C8	2.42	0.55
12:I:189:ARG:NH1	12:I:200:ILE:O	2.39	0.55
16:M:97:ALA:HB2	18:O:203:VAL:HB	1.89	0.55
1:5:3641:U:H5	1:5:3646:A:N7	2.03	0.55
4:9:1272:C:O2'	4:9:1274:G:N2	2.40	0.55
1:5:1177:U:H2'	1:5:1178:G:C8	2.42	0.55
3:8:127:U:H2'	3:8:128:C:C6	2.41	0.55
18:O:10:ASP:OD1	18:O:37:ARG:HD3	2.07	0.55
1:5:4039:G:H4'	1:5:4049:U:H2'	1.87	0.55
3:8:123:U:O2'	3:8:126:C:N4	2.40	0.55
9:E:96:THR:HG22	9:E:109:VAL:HG22	1.89	0.55
11:H:140:GLN:NE2	11:H:143:GLU:OE1	2.33	0.55
4:9:1780:G:H2'	4:9:1781:A:C8	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:P:36:ILE:HD11	19:P:48:LEU:HD21	1.89	0.54
52:GG:58:LYS:HA	52:GG:107:SER:HB2	1.88	0.54
1:5:3868:G:H22	1:5:3900:G:H1'	1.72	0.54
1:5:4146:G:H5'	1:5:4146:G:H8	1.72	0.54
1:5:4459:U:H2'	1:5:4460:U:C6	2.42	0.54
37:h:12:LYS:HD3	37:h:16:GLU:HG3	1.89	0.54
49:DD:70:THR:HG22	49:DD:86:LEU:HD13	1.89	0.54
1:5:966:A:H5''	1:5:967:C:C6	2.42	0.54
1:5:3723:A:OP2	38:i:68:ARG:NH2	2.37	0.54
1:5:4726:G:O2'	6:B:129:ALA:O	2.12	0.54
13:J:111:GLU:OE1	64:SS:14:ARG:NH2	2.40	0.54
53:HH:10:LYS:HD2	53:HH:16:PRO:HA	1.88	0.54
59:NN:55:ARG:NH1	59:NN:56:ASP:OD1	2.40	0.54
64:SS:86:ARG:NH2	64:SS:89:ASP:OD1	2.30	0.54
4:9:886:A:H3'	4:9:887:U:H5''	1.90	0.54
8:D:146:LEU:HD21	8:D:159:VAL:HG12	1.89	0.54
38:i:19:LYS:HE2	38:i:21:VAL:HG12	1.88	0.54
1:5:10:A:H2'	1:5:11:G:H8	1.72	0.54
1:5:1308:C:H2'	1:5:1309:C:C6	2.42	0.54
3:8:123:U:H5''	3:8:124:U:C5	2.42	0.54
4:9:74:G:N2	4:9:78:C:OP2	2.20	0.54
29:Z:100:VAL:HG13	29:Z:107:LYS:HA	1.88	0.54
4:9:536:A:H61	4:9:547:G:H1	1.56	0.54
4:9:1567:G:P	4:9:1567:G:H21	2.30	0.54
23:T:28:ALA:HA	23:T:31:MET:HG2	1.90	0.54
1:5:1237:C:H4'	1:5:1238:A:O5'	2.08	0.54
1:5:1432:G:HO2'	1:5:1451:G:H22	1.55	0.54
4:9:536:A:H61	4:9:547:G:H22	1.54	0.54
4:9:1323:U:H2'	4:9:1324:G:C8	2.42	0.54
4:9:1834:A:H2	4:9:1837:G:N1	2.04	0.54
29:Z:77:TYR:CD1	29:Z:77:TYR:C	2.86	0.54
1:5:2601:A:N6	1:5:2744:A:OP2	2.38	0.54
2:7:24:C:H2'	2:7:25:G:O4'	2.08	0.54
4:9:1139:C:H2'	4:9:1140:G:O4'	2.08	0.54
17:N:155:VAL:O	17:N:162:ARG:NH2	2.41	0.54
51:FF:102:LEU:HD22	71:ZZ:110:THR:HG21	1.89	0.54
1:5:2020:U:H2'	1:5:2021:G:H8	1.73	0.54
1:5:717:U:H2'	1:5:718:C:C6	2.43	0.54
61:PP:18:ARG:NH1	64:SS:88:LYS:O	2.40	0.54
80:13:69:U:H2'	80:13:70:G:H8	1.72	0.54
80:11:16:G:OP2	80:11:17:C:N4	2.36	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:1964:A:H3'	1:5:1965:G:H8	1.73	0.53
1:5:3788:C:N4	1:5:3812:C:OP2	2.40	0.53
1:5:2345:G:N7	30:a:9:ARG:NH2	2.56	0.53
1:5:3707:U:H2'	1:5:3708:C:C6	2.44	0.53
1:5:4169:G:H4'	1:5:4171:C:C2	2.44	0.53
4:9:107:A:H2'	4:9:108:G:C8	2.43	0.53
1:5:173:C:OP1	15:L:129:ARG:NH1	2.33	0.53
1:5:4935:C:H2'	1:5:4936:G:H8	1.74	0.53
72:aa:87:ARG:NH2	72:aa:94:ASP:O	2.27	0.53
80:11:71:C:H2'	80:11:72:U:H6	1.73	0.53
1:5:3760:A:N6	4:9:1824:A:O2'	2.41	0.53
1:5:3860:A:H61	1:5:4560:C:H5	1.53	0.53
1:5:4260:U:H2'	1:5:4261:C:C6	2.43	0.53
1:5:4935:C:H2'	1:5:4936:G:C8	2.43	0.53
4:9:943:U:O2'	60:OO:135:ILE:O	2.20	0.53
4:9:1507:G:O2'	77:ff:85:TYR:OH	2.25	0.53
4:9:1658:G:OP2	4:9:1660:C:N4	2.41	0.53
22:S:82:LEU:HD21	22:S:109:CYS:SG	2.48	0.53
80:11:51:U:H2'	80:11:52:G:H8	1.74	0.53
4:9:67:C:H41	52:GG:163:ASN:HA	1.73	0.53
4:9:1404:U:P	66:UU:21:ARG:HH22	2.31	0.53
46:AA:17:LYS:HB3	46:AA:173:LEU:HD11	1.90	0.53
79:10:22:U:O2'	79:10:23:A:OP1	2.25	0.53
1:5:4051:C:H2'	1:5:4052:C:C6	2.44	0.53
4:9:1856:C:H2'	4:9:1857:G:C8	2.44	0.53
73:bb:42:LYS:HD2	73:bb:57:VAL:HG11	1.89	0.53
1:5:1534:A:C8	81:j:15:THR:HG23	2.44	0.53
4:9:1314:U:H2'	56:KK:2:LEU:HD23	1.91	0.53
77:ff:133:ALA:N	77:ff:140:TYR:O	2.41	0.53
1:5:484:U:O2'	1:5:485:C:OP1	2.27	0.53
1:5:2440:U:O2'	1:5:2441:C:OP1	2.27	0.53
4:9:1400:U:P	78:gg:100:ARG:HH12	2.32	0.53
27:X:92:ASP:C	27:X:93:ASN:HD22	2.17	0.53
67:VV:14:PRO:HG2	67:VV:23:ILE:HD11	1.91	0.53
4:9:959:G:OP2	60:OO:38:ASN:ND2	2.41	0.53
11:H:51:LYS:HB2	11:H:53:LYS:HG3	1.91	0.53
1:5:294:G:O2'	30:a:59:ARG:NH2	2.42	0.52
80:13:3:G:C8	84:13:101:ATP:H3'	2.45	0.52
1:5:1502:G:H22	30:a:77:LYS:HE2	1.74	0.52
1:5:1846:G:H2'	1:5:1847:C:C6	2.45	0.52
1:5:4303:C:H2'	1:5:4305:G:H8	1.71	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:9:332:G:O6	52:GG:189:ARG:NH2	2.36	0.52
4:9:751:G:OP2	52:GG:230:LYS:NZ	2.42	0.52
1:5:4942:C:H4'	1:5:4943:A:OP1	2.09	0.52
4:9:1693:G:N2	4:9:1834:A:H8	2.04	0.52
1:5:229:G:OP1	28:Y:11:ARG:NH1	2.37	0.52
1:5:2822:G:N7	21:R:20:LYS:NZ	2.46	0.52
17:N:178:HIS:HA	17:N:181:HIS:NE2	2.24	0.52
1:5:910:G:H2'	1:5:911:U:C6	2.45	0.52
1:5:945:U:OP1	7:C:342:ARG:NH2	2.42	0.52
9:E:139:HIS:O	9:E:141:ARG:NH1	2.43	0.52
47:BB:107:ARG:NH1	60:OO:133:THR:O	2.31	0.52
1:5:424:U:H2'	1:5:425:U:H6	1.73	0.52
1:5:2293:U:H2'	1:5:2294:G:C8	2.44	0.52
1:5:3911:C:H2'	1:5:3912:U:C6	2.45	0.52
1:5:4572:U:H2'	1:5:4573:G:C8	2.45	0.52
2:7:3:C:H2'	2:7:4:U:C6	2.45	0.52
9:E:185:ASN:ND2	9:E:274:LEU:O	2.43	0.52
12:I:48:LEU:O	12:I:139:ARG:HA	2.10	0.52
1:5:1809:C:H2'	1:5:1810:G:H8	1.74	0.52
1:5:4413:C:H5	1:5:4429:C:N4	2.07	0.52
4:9:1740:C:H2'	4:9:1741:U:C6	2.45	0.52
29:Z:77:TYR:CE1	32:c:39:ARG:HG3	2.44	0.52
1:5:983:C:C5	9:E:73:ARG:HD3	2.44	0.52
4:9:446:G:OP2	54:II:47:ARG:NH2	2.43	0.52
4:9:1019:C:OP2	59:NN:70:LYS:NZ	2.36	0.52
4:9:1285:G:OP1	58:MM:107:SER:OG	2.28	0.52
78:gg:153:CYS:SG	78:gg:198:VAL:HG12	2.49	0.52
1:5:100:C:H2'	1:5:101:A:H8	1.74	0.52
1:5:2431:A:OP1	40:l:41:ARG:NH1	2.35	0.52
1:5:2616:C:OP1	21:R:60:ARG:NH1	2.43	0.52
17:N:135:ILE:HG23	17:N:142:ILE:HD13	1.91	0.52
52:GG:98:ARG:NH1	52:GG:99:GLY:O	2.43	0.52
80:13:62:C:H2'	80:13:63:A:H8	1.71	0.52
4:9:167:G:O3'	26:W:80:ARG:NH1	2.43	0.52
78:gg:79:LEU:HD22	78:gg:87:LEU:HD11	1.92	0.52
4:9:184:G:H2'	4:9:185:G:C8	2.40	0.51
4:9:1310:U:H2'	4:9:1311:C:C6	2.45	0.51
1:5:189:G:H2'	1:5:190:G:C8	2.43	0.51
2:7:3:C:H2'	2:7:4:U:H6	1.74	0.51
4:9:1228:A:H2'	4:9:1229:G:H8	1.75	0.51
49:DD:29:LEU:HB2	49:DD:34:TYR:HB2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:2478:C:H2'	1:5:2479:G:H8	1.75	0.51
1:5:2755:A:P	29:Z:65:ARG:HH22	2.33	0.51
1:5:4940:C:OP1	9:E:159:ARG:NH1	2.43	0.51
1:5:4944:C:H4'	1:5:4944:C:OP1	2.11	0.51
62:QQ:129:SER:O	62:QQ:131:LYS:HE3	2.11	0.51
80:11:53:G:H2'	80:11:54:A:H8	1.75	0.51
1:5:2465:C:H1'	1:5:3672:G:N2	2.23	0.51
1:5:3598:C:H2'	1:5:3599:A:C8	2.46	0.51
4:9:182:C:H5'	4:9:183:G:C8	2.46	0.51
4:9:1101:U:H2'	4:9:1102:G:C8	2.45	0.51
3:8:67:U:H2'	3:8:68:G:H8	1.74	0.51
70:YY:86:GLU:OE2	70:YY:90:ARG:NH1	2.35	0.51
4:9:1347:U:H2'	4:9:1348:G:N3	2.25	0.51
17:N:80:THR:HB	17:N:87:HIS:CB	2.41	0.51
1:5:1370:G:O6	7:C:239:LYS:NZ	2.38	0.51
1:5:1398:A:OP1	30:a:136:LYS:NZ	2.40	0.51
1:5:2487:G:O6	1:5:2489:C:O2'	2.21	0.51
4:9:1667:U:H2'	4:9:1668:U:C6	2.45	0.51
49:DD:66:ILE:O	49:DD:70:THR:HG23	2.10	0.51
67:VV:37:ALA:HB1	67:VV:46:PHE:CD1	2.45	0.51
77:ff:118:ARG:HB2	77:ff:131:PHE:CD1	2.46	0.51
80:11:43:G:H2'	80:11:44:A:C8	2.45	0.51
1:5:3958:G:O6	80:11:19:G:N1	2.43	0.51
58:MM:47:ALA:HB3	58:MM:74:ILE:HD13	1.93	0.51
1:5:173:C:OP1	15:L:129:ARG:HD3	2.11	0.51
1:5:257:C:H2'	1:5:258:G:C8	2.45	0.51
1:5:1072:C:O2'	1:5:1073:G:O5'	2.24	0.51
1:5:1191:C:H2'	1:5:1192:C:C6	2.46	0.51
1:5:1249:C:OP1	1:5:1250:C:H5	1.94	0.51
4:9:118:C:H1'	4:9:445:A:C5	2.46	0.51
4:9:202:G:OP2	54:II:143:LYS:NZ	2.44	0.51
74:cc:51:ARG:HG3	74:cc:51:ARG:HH11	1.75	0.51
1:5:1177:U:H2'	1:5:1178:G:H8	1.74	0.51
1:5:2361:G:N2	1:5:2362:U:O4	2.28	0.51
1:5:2664:G:H4'	1:5:2677:G:H4'	1.93	0.51
40:l:26:TRP:HA	40:l:29:MET:HE2	1.93	0.51
1:5:4053:A:H2'	1:5:4054:C:C6	2.46	0.50
1:5:4917:C:H2'	1:5:4918:C:C6	2.46	0.50
3:8:98:C:OP1	27:X:67:ARG:NH1	2.44	0.50
4:9:1593:C:H1'	65:TT:12:GLN:HE22	1.75	0.50
17:N:84:PRO:HA	17:N:87:HIS:NE2	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:KK:73:ASN:HA	56:KK:76:ILE:HD12	1.93	0.50
1:5:1554:A:OP2	44:p:4:ARG:NH1	2.38	0.50
4:9:907:G:H2'	4:9:908:A:C8	2.45	0.50
4:9:1863:A:H1'	72:aa:79:ILE:HD13	1.93	0.50
1:5:1312:A:O2'	34:e:44:ARG:NH2	2.45	0.50
1:5:1662:C:H2'	1:5:1663:C:C6	2.46	0.50
1:5:3938:G:N2	1:5:4171:C:OP2	2.43	0.50
4:9:804:U:H2'	4:9:805:U:C6	2.45	0.50
78:gg:57:ARG:NH1	78:gg:92:LEU:O	2.44	0.50
80:11:71:C:H2'	80:11:72:U:C6	2.46	0.50
1:5:3599:A:H2'	1:5:3600:G:C8	2.46	0.50
4:9:730:C:H2'	4:9:731:G:C8	2.46	0.50
5:A:234:LYS:HG2	5:A:238:ILE:HD12	1.94	0.50
14:K:114:ARG:NH1	20:Q:4:ASP:O	2.44	0.50
1:5:478:G:H2'	1:5:479:G:C8	2.45	0.50
1:5:1444:G:H2'	1:5:1445:U:C5	2.47	0.50
1:5:1472:C:H2'	1:5:1473:U:C6	2.46	0.50
1:5:2394:G:O2'	1:5:2819:U:O4	2.28	0.50
53:HH:52:GLU:O	53:HH:179:LYS:NZ	2.40	0.50
74:cc:24:GLN:OE1	74:cc:26:GLN:NE2	2.37	0.50
80:11:10:G:H5''	80:11:46:G:N3	2.27	0.50
1:5:477:C:H2'	1:5:478:G:H8	1.76	0.50
4:9:1692:U:H2'	4:9:1693:G:C8	2.47	0.50
1:5:3784:A:O2'	1:5:3785:A:H3'	2.11	0.50
7:C:2:ALA:O	7:C:29:LYS:NZ	2.42	0.50
17:N:84:PRO:HA	17:N:87:HIS:CD2	2.46	0.50
1:5:2517:A:N3	1:5:2539:C:O2'	2.43	0.50
1:5:3652:A:H2'	1:5:3653:A:C5	2.46	0.50
4:9:798:G:O2'	4:9:799:U:OP1	2.25	0.50
5:A:30:ARG:NH2	5:A:33:ASP:OD2	2.37	0.50
57:LL:89:ARG:NH1	57:LL:91:ASP:OD1	2.45	0.50
1:5:2313:A:O2'	1:5:2314:G:OP1	2.25	0.50
1:5:5053:U:H5'	1:5:5054:C:C5	2.47	0.50
52:GG:2:LYS:HB2	52:GG:108:VAL:HG22	1.92	0.50
1:5:52:G:H4'	1:5:1529:G:H4'	1.94	0.49
1:5:4950:U:O2'	1:5:4951:G:OP1	2.29	0.49
1:5:4978:G:H2'	1:5:4979:A:H5''	1.94	0.49
4:9:1203:G:H2'	4:9:1204:A:C8	2.47	0.49
9:E:287:HIS:CE1	9:E:288:LYS:HE2	2.47	0.49
43:o:26:TYR:CG	43:o:82:MET:HE1	2.47	0.49
1:5:2771:G:H2'	1:5:2772:C:O4'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:4274:A:H2'	1:5:4275:G:C8	2.47	0.49
1:5:4926:C:H5'	1:5:4926:C:O2	2.12	0.49
24:U:31:ASP:OD2	24:U:114:TYR:OH	2.18	0.49
45:r:97:ILE:HD13	45:r:107:ARG:HA	1.94	0.49
47:BB:73:ASP:OD1	60:OO:128:ARG:NH1	2.44	0.49
59:NN:55:ARG:HG2	59:NN:55:ARG:HH11	1.77	0.49
78:gg:270:LEU:HD13	78:gg:310:TRP:CD2	2.47	0.49
80:11:69:U:H2'	80:11:70:G:H8	1.76	0.49
1:5:264:C:H5''	1:5:265:C:OP2	2.12	0.49
1:5:2570:U:H2'	1:5:2571:C:C6	2.48	0.49
1:5:3688:U:OP2	5:A:198:ARG:NH2	2.42	0.49
7:C:29:LYS:HB2	7:C:267:TRP:HH2	1.76	0.49
80:13:47:U:H3'	80:13:48:C:H5'	1.94	0.49
1:5:477:C:H2'	1:5:478:G:C8	2.48	0.49
1:5:3635:A:H61	44:p:18:TYR:HA	1.78	0.49
1:5:5016:A:C2	1:5:5033:G:N2	2.71	0.49
68:WW:115:GLU:OE1	68:WW:118:ARG:NH2	2.36	0.49
80:13:12:C:H2'	80:13:13:G:C8	2.47	0.49
1:5:1:C:N4	3:8:156:U:H3	2.11	0.49
1:5:2065:G:H2'	1:5:2066:C:O4'	2.12	0.49
1:5:3965:A:N6	1:5:4045:G:H21	2.10	0.49
18:O:12:ARG:O	22:S:171:ARG:NH2	2.44	0.49
78:gg:269:GLU:HG2	78:gg:271:LYS:HE3	1.94	0.49
1:5:3923:A:H2'	1:5:3924:C:C6	2.46	0.49
1:5:4039:G:H5'	1:5:4042:G:O6	2.12	0.49
4:9:552:G:H2'	4:9:553:U:C6	2.47	0.49
4:9:895:G:H2'	4:9:896:U:C6	2.47	0.49
1:5:3873:G:H2'	1:5:3874:G:C8	2.47	0.49
1:5:4305:G:H22	23:T:87:LYS:CD	2.26	0.49
1:5:4957:C:H3'	1:5:4958:C:H5''	1.95	0.49
4:9:1302:G:N1	4:9:1306:U:O4	2.46	0.49
58:MM:85:LEU:O	58:MM:89:VAL:HG22	2.13	0.49
62:QQ:30:GLY:N	62:QQ:67:ASP:OD1	2.43	0.49
77:ff:100:LEU:HG	77:ff:103:LEU:HD13	1.95	0.49
1:5:2730:U:H2'	1:5:2731:C:C6	2.47	0.49
1:5:4323:A:OP1	8:D:179:ARG:NH2	2.35	0.49
4:9:878:G:H22	4:9:908:A:H2	1.58	0.49
4:9:1060:A:O2'	4:9:1062:A:N7	2.42	0.49
4:9:1778:C:H2'	4:9:1779:G:H8	1.77	0.49
31:b:40:LEU:O	31:b:44:ARG:HG3	2.12	0.49
48:CC:94:ILE:HG21	48:CC:162:ILE:HD12	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:HH:93:VAL:HG21	53:HH:133:LEU:HD12	1.94	0.49
1:5:2559:G:H2'	1:5:2560:C:C6	2.48	0.49
1:5:2566:G:H2'	1:5:2567:G:H8	1.76	0.49
1:5:517:C:H2'	1:5:518:G:H8	1.78	0.49
1:5:2580:U:OP1	29:Z:36:ARG:NH1	2.42	0.49
4:9:1292:C:C4	4:9:1293:A:C2	3.01	0.49
4:9:1489:A:H4'	4:9:1490:G:OP2	2.12	0.49
48:CC:88:ILE:HD13	48:CC:94:ILE:HD11	1.94	0.49
1:5:1298:C:H2'	1:5:1299:G:H8	1.78	0.48
1:5:1380:G:H4'	1:5:1381:U:O2	2.13	0.48
1:5:2495:U:H2'	1:5:2496:G:H8	1.77	0.48
4:9:986:G:C8	60:OO:137:SER:O	2.65	0.48
10:G:283:TYR:CZ	10:G:287:ARG:HD2	2.48	0.48
67:VV:15:ARG:NH1	67:VV:33:GLN:HB2	2.28	0.48
1:5:1442:C:H2'	1:5:1443:A:H8	1.77	0.48
4:9:1232:U:H2'	4:9:1233:G:H8	1.79	0.48
1:5:983:C:C6	9:E:73:ARG:HD3	2.48	0.48
1:5:1985:G:H1'	1:5:2003:G:H2'	1.95	0.48
1:5:4047:A:O2'	1:5:4048:A:OP1	2.27	0.48
4:9:943:U:OP1	47:BB:214:LYS:NZ	2.35	0.48
1:5:129:C:H2'	1:5:130:C:C6	2.48	0.48
1:5:1957:U:C2	1:5:1958:A:C8	3.02	0.48
1:5:2023:C:H2'	1:5:2024:G:C8	2.48	0.48
3:8:126:C:H1'	3:8:127:U:C6	2.48	0.48
4:9:792:C:H2'	4:9:793:G:H8	1.79	0.48
4:9:1010:G:H2'	4:9:1011:A:C8	2.48	0.48
4:9:1240:A:H2'	4:9:1241:A:C8	2.48	0.48
5:A:117:GLU:HG2	5:A:124:GLY:N	2.28	0.48
41:m:51:ILE:HG13	41:m:52:ILE:H	1.78	0.48
52:GG:121:ILE:HG21	52:GG:124:LEU:HD12	1.94	0.48
1:5:258:G:H2'	1:5:259:C:C6	2.48	0.48
1:5:667:A:N7	7:C:2:ALA:N	2.62	0.48
1:5:746:A:O2'	1:5:747:A:H5'	2.13	0.48
1:5:2490:U:H2'	1:5:2491:C:C6	2.48	0.48
1:5:3948:C:H5''	1:5:3949:A:OP2	2.13	0.48
4:9:521:A:OP1	55:JJ:45:ARG:NH1	2.46	0.48
4:9:880:G:C6	4:9:907:G:C6	3.01	0.48
46:AA:76:VAL:HG12	46:AA:123:VAL:CG2	2.44	0.48
1:5:4060:U:H2'	1:5:4061:G:C8	2.48	0.48
1:5:4239:A:H2'	1:5:4240:G:C8	2.48	0.48
4:9:1597:C:H4'	4:9:1603:G:O6	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J:35:ARG:NH1	13:J:123:ILE:O	2.47	0.48
1:5:490:C:H2'	1:5:491:G:C8	2.49	0.48
1:5:4508:C:N3	1:5:4512:U:H5	2.11	0.48
1:5:4759:C:H2'	1:5:4760:G:C8	2.49	0.48
3:8:111:U:H2'	3:8:111:U:O2	2.13	0.48
4:9:729:C:H2'	4:9:730:C:C6	2.48	0.48
4:9:862:A:C8	68:WW:107:SER:HA	2.49	0.48
4:9:1866:A:N1	72:aa:87:ARG:HD2	2.29	0.48
34:e:40:GLY:O	34:e:46:ARG:NH1	2.44	0.48
57:LL:103:GLU:OE2	69:XX:14:ARG:NH2	2.34	0.48
1:5:976:G:C2	1:5:977:C:C5	3.02	0.48
1:5:979:C:OP1	9:E:49:ASN:ND2	2.47	0.48
1:5:2412:A:H2'	1:5:2413:U:C6	2.49	0.48
3:8:86:U:O2'	3:8:87:G:OP1	2.32	0.48
8:D:62:CYS:HB3	8:D:105:LEU:HD22	1.96	0.48
21:R:160:GLU:OE1	21:R:163:ARG:NH2	2.41	0.48
22:S:93:MET:SD	22:S:113:MET:HE1	2.53	0.48
67:VV:40:ASP:HB2	67:VV:47:ASN:OD1	2.14	0.48
1:5:1440:U:H2'	1:5:1441:C:C6	2.49	0.48
1:5:1617:G:H1'	1:5:2513:A:N6	2.29	0.48
1:5:1883:G:OP1	34:e:47:ARG:NH1	2.43	0.48
1:5:2544:G:C6	1:5:2545:U:C4	3.02	0.48
1:5:3937:C:H2'	1:5:3938:G:C8	2.48	0.48
1:5:4061:G:H2'	1:5:4062:A:H8	1.78	0.48
4:9:367:U:H4'	4:9:371:A:C8	2.49	0.48
65:TT:33:TRP:HH2	65:TT:102:ARG:NH2	2.12	0.48
1:5:516:C:H2'	1:5:517:C:C6	2.49	0.48
1:5:1080:C:H2'	1:5:1081:C:C6	2.48	0.48
1:5:1788:A:H2'	12:I:22:PHE:CZ	2.49	0.48
3:8:67:U:H2'	3:8:68:G:C8	2.49	0.48
4:9:1098:C:H2'	4:9:1099:G:C8	2.49	0.48
4:9:1227:G:C2	4:9:1228:A:C8	3.02	0.48
4:9:1523:C:H2'	4:9:1524:G:H8	1.78	0.48
51:FF:78:MET:HG2	51:FF:79:HIS:H	1.79	0.48
1:5:488:G:H2'	1:5:489:C:C6	2.49	0.47
1:5:3770:U:H2'	1:5:3771:C:C6	2.49	0.47
4:9:164:A:H3'	4:9:165:G:H21	1.79	0.47
4:9:1139:C:H5	4:9:1149:A:H62	1.61	0.47
4:9:1845:A:H2'	4:9:1846:G:C8	2.48	0.47
5:A:108:PRO:HD3	44:p:90:LYS:HD2	1.95	0.47
8:D:41:LYS:HE3	23:T:32:ARG:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:11:5:A:H2'	80:11:6:G:H8	1.79	0.47
1:5:272:U:H2'	1:5:273:U:C6	2.49	0.47
1:5:2335:C:H2'	1:5:2336:G:H8	1.79	0.47
1:5:2361:G:N7	19:P:25:HIS:CE1	2.81	0.47
4:9:1101:U:H2'	4:9:1102:G:H8	1.79	0.47
7:C:237:ILE:HD12	7:C:237:ILE:H	1.79	0.47
24:U:100:LEU:HD13	24:U:112:LEU:HD23	1.94	0.47
49:DD:177:LEU:HD12	49:DD:182:LEU:HD13	1.96	0.47
78:gg:64:HIS:CD2	78:gg:65:PHE:H	2.32	0.47
80:13:35:A:H2'	80:13:36:U:C6	2.49	0.47
1:5:387:G:O2'	1:5:412:G:O6	2.24	0.47
1:5:495:C:H2'	1:5:496:G:C8	2.49	0.47
82:5:8701:SPD:H92	30:a:38:MET:HE1	1.96	0.47
4:9:562:U:H2'	4:9:563:G:C8	2.49	0.47
4:9:1538:C:H2'	4:9:1539:U:C6	2.49	0.47
58:MM:35:ILE:HD13	58:MM:61:TYR:HE1	1.80	0.47
1:5:64:A:N1	1:5:108:A:O2'	2.46	0.47
1:5:1756:U:H2'	1:5:1757:U:C6	2.49	0.47
1:5:1920:C:H3'	1:5:1921:C:H5''	1.97	0.47
1:5:2083:C:OP2	20:Q:14:ARG:NH2	2.43	0.47
1:5:4577:U:H2'	1:5:4578:G:H8	1.80	0.47
1:5:4637:G:H2'	1:5:4638:U:C6	2.49	0.47
4:9:115:U:H2'	4:9:116:U:C6	2.48	0.47
4:9:1714:U:H2'	4:9:1715:A:C8	2.50	0.47
22:S:9:GLU:OE2	22:S:31:ARG:NH1	2.38	0.47
36:g:41:ALA:O	36:g:52:ARG:NH1	2.40	0.47
1:5:407:A:O2'	1:5:410:A:OP1	2.25	0.47
4:9:562:U:H5'	55:JJ:134:HIS:HE2	1.80	0.47
4:9:792:C:H2'	4:9:793:G:C8	2.50	0.47
4:9:815:U:H2'	4:9:816:A:H8	1.79	0.47
34:e:89:LEU:HD13	34:e:118:LEU:HD22	1.95	0.47
50:EE:212:ASP:OD1	50:EE:213:ALA:N	2.47	0.47
51:FF:119:SER:OG	51:FF:189:ALA:HB1	2.15	0.47
80:13:74:C:HO2'	80:13:75:C:P	2.36	0.47
1:5:2396:A:N6	1:5:2814:C:O2	2.47	0.47
4:9:1120:U:H5''	73:bb:72:ARG:NH2	2.30	0.47
1:5:100:C:H2'	1:5:101:A:C8	2.49	0.47
1:5:1345:A:H2'	1:5:1346:C:C6	2.49	0.47
1:5:1435:G:O2'	1:5:2105:A:N1	2.43	0.47
1:5:2275:G:H2'	1:5:2276:A:C8	2.49	0.47
1:5:3917:A:H2'	1:5:3918:G:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:9:459:C:H2'	4:9:460:A:C8	2.50	0.47
4:9:1399:C:H5''	78:gg:100:ARG:HH11	1.80	0.47
4:9:1507:G:HO2'	77:ff:85:TYR:HH	1.61	0.47
4:9:1550:G:H3'	4:9:1579:A:H61	1.79	0.47
5:A:70:LYS:HE3	5:A:72:ARG:CZ	2.44	0.47
18:O:116:LYS:HE2	22:S:169:THR:HG21	1.95	0.47
45:r:105:ASP:OD1	45:r:105:ASP:N	2.47	0.47
56:KK:77:GLN:OE1	56:KK:80:ARG:NH1	2.46	0.47
61:PP:21:ASP:OD1	61:PP:22:LEU:N	2.47	0.47
78:gg:254:PRO:HA	78:gg:285:GLN:HA	1.96	0.47
1:5:4037:C:H2'	1:5:4038:C:C6	2.49	0.47
1:5:709:C:H1'	1:5:4942:C:C5	2.50	0.47
1:5:1442:C:H2'	1:5:1443:A:C8	2.50	0.47
1:5:2474:G:N2	1:5:2502:A:H2'	2.29	0.47
4:9:28:U:H2'	4:9:29:G:H8	1.80	0.47
4:9:53:C:O2'	4:9:507:G:N7	2.45	0.47
4:9:744:G:C6	4:9:798:G:N2	2.83	0.47
28:Y:54:GLU:OE1	28:Y:108:ARG:NH1	2.47	0.47
1:5:1411(A):G:H2'	1:5:1411(B):C:C6	2.50	0.47
1:5:4746:C:H2'	1:5:4747:C:C6	2.50	0.47
4:9:507:G:OP2	70:YY:104:ARG:NH2	2.43	0.47
80:11:69:U:H2'	80:11:70:G:C8	2.49	0.47
1:5:1341:U:H2'	1:5:1342:A:C8	2.50	0.46
1:5:1927:U:OP1	1:5:1949:U:O2'	2.31	0.46
1:5:2632:U:H2'	1:5:2633:U:C6	2.50	0.46
1:5:3960:A:N1	1:5:4047:A:N6	2.62	0.46
4:9:344:U:H2'	4:9:345:U:C6	2.50	0.46
4:9:380:G:P	54:II:56:ARG:HH21	2.37	0.46
4:9:1223:A:OP1	51:FF:79:HIS:HA	2.14	0.46
4:9:1611:G:OP2	64:SS:121:ARG:NH2	2.42	0.46
6:B:213:GLN:NE2	6:B:285:TYR:O	2.39	0.46
56:KK:91:PRO:HD2	56:KK:94:LEU:HD12	1.97	0.46
1:5:3926:C:O2'	17:N:87:HIS:HE1	1.99	0.46
1:5:3961:G:N1	1:5:3963:A:H2'	2.29	0.46
4:9:1614:A:P	61:PP:42:ARG:HH21	2.38	0.46
9:E:191:ARG:NH1	9:E:217:ASP:OD1	2.47	0.46
1:5:1197:C:H2'	1:5:1198:G:C8	2.50	0.46
1:5:3673:C:O2'	1:5:3674:G:OP1	2.29	0.46
1:5:4232:U:H4'	1:5:4233:A:O5'	2.15	0.46
1:5:4586:G:C6	1:5:4717:A:C6	3.04	0.46
1:5:4967:A:H2'	1:5:4968:A:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:9:1348:G:H2'	4:9:1349:G:H8	1.79	0.46
30:a:15:VAL:O	30:a:16:SER:OG	2.31	0.46
50:EE:139:LEU:HG	50:EE:150:PRO:HB3	1.97	0.46
60:OO:19:PRO:HG2	60:OO:27:VAL:HG21	1.96	0.46
80:13:35:A:H2'	80:13:36:U:H6	1.81	0.46
1:5:3771:C:H4'	80:13:14:C:H4'	1.98	0.46
1:5:4064:C:H2'	1:5:4065:G:C8	2.51	0.46
42:n:2:ARG:HB3	42:n:5:TRP:CD1	2.51	0.46
80:11:12:C:H2'	80:11:13:G:C8	2.50	0.46
1:5:1411:C:H2'	1:5:1411(A):G:C8	2.51	0.46
1:5:1483:C:H5''	1:5:1483:C:O2	2.16	0.46
4:9:942:G:H2'	4:9:943:U:C6	2.50	0.46
4:9:1844:U:O4	42:n:4:LYS:HE3	2.15	0.46
9:E:164:ARG:NH1	16:M:106:ASP:OD2	2.49	0.46
46:AA:44:ASP:HA	63:RR:128:PHE:HB3	1.98	0.46
48:CC:275:LYS:HG3	48:CC:276:THR:HG23	1.98	0.46
4:9:53:C:P	70:YY:112:ASN:HD22	2.39	0.46
4:9:1700:C:C2	4:9:1834:A:N6	2.84	0.46
45:r:46:ARG:HA	45:r:70:GLN:HE22	1.81	0.46
55:JJ:78:LEU:HG	55:JJ:92:MET:HG3	1.97	0.46
1:5:453:G:N1	1:5:1293:G:N7	2.55	0.46
1:5:2097:A:OP1	1:5:2107:A:N6	2.49	0.46
1:5:4591:U:H2'	1:5:4592:C:C6	2.50	0.46
4:9:1088:U:H4'	4:9:1089:G:OP2	2.16	0.46
78:gg:230:LEU:HD13	78:gg:259:TRP:CD2	2.51	0.46
1:5:457:G:H2'	1:5:458:C:C6	2.51	0.46
1:5:1298:C:H2'	1:5:1299:G:C8	2.51	0.46
1:5:3971:G:H2'	1:5:3972:A:C8	2.51	0.46
1:5:4594:U:H2'	1:5:4595:G:H8	1.80	0.46
4:9:1397:U:O4	62:QQ:12:VAL:HA	2.16	0.46
4:9:1698:C:O2'	4:9:1699:A:OP1	2.33	0.46
34:e:7:LEU:HB2	34:e:93:LYS:HB3	1.98	0.46
43:o:14:LYS:HB3	43:o:77:CYS:SG	2.55	0.46
1:5:179:G:H2'	1:5:180:C:C6	2.51	0.46
1:5:2517:A:O2'	36:g:66:ARG:NH2	2.49	0.46
4:9:674:C:H2'	4:9:675:U:C6	2.51	0.46
6:B:189:THR:HG23	6:B:192:GLU:H	1.81	0.46
26:W:35:LYS:HE2	26:W:51:TRP:CZ2	2.50	0.46
80:11:10:G:O2'	80:11:12:C:N4	2.39	0.46
1:5:172:C:O2'	1:5:173:C:O5'	2.34	0.46
1:5:260:C:H2'	1:5:261:G:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:2491:C:H2'	1:5:2492:C:C6	2.51	0.46
1:5:4577:U:H2'	1:5:4578:G:C8	2.51	0.46
4:9:145:G:H2'	4:9:146:G:C8	2.51	0.46
58:MM:19:GLN:HE21	58:MM:88:TRP:NE1	2.13	0.46
74:cc:21:THR:HG22	74:cc:68:LEU:HD21	1.98	0.46
1:5:1558:A:H2'	1:5:1559:G:H8	1.81	0.45
1:5:2539:C:H2'	1:5:2540:C:C6	2.51	0.45
4:9:129:C:H3'	4:9:214:U:O4	2.16	0.45
4:9:151:C:H1'	52:GG:132:ARG:NH2	2.31	0.45
4:9:693:A:H2'	4:9:694:G:H8	1.80	0.45
5:A:142:GLU:HG2	5:A:143:THR:HG23	1.98	0.45
17:N:49:ARG:HH11	17:N:49:ARG:HG2	1.81	0.45
46:AA:30:LEU:HD13	46:AA:38:ILE:HD12	1.98	0.45
46:AA:140:VAL:O	46:AA:142:LEU:N	2.49	0.45
1:5:1398:A:C6	1:5:1420:A:C8	3.04	0.45
1:5:2293:U:H2'	1:5:2294:G:H8	1.80	0.45
1:5:4266:G:N3	1:5:4266:G:H2'	2.31	0.45
1:5:4504:C:H2'	1:5:4505:C:C6	2.51	0.45
4:9:656:G:HO2'	48:CC:227:ARG:HH11	1.63	0.45
4:9:857:U:H2'	4:9:858:A:C8	2.51	0.45
20:Q:43:PHE:CD2	20:Q:133:GLY:HA3	2.51	0.45
26:W:23:ARG:NH2	26:W:25:ASP:OD2	2.39	0.45
34:e:84:GLU:CD	45:r:20:ARG:HH22	2.24	0.45
47:BB:126:ASP:OD1	47:BB:136:ARG:HD3	2.16	0.45
70:YY:86:GLU:OE2	70:YY:90:ARG:HD2	2.16	0.45
1:5:1411:C:H2'	1:5:1411(A):G:H8	1.82	0.45
1:5:1472:C:H2'	1:5:1473:U:H6	1.80	0.45
1:5:1534:A:C4	81:j:13:ASN:O	2.70	0.45
1:5:1804:A:H5'	1:5:1805:A:H2'	1.99	0.45
1:5:4638:U:H2'	1:5:4639:G:N3	2.31	0.45
4:9:851:C:O2'	4:9:852:G:N2	2.50	0.45
4:9:1508:A:H3'	77:ff:83:LYS:NZ	2.31	0.45
8:D:119:TYR:OH	8:D:139:PRO:O	2.32	0.45
60:OO:103:ASN:HB3	60:OO:139:SER:OG	2.17	0.45
61:PP:22:LEU:HA	61:PP:25:LEU:HD12	1.98	0.45
1:5:489:C:H2'	1:5:490:C:C6	2.52	0.45
1:5:2276:A:H2'	1:5:2277:C:O4'	2.16	0.45
4:9:1374:C:H2'	4:9:1375:G:O4'	2.17	0.45
4:9:1553:C:H2'	4:9:1554:C:C6	2.51	0.45
5:A:142:GLU:CD	5:A:142:GLU:H	2.24	0.45
48:CC:106:VAL:HG22	48:CC:128:VAL:HG22	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:FF:73:THR:O	51:FF:89:THR:HG21	2.16	0.45
55:JJ:60:LEU:HD22	55:JJ:70:ARG:HA	1.97	0.45
1:5:280:G:H5''	17:N:14:LYS:HE2	1.99	0.45
1:5:664:G:H2'	1:5:665:C:C6	2.51	0.45
8:D:41:LYS:HE2	23:T:93:ILE:CD1	2.46	0.45
16:M:6:PHE:O	16:M:11:ARG:NE	2.46	0.45
52:GG:1:MET:HE2	52:GG:24:LEU:HD22	1.98	0.45
1:5:1080:C:H2'	1:5:1081:C:H6	1.82	0.45
1:5:4083:U:OP1	5:A:123:ARG:NH2	2.45	0.45
1:5:941:C:OP2	14:K:241:ARG:NE	2.41	0.45
1:5:4452:U:OP2	1:5:4522:G:N2	2.44	0.45
4:9:379:C:H5'	54:II:33:ALA:HA	1.98	0.45
4:9:909:G:OP2	21:R:172:ARG:NH1	2.50	0.45
12:I:17:TYR:H	12:I:95:HIS:CD2	2.34	0.45
80:13:53:G:H2'	80:13:54:A:H8	1.82	0.45
1:5:62:A:N3	1:5:77:U:O2'	2.37	0.45
1:5:2479:G:H2'	1:5:2480:G:H8	1.81	0.45
4:9:523:A:P	55:JJ:127:ARG:HH21	2.40	0.45
4:9:881:G:H2'	4:9:882:U:C6	2.52	0.45
4:9:898:U:H2'	4:9:899:U:C6	2.52	0.45
4:9:1147:C:OP1	72:aa:6:ARG:NH1	2.47	0.45
4:9:1839:U:H1'	4:9:1863:A:C2	2.50	0.45
51:FF:80:GLY:HA2	51:FF:83:ASN:OD1	2.17	0.45
54:II:177:SER:OG	54:II:184:ARG:O	2.29	0.45
80:11:47:U:H3'	80:11:48:C:H5'	1.99	0.45
1:5:2725:A:N6	21:R:88:ARG:O	2.50	0.45
1:5:3910:C:H2'	1:5:3911:C:H6	1.82	0.45
1:5:4948:C:O2	1:5:4949:G:H2'	2.17	0.45
4:9:168:C:H4'	52:GG:131:ARG:HD2	1.98	0.45
41:m:89:CYS:O	41:m:92:THR:HG23	2.17	0.45
73:bb:33:MET:HE2	73:bb:48:SER:HA	1.98	0.45
1:5:48:G:H5'	17:N:192:TRP:NE1	2.32	0.45
1:5:2088:A:H5''	1:5:2089:G:C3'	2.46	0.45
1:5:2409:U:H5	1:5:2783:A:N1	2.15	0.45
1:5:3641:U:C5	1:5:3646:A:N7	2.85	0.45
4:9:1507:G:H1	77:ff:88:PRO:HA	1.81	0.45
6:B:59:GLU:HG3	6:B:366:LYS:HE3	1.98	0.45
13:J:161:GLU:HA	13:J:164:ARG:HG2	1.99	0.45
20:Q:42:THR:O	20:Q:46:VAL:HG23	2.17	0.45
55:JJ:33:GLY:HA3	76:ee:111:TYR:CD1	2.52	0.45
57:LL:85:THR:HG22	57:LL:112:HIS:HA	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:1645:C:H2'	1:5:1646:A:C8	2.52	0.44
1:5:1949:U:OP1	11:H:64:ARG:NH1	2.49	0.44
1:5:2749:C:H2'	1:5:2750:G:H8	1.81	0.44
1:5:4776:G:C6	1:5:4860:G:C6	3.04	0.44
4:9:1118:C:H2'	4:9:1119:A:O4'	2.17	0.44
4:9:1619:A:P	61:PP:47:ARG:HH11	2.39	0.44
15:L:178:ALA:N	30:a:134:GLU:OE2	2.42	0.44
36:g:15:THR:HG22	36:g:16:ALA:N	2.33	0.44
51:FF:39:ILE:HG23	51:FF:68:ILE:HG21	1.99	0.44
1:5:63:G:P	17:N:169:ARG:HH22	2.38	0.44
1:5:1984:A:O2'	1:5:1985:G:OP1	2.32	0.44
1:5:2640:G:H2'	1:5:2641:A:C8	2.52	0.44
1:5:2899:C:H2'	1:5:2900:U:H6	1.77	0.44
1:5:3642:A:C4	81:j:3:LYS:HB3	2.53	0.44
1:5:3727:A:H2'	1:5:3728:A:C8	2.52	0.44
1:5:4305:G:H22	23:T:87:LYS:NZ	2.15	0.44
3:8:94:G:H1'	81:j:82:THR:O	2.17	0.44
4:9:1623:A:H5''	64:SS:133:GLY:HA3	1.99	0.44
1:5:1088:C:H2'	1:5:1089:G:H8	1.81	0.44
1:5:1989:G:C2	1:5:1990:A:C5	3.05	0.44
1:5:2672:C:OP1	44:p:44:LYS:NZ	2.44	0.44
1:5:2709:C:OP2	21:R:43:LYS:HG3	2.18	0.44
1:5:4233:A:C4	1:5:4235:G:N7	2.85	0.44
1:5:4233:A:C8	1:5:4235:G:C8	3.06	0.44
4:9:1113:A:H2'	4:9:1114:U:C6	2.52	0.44
11:H:105:ILE:CG2	11:H:109:GLY:HA2	2.48	0.44
13:J:99:PHE:HB2	13:J:159:LYS:HE3	1.98	0.44
53:HH:91:HIS:ND1	53:HH:172:THR:OG1	2.35	0.44
59:NN:99:ARG:NH2	59:NN:119:GLU:OE2	2.32	0.44
1:5:64:A:H4'	1:5:65:A:O5'	2.18	0.44
1:5:1835:G:C8	1:5:1835:G:H5'	2.52	0.44
1:5:2412:A:H2'	1:5:2413:U:H6	1.83	0.44
1:5:3625:G:O2'	1:5:3626:G:OP1	2.32	0.44
1:5:3949:A:H2'	1:5:3950:U:C6	2.52	0.44
1:5:4586:G:O6	1:5:4717:A:N6	2.50	0.44
1:5:4916:G:C6	1:5:4917:C:C4	3.06	0.44
4:9:563:G:N3	4:9:564:A:C8	2.85	0.44
4:9:669:A:H5'	4:9:669:A:H8	1.82	0.44
26:W:114:GLU:O	26:W:118:ALA:CB	2.64	0.44
1:5:1440:U:H2'	1:5:1441:C:C5	2.53	0.44
1:5:2466:G:O5'	1:5:2466:G:H8	2.01	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:2602:G:H2'	1:5:2603:C:C6	2.52	0.44
1:5:4068:U:H2'	1:5:4069:U:O4'	2.17	0.44
4:9:464:A:H4'	4:9:465:A:OP2	2.18	0.44
4:9:506:G:OP1	70:YY:108:LYS:NZ	2.41	0.44
4:9:928:G:H21	73:bb:68:GLY:HA2	1.82	0.44
4:9:1303:C:O2	4:9:1303:C:H5'	2.16	0.44
4:9:1798:C:H2'	4:9:1799:G:O4'	2.18	0.44
12:I:31:ILE:HG22	12:I:62:SER:HB2	1.99	0.44
28:Y:24:HIS:CE1	28:Y:25:ILE:HG12	2.52	0.44
48:CC:196:ILE:HB	48:CC:223:TYR:CB	2.46	0.44
1:5:665:C:H5''	1:5:666:G:O5'	2.17	0.44
1:5:1437:C:N3	31:b:106:ARG:NE	2.59	0.44
1:5:4585:U:H2'	1:5:4586:G:H8	1.83	0.44
4:9:1447:G:P	66:UU:87:ARG:HH22	2.41	0.44
35:f:41:PHE:HE1	35:f:110:ILE:HD11	1.83	0.44
36:g:98:GLU:OE2	36:g:101:LYS:NZ	2.42	0.44
49:DD:65:ARG:HG2	49:DD:65:ARG:HH11	1.82	0.44
62:QQ:58:LEU:HB3	62:QQ:62:ARG:HD2	1.98	0.44
1:5:302:C:H2'	1:5:303:C:C6	2.53	0.44
1:5:1188:C:H2'	1:5:1189:G:C8	2.47	0.44
1:5:1370:G:O2'	1:5:1371:A:OP2	2.31	0.44
1:5:1964:A:H3'	1:5:1965:G:C8	2.51	0.44
1:5:2008:U:C5	1:5:2010:A:H3'	2.53	0.44
1:5:4700:A:N1	11:H:72:THR:HG21	2.33	0.44
1:5:4918:C:H2'	1:5:4919:G:O4'	2.17	0.44
4:9:562:U:OP1	55:JJ:134:HIS:NE2	2.47	0.44
4:9:877:C:H2'	4:9:878:G:C8	2.53	0.44
4:9:1536:G:H2'	4:9:1537:A:C8	2.53	0.44
4:9:1713:C:H2'	4:9:1714:U:C6	2.52	0.44
16:M:65:PRO:HG2	16:M:68:ALA:HB2	2.00	0.44
1:5:1847:C:H4'	20:Q:152:PHE:CE2	2.53	0.44
1:5:2455:G:H1'	1:5:2471:G:C2	2.52	0.44
4:9:754:G:H2'	4:9:755:C:C6	2.52	0.44
4:9:1253:A:H4'	4:9:1254:C:H5''	2.00	0.44
4:9:1289:U:OP2	77:ff:95:ARG:NH1	2.51	0.44
40:l:24:PRO:HD2	40:l:27:ILE:HD12	2.00	0.44
80:11:36:U:H2'	80:11:37:A:O4'	2.17	0.44
1:5:48:G:H5'	17:N:192:TRP:CD1	2.53	0.44
1:5:396:A:H2'	1:5:397:G:C8	2.53	0.44
1:5:1195:G:C6	1:5:1196:G:C6	3.06	0.44
1:5:1767:A:H2'	1:5:1768:C:H5''	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:9:572:U:H5'	70:YY:60:PHE:O	2.18	0.44
10:G:217:ILE:O	10:G:221:VAL:HG13	2.17	0.44
1:5:63:G:OP1	17:N:169:ARG:NH2	2.33	0.43
1:5:2569:G:H2'	1:5:2570:U:C6	2.53	0.43
4:9:65:C:O2'	4:9:67:C:OP2	2.32	0.43
4:9:823:U:H5	55:JJ:143:ASN:HB3	1.83	0.43
62:QQ:53:GLU:OE1	62:QQ:85:ARG:NH1	2.45	0.43
65:TT:5:THR:OG1	65:TT:65:TYR:OH	2.34	0.43
71:ZZ:79:ILE:HB	71:ZZ:83:LEU:HD23	1.99	0.43
80:13:69:U:H2'	80:13:70:G:C8	2.51	0.43
1:5:517:C:H2'	1:5:518:G:C8	2.54	0.43
1:5:1437:C:O2'	1:5:1438:U:O5'	2.34	0.43
1:5:3907:G:N7	1:5:4447:C:H4'	2.33	0.43
1:5:4862:G:H2'	1:5:4863:G:C8	2.53	0.43
4:9:1397:U:H2'	4:9:1397:U:O2	2.18	0.43
4:9:1656:G:C2	4:9:1657:G:C8	3.06	0.43
23:T:69:GLN:OE1	23:T:69:GLN:N	2.51	0.43
34:e:35:TRP:CZ2	34:e:56:PRO:HD2	2.53	0.43
46:AA:2:SER:OG	67:VV:80:SER:HB2	2.17	0.43
46:AA:6:ASP:HA	46:AA:9:GLN:HG2	2.00	0.43
1:5:123:C:H2'	1:5:124:C:C6	2.53	0.43
1:5:269:G:C6	1:5:270:U:C4	3.06	0.43
1:5:490:C:H2'	1:5:491:G:H8	1.83	0.43
1:5:4975:G:H4'	1:5:4976:U:O5'	2.18	0.43
4:9:141:A:H61	4:9:177:G:H1'	1.83	0.43
4:9:200:G:H2'	4:9:201:C:C6	2.52	0.43
4:9:815:U:H2'	4:9:816:A:C8	2.53	0.43
6:B:56:ILE:HG21	6:B:365:LEU:HD22	2.00	0.43
31:b:101:HIS:CD2	31:b:102:PRO:HD2	2.54	0.43
58:MM:93:LYS:HD2	58:MM:102:LYS:HD3	2.00	0.43
78:gg:237:ASN:ND2	78:gg:286:CYS:O	2.39	0.43
80:13:31:G:H2'	80:13:32:C:H6	1.82	0.43
1:5:2109:A:H2'	1:5:2110:G:O4'	2.18	0.43
1:5:2318:G:N2	1:5:2321:G:OP2	2.37	0.43
1:5:4061:G:H2'	1:5:4062:A:C8	2.53	0.43
2:7:2:U:H2'	2:7:3:C:C6	2.53	0.43
2:7:7:G:OP1	8:D:33:ARG:NE	2.42	0.43
46:AA:30:LEU:HD13	46:AA:38:ILE:CD1	2.48	0.43
50:EE:54:TYR:OH	50:EE:97:GLU:OE1	2.22	0.43
60:OO:43:HIS:NE2	60:OO:52:THR:OG1	2.48	0.43
1:5:279:A:OP2	17:N:8:GLN:NE2	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:4300:U:OP1	23:T:87:LYS:NZ	2.51	0.43
1:5:4345:C:H2'	1:5:4346:U:H6	1.83	0.43
1:5:4694:G:N3	1:5:4694:G:H2'	2.34	0.43
4:9:1305:C:OP2	77:ff:93:HIS:ND1	2.47	0.43
4:9:1570:G:N7	65:TT:97:LYS:NZ	2.56	0.43
4:9:1856:C:H2'	4:9:1857:G:H8	1.82	0.43
9:E:118:TYR:CE1	45:r:119:ARG:HD3	2.53	0.43
28:Y:2:LYS:HE3	28:Y:2:LYS:HB3	1.92	0.43
52:GG:7:PHE:CE2	52:GG:125:THR:HG22	2.54	0.43
52:GG:44:GLU:H	52:GG:44:GLU:CD	2.27	0.43
79:10:13:A:N6	80:11:34:C:H42	2.17	0.43
80:13:23:C:H2'	80:13:24:G:C8	2.53	0.43
1:5:259:C:H2'	1:5:260:C:C6	2.53	0.43
1:5:510:U:H5''	30:a:86:THR:HG22	2.00	0.43
1:5:1364:U:P	15:L:36:ARG:HH22	2.40	0.43
1:5:1890:G:H22	1:5:1939:A:H61	1.66	0.43
1:5:4173:G:H2'	1:5:4174:U:C6	2.53	0.43
1:5:4967:A:H2'	1:5:4968:A:H8	1.82	0.43
4:9:634:A:H2'	4:9:635:G:H8	1.82	0.43
4:9:886:A:C6	4:9:901:G:C4	3.07	0.43
4:9:1010:G:H2'	4:9:1011:A:H8	1.82	0.43
4:9:1232:U:H2'	4:9:1233:G:C8	2.53	0.43
7:C:142:HIS:CE1	7:C:204:ARG:HH22	2.37	0.43
26:W:50:ASN:HA	26:W:55:TYR:CD1	2.53	0.43
80:13:12:C:H2'	80:13:13:G:H8	1.82	0.43
1:5:165:A:H2'	1:5:166:C:H6	1.82	0.43
1:5:910:G:H2'	1:5:911:U:H6	1.83	0.43
1:5:2385:U:H2'	1:5:2386:U:C6	2.53	0.43
1:5:2520:C:O2	1:5:2640:G:N2	2.52	0.43
1:5:3732:A:H2'	1:5:3733:A:C8	2.54	0.43
1:5:4163:U:OP1	10:G:106:ARG:NH1	2.49	0.43
25:V:35:LYS:HB2	25:V:67:LYS:HG3	2.00	0.43
40:l:43:HIS:CG	40:l:46:ARG:HH21	2.36	0.43
41:m:51:ILE:HD12	41:m:51:ILE:HA	1.90	0.43
45:r:65:LYS:HE2	45:r:70:GLN:OE1	2.18	0.43
68:WW:3:ARG:HD3	68:WW:6:VAL:HG22	2.01	0.43
70:YY:86:GLU:CD	70:YY:87:PRO:HD2	2.44	0.43
78:gg:192:THR:OG1	78:gg:213:ASP:OD2	2.29	0.43
1:5:1690:C:OP2	20:Q:11:ARG:NH2	2.47	0.43
1:5:4524:G:C2	6:B:252:ALA:HB1	2.53	0.43
4:9:1279:C:H2'	4:9:1280:G:H8	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:9:1823:A:H3'	4:9:1824:A:C5'	2.49	0.43
17:N:80:THR:HB	17:N:87:HIS:HB2	2.01	0.43
46:AA:63:ARG:HG3	46:AA:185:MET:HE1	2.01	0.43
49:DD:63:GLY:O	49:DD:66:ILE:HG22	2.19	0.43
80:13:4:C:H2'	80:13:5:A:H8	1.83	0.43
1:5:1502:G:C8	1:5:1502:G:H5''	2.54	0.43
1:5:1534:A:H8	81:j:15:THR:HG23	1.83	0.43
1:5:2520:C:H2'	1:5:2521:G:H8	1.84	0.43
4:9:816:A:P	55:JJ:10:ARG:HH22	2.39	0.43
17:N:49:ARG:HG2	17:N:49:ARG:NH1	2.34	0.43
32:c:44:LYS:HD2	32:c:99:PRO:HD3	2.01	0.43
32:c:64:ALA:O	32:c:68:LYS:N	2.52	0.43
50:EE:141:THR:OG1	50:EE:143:ASP:OD1	2.35	0.43
58:MM:52:LEU:HD13	58:MM:65:VAL:HG11	2.01	0.43
1:5:333:U:H5''	1:5:334:A:OP1	2.18	0.43
1:5:1307:A:H2'	1:5:1308:C:C6	2.54	0.43
1:5:1341:U:H2'	1:5:1342:A:H8	1.83	0.43
1:5:1457:G:O2'	1:5:1458:C:H5''	2.18	0.43
1:5:1567:U:H2'	1:5:1568:C:C6	2.54	0.43
1:5:2544:G:C6	3:8:126:C:N4	2.87	0.43
3:8:6:C:H2'	3:8:7:U:C6	2.53	0.43
4:9:28:U:H2'	4:9:29:G:C8	2.53	0.43
4:9:536:A:N6	4:9:547:G:H1	2.15	0.43
4:9:589:G:C6	4:9:591:U:C4	3.07	0.43
4:9:913:A:OP1	53:HH:99:ARG:NE	2.42	0.43
4:9:1508:A:H3'	77:ff:83:LYS:HZ1	1.84	0.43
4:9:1866:A:N6	72:aa:84:VAL:HB	2.34	0.43
12:I:166:HIS:CE1	23:T:160:ALA:HB3	2.54	0.43
15:L:62:PRO:O	15:L:63:THR:HB	2.19	0.43
19:P:36:ILE:HD12	19:P:91:LEU:HD13	2.00	0.43
45:r:46:ARG:HA	45:r:70:GLN:NE2	2.33	0.43
80:11:35:A:H2'	80:11:36:U:C6	2.54	0.43
1:5:233:U:H3'	1:5:234:G:H5''	2.00	0.42
1:5:385:A:N3	1:5:387:G:H5''	2.34	0.42
1:5:433:A:C2	1:5:3867:A:H4'	2.54	0.42
1:5:2487:G:O6	1:5:2489:C:H1'	2.18	0.42
1:5:2520:C:H2'	1:5:2521:G:C8	2.54	0.42
1:5:4045:G:H2'	1:5:4046:A:H3'	2.01	0.42
2:7:38:U:H2'	2:7:40:U:C5	2.54	0.42
4:9:1267:C:H2'	4:9:1268:C:C6	2.54	0.42
29:Z:87:VAL:HG12	29:Z:89:ILE:HB	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:11:5:A:H2'	80:11:6:G:C8	2.54	0.42
1:5:972:C:O2'	1:5:973:G:OP2	2.35	0.42
1:5:1444:G:O5'	1:5:1444:G:H8	2.02	0.42
1:5:1803:G:H2'	1:5:1836:G:N2	2.34	0.42
1:5:2045:G:O6	1:5:3870:C:O2'	2.32	0.42
1:5:2392:C:C2	1:5:2393:C:C5	3.06	0.42
1:5:3860:A:N3	19:P:131:ARG:NH1	2.57	0.42
4:9:1252:C:N4	62:QQ:146:ARG:O	2.45	0.42
19:P:94:MET:HE1	19:P:146:ILE:HB	2.01	0.42
21:R:105:LEU:HD23	21:R:138:LEU:HD23	2.01	0.42
27:X:117:TYR:HB3	27:X:119:ILE:HD12	2.01	0.42
46:AA:170:SER:O	46:AA:174:MET:HG2	2.20	0.42
51:FF:140:ASP:OD1	74:cc:44:ARG:NH1	2.51	0.42
1:5:1088:C:H2'	1:5:1089:G:C8	2.55	0.42
1:5:1214:C:N3	31:b:91:ARG:NH2	2.67	0.42
1:5:2404:A:OP2	40:l:2:SER:OG	2.27	0.42
1:5:4994:G:H2'	1:5:4995:U:H6	1.84	0.42
2:7:88:A:H2'	2:7:89:G:O4'	2.19	0.42
4:9:881:G:H2'	4:9:882:U:H6	1.83	0.42
4:9:1531:A:H2'	4:9:1532:C:C6	2.54	0.42
30:a:103:VAL:CG1	30:a:108:TYR:HB2	2.49	0.42
50:EE:148:ARG:NH2	52:GG:202:ASN:OD1	2.51	0.42
62:QQ:38:PRO:HG2	62:QQ:41:MET:HG2	2.01	0.42
81:j:28:HIS:HE1	81:j:30:GLN:HB2	1.84	0.42
1:5:460:C:H2'	1:5:461:G:H8	1.84	0.42
1:5:956:A:C8	1:5:957:G:C8	3.05	0.42
1:5:1604:G:H2'	1:5:1605:G:C8	2.53	0.42
1:5:2385:U:H2'	1:5:2386:U:H6	1.83	0.42
1:5:3710:G:H1'	1:5:3712:A:N6	2.34	0.42
4:9:634:A:H2'	4:9:635:G:C8	2.55	0.42
4:9:913:A:N6	53:HH:98:ARG:HB3	2.35	0.42
4:9:1019:C:H2'	4:9:1020:A:O4'	2.20	0.42
23:T:93:ILE:HA	23:T:96:ILE:HG12	2.01	0.42
46:AA:85:ARG:NH2	63:RR:82:ASP:O	2.51	0.42
55:JJ:35:TYR:CD2	55:JJ:106:LEU:HD23	2.54	0.42
61:PP:41:GLN:NE2	61:PP:113:GLY:O	2.51	0.42
69:XX:51:VAL:HG13	69:XX:70:VAL:CG2	2.49	0.42
1:5:1683:U:H2'	1:5:1684:A:C8	2.54	0.42
1:5:1962:A:C5	1:5:1963:C:C5	3.08	0.42
1:5:1963:C:H5''	1:5:1964:A:OP2	2.19	0.42
1:5:1973:G:H2'	1:5:1974:U:C5	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:8:60:G:N2	3:8:64:U:C2	2.87	0.42
4:9:368:U:O2'	4:9:369:C:OP1	2.32	0.42
4:9:561:A:H2'	4:9:562:U:C6	2.54	0.42
4:9:1199:A:H2'	4:9:1200:A:C8	2.54	0.42
4:9:1335:G:OP1	49:DD:185:LYS:HE3	2.19	0.42
15:L:63:THR:HG21	30:a:66:ASN:HD22	1.83	0.42
17:N:9:GLU:HB2	38:i:44:ILE:HG13	2.02	0.42
19:P:25:HIS:CE1	19:P:27:LYS:HG3	2.55	0.42
38:i:45:ARG:NH1	38:i:49:GLY:O	2.52	0.42
48:CC:146:GLU:OE1	49:DD:120:TYR:OH	2.24	0.42
51:FF:76:MET:HB3	51:FF:89:THR:HG21	2.01	0.42
56:KK:3:MET:HE3	56:KK:44:HIS:HB3	2.02	0.42
58:MM:92:CYS:SG	58:MM:103:VAL:HG13	2.59	0.42
78:gg:23:THR:HG22	78:gg:31:ILE:HD12	2.02	0.42
1:5:67:C:OP2	1:5:312:G:N2	2.53	0.42
1:5:2007:G:C2'	1:5:2012:A:H61	2.31	0.42
1:5:3684:G:H2'	1:5:3685:C:C6	2.54	0.42
4:9:1119:A:H2'	4:9:1120:U:H6	1.81	0.42
6:B:36:ASP:HB2	6:B:39:LYS:HG2	2.02	0.42
1:5:350:C:OP2	7:C:199:ARG:NH2	2.50	0.42
1:5:969:C:N4	1:5:2095:A:H61	2.17	0.42
1:5:973:G:N2	1:5:1282:G:C8	2.87	0.42
1:5:2411:C:H2'	1:5:2412:A:H8	1.85	0.42
1:5:2483:G:C6	1:5:2496:G:C6	3.08	0.42
1:5:3893:C:H2'	1:5:3894:A:C8	2.55	0.42
1:5:4915:G:N1	1:5:4916:G:C5	2.87	0.42
4:9:318:A:H61	52:GG:186:GLN:NE2	2.11	0.42
4:9:796:G:O6	4:9:797:C:N4	2.51	0.42
46:AA:2:SER:N	46:AA:8:LEU:O	2.53	0.42
47:BB:133:TYR:CE1	47:BB:221:PRO:HD2	2.55	0.42
51:FF:80:GLY:HA2	51:FF:83:ASN:CG	2.44	0.42
1:5:1447:C:H2'	1:5:1448:G:O4'	2.20	0.42
1:5:1960:A:H4'	1:5:1961:G:OP2	2.20	0.42
1:5:2553:A:O2'	1:5:2554:U:P	2.77	0.42
1:5:4271:A:H3'	1:5:4272:G:N2	2.34	0.42
3:8:89:U:H2'	3:8:90:C:C6	2.54	0.42
4:9:1017:U:H2'	4:9:1018:U:C6	2.55	0.42
4:9:1507:G:N2	77:ff:87:THR:O	2.43	0.42
7:C:140:LYS:HE2	7:C:245:HIS:HB2	2.01	0.42
58:MM:113:ASP:OD2	58:MM:121:LYS:HD3	2.20	0.42
77:ff:125:GLU:OE2	77:ff:143:LYS:NZ	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:gg:64:HIS:CG	78:gg:65:PHE:H	2.37	0.42
80:11:65:C:H2'	80:11:66:C:C6	2.55	0.42
1:5:465:G:H2'	1:5:466:A:H8	1.81	0.42
1:5:2505:C:N4	1:5:4084:G:H4'	2.35	0.42
1:5:2553:A:HO2'	1:5:2554:U:P	2.41	0.42
1:5:4458:C:H2'	1:5:4459:U:C6	2.54	0.42
1:5:4585:U:H2'	1:5:4586:G:C8	2.55	0.42
4:9:398:A:H5'	4:9:398:A:C8	2.54	0.42
4:9:1260:A:C2	4:9:1620:A:C8	3.07	0.42
6:B:223:THR:O	6:B:274:TYR:HA	2.19	0.42
22:S:86:SER:N	22:S:89:GLY:O	2.53	0.42
53:HH:135:PHE:CG	53:HH:136:PRO:HA	2.55	0.42
63:RR:53:TYR:CE2	63:RR:57:LEU:HD11	2.54	0.42
1:5:1837:A:OP1	23:T:130:ARG:NH1	2.53	0.42
1:5:2056:G:C8	1:5:2058:G:C8	3.08	0.42
1:5:3759:A:H5'	1:5:3765:G:H22	1.85	0.42
1:5:3969:G:H2'	1:5:3970:G:C8	2.54	0.42
1:5:4122:G:O2'	29:Z:136:PHE:OXT	2.37	0.42
1:5:4239:A:H2'	1:5:4240:G:H8	1.85	0.42
1:5:4291:G:H5''	1:5:4293:U:C6	2.54	0.42
4:9:1476:A:H4'	4:9:1477:U:OP2	2.19	0.42
9:E:69:ALA:HA	9:E:71:TYR:CE2	2.55	0.42
19:P:64:ASN:ND2	19:P:80:GLN:OE1	2.47	0.42
36:g:85:LYS:HE2	36:g:85:LYS:HB2	1.93	0.42
42:n:1:MET:HB2	42:n:6:ARG:NH2	2.34	0.42
1:5:1077:C:OP1	1:5:1215:C:O2'	2.36	0.41
1:5:1403:G:C6	1:5:1415:G:C6	3.08	0.41
1:5:1771:U:H2'	1:5:1772:C:C5	2.55	0.41
1:5:1961:G:O2'	1:5:1962:A:H8	2.03	0.41
1:5:2093:G:N2	1:5:2262:G:H1	2.17	0.41
1:5:2711:G:O2'	1:5:2712:G:OP1	2.37	0.41
3:8:52:A:H62	40:l:27:ILE:HD13	1.85	0.41
4:9:495:U:H2'	4:9:496:C:O4'	2.20	0.41
6:B:29:VAL:HG23	6:B:346:THR:HG21	2.02	0.41
29:Z:68:ILE:O	29:Z:115:LYS:NZ	2.35	0.41
52:GG:142:ARG:HE	52:GG:153:VAL:CG2	2.29	0.41
55:JJ:170:PRO:HB3	55:JJ:174:LYS:HG2	2.00	0.41
61:PP:57:LEU:HD23	61:PP:57:LEU:HA	1.89	0.41
1:5:978:G:OP2	9:E:61:ARG:NH1	2.49	0.41
1:5:1295:U:H4'	1:5:1296:G:O5'	2.20	0.41
1:5:1971:U:C5	1:5:2000:G:H2'	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:2749:C:H2'	1:5:2750:G:C8	2.55	0.41
1:5:4174:U:H2'	1:5:4175:G:H8	1.85	0.41
1:5:4870:G:H2'	16:M:91:TRP:CZ2	2.54	0.41
1:5:4910:A:H4'	6:B:95:THR:HB	2.01	0.41
4:9:533:A:H2'	4:9:534:G:C8	2.55	0.41
4:9:1069:U:H4'	5:A:247:ARG:HD3	2.02	0.41
19:P:36:ILE:HD11	19:P:48:LEU:HD11	2.01	0.41
24:U:42:PHE:CZ	24:U:46:ARG:HD2	2.55	0.41
1:5:126:C:H2'	1:5:127:G:C8	2.46	0.41
1:5:1087:A:H2'	1:5:1088:C:C6	2.55	0.41
1:5:1251:C:H2'	1:5:1252:C:C5	2.55	0.41
1:5:1761:G:N2	1:5:1772:C:C2	2.88	0.41
1:5:1884:C:H4'	1:5:2070:U:C4	2.55	0.41
1:5:3947:A:H2'	1:5:3948:C:C6	2.56	0.41
1:5:4537:C:H2'	1:5:4538:G:C8	2.55	0.41
4:9:1423:C:H2'	4:9:1424:G:O4'	2.19	0.41
11:H:41:ILE:HG22	11:H:43:VAL:HG13	2.02	0.41
25:V:87:SER:HA	25:V:97:TYR:HB3	2.01	0.41
46:AA:2:SER:O	46:AA:8:LEU:HB2	2.21	0.41
1:5:262:G:H2'	1:5:263:G:H8	1.85	0.41
1:5:1812:C:O2'	31:b:53:GLY:HA3	2.20	0.41
1:5:2262:G:OP2	45:r:98:ARG:NH2	2.44	0.41
1:5:2553:A:H1'	1:5:2554:U:O4'	2.20	0.41
1:5:4395:U:H5'	1:5:4395:U:C6	2.52	0.41
4:9:175:A:H2'	4:9:176:U:C6	2.56	0.41
19:P:29:THR:HG21	19:P:146:ILE:HD11	2.03	0.41
39:k:37:ARG:HD3	39:k:38:CYS:O	2.20	0.41
81:j:55:ARG:HH11	81:j:55:ARG:HB3	1.85	0.41
1:5:520:U:H2'	1:5:521:C:C6	2.55	0.41
1:5:966:A:H1'	1:5:968:C:N4	2.35	0.41
1:5:1238:A:O2'	1:5:1239:C:OP1	2.38	0.41
1:5:2503:G:H5''	1:5:2503:G:H8	1.84	0.41
1:5:2559:G:H2'	1:5:2560:C:H6	1.86	0.41
1:5:4291:G:H5''	1:5:4293:U:C5	2.55	0.41
1:5:4431:U:OP2	12:I:3:ARG:NH2	2.47	0.41
3:8:93:C:OP1	81:j:76:HIS:HE1	2.04	0.41
4:9:649:U:H2'	4:9:650:A:C8	2.55	0.41
4:9:791:C:H2'	4:9:792:C:H6	1.83	0.41
4:9:1286:G:N1	58:MM:37:GLU:OE2	2.46	0.41
4:9:1337:C:H2'	4:9:1338:G:C8	2.55	0.41
4:9:1553:C:H41	75:dd:22:ARG:CZ	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:B:312:LYS:HD3	6:B:370:THR:HG21	2.03	0.41
10:G:131:PRO:HD3	10:G:290:TRP:CE2	2.55	0.41
17:N:31:ARG:NH1	17:N:124:ASP:OD2	2.52	0.41
78:gg:101:PHE:CE2	78:gg:136:GLY:HA2	2.56	0.41
1:5:314:G:O2'	1:5:4355:G:OP1	2.30	0.41
1:5:496:G:H2'	1:5:497:G:C5'	2.51	0.41
1:5:1337:A:H5''	7:C:102:PHE:CD2	2.55	0.41
1:5:1947:U:C4	41:m:82:VAL:HG21	2.55	0.41
1:5:2478:C:N3	1:5:2479:G:C5	2.88	0.41
1:5:3760:A:H62	4:9:1825:A:H5'	1.84	0.41
1:5:4075:U:H2'	1:5:4169:G:H1	1.85	0.41
1:5:4274:A:H2'	1:5:4275:G:H8	1.84	0.41
4:9:569:A:H2'	4:9:570:C:O4'	2.21	0.41
4:9:649:U:H2'	4:9:650:A:H8	1.86	0.41
5:A:117:GLU:HA	5:A:124:GLY:HA2	2.03	0.41
12:I:101:LYS:NZ	84:l:101:ATP:O1G	2.44	0.41
40:l:43:HIS:CD2	40:l:46:ARG:HH21	2.39	0.41
45:r:90:LEU:HG	45:r:111:ILE:HG23	2.01	0.41
80:13:31:G:H2'	80:13:32:C:C6	2.54	0.41
1:5:25:A:H4'	1:5:340:C:H2'	2.01	0.41
1:5:459:C:OP1	9:E:114:LYS:HG2	2.21	0.41
1:5:492:U:H4'	1:5:493:G:OP2	2.19	0.41
1:5:1591:U:O4	1:5:4556:U:H5	2.03	0.41
1:5:2404:A:H61	1:5:2787:A:N6	2.18	0.41
1:5:2702:C:H5''	24:U:101:ARG:HH22	1.85	0.41
1:5:4884:G:H2'	1:5:4885:U:O4'	2.21	0.41
4:9:1863:A:H8	72:aa:79:ILE:HG21	1.84	0.41
29:Z:77:TYR:CZ	32:c:39:ARG:CG	3.00	0.41
60:OO:149:ARG:NH1	60:OO:151:LEU:HD11	2.36	0.41
70:YY:110:ARG:NE	70:YY:126:GLY:O	2.47	0.41
1:5:1460:C:H2'	1:5:1461:C:C6	2.55	0.41
1:5:1468:C:H2'	1:5:1469:C:C6	2.56	0.41
1:5:2016:C:H2'	1:5:2017:A:H8	1.86	0.41
1:5:2747:U:H2'	1:5:2748:C:C6	2.56	0.41
1:5:4301:U:H4'	23:T:54:HIS:CD2	2.56	0.41
1:5:4584:A:H2'	1:5:4585:U:O4'	2.21	0.41
1:5:4761:G:H2'	1:5:4762:A:H8	1.86	0.41
1:5:5016:A:H5''	1:5:5017:G:OP2	2.21	0.41
4:9:731:G:H2'	4:9:732:U:C6	2.55	0.41
4:9:809:A:H2'	4:9:810:A:O4'	2.20	0.41
4:9:898:U:H2'	4:9:899:U:H6	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:B:80:GLU:OE1	6:B:323:TYR:OH	2.17	0.41
60:OO:75:MET:HG2	60:OO:118:ALA:HB2	2.02	0.41
1:5:37:U:H4'	30:a:32:ARG:HD2	2.01	0.41
1:5:485:C:O2'	1:5:486:C:OP1	2.36	0.41
1:5:959:G:C8	1:5:959:G:H5'	2.55	0.41
1:5:1633:G:H5'	1:5:1634:A:OP1	2.21	0.41
1:5:1645:C:OP1	7:C:80:ARG:NH1	2.54	0.41
1:5:2732:G:H2'	1:5:2733:C:C6	2.56	0.41
1:5:3598:C:H2'	1:5:3599:A:H8	1.84	0.41
1:5:4322:G:N2	1:5:4325:A:OP2	2.49	0.41
4:9:399:C:H5	4:9:680:G:H5''	1.86	0.41
4:9:635:G:H2'	4:9:636:C:C6	2.55	0.41
4:9:669:A:H2'	4:9:670:A:C8	2.55	0.41
4:9:1144:A:H2'	4:9:1145:A:C8	2.56	0.41
4:9:1466:G:H2'	4:9:1467:C:C6	2.55	0.41
4:9:1523:C:H2'	4:9:1524:G:C8	2.56	0.41
47:BB:129:THR:OG1	47:BB:131:ASP:OD1	2.33	0.41
47:BB:146:ARG:HA	47:BB:146:ARG:HD2	1.92	0.41
52:GG:52:ILE:HG23	52:GG:52:ILE:O	2.21	0.41
52:GG:57:ASP:OD1	52:GG:58:LYS:N	2.52	0.41
61:PP:37:TYR:HB3	61:PP:41:GLN:HB2	2.03	0.41
64:SS:14:ARG:HD2	64:SS:14:ARG:HA	1.78	0.41
78:gg:54:ILE:HG23	78:gg:55:PRO:HD2	2.02	0.41
78:gg:121:VAL:HG12	78:gg:154:VAL:HG11	2.03	0.41
80:11:43:G:H2'	80:11:44:A:H8	1.85	0.41
1:5:164:G:H2'	1:5:165:A:C8	2.56	0.41
1:5:209:U:H6	1:5:209:U:H2'	1.70	0.41
1:5:1173:G:C6	1:5:1189:G:C6	3.09	0.41
1:5:2502:A:H4'	1:5:2503:G:OP1	2.21	0.41
1:5:2864:A:H2'	1:5:2865:U:C6	2.56	0.41
1:5:3880:G:H2'	1:5:3881:G:C8	2.56	0.41
4:9:1083:A:H4'	4:9:1085:C:C4	2.56	0.41
4:9:1713:C:H2'	4:9:1714:U:H6	1.86	0.41
10:G:187:PRO:HB3	10:G:259:GLN:HB2	2.02	0.41
11:H:4:ILE:HD11	22:S:152:PHE:CD2	2.56	0.41
20:Q:82:VAL:O	20:Q:102:ALA:HA	2.21	0.41
80:13:23:C:H2'	80:13:24:G:H8	1.86	0.41
1:5:48:G:O2'	1:5:49:U:OP2	2.36	0.40
1:5:966:A:H4'	1:5:967:C:O5'	2.20	0.40
1:5:4751:G:N1	1:5:4948:C:H5	2.07	0.40
2:7:40:U:O2	13:J:75:ARG:NH1	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:9:1441:U:O2	4:9:1443:C:N4	2.44	0.40
6:B:122:TRP:CE2	6:B:127:LYS:HE2	2.56	0.40
10:G:230:MET:HE2	38:i:39:PHE:CZ	2.56	0.40
17:N:65:ARG:HD3	17:N:127:TYR:CD2	2.56	0.40
20:Q:92:VAL:O	20:Q:112:ARG:NH2	2.44	0.40
60:OO:78:ALA:HB3	60:OO:118:ALA:HB3	2.03	0.40
1:5:150:U:H4'	1:5:151:G:OP2	2.21	0.40
1:5:257:C:H2'	1:5:258:G:H8	1.84	0.40
1:5:423:G:H2'	1:5:424:U:O4'	2.21	0.40
1:5:971(A):G:H4'	1:5:972:C:O5'	2.20	0.40
1:5:974:C:H2'	1:5:975:C:C6	2.56	0.40
1:5:2503:G:H1'	1:5:4084:G:N2	2.36	0.40
1:5:4897:G:C6	1:5:4924:C:N3	2.89	0.40
4:9:730:C:H2'	4:9:731:G:H8	1.86	0.40
7:C:209:VAL:O	7:C:229:LEU:HA	2.22	0.40
27:X:63:LYS:HB3	27:X:63:LYS:HE3	1.81	0.40
36:g:15:THR:HG22	36:g:16:ALA:H	1.86	0.40
48:CC:271:ASP:O	48:CC:275:LYS:HE3	2.20	0.40
52:GG:201:LYS:HE2	52:GG:201:LYS:HB3	1.96	0.40
80:11:65:C:H2'	80:11:66:C:H6	1.86	0.40
1:5:4460:U:H2'	1:5:4461:C:C6	2.56	0.40
1:5:4525:C:H2'	1:5:4526:U:H6	1.87	0.40
4:9:129:C:O2'	4:9:184:G:O6	2.33	0.40
4:9:1279:C:H2'	4:9:1280:G:C8	2.57	0.40
43:o:97:LYS:HB3	43:o:97:LYS:HE3	1.93	0.40
46:AA:173:LEU:C	46:AA:173:LEU:HD23	2.46	0.40
53:HH:69:LEU:HD22	53:HH:96:ALA:HB2	2.03	0.40
65:TT:71:GLY:O	65:TT:75:MET:HG2	2.22	0.40
69:XX:63:ASN:HD22	69:XX:114:ASP:CG	2.21	0.40
80:13:16:G:O2'	80:13:17:C:OP1	2.33	0.40
1:5:1772:C:H2'	1:5:1773:U:O4'	2.22	0.40
1:5:1882:U:C4	1:5:2279:A:C2	3.10	0.40
1:5:1957:U:O2'	1:5:1958:A:O5'	2.34	0.40
1:5:2015:U:H2'	1:5:2016:C:C6	2.56	0.40
1:5:4236:G:H2'	1:5:4237:C:C6	2.57	0.40
1:5:4525:C:H2'	1:5:4526:U:C6	2.56	0.40
1:5:4994:G:H2'	1:5:4995:U:C6	2.57	0.40
4:9:693:A:H2'	4:9:694:G:C8	2.56	0.40
4:9:1809:A:H2'	4:9:1810:U:C6	2.57	0.40
9:E:216:THR:O	9:E:219:TYR:HB3	2.20	0.40
16:M:36:ALA:HB2	16:M:52:PHE:CZ	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:103:VAL:HG12	30:a:108:TYR:HB2	2.03	0.40
54:II:23:LYS:HB3	54:II:23:LYS:HE2	1.83	0.40
65:TT:134:ILE:O	65:TT:138:VAL:HG23	2.22	0.40
80:11:12:C:H2'	80:11:13:G:H8	1.86	0.40
80:11:63:A:H2'	80:11:64:U:C6	2.57	0.40
1:5:3717:A:H2'	1:5:3718:A:H8	1.82	0.40
1:5:3823:G:H8	1:5:3823:G:O5'	2.04	0.40
1:5:3926:C:O2'	17:N:87:HIS:CE1	2.75	0.40
1:5:4896:G:H2'	1:5:4897:G:H8	1.86	0.40
2:7:92:C:H2'	2:7:93:G:H8	1.87	0.40
4:9:128:U:H3'	4:9:129:C:C6	2.56	0.40
4:9:612:U:H4'	76:ee:88:GLN:OE1	2.21	0.40
6:B:56:ILE:O	6:B:73:VAL:HA	2.22	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%)	240 (98%)	6 (2%)	0	100	100
6	B	392/403 (97%)	377 (96%)	15 (4%)	0	100	100
7	C	360/425 (85%)	352 (98%)	8 (2%)	0	100	100
8	D	291/297 (98%)	283 (97%)	8 (3%)	0	100	100
9	E	208/291 (72%)	196 (94%)	12 (6%)	0	100	100
10	G	229/319 (72%)	223 (97%)	6 (3%)	0	100	100
11	H	188/192 (98%)	184 (98%)	4 (2%)	0	100	100
12	I	201/214 (94%)	198 (98%)	3 (2%)	0	100	100
13	J	168/178 (94%)	166 (99%)	2 (1%)	0	100	100
14	K	223/247 (90%)	216 (97%)	7 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	L	208/211 (99%)	204 (98%)	4 (2%)	0	100	100
16	M	136/218 (62%)	134 (98%)	2 (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
19	P	151/184 (82%)	146 (97%)	5 (3%)	0	100	100
20	Q	185/188 (98%)	176 (95%)	9 (5%)	0	100	100
21	R	178/196 (91%)	175 (98%)	3 (2%)	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%)	95 (98%)	2 (2%)	0	100	100
25	V	127/140 (91%)	124 (98%)	3 (2%)	0	100	100
26	W	102/157 (65%)	101 (99%)	1 (1%)	0	100	100
27	X	116/156 (74%)	116 (100%)	0	0	100	100
28	Y	132/145 (91%)	129 (98%)	3 (2%)	0	100	100
29	Z	133/136 (98%)	132 (99%)	1 (1%)	0	100	100
30	a	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
31	b	94/245 (38%)	90 (96%)	4 (4%)	0	100	100
32	c	96/115 (84%)	93 (97%)	3 (3%)	0	100	100
33	d	105/125 (84%)	102 (97%)	3 (3%)	0	100	100
34	e	126/135 (93%)	123 (98%)	3 (2%)	0	100	100
35	f	107/110 (97%)	105 (98%)	2 (2%)	0	100	100
36	g	112/116 (97%)	111 (99%)	1 (1%)	0	100	100
37	h	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
38	i	100/105 (95%)	98 (98%)	2 (2%)	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%)	48 (96%)	2 (4%)	0	100	100
42	n	23/25 (92%)	23 (100%)	0	0	100	100
43	o	102/106 (96%)	98 (96%)	4 (4%)	0	100	100
44	p	89/92 (97%)	86 (97%)	3 (3%)	0	100	100
45	r	122/137 (89%)	120 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	AA	215/295 (73%)	210 (98%)	5 (2%)	0	100	100
47	BB	211/264 (80%)	207 (98%)	4 (2%)	0	100	100
48	CC	219/293 (75%)	215 (98%)	4 (2%)	0	100	100
49	DD	222/243 (91%)	218 (98%)	4 (2%)	0	100	100
50	EE	260/263 (99%)	250 (96%)	10 (4%)	0	100	100
51	FF	180/204 (88%)	171 (95%)	9 (5%)	0	100	100
52	GG	235/249 (94%)	231 (98%)	4 (2%)	0	100	100
53	HH	181/194 (93%)	177 (98%)	4 (2%)	0	100	100
54	II	194/208 (93%)	190 (98%)	4 (2%)	0	100	100
55	JJ	179/194 (92%)	176 (98%)	3 (2%)	0	100	100
56	KK	94/165 (57%)	93 (99%)	1 (1%)	0	100	100
57	LL	139/158 (88%)	135 (97%)	4 (3%)	0	100	100
58	MM	108/132 (82%)	102 (94%)	6 (6%)	0	100	100
59	NN	147/151 (97%)	144 (98%)	3 (2%)	0	100	100
60	OO	134/168 (80%)	131 (98%)	3 (2%)	0	100	100
61	PP	127/145 (88%)	121 (95%)	6 (5%)	0	100	100
62	QQ	140/146 (96%)	138 (99%)	2 (1%)	0	100	100
63	RR	130/135 (96%)	126 (97%)	4 (3%)	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%)	124 (98%)	3 (2%)	0	100	100
69	XX	138/143 (96%)	135 (98%)	3 (2%)	0	100	100
70	YY	122/130 (94%)	119 (98%)	3 (2%)	0	100	100
71	ZZ	73/125 (58%)	71 (97%)	2 (3%)	0	100	100
72	aa	99/115 (86%)	96 (97%)	3 (3%)	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%)	51 (96%)	2 (4%)	0	100	100
76	ee	53/133 (40%)	52 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
77	ff	66/156 (42%)	61 (92%)	5 (8%)	0	100	100
78	gg	311/317 (98%)	296 (95%)	15 (5%)	0	100	100
81	j	84/97 (87%)	80 (95%)	4 (5%)	0	100	100
All	All	11148/12891 (86%)	10852 (97%)	296 (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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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%)	83 (99%)	1 (1%)	63	86
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%)	97 (99%)	1 (1%)	68	89
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%)	224 (100%)	0	100	100
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
60	OO	106/130 (82%)	105 (99%)	1 (1%)	70	90
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%)	9735 (100%)	3 (0%)	100	100

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	c	92	CYS
36	g	73	HIS

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Mol	Chain	Res	Type
60	OO	46	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (111) such sidechains are listed below:

Mol	Chain	Res	Type
5	A	22	HIS
6	B	55	HIS
6	B	109	HIS
6	B	167	GLN
6	B	184	GLN
6	B	204	GLN
6	B	236	HIS
6	B	376	HIS
7	C	198	ASN
7	C	212	ASN
9	E	170	GLN
9	E	253	GLN
10	G	134	ASN
10	G	135	GLN
10	G	153	HIS
10	G	194	ASN
10	G	278	ASN
11	H	42	ASN
12	I	59	GLN
12	I	73	ASN
12	I	100	ASN
12	I	144	ASN
13	J	71	HIS
13	J	104	ASN
14	K	57	HIS
14	K	62	GLN
14	K	79	ASN
14	K	199	HIS
16	M	20	HIS
16	M	70	GLN
17	N	8	GLN
17	N	37	HIS
17	N	87	HIS
17	N	145	ASN
17	N	182	HIS
18	O	50	ASN
18	O	150	GLN

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Mol	Chain	Res	Type
18	O	167	HIS
19	P	25	HIS
19	P	56	GLN
20	Q	7	HIS
20	Q	57	ASN
21	R	40	GLN
21	R	141	HIS
23	T	3	ASN
25	V	27	ASN
25	V	77	HIS
26	W	17	HIS
26	W	104	GLN
27	X	93	ASN
28	Y	20	ASN
28	Y	56	GLN
30	a	28	HIS
30	a	39	HIS
31	b	27	GLN
33	d	121	ASN
34	e	126	ASN
35	f	20	ASN
36	g	110	GLN
37	h	98	HIS
38	i	80	HIS
40	l	4	HIS
41	m	61	GLN
45	r	70	GLN
45	r	103	HIS
48	CC	272	HIS
49	DD	57	ASN
49	DD	159	HIS
50	EE	201	HIS
50	EE	260	GLN
51	FF	31	ASN
51	FF	82	ASN
51	FF	83	ASN
51	FF	137	GLN
52	GG	59	GLN
52	GG	186	GLN
53	HH	44	ASN
53	HH	73	GLN
53	HH	76	GLN

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Mol	Chain	Res	Type
53	HH	114	GLN
53	HH	186	ASN
54	II	88	ASN
54	II	146	GLN
54	II	181	GLN
55	JJ	124	HIS
56	KK	66	HIS
56	KK	84	HIS
57	LL	18	GLN
57	LL	94	HIS
57	LL	106	HIS
58	MM	19	GLN
59	NN	58	HIS
59	NN	105	ASN
59	NN	123	HIS
60	OO	26	ASN
61	PP	54	HIS
64	SS	135	HIS
65	TT	12	GLN
66	UU	92	HIS
67	VV	35	ASN
69	XX	16	HIS
69	XX	46	HIS
69	XX	77	ASN
70	YY	63	HIS
75	dd	4	GLN
77	ff	111	ASN
78	gg	51	ASN
78	gg	117	ASN
78	gg	119	GLN
81	j	57	ASN
81	j	76	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3582/3601 (99%)	550 (15%)	180 (5%)
2	7	118/120 (98%)	7 (5%)	1 (0%)
3	8	149/156 (95%)	21 (14%)	5 (3%)
4	9	1685/1869 (90%)	228 (13%)	64 (3%)
79	10	10/185 (5%)	3 (30%)	1 (10%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
80	11	73/75 (97%)	10 (13%)	4 (5%)
80	13	73/75 (97%)	7 (9%)	3 (4%)
All	All	5690/6081 (93%)	826 (14%)	258 (4%)

All (826) 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	73	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	136	C
1	5	143	C
1	5	144	G
1	5	159	C
1	5	160	G
1	5	171	U
1	5	172	C
1	5	173	C
1	5	197	A
1	5	200	U
1	5	209	U
1	5	217	C
1	5	218	A
1	5	219	G
1	5	220	C
1	5	224	U
1	5	225	G
1	5	226	G

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Mol	Chain	Res	Type
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
1	5	280	G
1	5	297	U
1	5	309	C
1	5	315	G
1	5	316	U
1	5	334	A
1	5	340	C
1	5	386	A
1	5	387	G
1	5	408	A
1	5	409	G
1	5	412	G
1	5	413	G
1	5	431	G
1	5	432	U
1	5	433	A
1	5	449	C
1	5	450	G
1	5	453	G
1	5	454	U
1	5	464	G
1	5	468	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	493	G
1	5	497	G
1	5	498	C

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Mol	Chain	Res	Type
1	5	499	G
1	5	505	G
1	5	649	A
1	5	650	C
1	5	666	G
1	5	683	C
1	5	685	C
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	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	926	G
1	5	929	A
1	5	931	C
1	5	932	A
1	5	934	C
1	5	935	A
1	5	935(A)	G
1	5	936	C
1	5	937	U
1	5	943	A
1	5	944	A
1	5	945	U
1	5	959	G
1	5	960	A
1	5	961	G
1	5	967	C

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Mol	Chain	Res	Type
1	5	969	C
1	5	972	C
1	5	983	C
1	5	1065	G
1	5	1070	G
1	5	1072	C
1	5	1073	G
1	5	1076	C
1	5	1079	C
1	5	1195	G
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	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	1302	U
1	5	1304	C
1	5	1324	A
1	5	1325	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

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Mol	Chain	Res	Type
1	5	1370	G
1	5	1371	A
1	5	1377	G
1	5	1380	G
1	5	1381	U
1	5	1387	A
1	5	1388	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	1455	G
1	5	1456	C
1	5	1458	C
1	5	1477	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	1547	A
1	5	1566	C
1	5	1578	U
1	5	1591	U
1	5	1596	U
1	5	1612	G
1	5	1613	A
1	5	1614	C
1	5	1624	G
1	5	1625	G
1	5	1626	G
1	5	1631	A

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Mol	Chain	Res	Type
1	5	1633	G
1	5	1634	A
1	5	1641	G
1	5	1654	G
1	5	1661	C
1	5	1676	C
1	5	1677	U
1	5	1691	G
1	5	1724	G
1	5	1733	G
1	5	1734	G
1	5	1742	A
1	5	1750	G
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	1805	A
1	5	1819	G
1	5	1821	G
1	5	1822	U
1	5	1834	U
1	5	1835	G
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	1920	C
1	5	1921	C
1	5	1922	G
1	5	1930	U
1	5	1940	G
1	5	1948	G
1	5	1958	A

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Mol	Chain	Res	Type
1	5	1959	U
1	5	1962	A
1	5	1964	A
1	5	1971	U
1	5	1978	C
1	5	1980	U
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	2008	U
1	5	2011	C
1	5	2023	C
1	5	2024	G
1	5	2026	A
1	5	2044	U
1	5	2046	G
1	5	2048	U
1	5	2052	G
1	5	2055	G
1	5	2056	G
1	5	2068	C
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	2102	G
1	5	2104	A
1	5	2105	A
1	5	2106	G
1	5	2107	A

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Mol	Chain	Res	Type
1	5	2108	G
1	5	2259	G
1	5	2260	C
1	5	2266	C
1	5	2267	U
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	2421	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	2493	G
1	5	2503	G
1	5	2504	C
1	5	2505	C
1	5	2506	G
1	5	2513	A
1	5	2544	G
1	5	2545	U
1	5	2546	G
1	5	2547	G
1	5	2553	A
1	5	2554	U
1	5	2555	G

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Mol	Chain	Res	Type
1	5	2583	C
1	5	2587	A
1	5	2601	A
1	5	2627	C
1	5	2669	C
1	5	2686	G
1	5	2687	U
1	5	2695	A
1	5	2696	A
1	5	2705	G
1	5	2708	U
1	5	2709	C
1	5	2710	C
1	5	2711	G
1	5	2712	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	2763	U
1	5	2764	A
1	5	2772	C
1	5	2787	A
1	5	2788	U
1	5	2789	A
1	5	2790	U
1	5	2794	C
1	5	2795	A
1	5	2826	U
1	5	2827	G
1	5	2855	G
1	5	3598	C
1	5	3604	A
1	5	3605	C
1	5	3606	U
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	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	3750	G
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	3960	A
1	5	3963	A
1	5	3964	U
1	5	3966	A
1	5	3967	G

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Mol	Chain	Res	Type
1	5	3969	G
1	5	3972	A
1	5	3973	G
1	5	4041	C
1	5	4042	G
1	5	4047	A
1	5	4048	A
1	5	4049	U
1	5	4069	U
1	5	4070	U
1	5	4076	G
1	5	4084	G
1	5	4119	C
1	5	4120	U
1	5	4122	G
1	5	4127	A
1	5	4147	G
1	5	4157	A
1	5	4163	U
1	5	4170	A
1	5	4171	C
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	4266	G
1	5	4267	G
1	5	4268	A
1	5	4271	A
1	5	4273	A
1	5	4281	A
1	5	4282	A
1	5	4291	G
1	5	4292	A
1	5	4305	G
1	5	4306	U
1	5	4330	G
1	5	4339	A

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Mol	Chain	Res	Type
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	4387	C
1	5	4394	A
1	5	4395	U
1	5	4396	A
1	5	4422	A
1	5	4438	U
1	5	4448	G
1	5	4449	A
1	5	4464	A
1	5	4475	G
1	5	4476	C
1	5	4488	A
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	4567	G
1	5	4572	U
1	5	4573	G
1	5	4590	A
1	5	4627	U
1	5	4635	A
1	5	4636	U
1	5	4637	G
1	5	4656	A
1	5	4670	C
1	5	4672	A
1	5	4677	U
1	5	4700	A
1	5	4708	A
1	5	4709	U
1	5	4719	G

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Mol	Chain	Res	Type
1	5	4720	C
1	5	4721	G
1	5	4736	C
1	5	4737	G
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	4765	G
1	5	4771	C
1	5	4870	G
1	5	4871	C
1	5	4875	G
1	5	4876	A
1	5	4877	G
1	5	4882	U
1	5	4883	C
1	5	4885	U
1	5	4902	C
1	5	4909	A
1	5	4910	A
1	5	4913	G
1	5	4914	G
1	5	4915	G
1	5	4926	C
1	5	4931	G
1	5	4937	C
1	5	4943	A
1	5	4944	C
1	5	4948	C
1	5	4949	G
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

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Mol	Chain	Res	Type
1	5	4991	U
1	5	5013	C
1	5	5014	A
1	5	5017	G
1	5	5041	G
1	5	5047	C
1	5	5048	A
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	3	A
3	8	34	U
3	8	59	A
3	8	62	A
3	8	63	U
3	8	87	G
3	8	94	G
3	8	95	A
3	8	104	A
3	8	105	C
3	8	110	U
3	8	111	U
3	8	112	G
3	8	123	U
3	8	124	U
3	8	125	C
3	8	126	C
3	8	127	U
3	8	128	C
3	8	137	A
4	9	4	C
4	9	17	C
4	9	25	A

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Mol	Chain	Res	Type
4	9	33	G
4	9	41	G
4	9	46	A
4	9	56	G
4	9	67	C
4	9	68	A
4	9	73	C
4	9	74	G
4	9	75	G
4	9	79	A
4	9	103	A
4	9	111	A
4	9	113	G
4	9	115	U
4	9	126	G
4	9	127	C
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	294	U
4	9	308	G
4	9	309	G
4	9	312	G
4	9	318	A
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	383	G
4	9	385	G
4	9	386	C
4	9	400	C
4	9	408	A
4	9	409	C

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Mol	Chain	Res	Type
4	9	418	A
4	9	448	A
4	9	449	A
4	9	450	C
4	9	452	G
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	502	C
4	9	516	A
4	9	517	C
4	9	531	A
4	9	532	C
4	9	533	A
4	9	541	U
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	561	A
4	9	562	U
4	9	564	A
4	9	569	A
4	9	587	A
4	9	588	G
4	9	590	A
4	9	591	U
4	9	606	G
4	9	608	C
4	9	614	C
4	9	620	G
4	9	621	C
4	9	628	A
4	9	643	A

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Mol	Chain	Res	Type
4	9	644	G
4	9	655	A
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	869	A
4	9	870	A
4	9	872	A
4	9	873	G
4	9	874	G
4	9	875	A
4	9	876	C
4	9	887	U
4	9	888	U
4	9	889	U
4	9	891	G
4	9	912	C
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	1017	U
4	9	1023	A

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Mol	Chain	Res	Type
4	9	1062	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	1138	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	1224	G
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	1293	A
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	1406	G
4	9	1454	A
4	9	1455	A
4	9	1462	U

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Mol	Chain	Res	Type
4	9	1463	U
4	9	1476	A
4	9	1477	U
4	9	1490	G
4	9	1497	G
4	9	1498	A
4	9	1520	G
4	9	1521	C
4	9	1522	A
4	9	1533	A
4	9	1548	G
4	9	1553	C
4	9	1554	C
4	9	1556	A
4	9	1557	C
4	9	1558	C
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
4	9	1639	G
4	9	1648	G
4	9	1654	G
4	9	1665	G
4	9	1671	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

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Mol	Chain	Res	Type
4	9	1823	A
4	9	1824	A
4	9	1829	G
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	1851	A
4	9	1852	C
4	9	1861	G
4	9	1863	A
4	9	1865	C
4	9	1869	A
79	10	19	U
79	10	20	U
79	10	23	A
80	13	17	C
80	13	18	G
80	13	20	A
80	13	22	G
80	13	48	C
80	13	75	C
80	13	76	A
80	11	10	G
80	11	17	C
80	11	18	G
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 (258) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	42	A
1	5	64	A
1	5	65	A

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Mol	Chain	Res	Type
1	5	125	C
1	5	134	G
1	5	172	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	432	U
1	5	449	C
1	5	466	A
1	5	480	C
1	5	481(A)	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	696	C
1	5	747	A
1	5	749	G
1	5	913	U
1	5	915	A
1	5	916	C
1	5	924	C
1	5	930	G
1	5	933	G
1	5	935(A)	G
1	5	936	C
1	5	955	G
1	5	959	G
1	5	960	A
1	5	966	A

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Mol	Chain	Res	Type
1	5	971(A)	G
1	5	1064	G
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	1271	G
1	5	1283	G
1	5	1292	C
1	5	1301	C
1	5	1324	A
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	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
1	5	1590	C
1	5	1613	A
1	5	1625	G
1	5	1633	G
1	5	1678	C
1	5	1733	G
1	5	1804	A
1	5	1818	G
1	5	1834	U
1	5	1835	G
1	5	1898	C
1	5	1921	C
1	5	1929	A

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Mol	Chain	Res	Type
1	5	1958	A
1	5	1992	U
1	5	2001	G
1	5	2010	A
1	5	2023	C
1	5	2068	C
1	5	2088	A
1	5	2089	G
1	5	2093	G
1	5	2106	G
1	5	2265	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	2467	U
1	5	2474	G
1	5	2490	U
1	5	2502	A
1	5	2505	C
1	5	2506	G
1	5	2529	A
1	5	2544	G
1	5	2546	G
1	5	2553	A
1	5	2587	A
1	5	2696	A
1	5	2709	C
1	5	2724	G
1	5	2794	C
1	5	3603	G
1	5	3625	G
1	5	3672	G
1	5	3673	C
1	5	3710	G
1	5	3810	C
1	5	3876	A
1	5	3878	C

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Mol	Chain	Res	Type
1	5	3888	G
1	5	3904	G
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	4069	U
1	5	4075	U
1	5	4076	G
1	5	4118	U
1	5	4119	C
1	5	4121	G
1	5	4146	G
1	5	4170	A
1	5	4232	U
1	5	4254	G
1	5	4266	G
1	5	4281	A
1	5	4291	G
1	5	4305	G
1	5	4373	G
1	5	4395	U
1	5	4448	G
1	5	4464	A
1	5	4475	G
1	5	4527	G
1	5	4548	A
1	5	4572	U
1	5	4626	A
1	5	4635	A
1	5	4656	A
1	5	4699	U
1	5	4870	G
1	5	4876	A
1	5	4884	G
1	5	4904	G
1	5	4909	A
1	5	4920	C
1	5	4925	U

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Mol	Chain	Res	Type
1	5	4936	G
1	5	4942	C
1	5	4947	U
1	5	4949	G
1	5	4965	U
1	5	4990	C
1	5	5013	C
1	5	5047	C
1	5	5061	A
2	7	109	U
3	8	2	G
3	8	62	A
3	8	94	G
3	8	110	U
3	8	124	U
4	9	24	C
4	9	72	C
4	9	110	U
4	9	126	G
4	9	143	U
4	9	160	U
4	9	182	C
4	9	318	A
4	9	398	A
4	9	400	C
4	9	448	A
4	9	465	A
4	9	516	A
4	9	532	C
4	9	550	C
4	9	553	U
4	9	555	A
4	9	561	A
4	9	587	A
4	9	591	U
4	9	606	G
4	9	620	G
4	9	631	U
4	9	752	G
4	9	821	G
4	9	858	A
4	9	867	G

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Mol	Chain	Res	Type
4	9	869	A
4	9	872	A
4	9	874	G
4	9	875	A
4	9	912	C
4	9	919	A
4	9	1016	U
4	9	1061	U
4	9	1115	U
4	9	1117	C
4	9	1137	U
4	9	1153	C
4	9	1215	C
4	9	1253	A
4	9	1284	A
4	9	1302	G
4	9	1308	U
4	9	1395	C
4	9	1396	A
4	9	1454	A
4	9	1476	A
4	9	1489	A
4	9	1497	G
4	9	1519	U
4	9	1520	G
4	9	1553	C
4	9	1556	A
4	9	1580	A
4	9	1636	G
4	9	1637	A
4	9	1638	G
4	9	1664	A
4	9	1679	A
4	9	1757	G
4	9	1835	A
4	9	1837	G
4	9	1868	U
79	10	22	U
80	13	16	G
80	13	19	G
80	13	74	C
80	11	10	G

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Mol	Chain	Res	Type
80	11	16	G
80	11	19	G
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	$\# Z > 2$
82	SPD	5	8701	-	9,9,9	0.33	0	8,8,8	0.46	0
84	ATP	13	101	80	32,33,33	0.36	0	48,52,52	0.49	0
84	ATP	11	101	80	32,33,33	0.38	0	48,52,52	0.48	0
85	MET	13	102	80	6,7,8	0.46	0	2,7,9	0.21	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
82	SPD	5	8701	-	-	0/7/7/7	-
84	ATP	13	101	80	-	1/22/38/38	0/3/3/3
84	ATP	11	101	80	-	0/22/38/38	0/3/3/3
85	MET	13	102	80	-	0/5/6/8	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

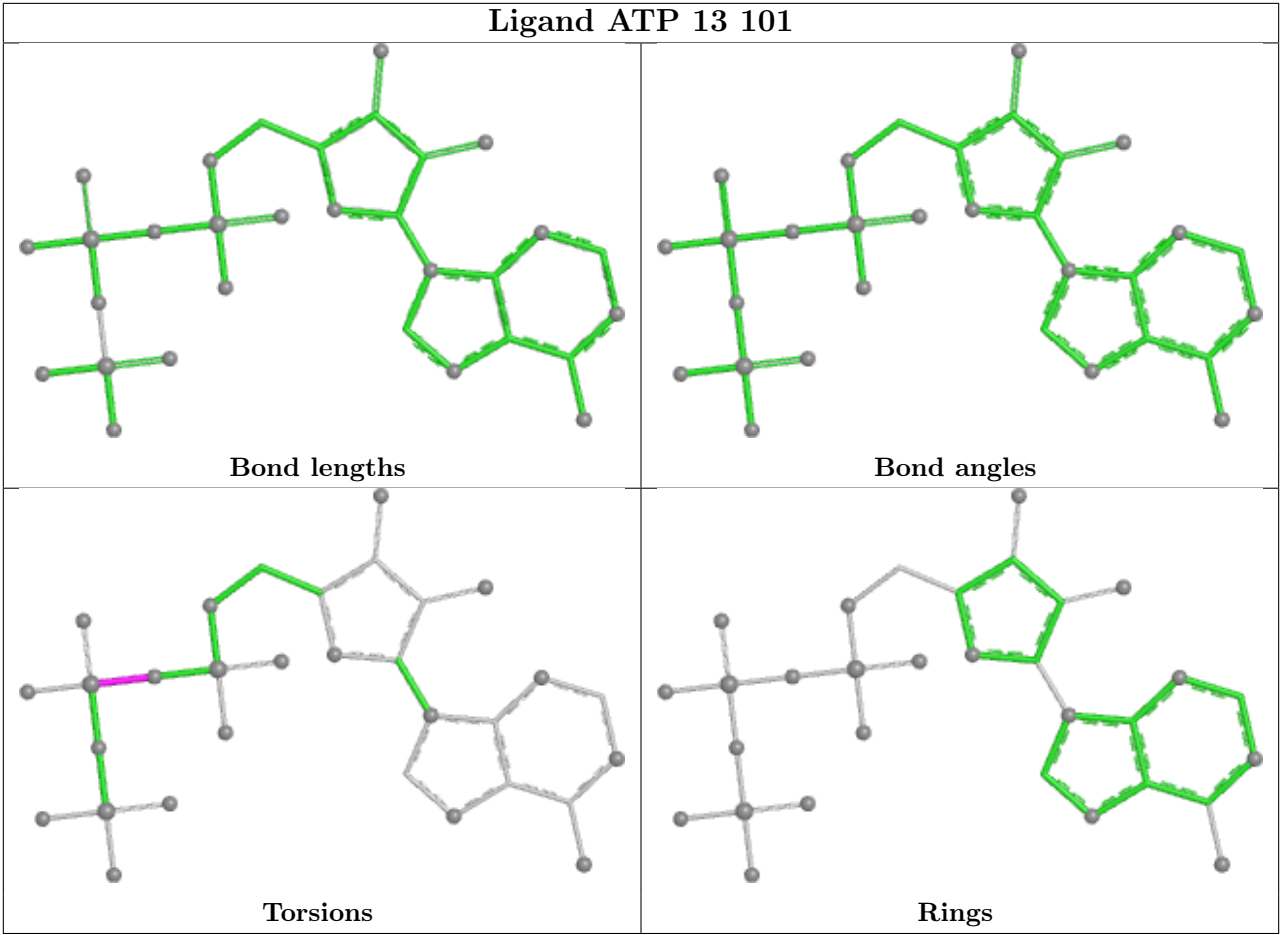
Mol	Chain	Res	Type	Atoms
84	13	101	ATP	PA-O3A-PB-O2B

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
82	5	8701	SPD	1	0
84	13	101	ATP	3	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	41.75
1	5	1252:C	O3'	1271:G	P	35.76
1	5	1219:G	O3'	1233:G	P	21.95
1	5	3976:C	O3'	4035:G	P	18.65
1	5	1406(C):G	O3'	1411:C	P	17.74

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	4777:C	O3'	4859:C	P	17.51
1	5	523:C	O3'	638:G	P	17.17
1	5	4101:C	O3'	4107:G	P	17.05
1	5	4138:C	O3'	4146:G	P	16.93
1	5	990:C	O3'	1064:G	P	16.15
1	5	1696:C	O3'	1720:C	P	15.21
1	5	5022:U	O3'	5028:G	P	14.55
1	5	1364:U	O3'	1368:A	P	14.26
1	5	760:G	O3'	904:C	P	14.12
1	5	2901:G	O3'	3597:G	P	12.51
1	5	182:G	O3'	189:G	P	11.57
1	5	1180:C	O3'	1183:C	P	10.05
1	5	4729:A	O3'	4735:G	P	9.78
1	5	512:U	O3'	515:C	P	7.65
1	5	4740:G	O3'	4743:G	P	5.89
1	5	1100:U	O3'	1168:G	P	4.81
1	5	500:G	O3'	504:G	P	4.80
1	5	4899:G	O3'	4902:C	P	3.12

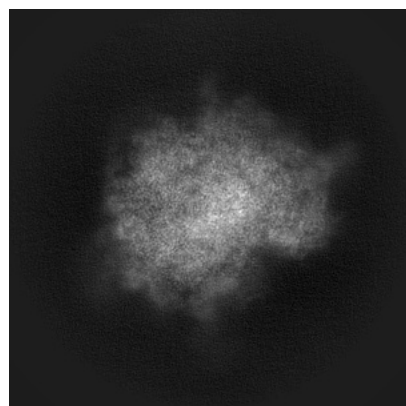
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-73315. These allow visual inspection of the internal detail of the map and identification of artifacts.

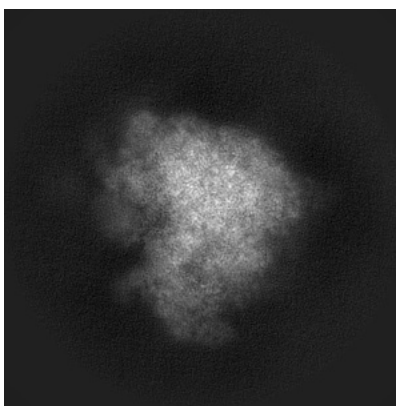
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

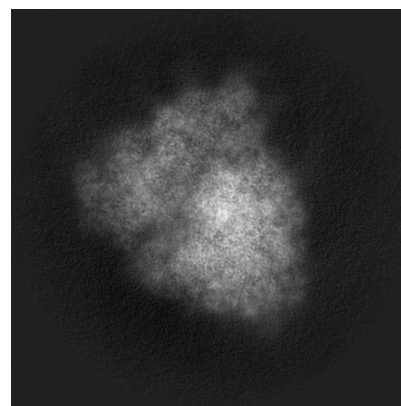
6.1.1 Primary map



X

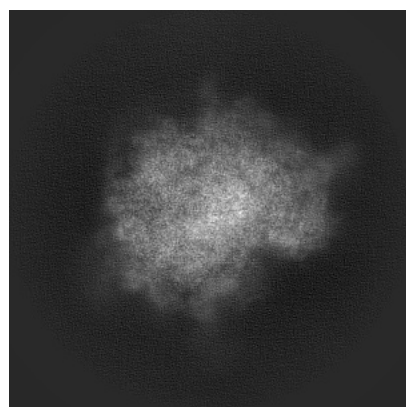


Y

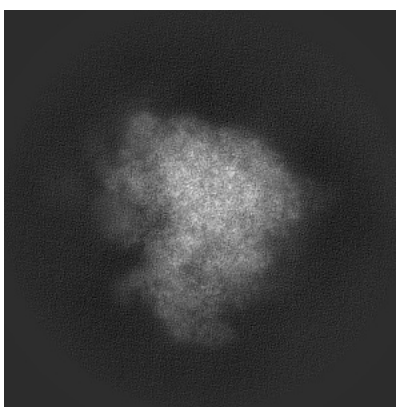


Z

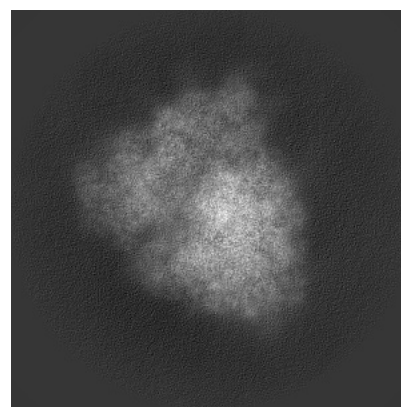
6.1.2 Raw map



X



Y

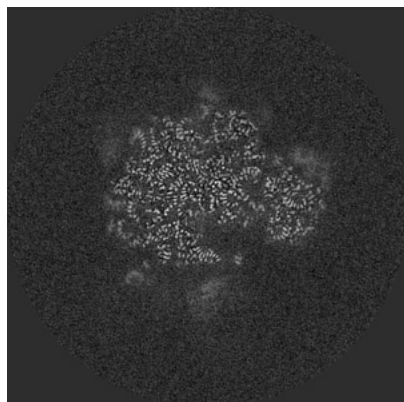


Z

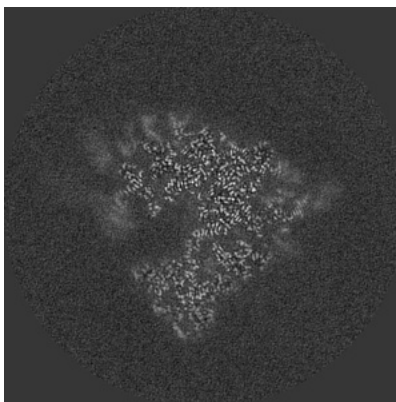
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

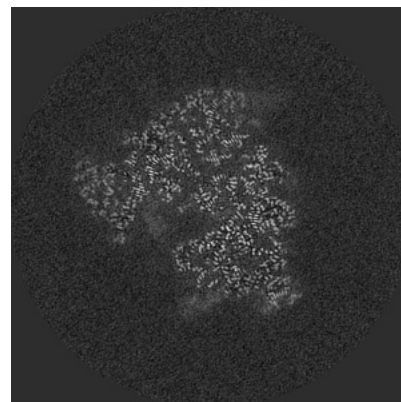
6.2.1 Primary map



X Index: 200

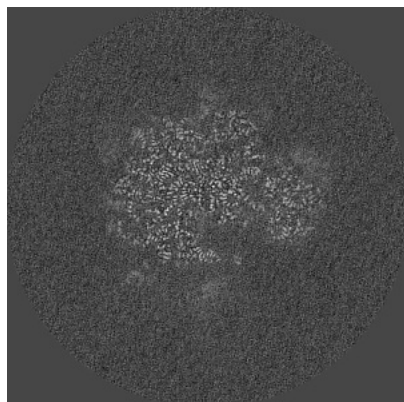


Y Index: 200

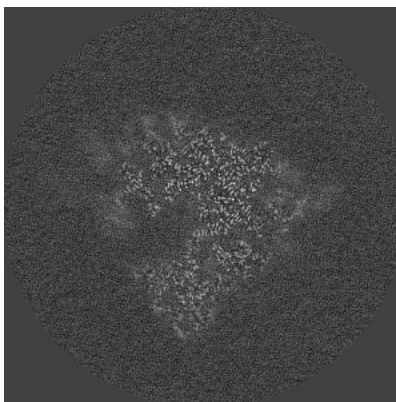


Z Index: 200

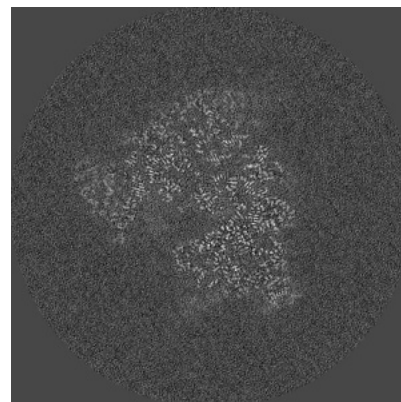
6.2.2 Raw map



X Index: 200



Y Index: 200

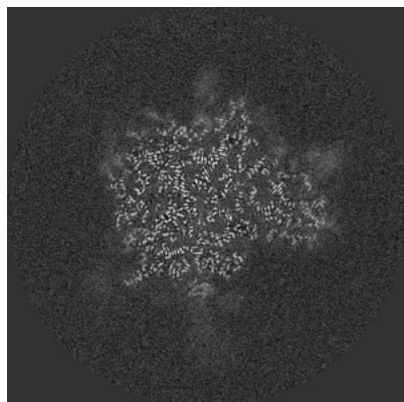


Z Index: 200

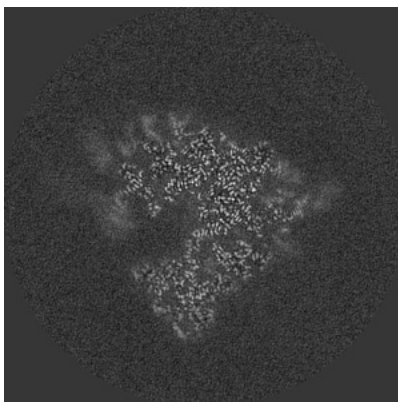
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

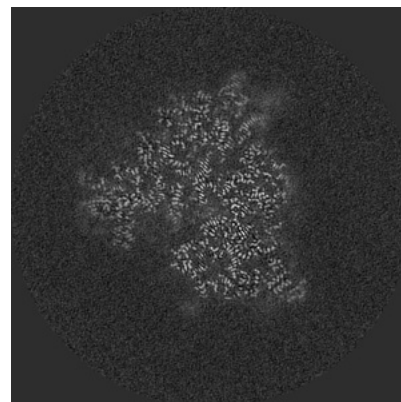
6.3.1 Primary map



X Index: 214

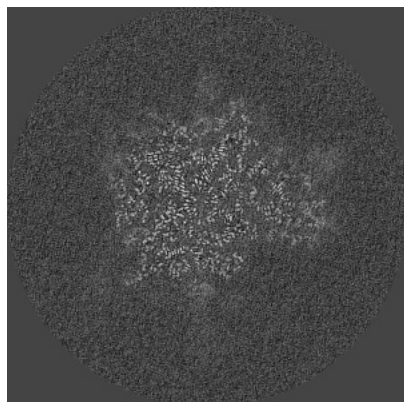


Y Index: 200

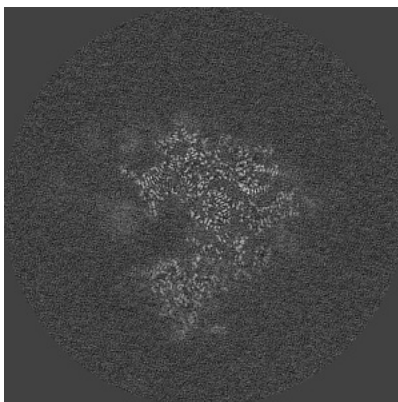


Z Index: 192

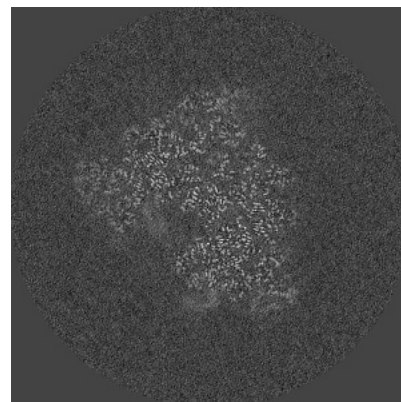
6.3.2 Raw map



X Index: 214



Y Index: 209

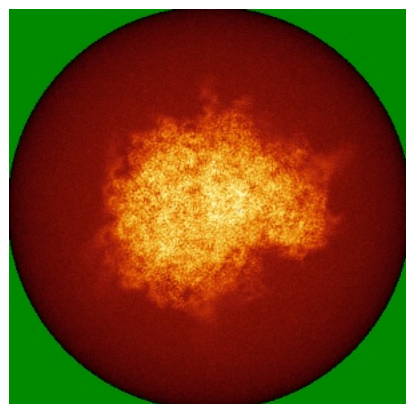


Z Index: 204

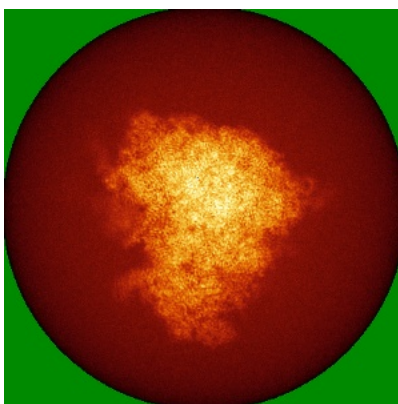
The images above show the largest variance slices of the map in three orthogonal directions.

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

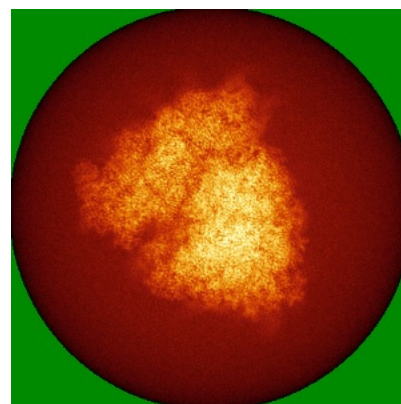
6.4.1 Primary map



X

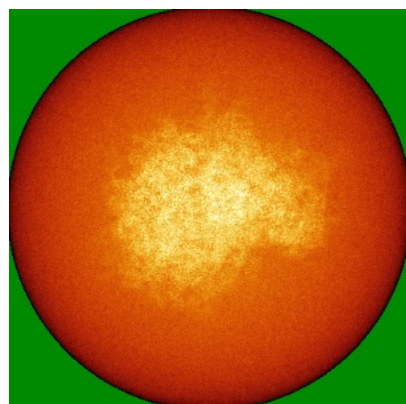


Y

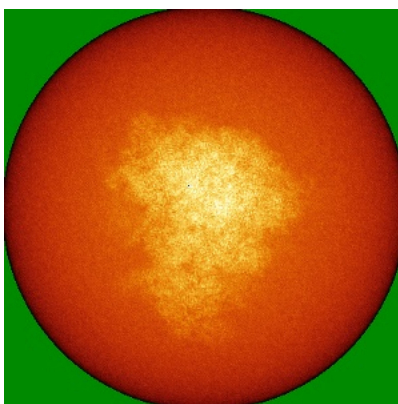


Z

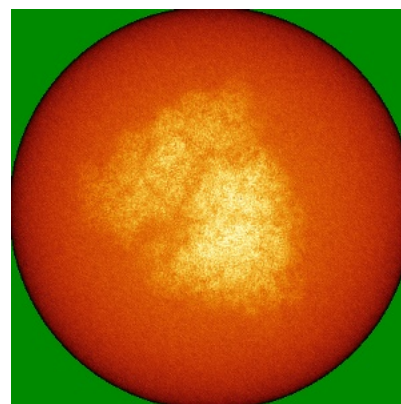
6.4.2 Raw map



X



Y

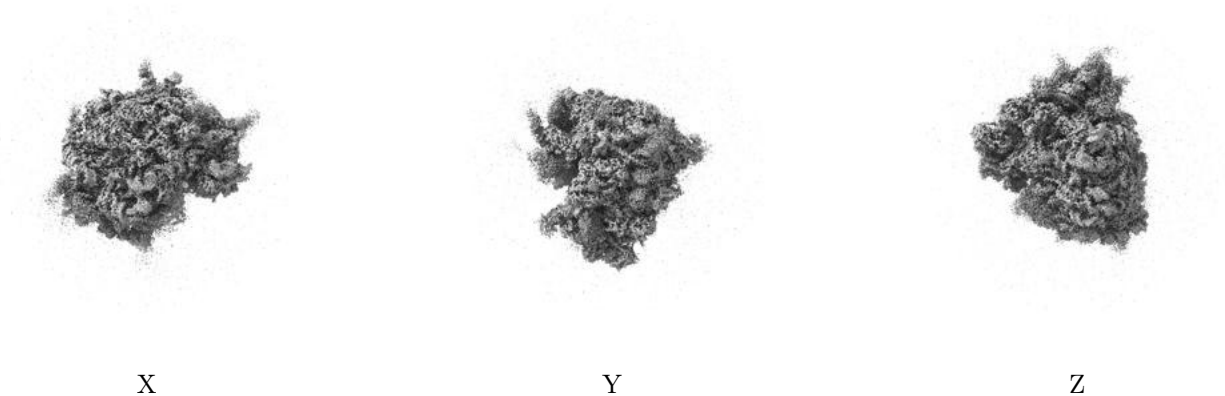


Z

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

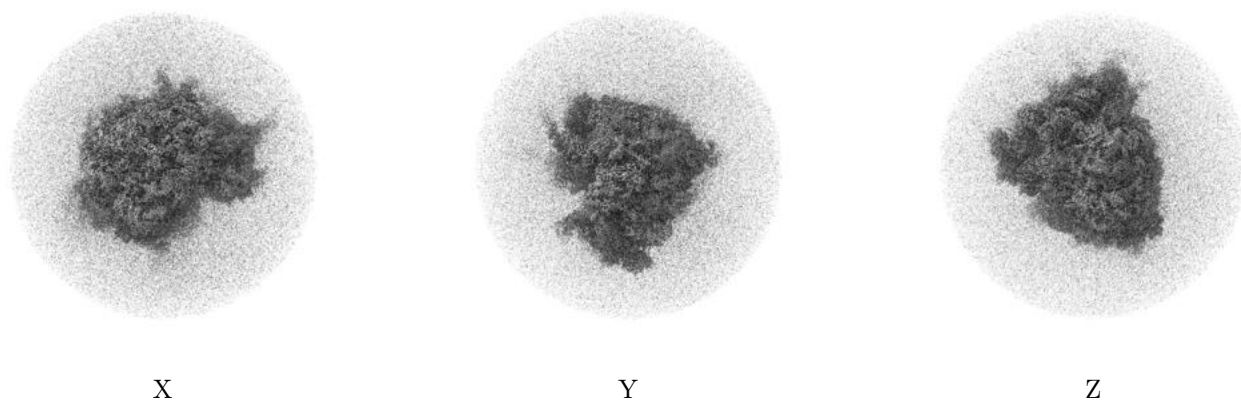
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.015. 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



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.

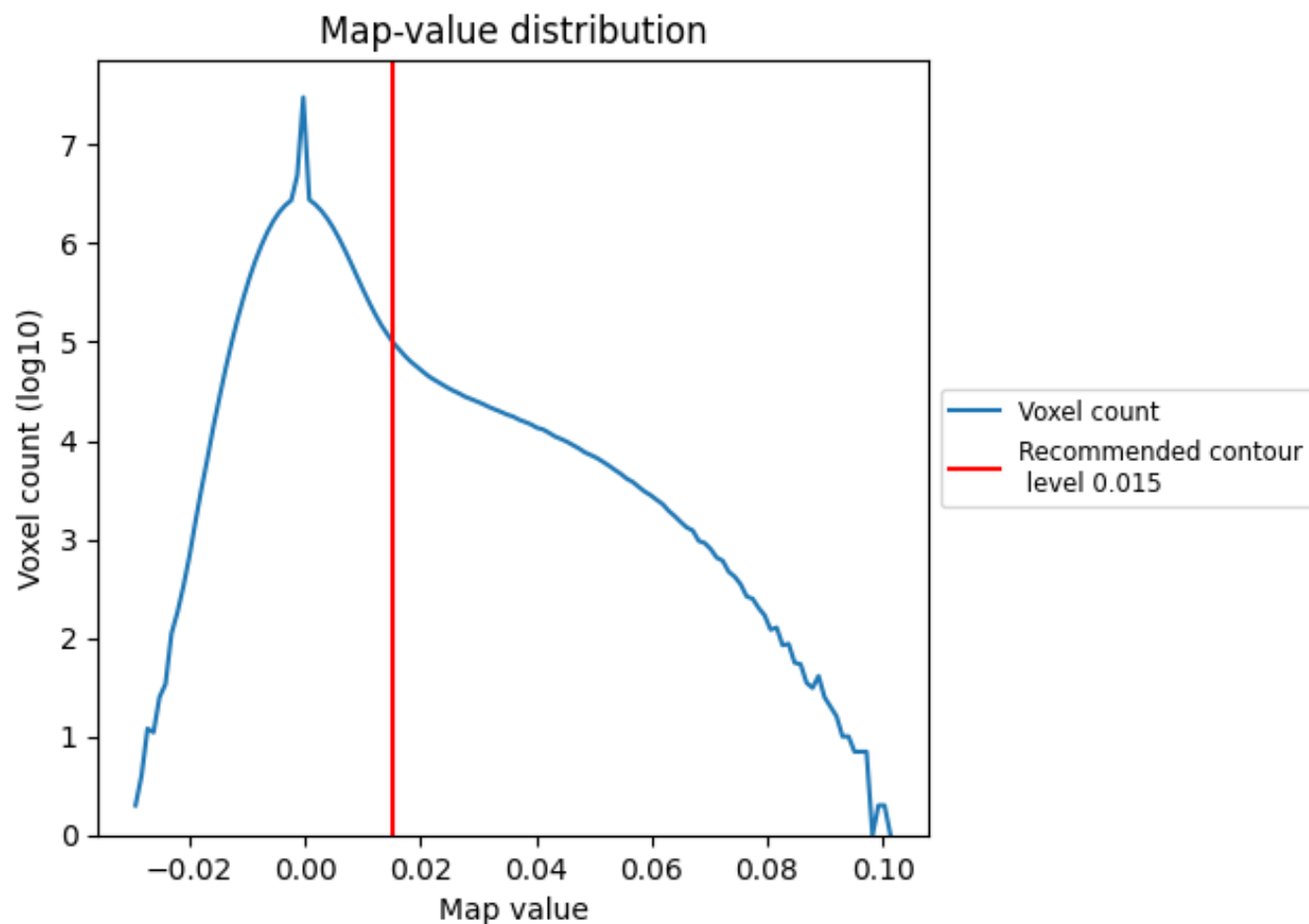
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

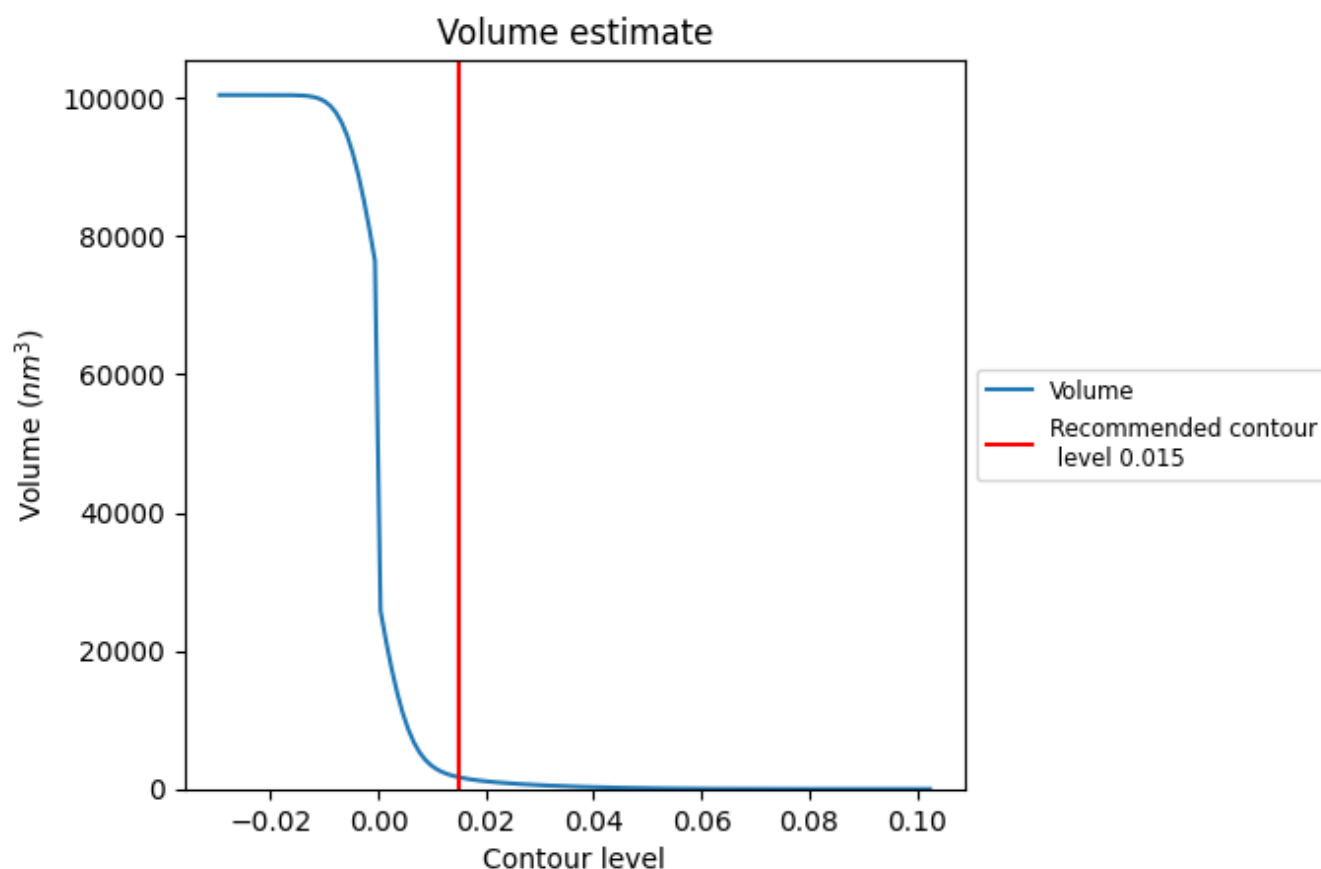
This section contains the results of statistical analysis of the map.

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.

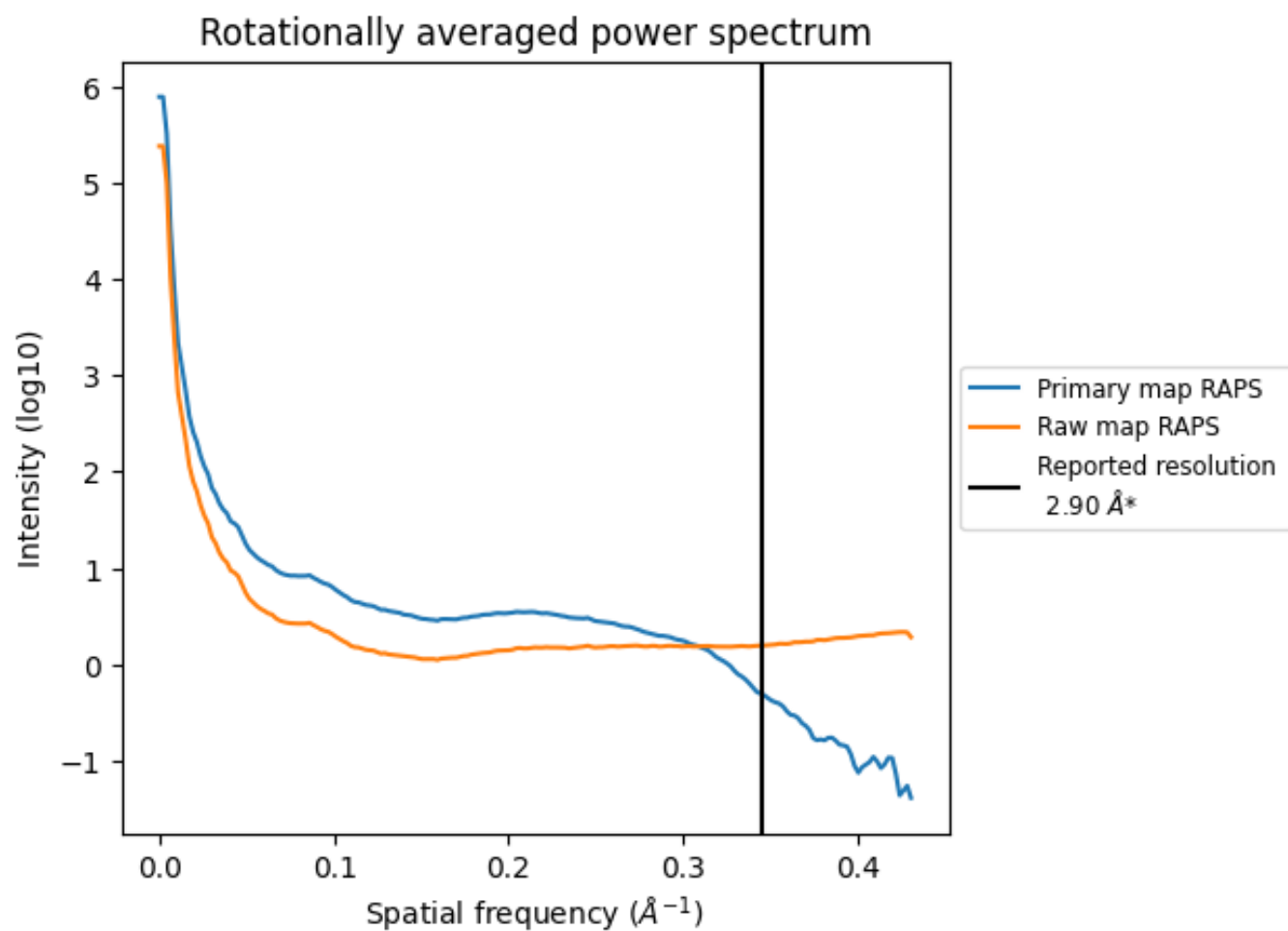
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1698 nm^3 ; this corresponds to an approximate mass of 1534 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 ⓘ

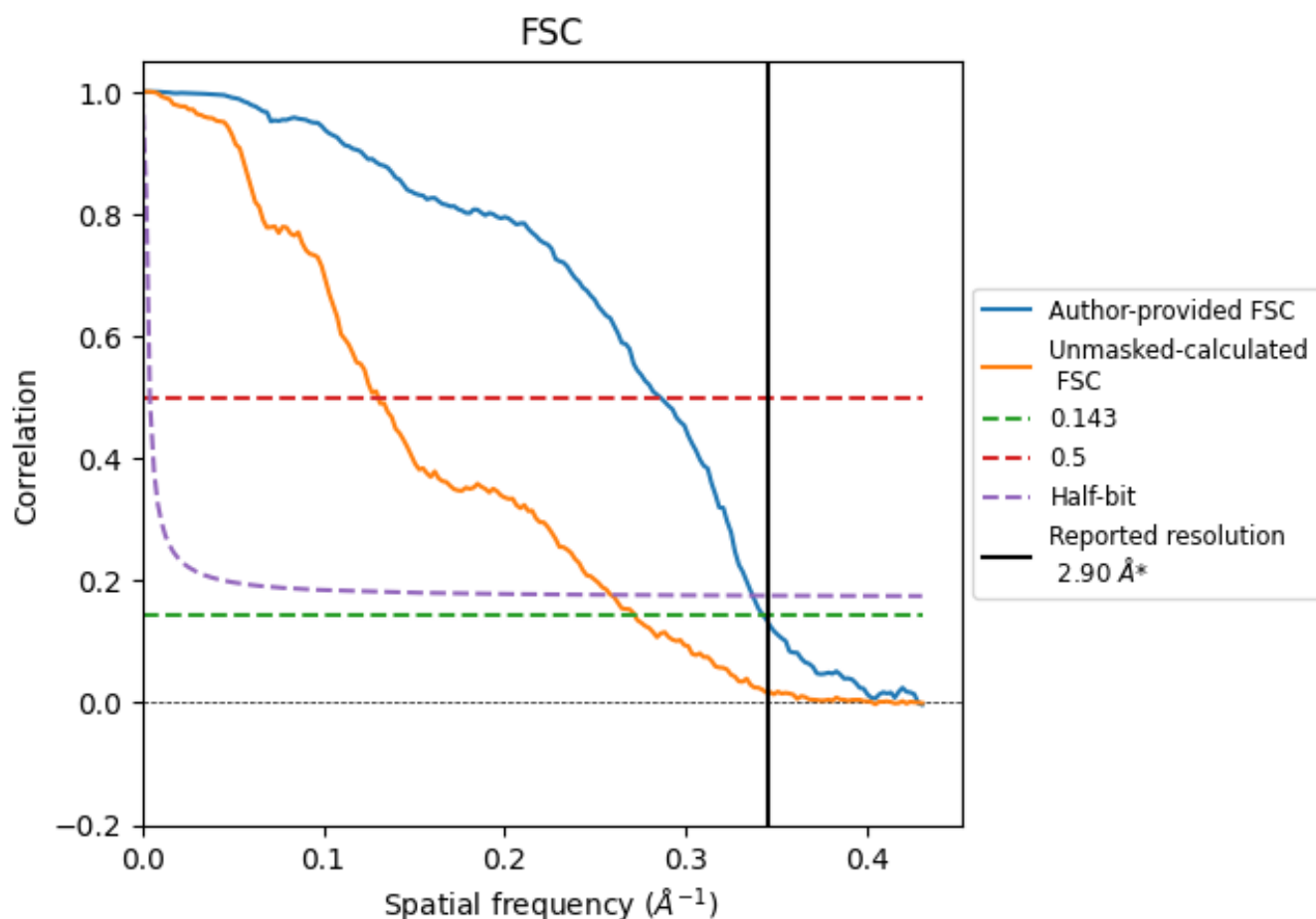


*Reported resolution corresponds to spatial frequency of 0.345 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

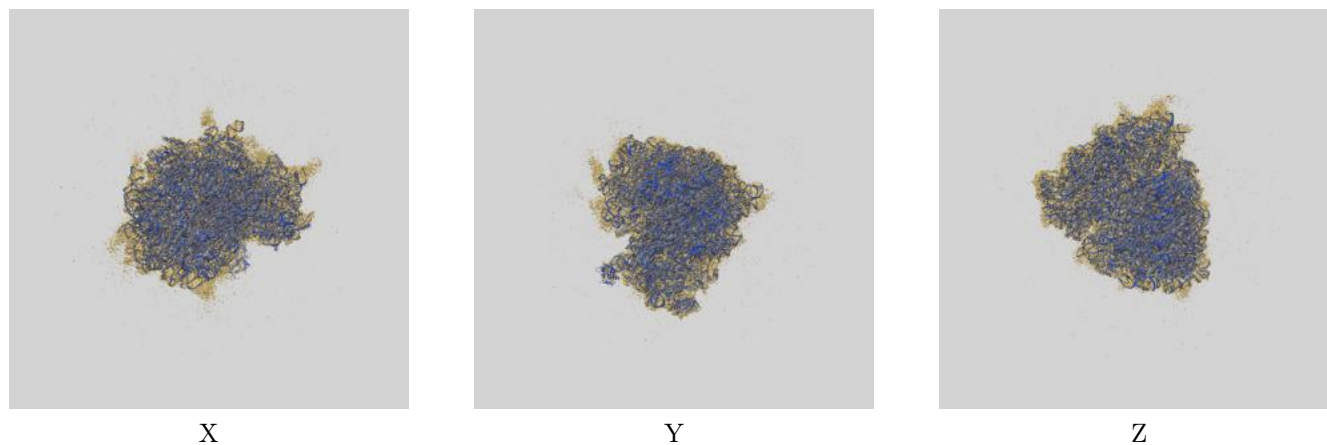
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.92	3.50	2.97
Unmasked-calculated*	3.68	7.69	3.87

*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 3.68 differs from the reported value 2.9 by more than 10 %

9 Map-model fit [i](#)

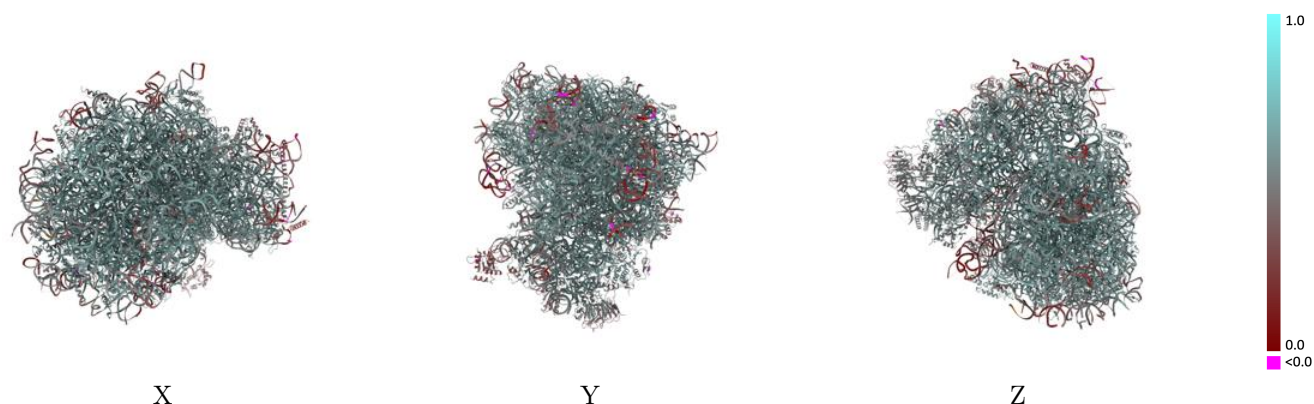
This section contains information regarding the fit between EMDB map EMD-73315 and PDB model 9YPZ. Per-residue inclusion information can be found in [section 3](#) on [page 27](#).

9.1 Map-model overlay [i](#)



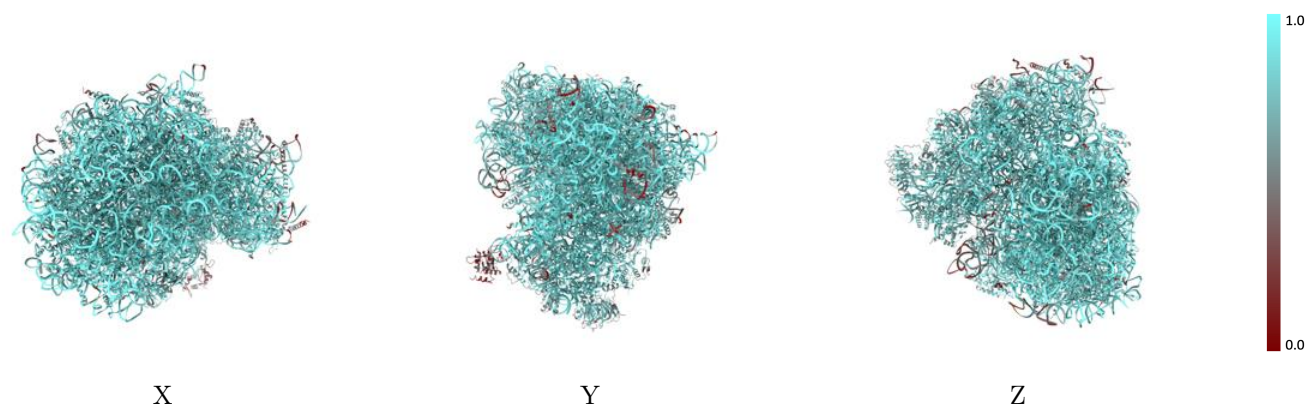
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



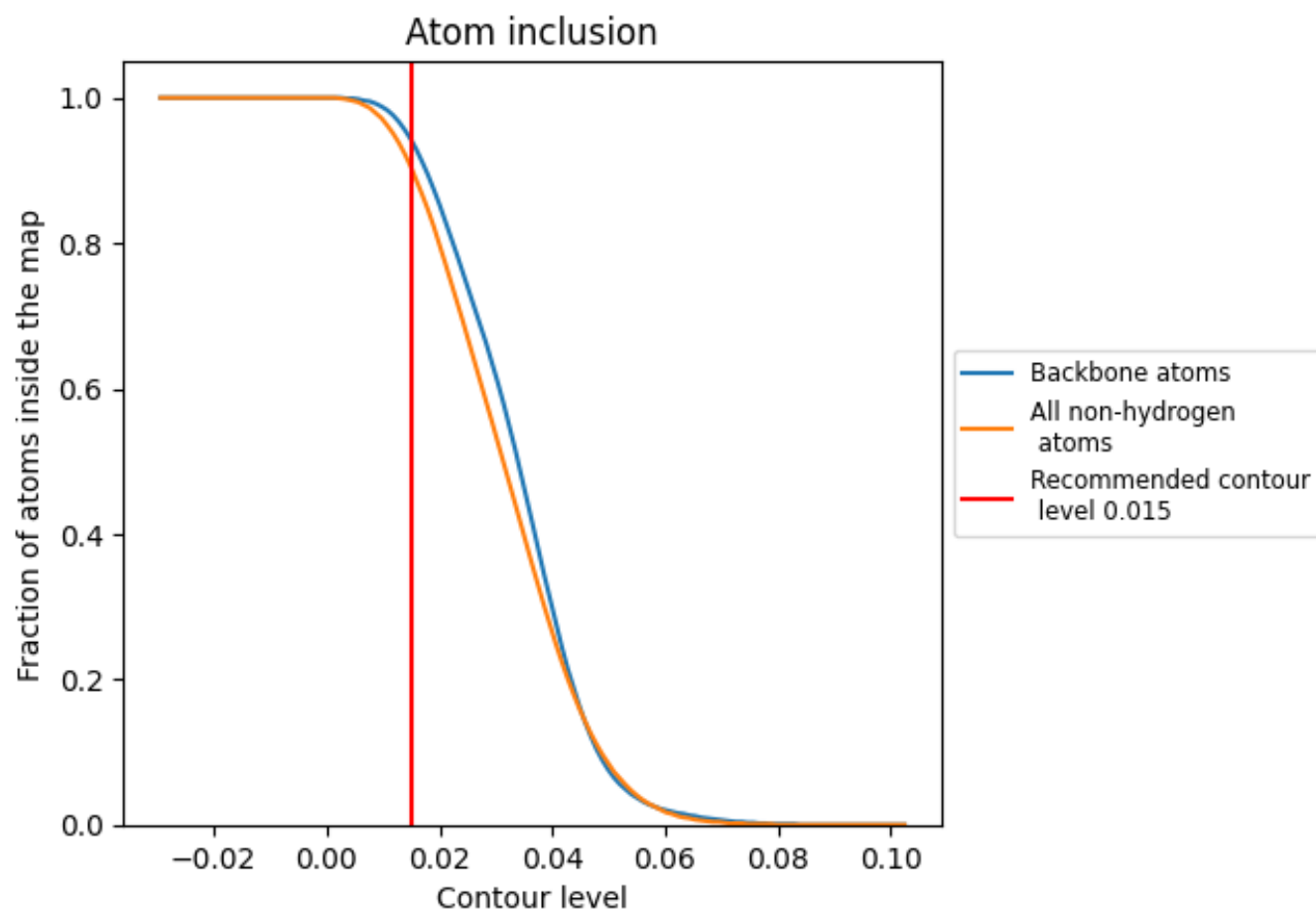
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.9040	 0.5550
10	 0.7990	 0.4520
11	 0.6450	 0.2860
13	 0.9210	 0.5100
5	 0.9380	 0.5560
7	 0.9940	 0.6070
8	 0.9680	 0.5780
9	 0.9390	 0.5530
A	 0.9590	 0.6180
AA	 0.8440	 0.5530
B	 0.9230	 0.5990
BB	 0.8530	 0.5630
C	 0.9260	 0.5980
CC	 0.8920	 0.5740
D	 0.8770	 0.5730
DD	 0.7840	 0.5060
E	 0.8700	 0.5550
EE	 0.8840	 0.5630
FF	 0.8390	 0.5420
G	 0.8270	 0.5460
GG	 0.7750	 0.4940
H	 0.8710	 0.5710
HH	 0.7130	 0.4980
I	 0.9080	 0.5860
II	 0.8780	 0.5640
J	 0.8610	 0.5520
JJ	 0.8700	 0.5610
K	 0.9410	 0.6030
KK	 0.7770	 0.4860
L	 0.8690	 0.5710
LL	 0.8960	 0.5780
M	 0.8960	 0.5730
MM	 0.2260	 0.2950
N	 0.9700	 0.6160
NN	 0.8900	 0.5740



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Chain	Atom inclusion	Q-score
O	 0.9300	 0.6000
OO	 0.8670	 0.5700
P	 0.9230	 0.6010
PP	 0.7560	 0.5060
Q	 0.9430	 0.6100
QQ	 0.8370	 0.5380
R	 0.8680	 0.5680
RR	 0.7640	 0.5120
S	 0.9300	 0.6040
SS	 0.8090	 0.5240
T	 0.8980	 0.5820
TT	 0.8150	 0.5250
U	 0.7960	 0.5230
UU	 0.7350	 0.4740
V	 0.9380	 0.6060
VV	 0.8330	 0.5500
W	 0.7520	 0.4890
WW	 0.9290	 0.5870
X	 0.8890	 0.5760
XX	 0.9160	 0.5870
Y	 0.8900	 0.5740
YY	 0.8430	 0.5440
Z	 0.8840	 0.5630
ZZ	 0.7740	 0.5170
a	 0.9460	 0.6080
aa	 0.8990	 0.5730
b	 0.8560	 0.5540
bb	 0.8140	 0.5270
c	 0.8580	 0.5670
cc	 0.8170	 0.5380
d	 0.8930	 0.5810
dd	 0.8850	 0.5520
e	 0.9380	 0.6070
ee	 0.7680	 0.5150
f	 0.9540	 0.6100
ff	 0.2940	 0.3180
g	 0.8850	 0.5820
gg	 0.6840	 0.4490
h	 0.8880	 0.5710
i	 0.8690	 0.5600
j	 0.9700	 0.6150
k	 0.7610	 0.5350

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Chain	Atom inclusion	Q-score
l	 0.9510	 0.5970
m	 0.9130	 0.5860
n	 0.9410	 0.6080
o	 0.9220	 0.5940
p	 0.9000	 0.5970
r	 0.9230	 0.5970