



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 12:07 PM UTC

PDB ID : 6Q95 / pdb_00006q95
EMDB ID : EMD-4475
Title : Structure of tmRNA SmpB bound in A site of T. thermophilus 70S ribosome
Authors : Rae, C.D.
Deposited on : 2018-12-17
Resolution : 3.70 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

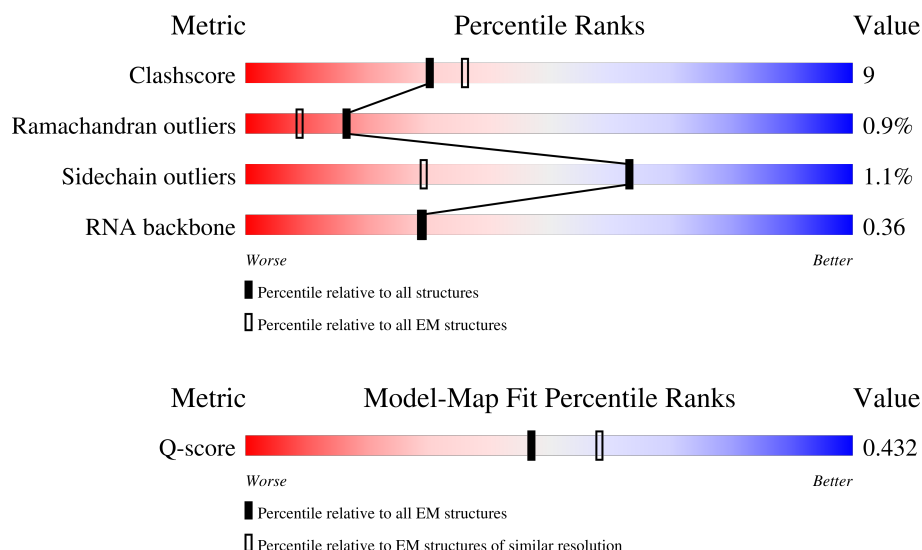
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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	11569 (3.20 - 4.20)

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	2	1522	13% 49% 41% 8%
2	g	235	72% 27%
3	h	207	8% 73% 26%

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Mol	Chain	Length	Quality of chain
4	i	208	
5	j	151	
6	k	101	
7	l	155	
8	m	138	
9	n	127	
10	o	99	
11	p	119	
12	q	125	
13	r	120	
14	s	60	
15	t	88	
16	u	84	
17	v	100	
18	w	70	
19	x	79	
20	y	99	
21	z	25	
22	7	77	
23	8	76	
24	9	6	
25	W	85	
26	X	89	
27	Y	51	
28	Z	60	

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Mol	Chain	Length	Quality of chain
29	a	58	
30	b	59	
31	c	45	
32	d	49	
33	e	64	
34	1	2915	
35	3	119	
36	A	229	
37	B	272	
38	C	205	
39	D	208	
40	E	181	
41	F	160	
42	G	60	
43	J	139	
44	K	122	
45	L	146	
46	M	136	
47	N	117	
48	O	99	
49	P	138	
50	Q	117	
51	R	101	
52	S	113	
53	T	93	

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Mol	Chain	Length	Quality of chain
54	U	101	11% 66% 30%
55	V	92	76% 24%
56	5	144	34% 76% 23%
57	6	2	100%
58	f	37	8% 70% 30%
59	H	140	51% 89% 7%
59	I	140	87% 99%
60	4	349	37% 20% 53% 18% 9%

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 154751 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 16S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1504	Total	C	N	O	P	0	0
			32329	14390	5992	10444	1503		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	g	235	Total	C	N	O	S	0	1
			1901	1213	342	341	5		

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	h	207	Total	C	N	O	S	0	1
			1613	1016	315	281	1		

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	i	208	Total	C	N	O	S	0	0
			1703	1066	339	291	7		

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	j	151	Total	C	N	O	S	0	1
			1147	724	218	201	4		

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	k	101	Total	C	N	O	S	0	0
			843	531	155	154	3		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	l	155	Total	C	N	O	S	0	0
			1257	781	252	218	6		

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	m	138	Total	C	N	O	S	0	0
			1116	705	215	193	3		

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	n	127	Total	C	N	O	0	0
			1011	639	198	174		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	58	ARG	HIS	conflict	UNP P80374

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	o	99	Total	C	N	O	S	0	1
			795	499	157	138	1		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	p	119	Total	C	N	O	S	0	0
			885	549	168	165	3		

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	q	125	Total	C	N	O	S	0	1
			971	611	196	163	1		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	r	120	Total	C	N	O	S	0	0
			955	591	197	165	2		

- Molecule 14 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	s	60	Total	C	N	O	S	0	0
			492	312	104	72	4		

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	t	88	Total	C	N	O	S	0	0
			734	459	147	126	2		

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	u	84	Total	C	N	O	S	0	1
			701	443	140	117	1		

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	v	100	Total	C	N	O	S	0	1
			824	528	152	142	2		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	w	70	Total	C	N	O	0	0
			574	367	112	95		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	x	79	Total	C	N	O	S	0	1
			630	403	115	110	2		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	y	99	Total	C	N	O	S	0	0
			763	470	162	129	2		

- Molecule 21 is a protein called 30S ribosomal protein Thx.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	z	25	Total	C	N	O	0	1
			209	128	51	30		

- Molecule 22 is a RNA chain called tRNA-fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	7	77	Total	C	N	O	P	0	0
			1645	733	297	538	77		

- Molecule 23 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	8	76	Total	C	N	O	P	0	0
			1616	720	281	539	76		

- Molecule 24 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	9	6	Total	C	N	O	P	0	0
			125	56	19	44	6		

- Molecule 25 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W	85	Total	C	N	O	S	0	0
			650	401	137	111	1		

- Molecule 26 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	X	89	Total	C	N	O	0	1
			693	435	140	118		

- Molecule 27 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Y	51	Total	C	N	O	S	0	1
			421	263	85	72	1		

- Molecule 28 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Z	60	Total	C	N	O	S	0	1
			468	298	91	78	1		

- Molecule 29 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	a	58	Total	C	N	O	S	0	0
			464	295	81	84	4		

- Molecule 30 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	b	59	Total	C	N	O	S	0	0
			459	288	90	76	5		

- Molecule 31 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	c	45	Total	C	N	O	S	0	1
			381	235	78	64	4		

- Molecule 32 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	49	Total	C	N	O	S	0	1
			419	257	105	55	2		

- Molecule 33 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	e	64	Total	C	N	O	S	0	1
			508	326	102	78	2		

- Molecule 34 is a RNA chain called 23S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	1	2831	Total	C	N	O	P	0	0
			60977	27139	11405	19603	2830		

- Molecule 35 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	3	119	Total	C	N	O	P	0	0
			2551	1136	471	826	118		

- Molecule 36 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	A	191	Total	C	N	O	0	1
			1142	691	221	230		

- Molecule 37 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	B	272	Total	C	N	O	S	0	1
			2105	1329	417	356	3		

- Molecule 38 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	C	205	Total	C	N	O	S	0	1
			1564	988	300	270	6		

- Molecule 39 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	D	208	Total	C	N	O	S	0	1
			1624	1035	304	282	3		

- Molecule 40 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	E	181	Total	C	N	O	S	0	0
			1474	942	268	260	4		

- Molecule 41 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	F	160	Total	C	N	O	S	0	1
			1223	773	229	220	1		

- Molecule 42 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	G	60	Total	C	N	O	S	0	1
			454	289	84	80	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	146	ALA	GLU	conflict	UNP Q5SLQ1

- Molecule 43 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	J	139	Total	C	N	O	S	0	1
			1105	712	207	182	4		

- Molecule 44 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	K	122	Total	C	N	O	S	0	0
			933	588	171	170	4		

- Molecule 45 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	L	146	Total	C	N	O	S	0	0
			1114	692	227	193	2		

- Molecule 46 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	M	136	Total	C	N	O	S	0	0
			1080	688	204	183	5		

- Molecule 47 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	N	117	Total	C	N	O	0	0
			960	599	202	159		

- Molecule 48 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	O	99	Total	C	N	O	0	1
			771	486	155	130		

- Molecule 49 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	P	138	Total	C	N	O	S	0	1
			1142	710	235	196	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Q	117	Total	C	N	O	S	0	0
			958	604	202	151	1		

- Molecule 51 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	R	101	Total	C	N	O	S	0	0
			779	501	142	135	1		

- Molecule 52 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	S	113	Total	C	N	O	S	0	0
			896	563	176	155	2		

- Molecule 53 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	T	93	Total	C	N	O	0	1
			726	471	132	123		

- Molecule 54 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	U	101	Total	C	N	O	S	0	1
			776	500	149	123	4		

- Molecule 55 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	V	92	Total	C	N	O	S	0	1
			766	488	148	129	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	179	ASP	GLU	conflict	UNP Q5SHZ1

- Molecule 56 is a protein called SsrA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	5	144	Total	C	N	O	S	0	0
			1184	754	219	210	1		

- Molecule 57 is a protein called Nascent peptide MET-ALA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	6	2	Total	C	N	O	S	0	0
			13	8	2	2	1		

- Molecule 58 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	f	37	Total	C	N	O	S	0	0
			307	188	68	47	4		

- Molecule 59 is a protein called 50S RIBOSOMAL PROTEIN L10 AND L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	H	130	Total	C	N	O		0	0
			650	390	130	130			
59	I	140	Total	C	N	O		0	0
			701	420	140	141			

- Molecule 60 is a RNA chain called transfer-messenger RNA (tmRNA).

Mol	Chain	Residues	Atoms					AltConf	Trace
60	4	319	Total	C	N	O	P	0	0
			6834	3040	1259	2216	319		

- Molecule 61 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
61	2	189	Total	Mg	0
			189	189	
61	k	1	Total	Mg	0
			1	1	
61	l	2	Total	Mg	0
			2	2	
61	m	1	Total	Mg	0
			1	1	
61	q	1	Total	Mg	0
			1	1	
61	r	1	Total	Mg	0
			1	1	
61	7	4	Total	Mg	0
			4	4	
61	8	12	Total	Mg	0
			12	12	
61	9	3	Total	Mg	0
			3	3	
61	b	3	Total	Mg	0
			3	3	
61	1	397	Total	Mg	0
			397	397	
61	3	13	Total	Mg	0
			13	13	
61	C	1	Total	Mg	0
			1	1	
61	D	1	Total	Mg	0
			1	1	
61	J	2	Total	Mg	0
			2	2	
61	K	1	Total	Mg	0
			1	1	
61	L	2	Total	Mg	0
			2	2	
61	N	1	Total	Mg	0
			1	1	
61	O	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
61	5	1	Total 1	Mg 1	0

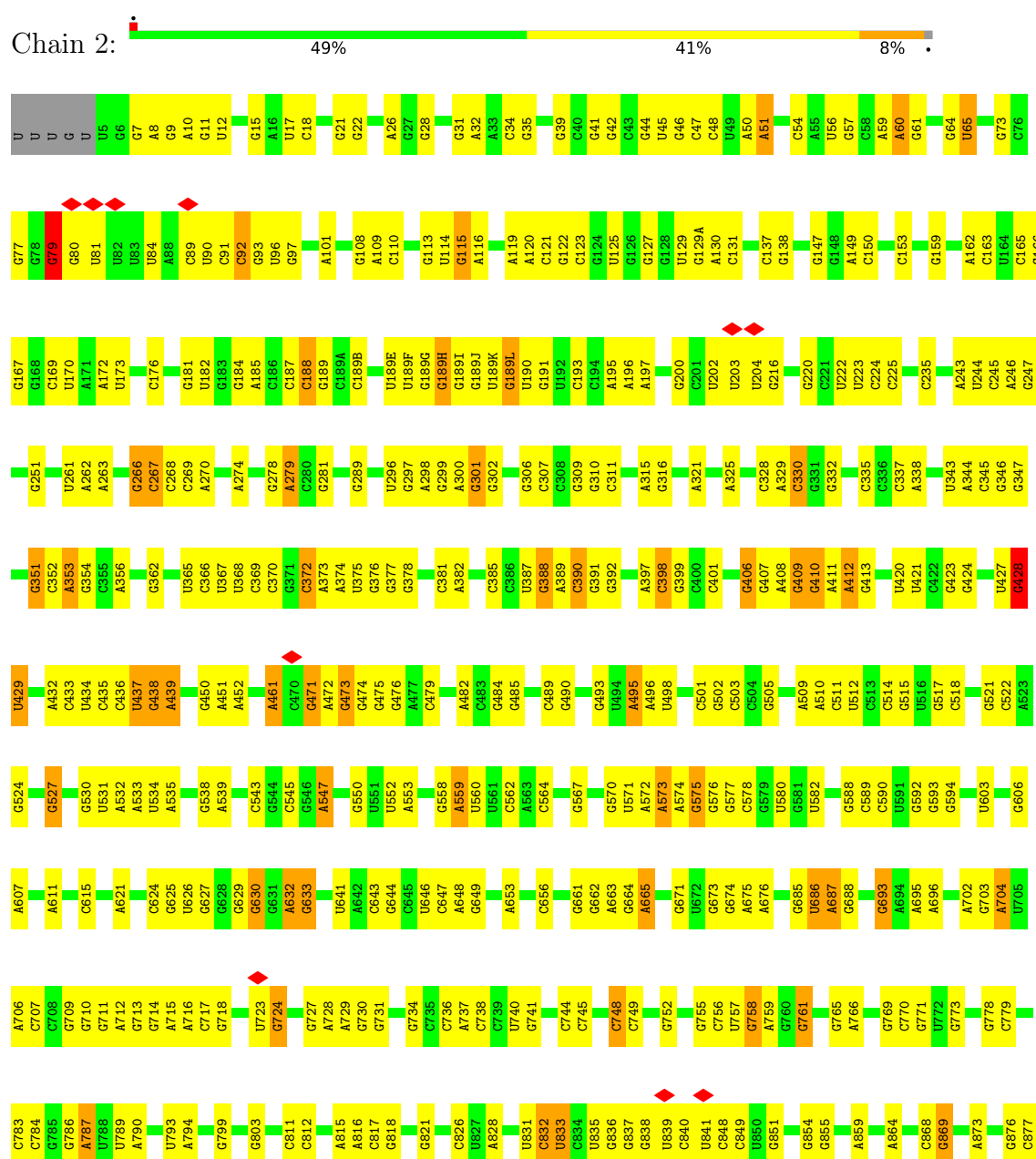
- Molecule 62 is ZINC ION (CCD ID: ZN) (formula: Zn).

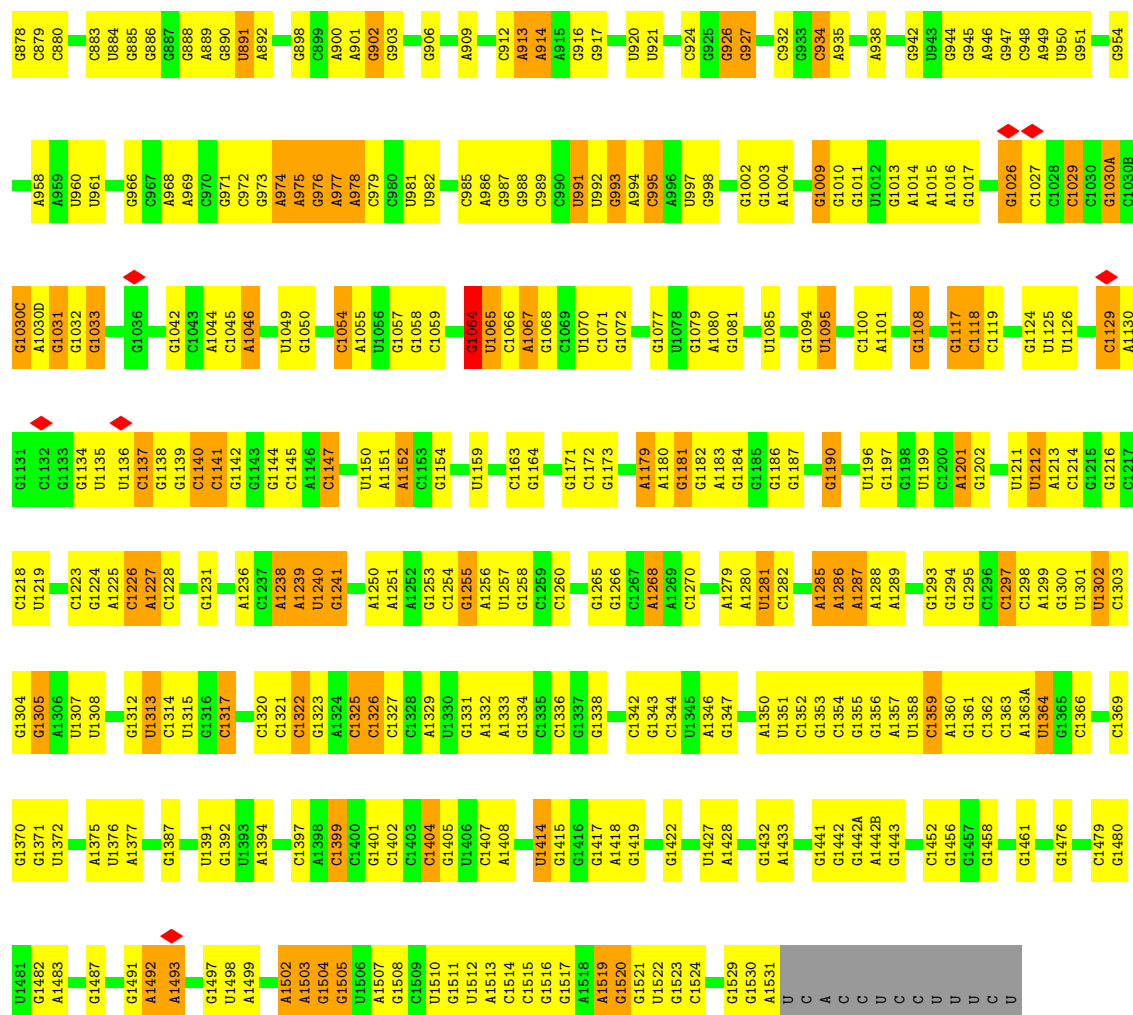
Mol	Chain	Residues	Atoms		AltConf
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62	s	1	Total 1	Zn 1	0
62	f	1	Total 1	Zn 1	0

3 Residue-property plots

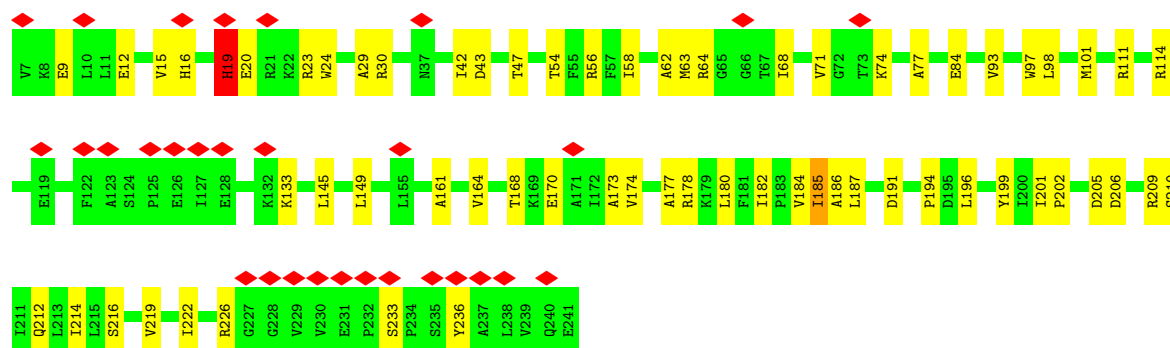
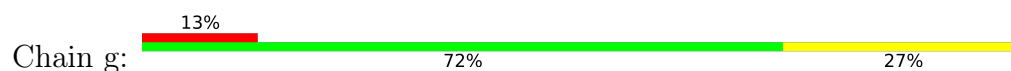
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 16S RIBOSOMAL RNA

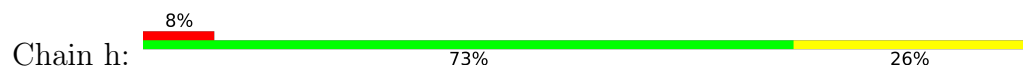


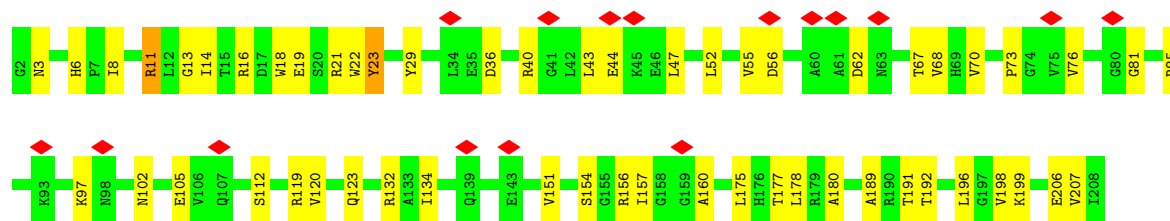


• Molecule 2: 30S ribosomal protein S2

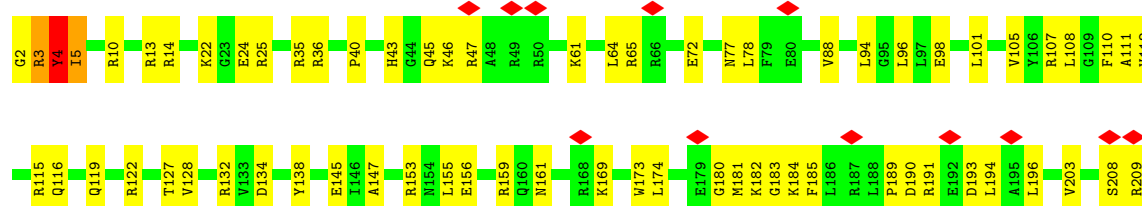


• Molecule 3: 30S ribosomal protein S3

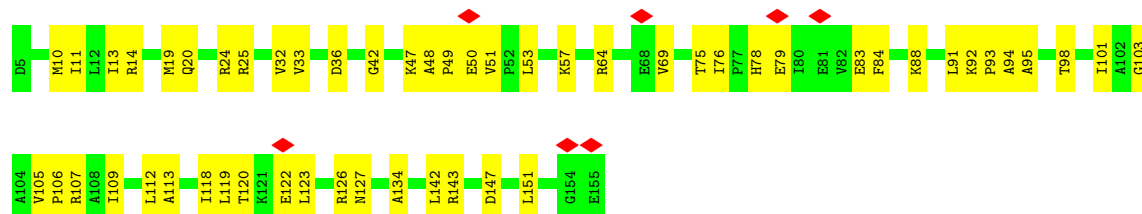




• Molecule 4: 30S ribosomal protein S4



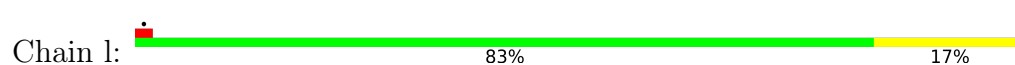
• Molecule 5: 30S ribosomal protein S5



• Molecule 6: 30S ribosomal protein S6

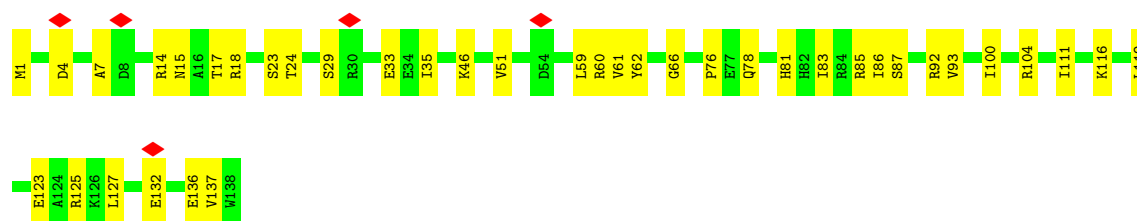


• Molecule 7: 30S ribosomal protein S7

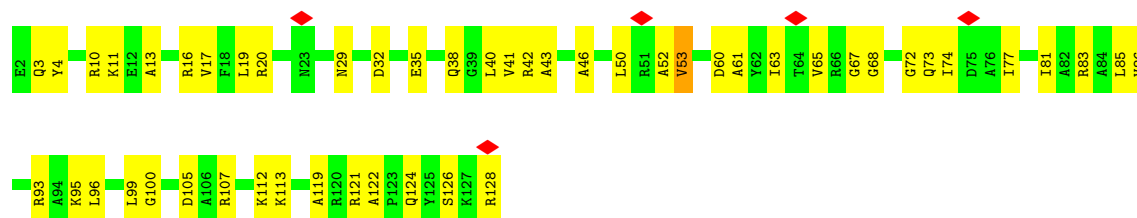


• Molecule 8: 30S ribosomal protein S8

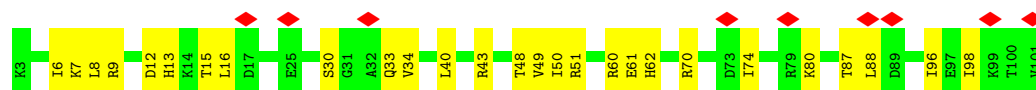




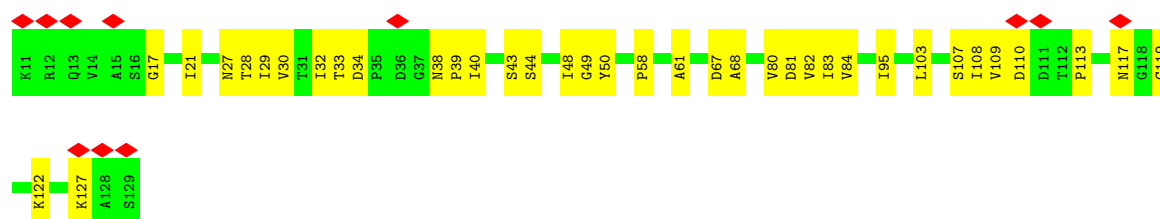
• Molecule 9: 30S ribosomal protein S9



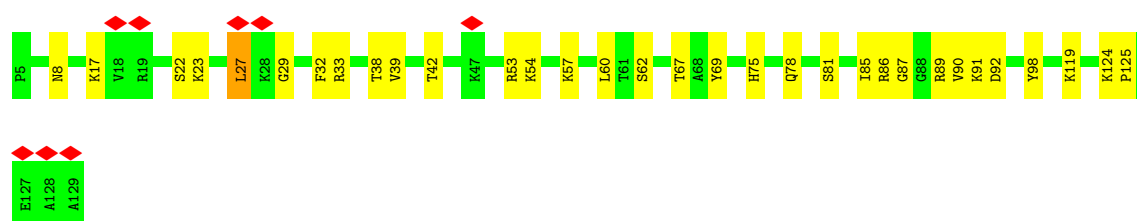
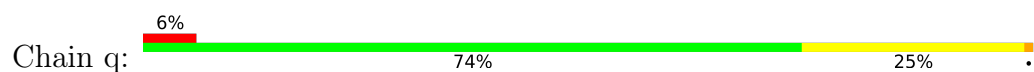
• Molecule 10: 30S ribosomal protein S10



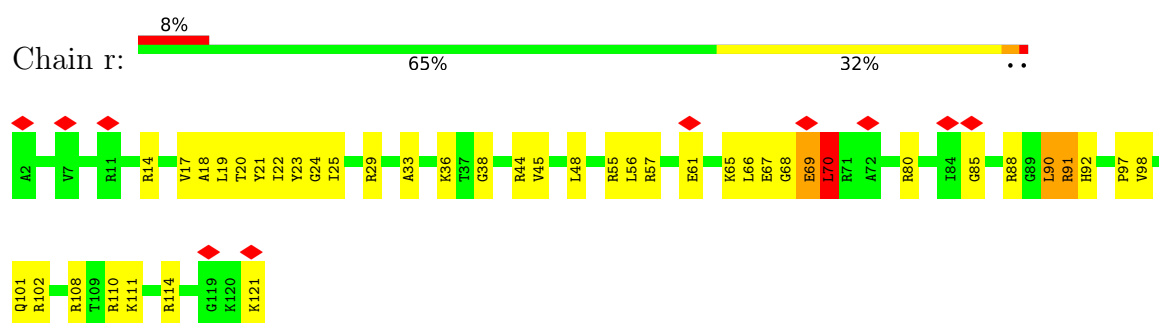
• Molecule 11: 30S ribosomal protein S11



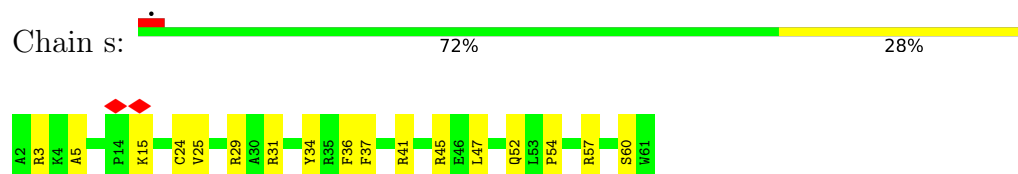
• Molecule 12: 30S ribosomal protein S12



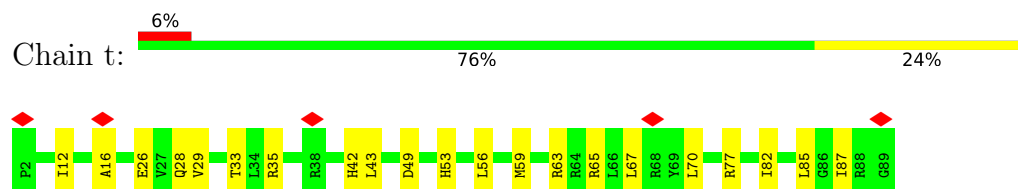
• Molecule 13: 30S ribosomal protein S13



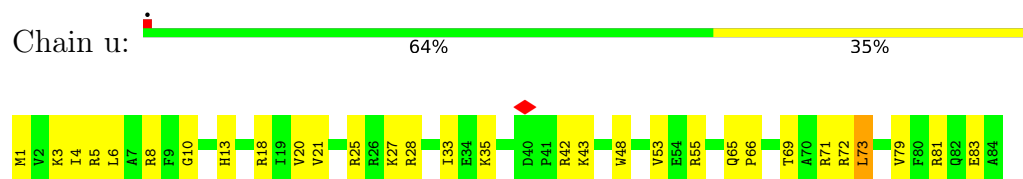
- Molecule 14: 30S ribosomal protein S14 type Z



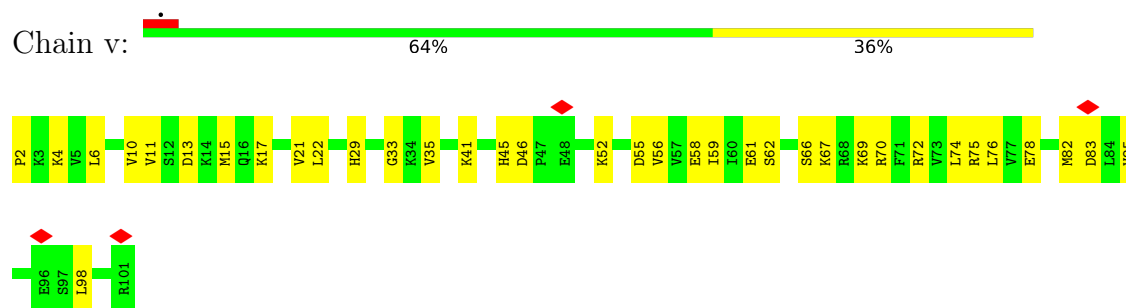
- Molecule 15: 30S ribosomal protein S15



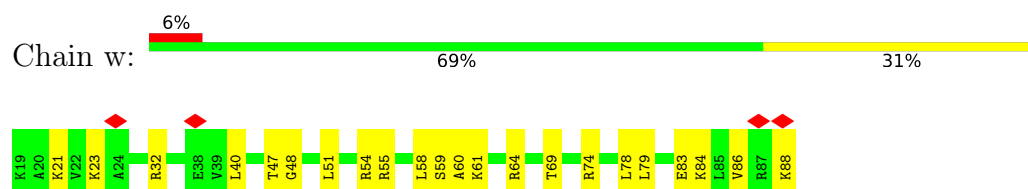
- Molecule 16: 30S ribosomal protein S16



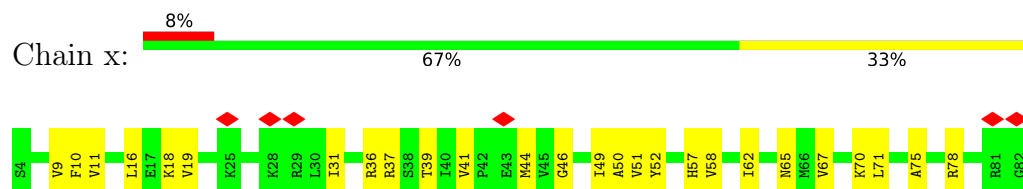
- Molecule 17: 30S ribosomal protein S17



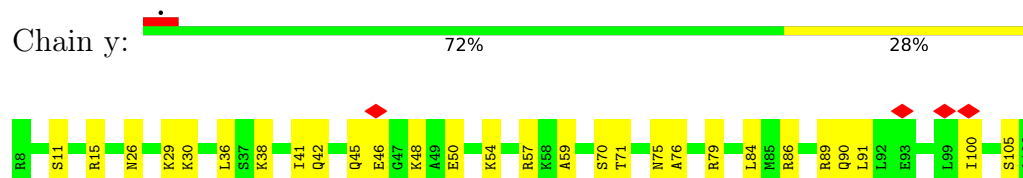
- Molecule 18: 30S ribosomal protein S18



- Molecule 19: 30S ribosomal protein S19



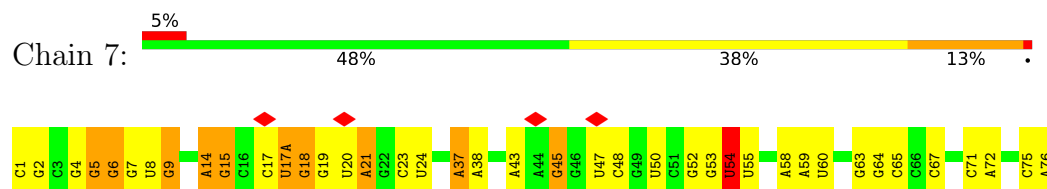
- Molecule 20: 30S ribosomal protein S20



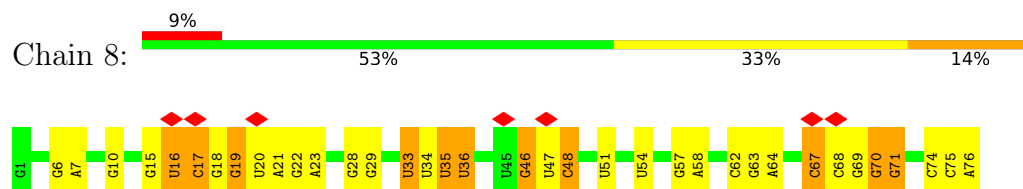
- Molecule 21: 30S ribosomal protein Thx



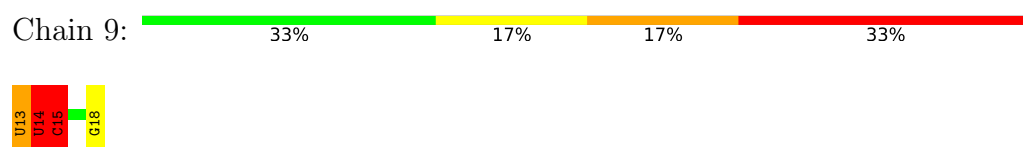
- Molecule 22: tRNA-fMet



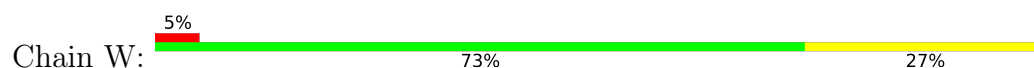
- Molecule 23: tRNA-Phe



- Molecule 24: mRNA

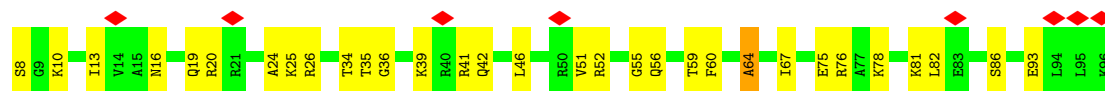


- Molecule 25: 50S ribosomal protein L27

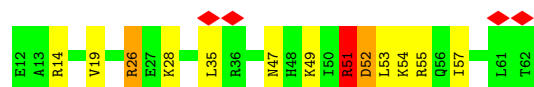
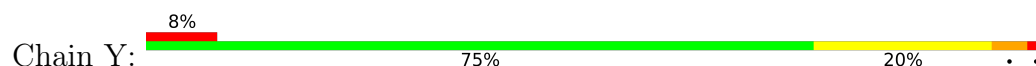




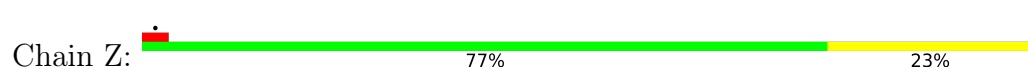
- Molecule 26: 50S ribosomal protein L28



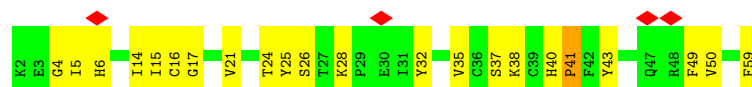
- Molecule 27: 50S ribosomal protein L29



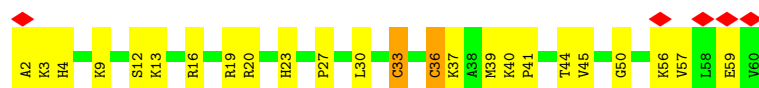
- Molecule 28: 50S ribosomal protein L30



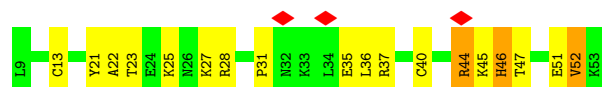
- Molecule 29: 50S ribosomal protein L31



- Molecule 30: 50S ribosomal protein L32

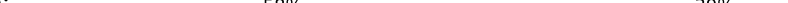


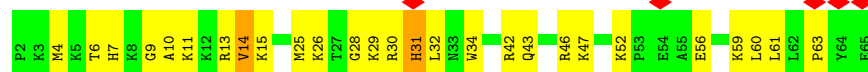
- Molecule 31: 50S ribosomal protein L33

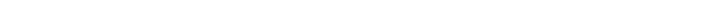


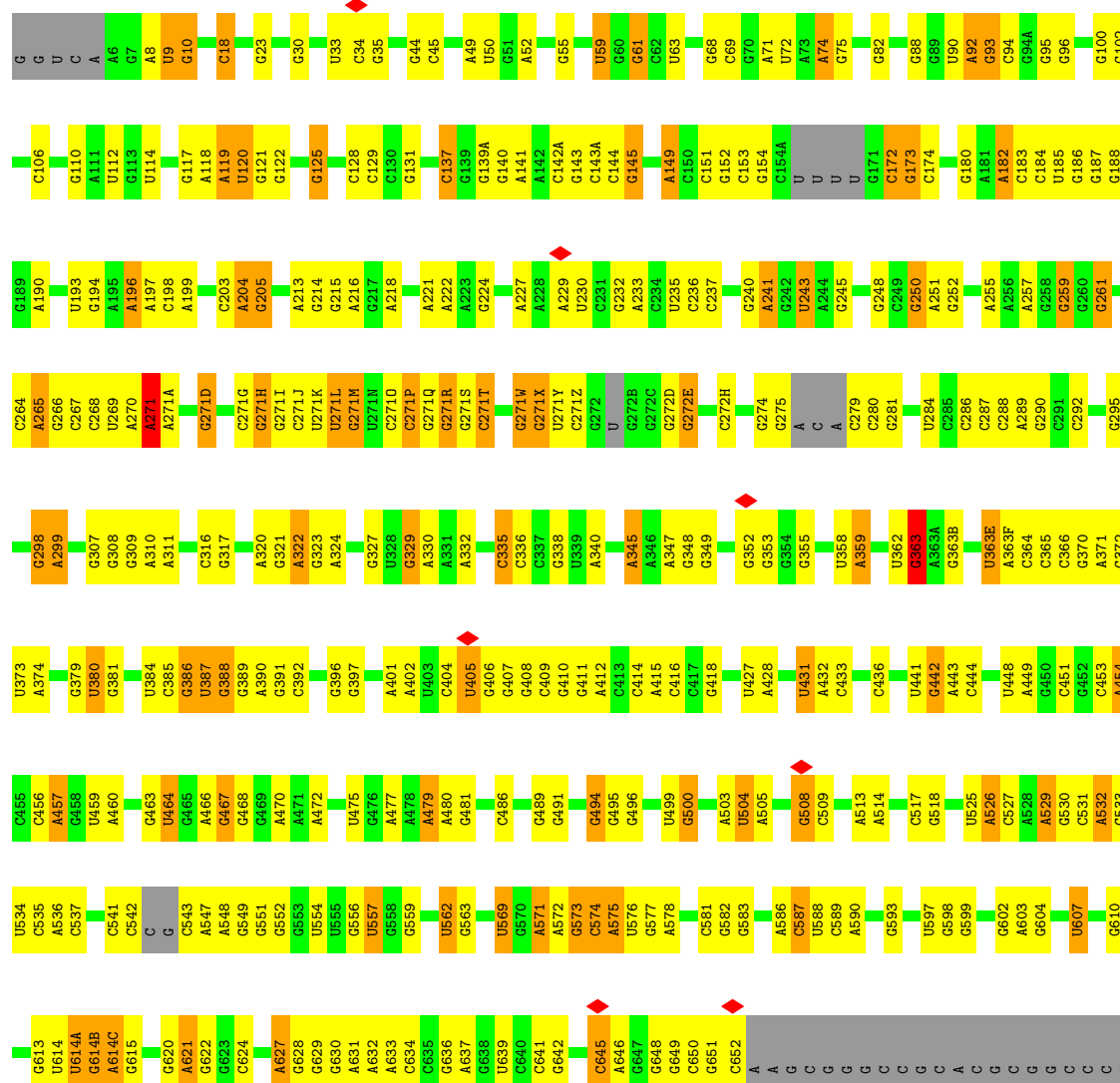
- Molecule 32: 50S ribosomal protein L34

M1	K2	R3	P7	N8	R9	R10	K11	R12	A13	K14	K37	G38	R39	R47	K48	R49
----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Chain e:  8% 58% 39%



- Chain 1:  45% 41% 11%

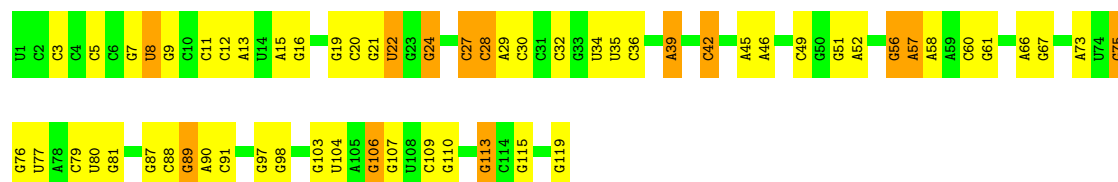






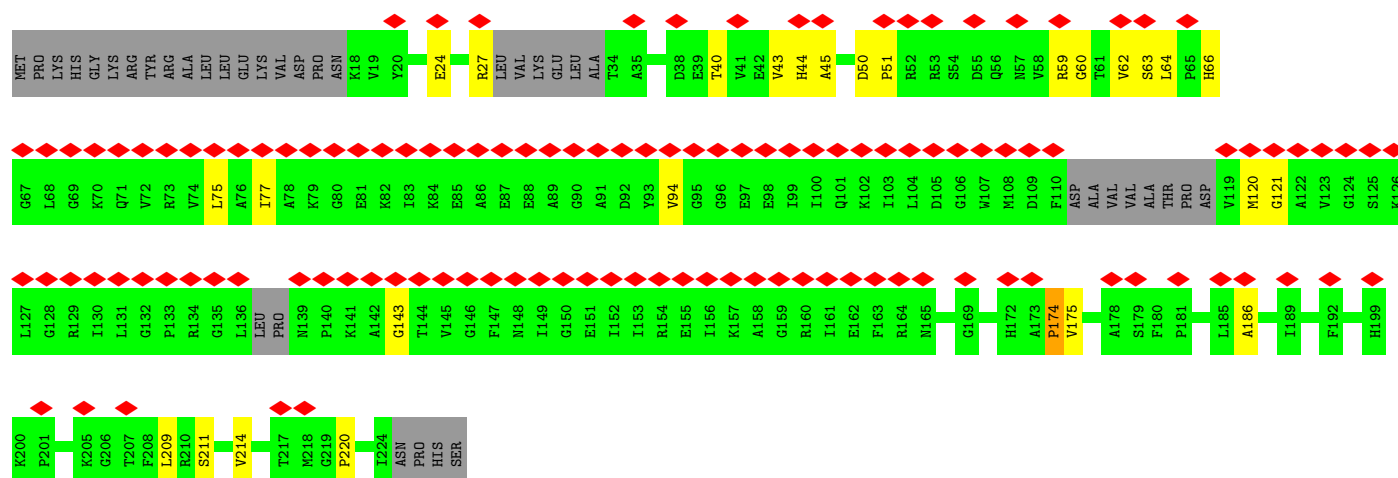
- Molecule 35: 5S RIBOSOMAL RNA

Chain 3: 



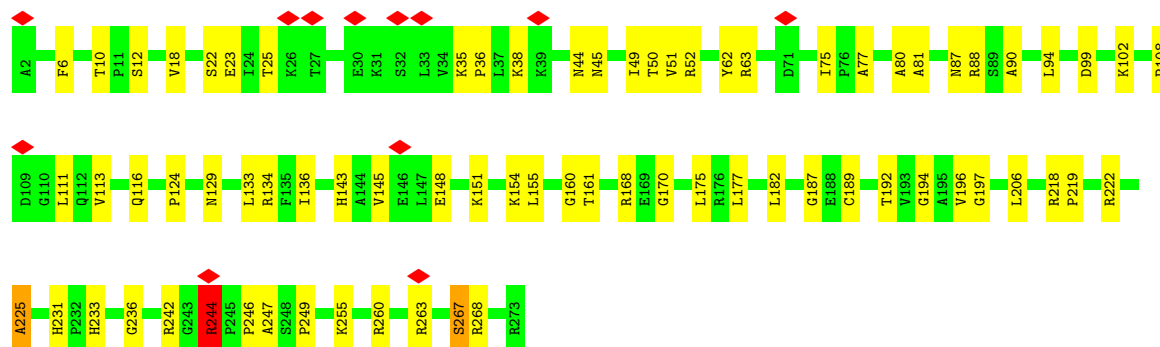
- Molecule 36: 50S ribosomal protein L1

Chain A: 



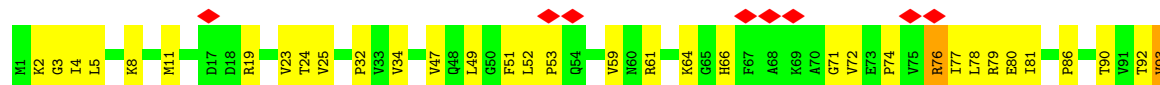
- Molecule 37: 50S ribosomal protein L2

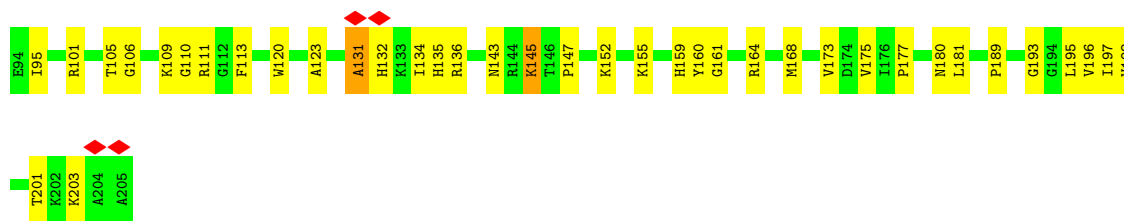
Chain B: 



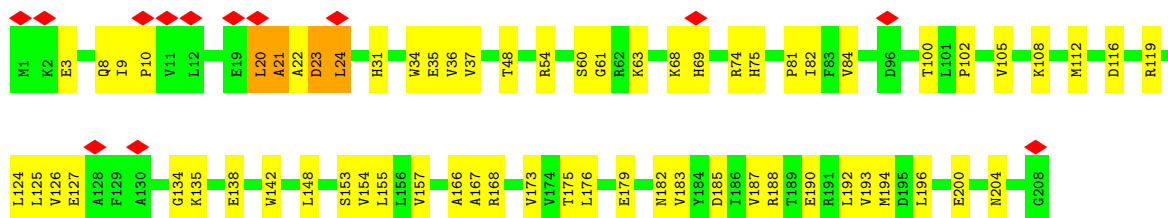
- Molecule 38: 50S ribosomal protein L3

Chain C: 

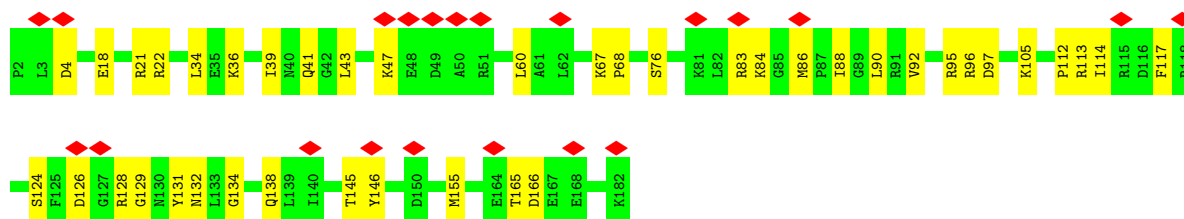
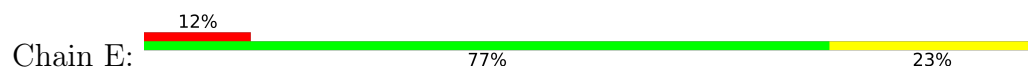




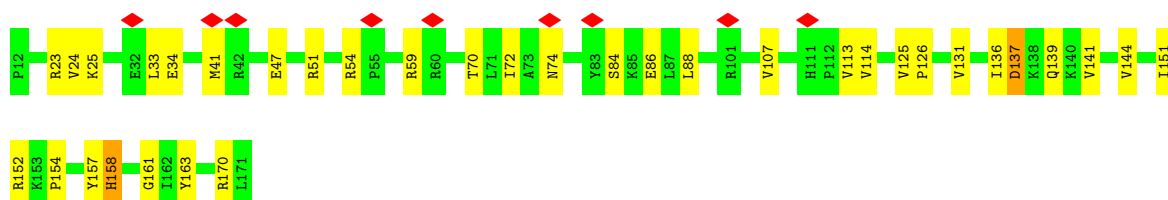
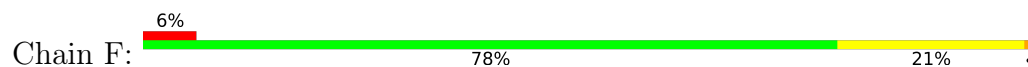
- Molecule 39: 50S ribosomal protein L4



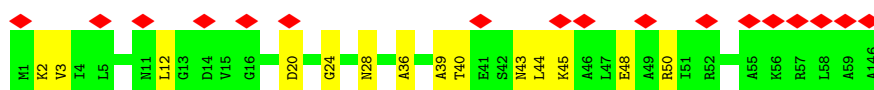
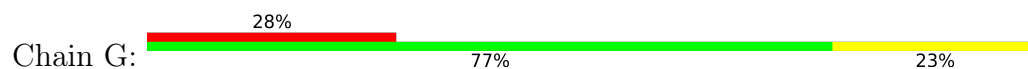
- Molecule 40: 50S ribosomal protein L5



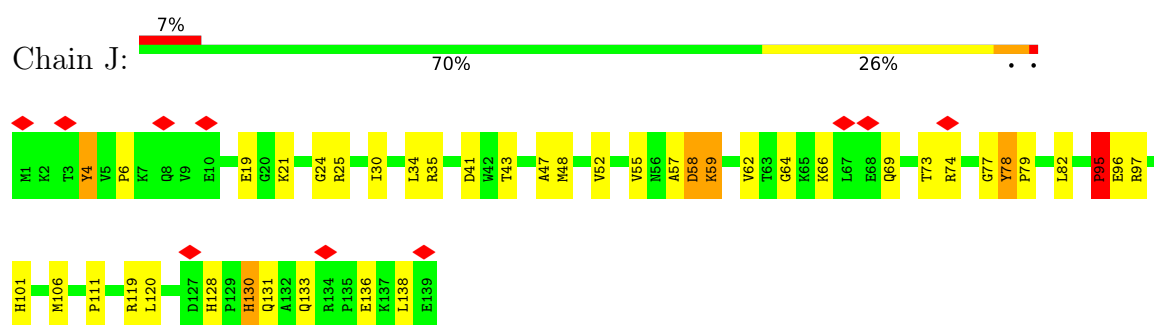
- Molecule 41: 50S ribosomal protein L6



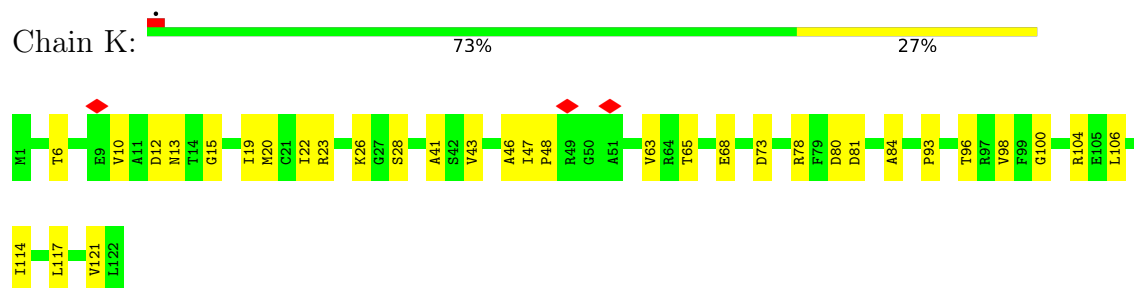
- Molecule 42: 50S ribosomal protein L9



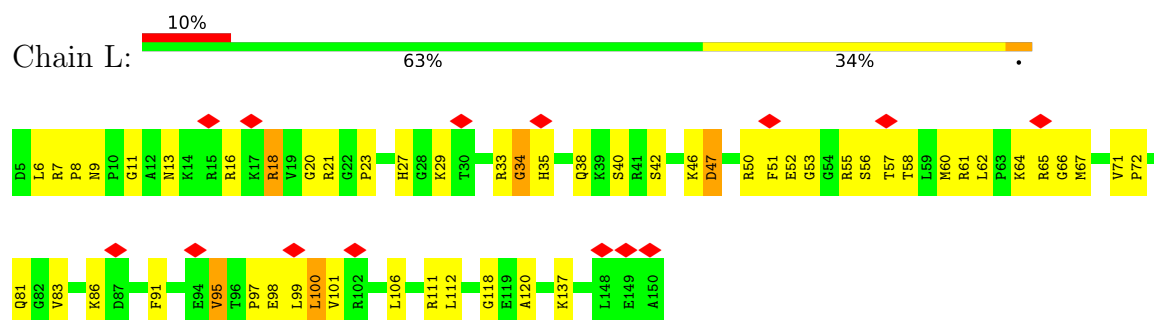
- Molecule 43: 50S ribosomal protein L13



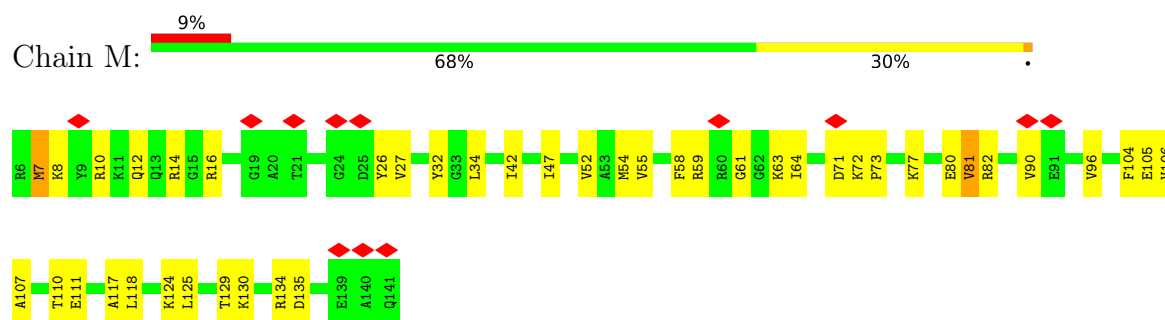
- Molecule 44: 50S ribosomal protein L14



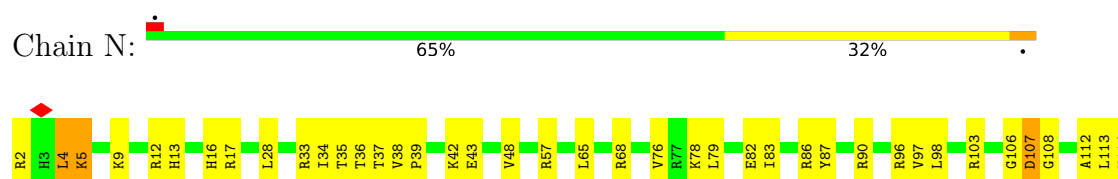
- Molecule 45: 50S ribosomal protein L15



- Molecule 46: 50S ribosomal protein L16

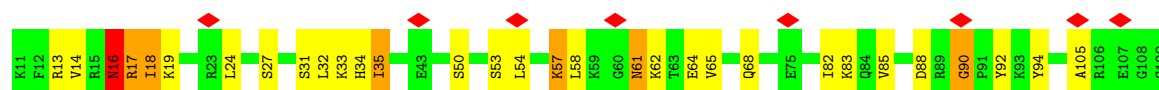


- Molecule 47: 50S ribosomal protein L17

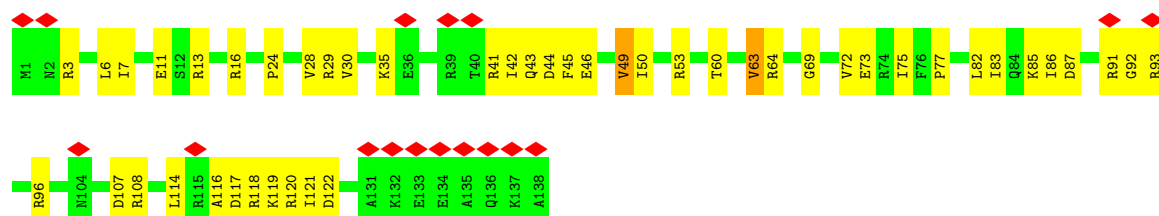




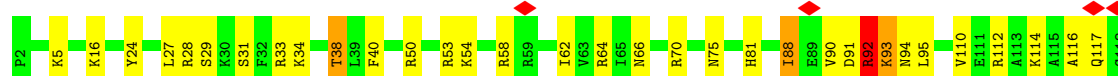
- Molecule 48: 50S ribosomal protein L18



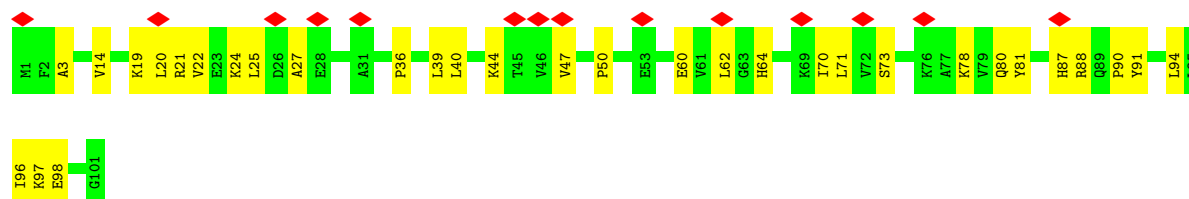
- Molecule 49: 50S ribosomal protein L19



- Molecule 50: 50S ribosomal protein L20



- Molecule 51: 50S ribosomal protein L21



- Molecule 52: 50S ribosomal protein L22

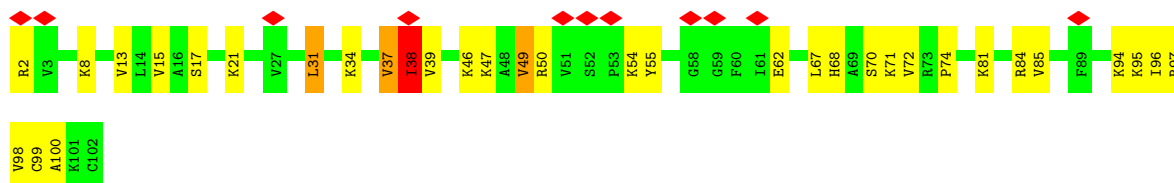




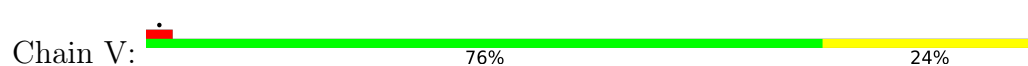
- Molecule 53: 50S ribosomal protein L23



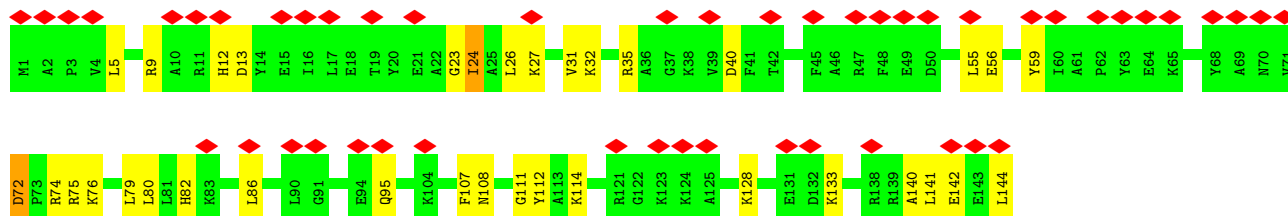
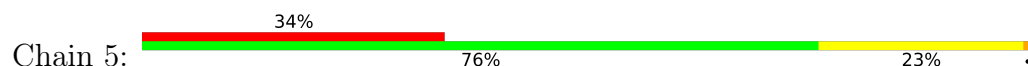
- Molecule 54: 50S ribosomal protein L24



- Molecule 55: 50S ribosomal protein L25



- Molecule 56: SsrA-binding protein



- Molecule 57: Nascent peptide MET-ALA



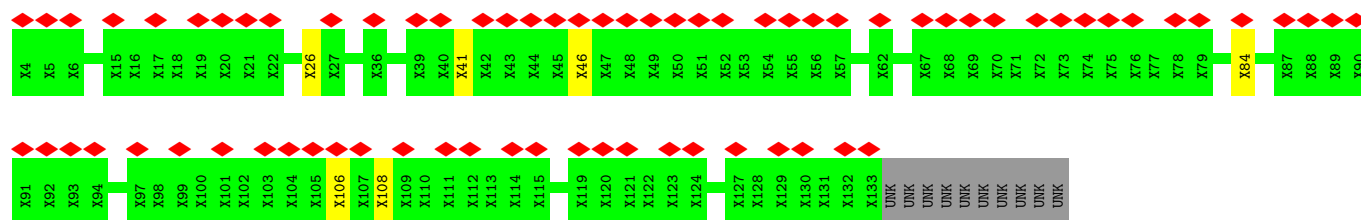
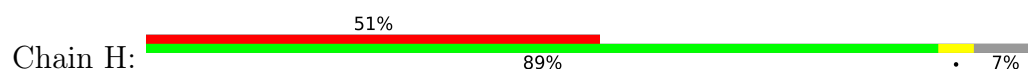
There are no outlier residues recorded for this chain.

- Molecule 58: 50S ribosomal protein L36

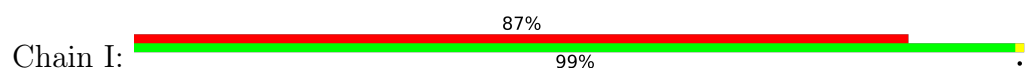




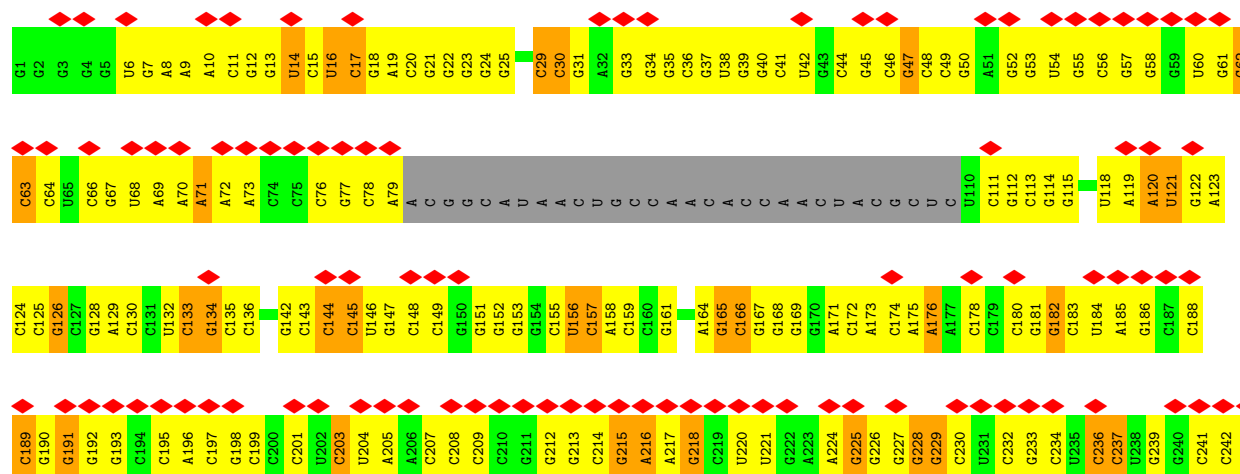
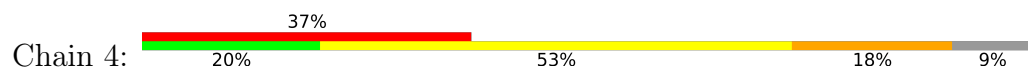
• Molecule 59: 50S RIBOSOMAL PROTEIN L10 AND L11

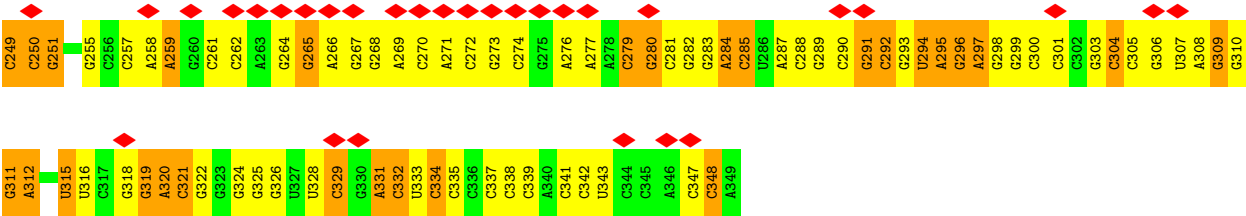


• Molecule 59: 50S RIBOSOMAL PROTEIN L10 AND L11



• Molecule 60: transfer-messenger RNA (tmRNA)





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	24400	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	42	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.420	Depositor
Minimum map value	-0.202	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	482.40002, 482.40002, 482.40002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.34, 1.34, 1.34	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 5MU, 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	2	0.61	0/36183	0.57	13/56458 (0.0%)
2	g	0.43	0/1935	0.64	0/2609
3	h	0.49	0/1637	0.67	0/2207
4	i	0.50	0/1733	0.74	4/2318 (0.2%)
5	j	0.58	0/1163	0.69	0/1566
6	k	0.41	0/856	0.57	0/1154
7	l	0.46	0/1276	0.64	0/1709
8	m	0.51	0/1136	0.67	0/1527
9	n	0.48	0/1029	0.76	0/1378
10	o	0.47	0/808	0.68	0/1087
11	p	0.47	0/900	0.58	0/1213
12	q	0.58	0/987	0.75	0/1322
13	r	0.51	0/963	0.86	4/1285 (0.3%)
14	s	0.57	0/501	0.73	0/664
15	t	0.49	0/745	0.59	0/992
16	u	0.56	0/717	0.65	0/965
17	v	0.53	0/837	0.64	0/1119
18	w	0.45	0/579	0.55	0/768
19	x	0.47	0/643	0.69	0/867
20	y	0.48	0/765	0.65	0/1007
21	z	0.54	0/213	0.63	0/279
22	7	0.51	0/1814	0.59	0/2825
23	8	0.45	3/1803 (0.2%)	0.58	0/2806
24	9	0.98	2/138 (1.4%)	0.76	0/212
25	W	0.68	0/658	0.71	0/878
26	X	0.53	0/700	0.88	0/931
27	Y	0.49	0/423	0.93	2/560 (0.4%)
28	Z	0.59	0/473	0.65	0/636
29	a	0.38	0/475	0.85	0/641
30	b	0.60	0/473	0.81	0/639
31	c	0.53	0/388	1.16	4/520 (0.8%)
32	d	0.67	0/427	0.68	0/563

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	e	0.61	0/516	0.92	0/681
34	1	0.76	20/68276 (0.0%)	0.66	33/106538 (0.0%)
35	3	0.53	0/2853	0.56	0/4451
36	A	0.25	0/1145	0.69	0/1556
37	B	0.67	0/2155	0.85	5/2907 (0.2%)
38	C	0.67	0/1597	0.84	0/2155
39	D	0.58	0/1659	0.73	0/2246
40	E	0.45	0/1498	0.74	0/2013
41	F	0.40	0/1246	0.74	1/1684 (0.1%)
42	G	0.34	0/457	0.66	0/617
43	J	0.56	0/1132	0.87	1/1527 (0.1%)
44	K	0.71	0/943	0.78	1/1269 (0.1%)
45	L	0.55	0/1131	1.18	10/1504 (0.7%)
46	M	0.64	0/1100	0.80	2/1470 (0.1%)
47	N	0.63	0/974	0.88	2/1302 (0.2%)
48	O	0.47	0/779	0.96	5/1038 (0.5%)
49	P	0.50	0/1156	0.82	0/1544
50	Q	0.66	0/975	0.76	0/1297
51	R	0.51	0/789	0.94	0/1054
52	S	0.59	0/907	0.73	0/1216
53	T	0.57	0/740	1.08	2/995 (0.2%)
54	U	0.45	0/789	1.09	3/1053 (0.3%)
55	V	0.47	0/782	0.68	0/1053
56	5	0.37	0/1203	0.64	0/1606
57	6	0.93	0/12	0.61	0/14
58	f	0.68	0/310	0.79	0/407
60	4	0.34	0/7639	0.64	1/11915 (0.0%)
All	All	0.64	25/166141 (0.0%)	0.67	93/248817 (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
2	g	0	1
3	h	0	2
4	i	0	2
9	n	0	1
12	q	0	1
13	r	0	1
20	y	0	2

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
26	X	0	3
27	Y	0	4
29	a	0	5
30	b	0	3
33	e	0	1
34	1	0	3
36	A	0	1
37	B	0	5
38	C	0	4
39	D	0	1
40	E	0	4
41	F	0	3
43	J	0	9
44	K	0	2
45	L	0	10
46	M	0	2
47	N	0	2
48	O	0	2
49	P	0	1
50	Q	0	5
52	S	0	1
53	T	0	4
54	U	0	5
All	All	0	90

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	1	271	A	C6-N1	39.36	2.14	1.35
34	1	1142	U	C4-C5	33.89	2.11	1.43
34	1	271	A	C6-N6	30.50	1.95	1.33
34	1	271	A	N9-C8	29.42	1.96	1.37
34	1	1142	U	N1-C2	24.50	1.87	1.38
34	1	1142	U	C2-O2	21.87	1.66	1.22
34	1	1142	U	C4-O4	16.56	1.56	1.23
34	1	271	A	C1'-N9	14.95	1.69	1.47
34	1	271	A	N3-C4	11.87	1.58	1.34
34	1	271	A	N9-C4	11.78	1.61	1.37
34	1	363	G	N9-C4	10.30	1.58	1.38
34	1	271	A	N7-C5	-10.04	1.19	1.39
34	1	1142	U	N3-C4	-9.02	1.20	1.38
34	1	363	G	N9-C8	-7.50	1.22	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	1	271	A	C5-C4	-6.19	1.26	1.38
34	1	1142	U	C5-C6	-6.16	1.21	1.34
23	8	36	U	C1'-N1	6.04	1.57	1.48
24	9	14	U	C1'-N1	6.03	1.57	1.48
24	9	15	C	C1'-N1	5.69	1.56	1.48
34	1	271	A	C8-N7	5.61	1.42	1.31
34	1	363	G	C5-C4	-5.53	1.27	1.38
34	1	1142	U	C1'-N1	5.37	1.56	1.48
23	8	35	U	C1'-N1	5.26	1.56	1.48
34	1	271	A	C5-C6	-5.23	1.30	1.41
23	8	34	U	C1'-N1	5.20	1.56	1.48

All (93) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	1	1142	U	C2-N3-C4	-31.37	32.90	127.00
34	1	363	G	C4-C5-N7	-25.60	34.00	110.80
34	1	271	A	C8-N9-C4	-25.01	30.78	105.80
34	1	363	G	N7-C8-N9	-24.26	40.33	113.10
34	1	1142	U	N3-C4-O4	-21.84	53.88	119.40
34	1	271	A	C5-C6-N6	-21.15	60.25	123.70
34	1	271	A	C4-C5-C6	-20.93	54.21	117.00
34	1	271	A	C5-N7-C8	-17.67	50.89	103.90
34	1	1142	U	C5-C6-N1	-17.44	70.37	122.70
34	1	363	G	C5-N7-C8	15.59	151.07	104.30
34	1	271	A	N1-C2-N3	-15.46	82.93	129.30
34	1	1142	U	N1-C2-N3	-15.26	69.11	114.90
34	1	271	A	C8-N9-C1'	12.32	164.66	127.70
34	1	363	G	C8-N9-C4	-12.26	69.61	106.40
34	1	1142	U	C5-C4-O4	12.14	162.32	125.90
34	1	271	A	N1-C6-N6	10.86	151.19	118.60
34	1	363	G	C4-N9-C1'	9.61	155.32	126.50
4	i	3	ARG	CA-C-N	8.77	138.28	121.54
4	i	3	ARG	C-N-CA	8.77	138.28	121.54
37	B	244	ARG	C-N-CD	-8.53	101.83	120.60
34	1	271	A	N7-C8-N9	8.30	138.69	113.80
54	U	31	LEU	C-N-CD	-8.23	102.50	120.60
37	B	244	ARG	CA-C-N	8.15	146.56	127.00
37	B	244	ARG	C-N-CA	8.15	146.56	127.00
47	N	106	GLY	CA-C-N	8.14	137.09	121.54
47	N	106	GLY	C-N-CA	8.14	137.09	121.54
54	U	31	LEU	CA-C-N	7.67	145.41	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	U	31	LEU	C-N-CA	7.67	145.41	127.00
34	1	1142	U	N1-C2-O2	7.46	145.19	122.80
43	J	78	TYR	N-CA-C	7.40	126.16	109.81
53	T	88	LYS	CA-C-N	7.28	135.07	121.97
53	T	88	LYS	C-N-CA	7.28	135.07	121.97
45	L	56	SER	CA-C-N	6.79	134.51	121.54
45	L	56	SER	C-N-CA	6.79	134.51	121.54
34	1	1142	U	C2-N1-C1'	6.71	137.82	117.70
34	1	271	A	C4-N9-C1'	6.64	146.23	126.30
45	L	47	ASP	CA-C-N	6.53	142.67	127.00
45	L	47	ASP	C-N-CA	6.53	142.67	127.00
34	1	1142	U	C6-N1-C1'	-6.30	102.29	121.20
48	O	16	ASN	CA-C-N	6.23	133.44	121.54
48	O	16	ASN	C-N-CA	6.23	133.44	121.54
4	i	4	TYR	CA-C-N	6.21	133.15	121.97
4	i	4	TYR	C-N-CA	6.21	133.15	121.97
31	c	31	PRO	CA-C-N	6.00	133.01	121.54
31	c	31	PRO	C-N-CA	6.00	133.01	121.54
45	L	38	GLN	CA-C-N	5.93	132.88	121.54
45	L	38	GLN	C-N-CA	5.93	132.88	121.54
13	r	69	GLU	CA-C-N	5.91	132.83	121.54
13	r	69	GLU	C-N-CA	5.91	132.83	121.54
45	L	46	LYS	CA-C-N	-5.75	107.76	121.80
45	L	46	LYS	C-N-CA	-5.75	107.76	121.80
34	1	271	A	C4-C5-N7	-5.73	93.52	110.70
34	1	1221(A)	C	O5'-P-OP1	5.71	125.12	108.00
34	1	1142	U	N3-C2-O2	5.70	139.31	122.20
48	O	18	ILE	N-CA-C	5.65	121.09	109.34
60	4	29	C	P-O3'-C3'	5.64	128.66	120.20
1	2	575	G	P-O3'-C3'	5.61	128.61	120.20
1	2	687	A	P-O3'-C3'	5.53	128.50	120.20
34	1	2126	A	P-O3'-C3'	5.53	128.50	120.20
31	c	27	LYS	CA-C-N	5.53	132.10	121.54
31	c	27	LYS	C-N-CA	5.53	132.10	121.54
34	1	1710	C	O5'-C5'-C4'	-5.52	103.22	111.50
44	K	26	LYS	N-CA-C	-5.47	99.15	110.80
46	M	7	MET	CA-C-N	5.43	131.91	121.54
46	M	7	MET	C-N-CA	5.43	131.91	121.54
34	1	2712	U	C2-N1-C1'	5.42	133.96	117.70
41	F	158	HIS	N-CA-C	5.40	122.31	110.80
34	1	1652	A	C2'-C3'-O3'	5.38	121.77	113.70
1	2	1064	G	C2'-C3'-O3'	5.32	117.48	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	79	G	P-O3'-C3'	5.32	128.17	120.20
1	2	1067	A	P-O3'-C3'	5.29	128.14	120.20
13	r	90	LEU	CA-C-N	5.25	131.56	121.54
13	r	90	LEU	C-N-CA	5.25	131.56	121.54
45	L	53	GLY	N-CA-C	-5.24	100.76	113.18
1	2	1064	G	P-O3'-C3'	5.20	128.00	120.20
48	O	57	LYS	CA-C-N	5.20	131.47	121.54
48	O	57	LYS	C-N-CA	5.20	131.47	121.54
34	1	1709	U	O3'-P-O5'	-5.14	96.30	104.00
1	2	575	G	C2'-C3'-O3'	5.13	117.19	109.50
27	Y	51	ARG	CA-C-N	5.12	135.23	126.32
27	Y	51	ARG	C-N-CA	5.12	135.23	126.32
1	2	913	A	P-O3'-C3'	5.10	127.86	120.20
34	1	1541	G	C2'-C3'-O3'	5.08	121.32	113.70
34	1	1558	A	P-O3'-C3'	5.07	127.80	120.20
1	2	1285	A	P-O3'-C3'	5.07	127.80	120.20
34	1	387	U	P-O3'-C3'	5.05	127.78	120.20
1	2	428	G	P-O3'-C3'	5.05	127.77	120.20
1	2	748	C	P-O3'-C3'	5.04	127.76	120.20
1	2	1065	U	P-O3'-C3'	5.04	127.75	120.20
1	2	1201	A	P-O3'-C3'	5.03	127.75	120.20
37	B	267	SER	CA-C-N	5.02	131.12	121.54
37	B	267	SER	C-N-CA	5.02	131.12	121.54
45	L	47	ASP	C-N-CD	-5.02	109.57	120.60

There are no chirality outliers.

All (90) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
34	1	1142	U	Sidechain
34	1	271	A	Sidechain
34	1	363	G	Sidechain
36	A	174	PRO	Peptide
37	B	12	SER	Peptide
37	B	197	GLY	Peptide
37	B	225	ALA	Peptide
37	B	25	THR	Peptide
37	B	35	LYS	Peptide
38	C	131	ALA	Peptide
38	C	71	GLY	Peptide
38	C	76	ARG	Peptide
38	C	80	GLU	Peptide

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Mol	Chain	Res	Type	Group
39	D	24	LEU	Peptide
40	E	129	GLY	Peptide
40	E	86	MET	Peptide
40	E	88	ILE	Peptide
40	E	95	ARG	Peptide
41	F	137	ASP	Peptide
41	F	144	VAL	Peptide
41	F	157	TYR	Peptide
43	J	130	HIS	Peptide
43	J	4	TYR	Peptide
43	J	58	ASP	Peptide
43	J	59	LYS	Peptide
43	J	64	GLY	Peptide
43	J	73	THR	Peptide
43	J	77	GLY	Peptide
43	J	82	LEU	Peptide
43	J	95	PRO	Peptide
44	K	100	GLY	Peptide
44	K	46	ALA	Peptide
45	L	111	ARG	Peptide
45	L	18	ARG	Peptide
45	L	20	GLY	Peptide
45	L	34	GLY	Peptide
45	L	40	SER	Peptide
45	L	51	PHE	Peptide
45	L	52	GLU	Peptide
45	L	57	THR	Peptide
45	L	9	ASN	Peptide
45	L	98	GLU	Peptide
46	M	10	ARG	Peptide
46	M	7	MET	Peptide
47	N	4	LEU	Peptide
47	N	5	LYS	Peptide
48	O	16	ASN	Peptide
48	O	61	ASN	Peptide
49	P	93	ARG	Peptide
50	Q	38	THR	Peptide
50	Q	88	ILE	Peptide
50	Q	91	ASP	Peptide
50	Q	92	ARG	Peptide
50	Q	95	LEU	Peptide
52	S	5	ALA	Peptide

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Mol	Chain	Res	Type	Group
53	T	25	LYS	Peptide
53	T	77	LYS	Peptide
53	T	84	ALA	Peptide
53	T	88	LYS	Peptide
54	U	100	ALA	Peptide
54	U	37	VAL	Peptide
54	U	38	ILE	Peptide
54	U	97	ARG	Peptide
54	U	98	VAL	Peptide
26	X	10	LYS	Peptide
26	X	55	GLY	Peptide
26	X	64	ALA	Peptide
27	Y	26	ARG	Peptide
27	Y	51	ARG	Peptide
27	Y	52	ASP	Peptide
27	Y	54	LYS	Peptide
29	a	37	SER	Peptide
29	a	38	LYS	Peptide
29	a	40	HIS	Peptide
29	a	41	PRO	Peptide
29	a	43	TYR	Peptide
30	b	2	ALA	Peptide
30	b	3	LYS	Peptide
30	b	36	CYS	Peptide
33	e	31	HIS	Peptide
2	g	19	HIS	Peptide
3	h	11	ARG	Peptide
3	h	23	TYR	Peptide
4	i	4	TYR	Peptide
4	i	5	ILE	Peptide
9	n	52	ALA	Peptide
12	q	27	LEU	Peptide
13	r	91	ARG	Peptide
20	y	11	SER	Peptide
20	y	48	LYS	Peptide

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	2	32329	0	16317	408	0
2	g	1901	0	1951	44	0
3	h	1613	0	1677	37	0
4	i	1703	0	1763	55	0
5	j	1147	0	1207	41	0
6	k	843	0	857	22	0
7	l	1257	0	1296	22	0
8	m	1116	0	1177	26	0
9	n	1011	0	1043	35	0
10	o	795	0	840	18	0
11	p	885	0	904	27	0
12	q	971	0	1057	22	0
13	r	955	0	1020	29	0
14	s	492	0	529	15	0
15	t	734	0	771	14	0
16	u	701	0	720	22	0
17	v	824	0	891	24	0
18	w	574	0	644	18	0
19	x	630	0	652	21	0
20	y	763	0	861	21	0
21	z	209	0	221	11	0
22	7	1645	0	838	11	0
23	8	1616	0	818	27	0
24	9	125	0	64	9	0
25	W	650	0	654	19	0
26	X	693	0	764	25	0
27	Y	421	0	461	11	0
28	Z	468	0	523	10	0
29	a	464	0	459	12	0
30	b	459	0	480	17	0
31	c	381	0	391	10	0
32	d	419	0	467	13	0
33	e	508	0	576	27	0
34	1	60977	0	30747	683	0
35	3	2551	0	1293	30	0
36	A	1142	0	865	14	0
37	B	2105	0	2182	50	0
38	C	1564	0	1629	54	0
39	D	1624	0	1677	46	0
40	E	1474	0	1534	27	0
41	F	1223	0	1282	19	0
42	G	454	0	494	9	0
43	J	1105	0	1180	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	K	933	0	996	23	0
45	L	1114	0	1187	42	0
46	M	1080	0	1127	27	0
47	N	960	0	1021	30	0
48	O	771	0	832	19	0
49	P	1142	0	1202	42	0
50	Q	958	0	1015	34	0
51	R	779	0	851	24	0
52	S	896	0	953	29	0
53	T	726	0	778	17	0
54	U	776	0	870	19	0
55	V	766	0	783	17	0
56	5	1184	0	1235	31	0
57	6	13	0	16	0	0
58	f	307	0	336	8	0
59	H	650	0	157	3	0
59	I	701	0	165	1	0
60	4	6834	0	3475	73	0
61	1	397	0	0	0	0
61	2	189	0	0	0	0
61	3	13	0	0	0	0
61	5	1	0	0	0	0
61	7	4	0	0	0	0
61	8	12	0	0	0	0
61	9	3	0	0	0	0
61	C	1	0	0	0	0
61	D	1	0	0	0	0
61	J	2	0	0	0	0
61	K	1	0	0	0	0
61	L	2	0	0	0	0
61	N	1	0	0	0	0
61	O	1	0	0	0	0
61	b	3	0	0	0	0
61	k	1	0	0	0	0
61	l	2	0	0	0	0
61	m	1	0	0	0	0
61	q	1	0	0	0	0
61	r	1	0	0	0	0
62	f	1	0	0	0	0
62	i	1	0	0	0	0
62	s	1	0	0	0	0
All	All	154751	0	102775	2144	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 9.

All (2144) 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)
34:1:271:A:N6	34:1:271:A:C5	1.72	1.56
34:1:271:A:N9	34:1:271:A:C1'	1.69	1.51
34:1:1142:U:C5	34:1:1142:U:C2	1.96	1.50
34:1:1142:U:C2	34:1:1142:U:O2	1.66	1.49
34:1:1142:U:C2	34:1:1142:U:N1	1.87	1.39
34:1:1142:U:C5	34:1:1142:U:C4	2.11	1.37
34:1:271:A:N6	34:1:271:A:C6	1.94	1.34
34:1:1142:U:N1	34:1:1142:U:C4	1.98	1.29
34:1:1142:U:O2	34:1:1142:U:C4	1.87	1.27
34:1:1142:U:N1	34:1:1142:U:N3	1.89	1.17
34:1:271:A:C6	34:1:271:A:N1	2.14	1.03
34:1:2747:G:N2	34:1:2757:A:H62	1.57	1.01
34:1:281:G:H21	34:1:359:A:H62	1.01	0.99
60:4:22:G:H1	60:4:316:U:H3	1.07	0.95
1:2:410:G:H21	1:2:432:A:H62	0.95	0.94
1:2:765:G:H1	1:2:812:C:HO2'	1.13	0.94
34:1:2747:G:H21	34:1:2757:A:N6	1.63	0.94
34:1:281:G:N2	34:1:359:A:H62	1.65	0.93
34:1:1418:G:N2	34:1:1580:A:C5	2.37	0.92
34:1:2747:G:H21	34:1:2757:A:H62	0.93	0.92
34:1:281:G:H21	34:1:359:A:N6	1.68	0.91
23:8:35:U:C5	23:8:36:U:O4	2.24	0.91
60:4:23:G:H1	60:4:315:U:H3	1.06	0.90
54:U:84:ARG:HB2	54:U:95:LYS:O	1.71	0.90
60:4:280:G:N7	60:4:296:G:C2	2.39	0.90
36:A:44:HIS:HB2	36:A:211:SER:O	1.72	0.90
1:2:410:G:N2	1:2:432:A:H62	1.71	0.88
34:1:2637:U:H3	34:1:2776:A:H62	1.26	0.83
1:2:1058:G:H1	1:2:1199:U:H3	1.24	0.83
1:2:410:G:H21	1:2:432:A:N6	1.77	0.83
34:1:676:A:H8	34:1:2069:G:H21	1.25	0.82
1:2:693:G:C8	24:9:13:U:O4	2.33	0.82
38:C:51:PHE:H	38:C:74:PRO:HG3	1.46	0.80
34:1:639:U:H3	34:1:649:G:H1	1.27	0.80
34:1:1311:G:H21	34:1:1603:A:H62	1.31	0.79
34:1:2096:U:H3	34:1:2193:G:H1	1.28	0.79
34:1:1418:G:H21	34:1:1580:A:N6	1.80	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:2098:U:H3	34:1:2191:G:H1	1.29	0.77
38:C:52:LEU:HB3	38:C:76:ARG:HG3	1.65	0.77
1:2:611:A:H61	1:2:629:G:H1	1.34	0.75
1:2:590:C:H42	1:2:649:G:H1	1.33	0.75
8:m:24:THR:O	8:m:60:ARG:HA	1.86	0.75
35:3:22:U:H3	35:3:61:G:H1	1.33	0.75
24:9:14:U:H5''	24:9:15:C:H5	1.51	0.74
34:1:2010:G:H5''	52:S:42:ARG:HB2	1.70	0.73
34:1:910:A:H62	46:M:12:GLN:HA	1.53	0.73
23:8:35:U:C5	23:8:36:U:C4	2.77	0.72
34:1:1658:C:OP1	38:C:132:HIS:ND1	2.22	0.72
3:h:19:GLU:O	3:h:56:ASP:HA	1.89	0.72
60:4:182:G:N7	60:4:215:G:N2	2.38	0.72
33:e:52:LYS:O	33:e:56:GLU:HB2	1.91	0.71
56:5:9:ARG:O	56:5:13:ASP:HB2	1.90	0.71
1:2:1493:A:H62	56:5:9:ARG:HA	1.56	0.71
34:1:877:U:N3	34:1:899:A:N1	2.37	0.70
34:1:574:C:N3	38:C:145:LYS:NZ	2.40	0.70
34:1:2098:U:O2	34:1:2191:G:N2	2.23	0.70
34:1:1142:U:N3	34:1:1142:U:C1'	2.55	0.70
51:R:36:PRO:HD2	51:R:60:GLU:H	1.57	0.70
2:g:54:THR:HG22	2:g:199:TYR:HB3	1.74	0.69
1:2:1502:A:H2	1:2:1505:G:H1	1.38	0.69
34:1:2060:A:N7	39:D:74:ARG:NH1	2.40	0.69
33:e:32:LEU:HB3	33:e:34:TRP:HB3	1.74	0.69
42:G:24:GLY:O	42:G:28:ASN:HB2	1.92	0.69
46:M:12:GLN:HE21	46:M:72:LYS:HD2	1.57	0.68
34:1:271(H):G:H1	34:1:271(P):C:H42	1.41	0.68
23:8:54:U:H3	23:8:58:A:H62	1.41	0.68
34:1:1817:G:OP1	37:B:88:ARG:NH2	2.27	0.68
43:J:66:LYS:HA	43:J:69:GLN:HB2	1.76	0.68
1:2:1363(A):A:H4'	1:2:1364:U:H5''	1.76	0.68
34:1:2427:C:H5''	34:1:2429:G:H5'	1.76	0.67
46:M:134:ARG:HE	46:M:135:ASP:H	1.43	0.67
50:Q:40:PHE:HB3	51:R:78:LYS:HD2	1.76	0.67
60:4:250:C:N4	60:4:284:A:N1	2.41	0.67
34:1:1212:G:O2'	34:1:1236:G:N2	2.24	0.67
34:1:1311:G:N2	34:1:1603:A:H62	1.93	0.67
35:3:104:U:HO2'	55:V:29:TYR:HH	1.36	0.67
1:2:413:G:N7	4:i:35:ARG:NH2	2.43	0.67
18:w:48:GLY:O	18:w:74:ARG:NH2	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Y:49:LYS:O	27:Y:53:LEU:HB2	1.95	0.67
34:1:1380:G:O2'	34:1:1569:A:N6	2.28	0.67
31:c:13:CYS:HA	31:c:51:GLU:HA	1.77	0.66
34:1:1142:U:N3	34:1:1142:U:O4'	2.28	0.66
34:1:2759:G:N2	41:F:139:GLN:OE1	2.29	0.66
9:n:20:ARG:HB2	9:n:60:ASP:HB3	1.78	0.66
17:v:21:VAL:HG11	17:v:59:ILE:HG13	1.77	0.66
34:1:2632:A:N3	38:C:61:ARG:NH1	2.44	0.66
1:2:522:C:H41	12:q:53:ARG:HH22	1.44	0.66
5:j:78:HIS:HE1	5:j:143:ARG:H	1.43	0.66
34:1:2287:A:H62	34:1:2344:U:H3	1.44	0.66
1:2:165:C:H2'	1:2:166:G:H8	1.61	0.65
26:X:42:GLN:NE2	34:1:2232:U:OP2	2.27	0.65
50:Q:27:LEU:O	50:Q:31:SER:HB3	1.96	0.65
26:X:26:ARG:HB3	26:X:35:THR:HG22	1.77	0.65
34:1:259:G:H21	34:1:621:A:H8	1.45	0.65
58:f:35:ARG:HH21	58:f:37:GLY:HA3	1.59	0.65
1:2:950:U:H3	1:2:1231:G:H1	1.45	0.65
55:V:26:GLY:HA2	55:V:86:VAL:O	1.97	0.65
56:5:31:VAL:HG11	60:4:320:A:H1'	1.79	0.65
1:2:594:G:N2	1:2:646:U:O2	2.29	0.65
36:A:121:GLY:HA2	36:A:143:GLY:H	1.61	0.65
30:b:4:HIS:O	34:1:2056:G:N2	2.29	0.65
34:1:571:A:H5'	34:1:2030:A:H62	1.60	0.65
34:1:2298:A:H62	34:1:2318:G:H8	1.43	0.65
34:1:270:A:N6	34:1:271:A:N7	2.44	0.65
34:1:2014:A:H4'	52:S:92:ARG:HH22	1.60	0.65
1:2:190:U:H3	20:y:105:SER:HG	0.70	0.65
34:1:1779:U:OP2	34:1:1784:A:N6	2.29	0.65
1:2:262:A:H4'	20:y:75:ASN:HB3	1.79	0.64
25:W:55:ARG:NH1	34:1:2387:U:OP1	2.31	0.64
34:1:527:C:N4	34:1:2779:U:OP1	2.30	0.64
44:K:68:GLU:OE1	44:K:78:ARG:NH1	2.30	0.64
34:1:1340:U:OP2	53:T:76:ARG:NH2	2.30	0.64
34:1:1682:G:OP2	34:1:1699:G:N2	2.30	0.64
34:1:2822:G:N7	47:N:2:ARG:NH2	2.46	0.64
1:2:429:U:H6	4:i:25:ARG:HH22	1.45	0.64
1:2:676:A:H5''	11:p:113:PRO:HB2	1.80	0.64
34:1:1283:G:N2	34:1:1286:A:OP2	2.30	0.64
45:L:86:LYS:HB3	45:L:118:GLY:HA3	1.80	0.64
1:2:977:A:OP1	14:s:31:ARG:NH1	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:2392:A:H2	34:1:2424:C:H42	1.45	0.64
33:e:30:ARG:HE	45:L:62:LEU:HD12	1.63	0.64
19:x:50:ALA:HB1	19:x:57:HIS:HB3	1.80	0.64
34:1:271:A:N6	34:1:271:A:N9	2.45	0.64
34:1:1282:U:H3	34:1:1286:A:H62	1.45	0.64
52:S:6:ILE:HA	52:S:103:ILE:O	1.98	0.64
1:2:1308:U:OP1	13:r:98:VAL:N	2.30	0.64
22:7:15:G:N2	22:7:21:A:N3	2.45	0.64
34:1:1902:C:O2	37:B:244:ARG:NH2	2.31	0.64
51:R:25:LEU:H	51:R:94:LEU:HD13	1.63	0.64
1:2:926:G:N2	24:9:15:C:OP2	2.31	0.63
2:g:98:LEU:H	2:g:101:MET:HE3	1.63	0.63
34:1:240:G:O2'	34:1:257:A:N6	2.32	0.63
1:2:1240:U:OP1	7:l:119:ARG:NH2	2.31	0.63
37:B:81:ALA:HB3	37:B:94:LEU:HB3	1.80	0.63
1:2:189(B):C:H42	1:2:189(J):G:H1	1.46	0.63
1:2:891:U:H2'	1:2:892:A:H8	1.63	0.63
9:n:40:LEU:HB2	9:n:43:ALA:HB2	1.80	0.63
41:F:23:ARG:HD3	41:F:34:GLU:HB3	1.78	0.63
34:1:2303:G:N3	40:E:132:ASN:ND2	2.45	0.63
8:m:18:ARG:NH2	8:m:81:HIS:O	2.31	0.63
34:1:1060:U:N3	34:1:1088:A:N7	2.44	0.63
34:1:495:G:H21	52:S:61:ASN:HD21	1.47	0.62
34:1:1540:U:H3'	34:1:1541:G:H3'	1.80	0.62
44:K:15:GLY:HA2	44:K:47:ILE:HB	1.79	0.62
53:T:27:THR:HG22	53:T:78:LYS:HB3	1.80	0.62
5:j:51:VAL:HG21	56:5:140:ALA:HB1	1.81	0.62
34:1:677:A:HO2'	34:1:2070:G:HO2'	1.45	0.62
1:2:437:U:H5''	4:i:155:LEU:HD11	1.81	0.62
34:1:392:C:H5''	34:1:409:C:H5''	1.80	0.62
23:8:54:U:N3	23:8:58:A:N6	2.47	0.62
23:8:75:C:H5''	23:8:76:A:H5'	1.80	0.62
54:U:50:ARG:NH2	54:U:55:TYR:O	2.33	0.62
1:2:1139:G:H1	1:2:1144:G:H1	1.48	0.62
1:2:1401:G:O6	1:2:1504:G:N2	2.33	0.62
34:1:2031:A:O2'	34:1:2454:G:N2	2.33	0.62
41:F:23:ARG:O	41:F:25:LYS:NZ	2.33	0.62
47:N:38:VAL:HG22	47:N:112:ALA:HB2	1.82	0.62
33:e:59:LYS:HD3	45:L:50:ARG:HG2	1.80	0.62
40:E:112:PRO:HA	40:E:113:ARG:HE	1.65	0.62
47:N:12:ARG:O	47:N:17:ARG:NH1	2.33	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:N:9:LYS:HG2	47:N:43:GLU:HG3	1.82	0.62
4:i:47:ARG:NH1	56:5:142:GLU:O	2.33	0.62
18:w:32:ARG:HA	18:w:69:THR:HG21	1.82	0.62
19:x:67:VAL:H	29:a:49:PHE:HE2	1.48	0.62
34:1:807:U:O2'	34:1:2060:A:N1	2.32	0.62
37:B:62:TYR:HA	37:B:87:ASN:HD21	1.65	0.61
34:1:271(A):A:N7	34:1:271(W):G:N2	2.47	0.61
60:4:249:C:N4	60:4:251:G:O6	2.32	0.61
1:2:1442:G:O6	1:2:1461:G:N2	2.33	0.61
10:o:48:THR:HG23	10:o:62:HIS:HB3	1.82	0.61
39:D:167:ALA:HB1	39:D:173:VAL:HG11	1.81	0.61
46:M:54:MET:HG2	46:M:117:ALA:HB1	1.81	0.61
1:2:429:U:OP2	4:i:36:ARG:NH2	2.32	0.61
1:2:831:U:N3	1:2:832:C:N4	2.49	0.61
1:2:1139:G:H4'	1:2:1140:C:H5'	1.83	0.61
24:9:14:U:H5''	24:9:15:C:C5	2.34	0.61
34:1:2099:U:O2	34:1:2190:G:N2	2.33	0.61
34:1:2305:A:H5''	40:E:134:GLY:HA3	1.82	0.61
35:3:30:C:H1'	35:3:57:A:H61	1.66	0.61
37:B:160:GLY:H	37:B:196:VAL:HB	1.65	0.61
1:2:656:C:O2	15:t:28:GLN:NE2	2.34	0.61
34:1:271(R):G:H2'	34:1:271(S):G:H8	1.65	0.61
34:1:1854:A:H62	34:1:1888:G:H8	1.48	0.61
34:1:2507:C:O2'	60:4:348:C:O2	2.16	0.61
34:1:2680:C:OP2	38:C:111:ARG:NH2	2.33	0.61
39:D:124:LEU:HB3	39:D:193:VAL:HG22	1.83	0.61
26:X:8:SER:N	34:1:1365:A:OP2	2.34	0.61
60:4:35:G:H21	60:4:36:C:H41	1.47	0.61
1:2:838:G:N2	1:2:849:C:O2	2.33	0.61
1:2:1417:G:O2'	1:2:1483:A:N6	2.34	0.61
34:1:1247:A:OP2	45:L:18:ARG:NH2	2.34	0.61
34:1:2473:U:OP1	34:1:2529:G:N2	2.33	0.61
1:2:315:A:O2'	1:2:330:C:O2'	2.19	0.60
1:2:429:U:O2'	4:i:22:LYS:NZ	2.34	0.60
34:1:323:G:HO2'	34:1:1205:U:H3	1.49	0.60
34:1:2571:C:H5''	34:1:2572:A:H5''	1.83	0.60
1:2:1433:A:OP1	49:P:108:ARG:NH2	2.34	0.60
13:r:80:ARG:NH1	19:x:65:ASN:O	2.34	0.60
34:1:1418:G:N2	34:1:1580:A:C6	2.54	0.60
15:t:12:ILE:O	15:t:16:ALA:HB2	2.02	0.60
30:b:9:LYS:NZ	34:1:2018:G:OP1	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:2822:G:OP2	47:N:2:ARG:NH1	2.34	0.60
2:g:42:ILE:HD11	2:g:202:PRO:HB2	1.82	0.60
30:b:13:LYS:HG3	30:b:16:ARG:HH21	1.65	0.60
32:d:10:ARG:NH2	34:1:125:G:O6	2.34	0.60
60:4:146:U:O2'	60:4:216:A:N6	2.35	0.60
25:W:47:PRO:HG3	25:W:53:MET:HB2	1.82	0.60
26:X:78:LYS:NZ	26:X:93:GLU:O	2.30	0.60
34:1:529:A:H62	34:1:2041:U:H3	1.49	0.60
40:E:41:GLN:HB2	40:E:90:LEU:HB2	1.82	0.60
43:J:4:TYR:HB3	50:Q:64:ARG:HH22	1.66	0.60
56:5:82:HIS:O	56:5:86:LEU:HB2	2.02	0.60
1:2:954:G:H21	1:2:1227:A:H62	1.49	0.60
9:n:95:LYS:HE3	9:n:96:LEU:HD23	1.83	0.60
33:e:43:GLN:NE2	34:1:2365:G:O6	2.33	0.60
34:1:768:G:O2'	34:1:1379:A:N6	2.31	0.60
23:8:54:U:H3	23:8:58:A:N6	2.00	0.60
25:W:24:LYS:NZ	34:1:2355:C:O2'	2.35	0.60
34:1:453:C:O2	34:1:457:A:O2'	2.20	0.60
34:1:1678:G:N2	34:1:1990:C:O2	2.32	0.60
1:2:924:C:O2'	1:2:1502:A:N6	2.29	0.60
9:n:13:ALA:HB2	9:n:68:GLY:HA3	1.83	0.60
34:1:994:C:OP2	50:Q:54:LYS:NZ	2.34	0.60
40:E:114:ILE:HB	40:E:117:PHE:HB2	1.84	0.60
54:U:84:ARG:O	54:U:94:LYS:HA	2.01	0.60
1:2:1003:G:H2'	1:2:1004:A:H4'	1.84	0.59
13:r:19:LEU:HD13	13:r:22:ILE:HD13	1.84	0.59
32:d:11:LYS:NZ	34:1:686:G:OP1	2.34	0.59
1:2:1307:U:OP1	13:r:101:GLN:NE2	2.35	0.59
9:n:96:LEU:O	9:n:100:GLY:N	2.34	0.59
23:8:54:U:O4	23:8:58:A:N7	2.36	0.59
26:X:52:ARG:HG2	26:X:59:THR:HG22	1.83	0.59
60:4:285:C:N4	60:4:294:U:O2'	2.35	0.59
1:2:1147:C:O2	9:n:16:ARG:NH2	2.36	0.59
26:X:20:ARG:NH2	26:X:39:LYS:O	2.35	0.59
34:1:993:G:OP1	50:Q:50:ARG:NH2	2.35	0.59
37:B:175:LEU:O	37:B:182:LEU:HA	2.03	0.59
45:L:81:GLN:HG2	45:L:106:LEU:HA	1.84	0.59
60:4:17:C:OP2	60:4:319:G:N2	2.35	0.59
60:4:318:G:OP1	60:4:321:C:N4	2.35	0.59
34:1:1112:G:N3	34:1:1113:U:N3	2.46	0.59
1:2:545:C:H5''	4:i:72:GLU:HG2	1.82	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1010:G:H2'	1:2:1011:G:H8	1.67	0.59
34:1:2701:C:H3'	34:1:2702:U:H5''	1.84	0.59
46:M:81:VAL:O	46:M:82:ARG:NH1	2.31	0.59
2:g:15:VAL:HG23	2:g:209:ARG:HH21	1.68	0.59
8:m:1:MET:N	8:m:1:MET:SD	2.74	0.59
34:1:993:G:N2	51:R:91:TYR:OH	2.32	0.59
34:1:1093:G:O2'	34:1:1100:C:N4	2.36	0.59
1:2:912:C:OP2	12:q:89:ARG:NH2	2.36	0.59
12:q:27:LEU:HD23	12:q:62:SER:HB3	1.84	0.59
24:9:14:U:H3'	24:9:15:C:C6	2.38	0.59
33:e:10:ALA:O	33:e:14:VAL:HB	2.02	0.59
34:1:1889:A:N3	34:1:2086:U:O2'	2.34	0.59
35:3:87:G:N2	35:3:90:A:OP2	2.35	0.59
1:2:261:U:OP2	20:y:79:ARG:NH2	2.34	0.59
1:2:884:U:H4'	1:2:885:G:H5''	1.84	0.59
2:g:63:MET:SD	2:g:64:ARG:NH1	2.76	0.59
3:h:13:GLY:HA3	14:s:57:ARG:HE	1.67	0.59
5:j:79:GLU:HG2	5:j:92:LYS:HE2	1.85	0.59
30:b:19:ARG:NH2	34:1:1264:G:OP1	2.28	0.59
34:1:1841:U:O2	37:B:244:ARG:NH2	2.36	0.59
34:1:2122:U:H3	34:1:2176:A:H61	1.51	0.59
1:2:1289:A:H5''	21:z:10:ARG:HH21	1.68	0.59
29:a:5:ILE:HG23	40:E:67:LYS:HE3	1.85	0.59
32:d:37:LYS:NZ	34:1:468:G:OP2	2.34	0.59
34:1:1141:U:HO3'	34:1:1142:U:HO2'	1.48	0.59
34:1:2099:U:H3	34:1:2190:G:H1	1.48	0.59
6:k:8:ILE:HB	6:k:61:LEU:HB2	1.85	0.58
31:c:13:CYS:O	31:c:21:TYR:HA	2.03	0.58
1:2:392:G:OP1	16:u:8:ARG:NH2	2.36	0.58
1:2:1286:A:H2'	1:2:1287:A:H4'	1.85	0.58
3:h:6:HIS:HD2	3:h:8:ILE:H	1.51	0.58
13:r:19:LEU:HD21	13:r:56:LEU:HD21	1.85	0.58
23:8:22:G:H2'	23:8:23:A:H8	1.68	0.58
34:1:897:C:H1'	34:1:899:A:H62	1.68	0.58
34:1:2199:A:H5'	34:1:2200:C:H5	1.68	0.58
41:F:41:MET:HG3	41:F:54:ARG:HA	1.85	0.58
44:K:6:THR:O	44:K:20:MET:HA	2.02	0.58
1:2:12:U:H3	1:2:22:G:H1	1.50	0.58
1:2:674:G:H2'	1:2:675:A:H8	1.67	0.58
2:g:93:VAL:HG11	2:g:97:TRP:HD1	1.67	0.58
20:y:26:ASN:HB2	20:y:71:THR:HG23	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:698:C:OP1	34:1:1634:A:N6	2.36	0.58
1:2:946:A:H2'	1:2:947:G:C8	2.39	0.58
8:m:18:ARG:NH1	8:m:78:GLN:OE1	2.36	0.58
12:q:90:VAL:O	12:q:92:ASP:N	2.37	0.58
34:1:1693:U:OP2	34:1:1694:C:N4	2.36	0.58
37:B:218:ARG:HG2	37:B:219:PRO:HD2	1.86	0.58
48:O:16:ASN:HB2	48:O:90:GLY:HA2	1.85	0.58
1:2:1254:C:OP2	10:o:43:ARG:NH2	2.36	0.58
33:e:31:HIS:O	34:1:2420:C:N4	2.34	0.58
34:1:1626:G:H5''	34:1:1627:G:H5'	1.86	0.58
1:2:189:G:H2'	1:2:189(L):G:H21	1.67	0.58
1:2:826:C:O2	8:m:15:ASN:ND2	2.36	0.58
1:2:976:G:OP2	1:2:1358:U:O2'	2.21	0.58
3:h:23:TYR:OH	10:o:9:ARG:NH1	2.37	0.58
6:k:55:ASP:HB2	6:k:86:ARG:HH12	1.69	0.58
34:1:404:C:H4'	34:1:405:U:H5'	1.86	0.58
34:1:629:G:N3	34:1:639:U:O2'	2.36	0.58
1:2:611:A:N6	1:2:629:G:H1	2.00	0.58
1:2:693:G:N7	24:9:13:U:O4	2.36	0.58
32:d:14:LYS:NZ	34:1:771:G:OP1	2.35	0.58
34:1:2547:U:O2	44:K:23:ARG:NH2	2.35	0.58
43:J:24:GLY:HA2	43:J:106:MET:HE1	1.86	0.58
43:J:128:HIS:NE2	43:J:131:GLN:OE1	2.37	0.58
1:2:1009:G:H2'	1:2:1010:G:H8	1.69	0.58
1:2:1359:C:O2'	1:2:1362:C:N4	2.33	0.58
3:h:119:ARG:NH1	3:h:123:GLN:OE1	2.36	0.58
4:i:145:GLU:HG2	4:i:184:LYS:HG2	1.85	0.58
19:x:41:VAL:HB	19:x:44:MET:HB2	1.86	0.58
1:2:1013:G:N2	1:2:1016:A:OP2	2.37	0.58
26:X:35:THR:OG1	26:X:36:GLY:N	2.37	0.58
34:1:366:C:H5'	34:1:370:G:H5'	1.86	0.58
34:1:1035:U:OP1	41:F:59:ARG:NH1	2.37	0.58
34:1:1500:G:N2	37:B:99:ASP:O	2.37	0.58
34:1:1568:G:OP1	37:B:63:ARG:NH1	2.33	0.58
34:1:2528:U:H2'	34:1:2530:A:H5''	1.86	0.58
39:D:116:ASP:OD1	39:D:119:ARG:NH2	2.37	0.58
52:S:97:LYS:HE2	52:S:99:ARG:HE	1.69	0.58
1:2:758:G:O6	15:t:65:ARG:NH2	2.36	0.58
2:g:9:GLU:HA	2:g:12:GLU:HB3	1.86	0.58
3:h:119:ARG:NH2	60:4:121:U:O4	2.36	0.58
13:r:65:LYS:HG3	13:r:70:LEU:HB2	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:1694:C:O2	34:1:1695:G:N2	2.37	0.58
38:C:101:ARG:O	38:C:201:THR:OG1	2.21	0.58
33:e:42:ARG:NH2	34:1:2348:U:OP2	2.37	0.57
34:1:956:G:OP2	46:M:14:ARG:NH2	2.37	0.57
34:1:1541:G:H1'	34:1:1542:A:C4	2.38	0.57
34:1:2061:G:OP1	39:D:68:LYS:NZ	2.37	0.57
1:2:606:G:O2'	1:2:632:A:N6	2.37	0.57
17:v:56:VAL:HB	17:v:78:GLU:HB3	1.86	0.57
34:1:942:G:O2'	34:1:1189:A:N3	2.36	0.57
34:1:2467:C:O2	46:M:124:LYS:NZ	2.37	0.57
53:T:53:LYS:HB3	53:T:80:ILE:HD12	1.85	0.57
1:2:624:C:H4'	16:u:10:GLY:HA2	1.85	0.57
1:2:673:G:H2'	1:2:674:G:C8	2.38	0.57
28:Z:49:LYS:NZ	34:1:850:C:O3'	2.37	0.57
31:c:40:CYS:SG	34:1:2370:G:N2	2.77	0.57
34:1:272(E):G:N1	34:1:363:G:O3'	2.36	0.57
34:1:1340:U:OP1	53:T:16:LYS:NZ	2.37	0.57
34:1:1448:G:H21	34:1:1528(A):A:H2	1.52	0.57
34:1:2680:C:H5'	38:C:189:PRO:HA	1.86	0.57
24:9:14:U:C5'	24:9:15:C:H5	2.16	0.57
34:1:614(A):U:H1'	34:1:614(B):G:H4'	1.87	0.57
34:1:840:C:OP2	34:1:932:G:N2	2.31	0.57
34:1:1710:C:O2'	34:1:2858:C:N3	2.37	0.57
1:2:727:G:N2	1:2:730:G:OP2	2.38	0.57
10:o:51:ARG:NH2	10:o:61:GLU:OE1	2.37	0.57
1:2:944:G:N1	1:2:1338:G:OP2	2.35	0.57
11:p:17:GLY:O	11:p:80:VAL:HA	2.04	0.57
34:1:1655:A:N6	34:1:2005:A:O2'	2.37	0.57
34:1:2258:C:O2'	34:1:2427:C:OP2	2.23	0.57
34:1:2472:G:H22	34:1:2477:C:H5'	1.69	0.57
36:A:24:GLU:HB3	36:A:27:ARG:HD3	1.86	0.57
42:G:40:THR:O	42:G:44:LEU:HB2	2.04	0.57
60:4:23:G:N2	60:4:315:U:O2	2.31	0.57
1:2:1179:A:OP2	9:n:93:ARG:NH2	2.38	0.57
12:q:38:THR:N	12:q:57:LYS:O	2.38	0.57
23:8:6:G:H1	23:8:67:C:H42	1.52	0.57
56:5:40:ASP:N	56:5:40:ASP:OD1	2.37	0.57
34:1:18:C:O2'	34:1:554:U:OP1	2.23	0.57
34:1:30:G:O2'	34:1:1214:A:N3	2.32	0.57
34:1:598:G:N2	39:D:35:GLU:OE2	2.36	0.57
35:3:106:G:H5'	55:V:31:ARG:HD2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:4:40:G:O6	60:4:300:C:N4	2.37	0.57
60:4:46:C:O2'	60:4:47:G:N7	2.34	0.57
1:2:974:A:OP2	14:s:41:ARG:NH1	2.37	0.57
6:k:50:TYR:OH	18:w:74:ARG:O	2.22	0.57
31:c:36:LEU:O	31:c:37:ARG:NH1	2.38	0.57
54:U:13:VAL:HG22	54:U:74:PRO:HA	1.86	0.57
1:2:34:C:H2'	1:2:35:G:H8	1.69	0.57
1:2:108:G:N2	1:2:109:A:N1	2.52	0.57
13:r:24:GLY:O	13:r:29:ARG:NH1	2.38	0.57
16:u:21:VAL:HG23	16:u:33:ILE:HB	1.87	0.57
33:e:46:ARG:NH2	34:1:631:A:OP2	2.38	0.57
34:1:960:A:H61	46:M:82:ARG:HH21	1.52	0.57
34:1:1827:C:OP2	37:B:222:ARG:NH1	2.34	0.57
41:F:47:GLU:OE2	41:F:51:ARG:NH1	2.36	0.57
45:L:58:THR:O	45:L:61:ARG:NE	2.36	0.57
59:H:26:UNK:HA	59:H:84:UNK:HA	1.87	0.57
1:2:65:U:H5'	1:2:200:G:H5'	1.87	0.56
8:m:46:LYS:HB2	8:m:62:TYR:HB2	1.87	0.56
17:v:10:VAL:HA	17:v:21:VAL:HA	1.87	0.56
34:1:562:U:O2'	34:1:572:A:O4'	2.22	0.56
1:2:505:G:H5'	1:2:534:U:H2'	1.87	0.56
34:1:1362:C:HO2'	34:1:1810:A:HO2'	1.49	0.56
34:1:2790:A:O2'	34:1:2893:G:N2	2.37	0.56
37:B:143:HIS:ND1	37:B:194:GLY:O	2.38	0.56
60:4:52:G:H1'	60:4:71:A:H62	1.68	0.56
1:2:28:G:O2'	1:2:296:U:OP1	2.24	0.56
1:2:346:G:OP1	49:P:41:ARG:NH2	2.38	0.56
1:2:1516:G:N2	1:2:1519:A:OP2	2.38	0.56
7:l:86:GLN:O	7:l:148:ASN:ND2	2.38	0.56
34:1:307:G:N2	34:1:310:A:OP2	2.38	0.56
34:1:2521:C:O2'	34:1:2564:A:N3	2.31	0.56
41:F:23:ARG:NH1	41:F:34:GLU:O	2.39	0.56
49:P:11:GLU:O	49:P:13:ARG:NH1	2.38	0.56
1:2:189(H):G:N2	1:2:189(I):G:O6	2.38	0.56
1:2:297:G:N2	1:2:300:A:OP2	2.38	0.56
1:2:995:C:N4	1:2:1046:A:N3	2.51	0.56
13:r:45:VAL:HG12	13:r:48:LEU:HD12	1.88	0.56
22:7:54:5MU:H72	22:7:55:U:C4	2.40	0.56
23:8:17:C:N4	34:1:2180:U:O3'	2.39	0.56
30:b:33:CYS:HB2	30:b:40:LYS:HG3	1.87	0.56
34:1:996:A:H5'	50:Q:94:ASN:HB2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:2245:U:H5'	34:1:2246:G:H5'	1.87	0.56
40:E:83:ARG:HG3	40:E:84:LYS:HG2	1.87	0.56
1:2:818:G:N2	1:2:873:A:OP1	2.36	0.56
1:2:1059:C:O3'	14:s:45:ARG:NH2	2.39	0.56
1:2:1134:G:N2	1:2:1141:C:O2	2.33	0.56
11:p:109:VAL:HG22	18:w:86:VAL:HG22	1.88	0.56
43:J:131:GLN:HG2	43:J:133:GLN:H	1.70	0.56
53:T:86:GLY:O	53:T:87:GLN:NE2	2.38	0.56
60:4:303:G:H3'	60:4:304:C:H4'	1.87	0.56
39:D:20:LEU:HD23	39:D:21:ALA:H	1.70	0.56
39:D:60:SER:OG	39:D:61:GLY:N	2.36	0.56
1:2:1492:A:H3'	1:2:1493:A:C5'	2.35	0.56
22:7:9:G:N2	22:7:45:G:N7	2.53	0.56
34:1:397:G:O2'	34:1:2230:G:N2	2.36	0.56
60:4:196:A:N6	60:4:225:G:OP2	2.39	0.56
1:2:110:C:O2'	16:u:25:ARG:O	2.24	0.56
1:2:193:C:OP1	20:y:57:ARG:NH1	2.39	0.56
1:2:1317:C:O2	19:x:37:ARG:NH1	2.38	0.56
4:i:153:ARG:NH2	4:i:180:GLY:O	2.36	0.56
8:m:92:ARG:NH1	8:m:132:GLU:OE2	2.38	0.56
11:p:81:ASP:OD1	11:p:107:SER:OG	2.23	0.56
16:u:4:ILE:HG12	16:u:21:VAL:HG12	1.88	0.56
34:1:1070:A:OP1	34:1:1075:C:N4	2.39	0.56
34:1:1696:G:N2	34:1:1977:A:O2'	2.38	0.56
34:1:1819:A:H5''	37:B:161:THR:HG21	1.87	0.56
9:n:3:GLN:HG2	9:n:20:ARG:HH12	1.71	0.56
10:o:30:SER:OG	10:o:80:LYS:O	2.24	0.56
10:o:33:GLN:NE2	10:o:34:VAL:O	2.39	0.56
19:x:46:GLY:H	19:x:62:ILE:HG13	1.71	0.56
30:b:16:ARG:HD3	34:1:1263:U:H5''	1.87	0.56
34:1:1586:A:H3'	34:1:1587:A:H8	1.71	0.56
38:C:4:ILE:HG22	38:C:198:VAL:HB	1.87	0.56
1:2:176:C:OP1	20:y:29:LYS:NZ	2.39	0.56
1:2:978:A:O2'	1:2:1322:C:N3	2.39	0.56
1:2:1239:A:H2'	1:2:1298:C:H42	1.71	0.56
2:g:209:ARG:NH1	2:g:236:TYR:OH	2.38	0.56
7:l:118:VAL:O	7:l:122:HIS:ND1	2.35	0.56
24:9:14:U:H3'	24:9:15:C:C5	2.40	0.56
34:1:270:A:OP2	34:1:271(X):G:N1	2.39	0.56
49:P:3:ARG:HB2	49:P:6:LEU:HB2	1.87	0.56
53:T:32:PRO:HB3	53:T:75:ASP:H	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:26:A:O2'	4:i:209:ARG:NH2	2.36	0.55
1:2:235:C:OP1	17:v:70:ARG:NH1	2.39	0.55
1:2:1305:G:OP2	21:z:2:GLY:N	2.39	0.55
19:x:9:VAL:HG21	29:a:59:PHE:HB3	1.88	0.55
34:1:975:C:O2'	34:1:976:C:OP2	2.23	0.55
34:1:1266:G:O2'	34:1:2012:G:O6	2.23	0.55
34:1:1902:C:OP1	37:B:242:ARG:NH1	2.39	0.55
34:1:2646:C:OP2	34:1:2732:G:O2'	2.21	0.55
58:f:11:CYS:SG	58:f:12:ASP:N	2.78	0.55
1:2:401:C:O2'	1:2:621:A:N3	2.36	0.55
1:2:1224:G:N2	1:2:1363:C:OP2	2.39	0.55
1:2:1493:A:N6	56:5:12:HIS:HB3	2.21	0.55
3:h:44:GLU:HA	3:h:52:LEU:HD21	1.89	0.55
18:w:47:THR:O	18:w:83:GLU:N	2.38	0.55
37:B:148:GLU:OE1	37:B:151:LYS:NZ	2.37	0.55
46:M:52:VAL:HA	46:M:55:VAL:HG12	1.87	0.55
56:5:72:ASP:N	56:5:72:ASP:OD1	2.39	0.55
1:2:1119:C:OP1	9:n:83:ARG:NH1	2.40	0.55
34:1:1192:G:OP2	45:L:21:ARG:NH1	2.39	0.55
41:F:24:VAL:HG21	41:F:72:ILE:HG12	1.88	0.55
23:8:16:U:N3	23:8:19:G:OP2	2.40	0.55
34:1:679:C:H2'	34:1:680:G:H8	1.71	0.55
34:1:987:G:O2'	34:1:1000:A:N3	2.36	0.55
44:K:98:VAL:HG12	44:K:117:LEU:HD23	1.88	0.55
60:4:30:C:H41	60:4:309:G:H21	1.54	0.55
1:2:880:C:OP1	12:q:8:ASN:ND2	2.39	0.55
1:2:1071:C:H2'	1:2:1072:G:H8	1.72	0.55
17:v:22:LEU:HD13	17:v:41:LYS:HG3	1.87	0.55
60:4:244:C:N4	60:4:255:G:O6	2.39	0.55
1:2:7:G:O2'	5:j:120:THR:O	2.25	0.55
34:1:863:A:H2'	34:1:864:G:C8	2.42	0.55
34:1:1012:U:OP1	50:Q:75:ASN:ND2	2.40	0.55
34:1:1020:A:N1	34:1:1141:U:O2'	2.31	0.55
34:1:1069:A:O2'	34:1:1074:G:O6	2.25	0.55
34:1:2681:C:H5	34:1:2725:A:H62	1.54	0.55
45:L:81:GLN:HB3	45:L:106:LEU:HD12	1.88	0.55
45:L:97:PRO:HA	45:L:100:LEU:HB2	1.89	0.55
48:O:33:LYS:O	48:O:62:LYS:NZ	2.39	0.55
1:2:779:C:OP1	11:p:122:LYS:NZ	2.39	0.55
21:z:17:THR:O	21:z:22:ARG:NH1	2.39	0.55
22:7:14:A:C5	22:7:15:G:H1'	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:W:12:ASN:ND2	34:1:2278:A:OP2	2.40	0.55
28:Z:29:ARG:NH2	34:1:931:G:OP1	2.40	0.55
34:1:1721:G:H8	34:1:1741:A:H62	1.53	0.55
44:K:104:ARG:NH2	44:K:121:VAL:O	2.39	0.55
46:M:34:LEU:HB2	46:M:118:LEU:HD22	1.89	0.55
1:2:757:U:O2'	1:2:879:C:O2	2.24	0.55
1:2:1493:A:C6	56:5:12:HIS:HB3	2.42	0.55
9:n:10:ARG:HD3	9:n:11:LYS:HB2	1.89	0.55
16:u:20:VAL:HG23	16:u:35:LYS:HA	1.88	0.55
23:8:35:U:C4	23:8:36:U:O4	2.60	0.55
34:1:321:G:O2'	34:1:340:A:N3	2.40	0.55
34:1:2345:G:O6	34:1:2371:G:N2	2.39	0.55
48:O:27:SER:HA	48:O:88:ASP:HB3	1.89	0.55
50:Q:90:VAL:HG12	51:R:39:LEU:HB3	1.87	0.55
1:2:159:G:N2	1:2:162:A:OP2	2.39	0.55
1:2:413:G:N2	1:2:429:U:OP2	2.40	0.55
1:2:715:A:H2'	1:2:716:A:C8	2.42	0.55
18:w:51:LEU:HD22	18:w:55:ARG:HG2	1.89	0.55
37:B:94:LEU:HD11	37:B:102:LYS:HB3	1.89	0.55
39:D:126:VAL:HG21	39:D:142:TRP:HZ2	1.72	0.55
1:2:269:C:H2'	1:2:270:A:H8	1.71	0.55
7:l:40:ALA:HB3	9:n:41:VAL:HG21	1.89	0.55
30:b:16:ARG:NH2	34:1:517:C:OP1	2.40	0.55
34:1:1000:A:OP2	34:1:1154:G:N1	2.35	0.55
34:1:2500:U:O2'	34:1:2504:U:OP1	2.25	0.55
36:A:62:VAL:HG23	36:A:64:LEU:HB2	1.89	0.55
39:D:127:GLU:HB2	39:D:196:LEU:HD23	1.88	0.55
1:2:427:U:OP1	4:i:13:ARG:NH2	2.40	0.54
1:2:1329:A:OP2	21:z:7:ARG:NH2	2.38	0.54
34:1:829:A:N7	34:1:2247:A:O2'	2.40	0.54
55:V:10:ARG:HH21	55:V:36:LYS:HD2	1.72	0.54
1:2:279:A:N6	17:v:98:LEU:O	2.40	0.54
1:2:543:C:OP2	4:i:10:ARG:NH2	2.41	0.54
18:w:21:LYS:NZ	18:w:54:ARG:O	2.39	0.54
34:1:814:C:OP2	45:L:27:HIS:ND1	2.31	0.54
34:1:1227:G:OP2	50:Q:16:LYS:NZ	2.40	0.54
34:1:2115:G:O2'	34:1:2117:A:N6	2.40	0.54
34:1:2315:G:OP1	40:E:36:LYS:NZ	2.40	0.54
49:P:60:THR:HG22	49:P:75:ILE:HG22	1.89	0.54
25:W:1:MET:N	34:1:2452:C:OP1	2.39	0.54
1:2:1281:U:H5'	1:2:1282:C:H5	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:j:20:GLN:OE1	5:j:25:ARG:NE	2.34	0.54
5:j:48:ALA:HB2	5:j:57:LYS:HD3	1.90	0.54
13:r:88:ARG:O	13:r:92:HIS:ND1	2.40	0.54
34:1:270:A:N1	34:1:365:C:O2'	2.41	0.54
34:1:577:G:O2'	34:1:1254:A:OP1	2.24	0.54
34:1:839:U:O2'	34:1:1191:G:N3	2.40	0.54
34:1:1353:A:H4'	37:B:38:LYS:HE2	1.90	0.54
35:3:24:G:N3	35:3:27:C:N4	2.55	0.54
40:E:145:THR:OG1	40:E:146:TYR:N	2.38	0.54
1:2:517:G:N2	1:2:530:G:OP1	2.41	0.54
9:n:96:LEU:HA	9:n:99:LEU:HB2	1.90	0.54
16:u:72:ARG:HE	16:u:73:LEU:HD22	1.72	0.54
16:u:81:ARG:NH1	16:u:83:GLU:OE2	2.39	0.54
34:1:2159:G:N2	34:1:2160:G:O6	2.39	0.54
53:T:77:LYS:HD2	53:T:78:LYS:HD3	1.89	0.54
53:T:77:LYS:HG3	53:T:78:LYS:HG2	1.89	0.54
1:2:890:G:O2'	1:2:906:G:O6	2.24	0.54
1:2:1071:C:H5''	5:j:49:PRO:HG2	1.88	0.54
8:m:14:ARG:NH2	8:m:83:ILE:O	2.41	0.54
26:X:86:SER:O	26:X:86:SER:OG	2.24	0.54
34:1:2867:G:OP2	49:P:119:LYS:NZ	2.32	0.54
53:T:63:LYS:HB2	53:T:70:LEU:HB2	1.89	0.54
1:2:362:G:N1	1:2:365:U:OP2	2.40	0.54
2:g:19:HIS:NE2	2:g:206:ASP:OD2	2.41	0.54
16:u:13:HIS:O	16:u:42:ARG:NH2	2.40	0.54
19:x:31:ILE:HG23	19:x:49:ILE:HA	1.90	0.54
34:1:327:G:N2	34:1:336:C:N3	2.55	0.54
34:1:1418:G:N2	34:1:1580:A:N6	2.51	0.54
56:5:55:LEU:HB2	56:5:79:LEU:HD13	1.89	0.54
2:g:84:GLU:HG2	2:g:233:SER:HB3	1.90	0.54
8:m:17:THR:O	8:m:78:GLN:NE2	2.41	0.54
11:p:109:VAL:HG11	18:w:84:LYS:HD2	1.89	0.54
23:8:54:U:C2	23:8:58:A:N6	2.75	0.54
34:1:1041:C:H2'	34:1:1042:G:H4'	1.89	0.54
34:1:1299:G:N1	34:1:1640:C:OP2	2.39	0.54
34:1:1853:A:N6	34:1:1889:A:N7	2.56	0.54
34:1:2666:C:O2	41:F:152:ARG:NH2	2.41	0.54
35:3:88:C:H41	35:3:89:G:H21	1.56	0.54
39:D:200:GLU:O	39:D:204:ASN:ND2	2.39	0.54
40:E:138:GLN:HB2	40:E:155:MET:HE3	1.89	0.54
1:2:643:C:H2'	1:2:644:G:H8	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:946:A:H2'	1:2:947:G:H8	1.73	0.54
1:2:1218:C:H2'	1:2:1219:U:C6	2.43	0.54
1:2:1325:C:OP2	21:z:6:ARG:NH2	2.42	0.54
4:i:61:LYS:HZ3	4:i:65:ARG:HD3	1.72	0.54
25:W:72:ARG:HB2	25:W:75:LEU:HB2	1.90	0.54
47:N:103:ARG:NH1	47:N:108:GLY:O	2.40	0.54
50:Q:66:ASN:HD21	50:Q:70:ARG:HH21	1.54	0.54
51:R:97:LYS:NZ	51:R:98:GLU:O	2.41	0.54
4:i:78:LEU:HD11	4:i:96:LEU:HB3	1.89	0.53
34:1:1798:U:H5''	37:B:260:ARG:HB2	1.90	0.53
34:1:2431:U:N3	34:1:2434:A:OP2	2.40	0.53
48:O:17:ARG:O	48:O:19:LYS:N	2.40	0.53
52:S:86:LEU:HD12	52:S:96:ILE:HD12	1.90	0.53
1:2:60:A:N7	1:2:108:G:O2'	2.40	0.53
1:2:888:G:O2'	1:2:909:A:N6	2.41	0.53
1:2:927:G:O2'	1:2:1503:A:N7	2.37	0.53
34:1:2104:G:O6	34:1:2186:G:O6	2.26	0.53
51:R:20:LEU:HG	51:R:21:ARG:HG3	1.90	0.53
60:4:234:C:N4	60:4:265:G:O6	2.41	0.53
1:2:938:A:N3	1:2:1376:U:O2'	2.35	0.53
34:1:2358:G:H22	45:L:55:ARG:HH22	1.57	0.53
34:1:2581:G:H1	34:1:2610:C:HO2'	1.56	0.53
41:F:126:PRO:HD2	41:F:131:VAL:HA	1.90	0.53
43:J:131:GLN:NE2	43:J:133:GLN:O	2.42	0.53
50:Q:28:ARG:NH1	50:Q:38:THR:OG1	2.41	0.53
1:2:1375:A:H4'	7:l:29:LYS:HD3	1.90	0.53
34:1:1311:G:H21	34:1:1603:A:N6	2.04	0.53
34:1:2804:C:H2'	34:1:2805:G:H8	1.74	0.53
4:i:64:LEU:HD23	4:i:203:VAL:HG11	1.89	0.53
7:l:144:MET:O	7:l:148:ASN:HB2	2.09	0.53
34:1:1902:C:H5'	37:B:246:PRO:HD3	1.91	0.53
48:O:14:VAL:HG23	48:O:17:ARG:HH12	1.72	0.53
55:V:41:LEU:HD11	55:V:83:PRO:HG2	1.90	0.53
3:h:191:THR:OG1	3:h:192:THR:N	2.39	0.53
34:1:389:G:H22	45:L:72:PRO:HD3	1.73	0.53
34:1:1666:G:H4'	44:K:6:THR:HG23	1.90	0.53
1:2:113:G:N3	1:2:353:A:O2'	2.41	0.53
1:2:1442(A):G:O2'	49:P:122:ASP:OD2	2.26	0.53
1:2:1522:U:H2'	1:2:1523:G:H8	1.72	0.53
8:m:33:GLU:HG3	8:m:59:LEU:HD21	1.89	0.53
19:x:36:ARG:NH2	19:x:75:ALA:O	2.40	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:906:G:OP1	46:M:26:TYR:OH	2.27	0.53
34:1:1071:G:H21	34:1:1089:G:H1	1.56	0.53
34:1:1175:U:H1'	34:1:1176:G:H2'	1.91	0.53
34:1:2572:A:OP1	34:1:2574:G:O2'	2.27	0.53
56:5:27:LYS:HB2	56:5:75:ARG:HH12	1.74	0.53
1:2:1029:C:H1'	1:2:1033:G:H22	1.73	0.53
1:2:1050:G:O2'	56:5:95:GLN:O	2.27	0.53
1:2:1422:G:H5''	44:K:48:PRO:HB3	1.90	0.53
4:i:94:LEU:HD13	4:i:196:LEU:HD12	1.91	0.53
6:k:3:ARG:HB3	6:k:66:GLU:HG3	1.91	0.53
22:7:5:G:H2'	22:7:6:G:H8	1.74	0.53
31:c:35:GLU:HB3	31:c:51:GLU:HB3	1.91	0.53
32:d:12:ARG:NH1	34:1:464:U:O2'	2.42	0.53
34:1:1028:A:OP2	34:1:1126:A:N6	2.42	0.53
34:1:1438:U:H2'	34:1:1439:A:H8	1.72	0.53
1:2:624:C:H2'	1:2:625:G:H8	1.74	0.53
25:W:27:GLU:HG3	25:W:68:GLU:HA	1.90	0.53
34:1:1995:U:N3	34:1:1996:C:N3	2.57	0.53
36:A:77:ILE:HD12	36:A:94:VAL:HG13	1.91	0.53
37:B:133:LEU:HD12	37:B:189:CYS:HB2	1.90	0.53
34:1:23:G:OP1	34:1:504:U:N3	2.39	0.53
40:E:76:SER:OG	40:E:84:LYS:N	2.42	0.53
48:O:62:LYS:HA	48:O:65:VAL:HG12	1.91	0.53
59:H:41:UNK:O	59:H:46:UNK:N	2.41	0.53
60:4:113:C:N4	60:4:114:G:O6	2.41	0.53
4:i:61:LYS:NZ	4:i:72:GLU:OE1	2.30	0.52
34:1:271(P):C:N4	34:1:271(Q):G:O6	2.42	0.52
48:O:31:SER:OG	48:O:32:LEU:N	2.41	0.52
1:2:45:U:H2'	1:2:46:G:C8	2.45	0.52
10:o:7:LYS:HE3	10:o:40:LEU:HD21	1.90	0.52
34:1:119:A:H4'	34:1:120:U:H5'	1.91	0.52
34:1:2816:C:O2	34:1:2883:A:O2'	2.25	0.52
2:g:58:ILE:HD11	2:g:185:ILE:HD13	1.90	0.52
23:8:17:C:N3	34:1:2180:U:O2'	2.42	0.52
34:1:613:G:O2'	34:1:614(C):A:N6	2.41	0.52
34:1:1206:G:O6	34:1:1240:U:O4	2.27	0.52
1:2:578:C:O2'	1:2:728:A:N3	2.41	0.52
1:2:1079:G:O2'	5:j:14:ARG:NH2	2.39	0.52
2:g:219:VAL:HA	2:g:222:ILE:HG22	1.91	0.52
3:h:81:GLY:O	3:h:85:ARG:NE	2.42	0.52
10:o:50:ILE:HB	14:s:41:ARG:HE	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:c:23:THR:HG21	34:1:2419:U:H5'	1.90	0.52
34:1:578:A:O2'	50:Q:33:ARG:NH2	2.43	0.52
34:1:1056:G:HO2'	34:1:1087:G:H22	1.54	0.52
49:P:13:ARG:HD3	49:P:13:ARG:H	1.74	0.52
60:4:191:G:H2'	60:4:192:G:C8	2.44	0.52
1:2:137:C:H2'	1:2:138:G:H8	1.74	0.52
1:2:885:G:H2'	1:2:886:G:H8	1.74	0.52
1:2:979:C:OP1	1:2:1223:C:N4	2.42	0.52
2:g:84:GLU:OE2	2:g:212:GLN:NE2	2.43	0.52
5:j:47:LYS:O	5:j:57:LYS:NZ	2.42	0.52
8:m:35:ILE:HG23	8:m:111:ILE:HD13	1.90	0.52
11:p:82:VAL:HG13	11:p:108:ILE:HA	1.91	0.52
19:x:36:ARG:HH21	19:x:75:ALA:HB3	1.75	0.52
33:e:13:ARG:NH2	34:1:250:G:OP2	2.43	0.52
34:1:143(A):C:H2'	34:1:144:C:H6	1.74	0.52
34:1:614(C):A:O2'	39:D:182:ASN:ND2	2.42	0.52
34:1:1509(A):A:H3'	34:1:1509(B):A:H8	1.74	0.52
34:1:2468:G:N2	34:1:2482:G:OP2	2.39	0.52
38:C:175:VAL:HG23	38:C:177:PRO:HD3	1.92	0.52
50:Q:62:ILE:HD13	50:Q:93:LYS:HG2	1.92	0.52
52:S:47:VAL:HA	52:S:50:VAL:HG12	1.92	0.52
55:V:5:LEU:HD13	55:V:47:VAL:HG21	1.90	0.52
1:2:376:G:H5''	16:u:5:ARG:HB2	1.90	0.52
1:2:1356:G:H2'	1:2:1357:A:C8	2.45	0.52
3:h:56:ASP:HB3	3:h:67:THR:HG23	1.90	0.52
13:r:19:LEU:HB3	13:r:25:ILE:HG21	1.92	0.52
30:b:36:CYS:SG	30:b:37:LYS:N	2.82	0.52
34:1:597:U:H2'	34:1:598:G:C8	2.45	0.52
34:1:2167:U:N3	34:1:2170:A:OP1	2.42	0.52
52:S:18:ARG:HG3	52:S:76:VAL:HG22	1.92	0.52
1:2:945:G:N2	1:2:1334:G:O2'	2.43	0.52
1:2:1298:C:OP2	7:l:114:ARG:NH1	2.42	0.52
1:2:1441:G:N1	1:2:1458:G:OP2	2.36	0.52
4:i:98:GLU:OE2	4:i:107:ARG:NE	2.39	0.52
5:j:79:GLU:HG3	5:j:93:PRO:HD2	1.91	0.52
5:j:84:PHE:HB2	5:j:134:ALA:HB2	1.92	0.52
12:q:57:LYS:NZ	12:q:67:THR:OG1	2.42	0.52
34:1:271(G):C:H42	34:1:271(Q):G:H1	1.56	0.52
34:1:661:C:O2'	45:L:16:ARG:O	2.22	0.52
34:1:2328:A:H2'	34:1:2329:G:C8	2.45	0.52
37:B:44:ASN:OD1	37:B:44:ASN:N	2.37	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:P:87:ASP:OD1	49:P:87:ASP:N	2.40	0.52
50:Q:70:ARG:NH1	50:Q:75:ASN:OD1	2.43	0.52
1:2:713:G:H2'	1:2:714:G:C8	2.44	0.52
1:2:993:G:O2'	1:2:994:A:N7	2.35	0.52
2:g:71:VAL:HA	2:g:93:VAL:HG23	1.92	0.52
2:g:177:ALA:HB1	2:g:182:ILE:HB	1.90	0.52
6:k:15:ASP:OD1	6:k:18:GLN:NE2	2.43	0.52
8:m:85:ARG:NH1	8:m:87:SER:O	2.43	0.52
32:d:10:ARG:HD2	34:1:770:G:H5''	1.90	0.52
34:1:457:A:N7	34:1:472:A:N6	2.56	0.52
34:1:581:C:H2'	34:1:582:G:H8	1.74	0.52
34:1:2052:G:O2'	38:C:143:ASN:O	2.26	0.52
34:1:2114:A:H61	34:1:2170:A:H61	1.58	0.52
37:B:136:ILE:O	37:B:168:ARG:NH2	2.42	0.52
51:R:70:ILE:HG23	51:R:90:PRO:HB3	1.92	0.52
1:2:316:G:OP2	1:2:351:G:O2'	2.22	0.52
1:2:370:C:O2	1:2:482:A:O2'	2.27	0.52
9:n:53:VAL:HG21	9:n:85:LEU:HD11	1.92	0.52
34:1:1470:G:N2	34:1:1520:G:OP2	2.34	0.52
34:1:2228:G:OP1	37:B:263:ARG:NH2	2.43	0.52
1:2:1304:G:N1	1:2:1332:A:OP2	2.36	0.52
1:2:1399:C:O2'	1:2:1502:A:N6	2.42	0.52
3:h:43:LEU:O	3:h:47:LEU:N	2.42	0.52
32:d:9:ARG:NH1	32:d:47:ARG:O	2.43	0.52
34:1:745:G:HO2'	34:1:748:G:HO2'	1.56	0.52
34:1:1215:G:H1	34:1:1234:U:H3	1.58	0.52
60:4:60:U:O2	60:4:63:C:N4	2.43	0.52
1:2:522:C:OP2	12:q:69:TYR:OH	2.27	0.51
6:k:3:ARG:HA	6:k:66:GLU:HA	1.91	0.51
22:7:1:C:H2'	22:7:2:G:C8	2.44	0.51
22:7:37:A:H3'	22:7:38:A:H8	1.74	0.51
34:1:614(C):A:N6	39:D:179:GLU:OE1	2.44	0.51
34:1:2882:A:OP1	47:N:96:ARG:NH1	2.43	0.51
39:D:8:GLN:HG3	39:D:9:ILE:HG22	1.93	0.51
39:D:155:LEU:HD11	39:D:176:LEU:HD22	1.90	0.51
17:v:66:SER:OG	17:v:67:LYS:N	2.43	0.51
34:1:289:A:H3'	34:1:290:G:H8	1.75	0.51
34:1:1288:U:O3'	34:1:1647:G:N2	2.42	0.51
34:1:1479:G:HO2'	34:1:1559:G:HO2'	1.54	0.51
37:B:267:SER:OG	37:B:268:ARG:N	2.44	0.51
43:J:6:PRO:HB3	43:J:41:ASP:HB3	1.90	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:J:95:PRO:O	43:J:97:ARG:N	2.35	0.51
45:L:118:GLY:O	45:L:137:LYS:NZ	2.36	0.51
1:2:123:C:OP1	1:2:311:C:O2'	2.28	0.51
6:k:100:ASN:ND2	18:w:23:LYS:O	2.43	0.51
20:y:36:LEU:HB3	20:y:59:ALA:HB2	1.92	0.51
47:N:86:ARG:NH2	47:N:87:TYR:OH	2.42	0.51
49:P:30:VAL:HA	49:P:44:ASP:HA	1.92	0.51
60:4:120:A:H3'	60:4:121:U:H2'	1.93	0.51
60:4:258:A:OP1	60:4:276:A:N6	2.43	0.51
1:2:514:C:H2'	1:2:515:G:H8	1.76	0.51
1:2:1135:U:H2'	1:2:1137:C:H1'	1.92	0.51
5:j:33:VAL:HA	5:j:42:GLY:O	2.10	0.51
34:1:862:G:H3'	34:1:863:A:H8	1.75	0.51
34:1:1309:G:O6	34:1:1606:G:N2	2.44	0.51
34:1:2048:G:H21	38:C:113:PHE:HZ	1.57	0.51
54:U:49:VAL:O	54:U:50:ARG:NH1	2.40	0.51
1:2:571:U:O4	1:2:864:A:N6	2.43	0.51
1:2:1077:G:N2	1:2:1080:A:OP2	2.38	0.51
1:2:1342:C:H2'	1:2:1343:G:H8	1.76	0.51
34:1:648:G:H2'	34:1:649:G:H8	1.75	0.51
34:1:1599:C:OP1	53:T:37:THR:N	2.43	0.51
37:B:88:ARG:HB3	37:B:90:ALA:H	1.76	0.51
54:U:31:LEU:HD23	54:U:34:LYS:HB2	1.93	0.51
55:V:10:ARG:HG2	55:V:12:GLY:H	1.76	0.51
1:2:1049:U:OP1	14:s:3:ARG:NH1	2.44	0.51
3:h:67:THR:HA	3:h:102:ASN:O	2.10	0.51
11:p:21:ILE:HG13	11:p:30:VAL:HG12	1.91	0.51
34:1:489:G:N2	34:1:1321:A:OP1	2.44	0.51
34:1:703:U:H3	34:1:728:G:H1	1.57	0.51
34:1:748:G:OP1	34:1:2612:C:N4	2.40	0.51
34:1:829:A:C8	34:1:2248:C:H5'	2.46	0.51
34:1:1070:A:H62	34:1:1096:A:H2'	1.75	0.51
44:K:19:ILE:HB	44:K:41:ALA:HB1	1.91	0.51
49:P:3:ARG:HG3	49:P:7:ILE:HG12	1.93	0.51
49:P:29:ARG:O	49:P:85:LYS:NZ	2.43	0.51
1:2:512:U:OP1	4:i:46:LYS:NZ	2.42	0.51
1:2:1080:A:H5'	5:j:14:ARG:HH21	1.74	0.51
1:2:1129:C:H41	1:2:1141:C:H42	1.58	0.51
1:2:1255:G:O2'	1:2:1258:G:N3	2.41	0.51
5:j:122:GLU:HB3	5:j:126:ARG:HG2	1.92	0.51
7:l:24:THR:O	7:l:28:ASN:ND2	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:l:84:ASN:N	7:l:84:ASN:OD1	2.44	0.51
10:o:8:LEU:HG	10:o:96:ILE:HG22	1.92	0.51
23:8:46:G:O2'	23:8:48:C:OP2	2.29	0.51
34:1:788:A:OP1	34:1:791:C:N4	2.39	0.51
34:1:2410:G:H2'	34:1:2411:A:C8	2.46	0.51
34:1:2576:G:O2'	34:1:2579:C:OP2	2.23	0.51
39:D:23:ASP:HB2	39:D:24:LEU:HD12	1.92	0.51
44:K:93:PRO:HB3	44:K:114:ILE:HD11	1.92	0.51
49:P:16:ARG:NH1	49:P:82:LEU:O	2.42	0.51
55:V:26:GLY:CA	55:V:86:VAL:O	2.58	0.51
1:2:7:G:H2'	5:j:119:LEU:HD12	1.93	0.51
1:2:1414:U:H2'	1:2:1415:G:H8	1.76	0.51
3:h:43:LEU:HA	3:h:47:LEU:HD13	1.92	0.51
10:o:12:ASP:OD2	10:o:15:THR:N	2.42	0.51
26:X:56:GLN:HB2	26:X:82:LEU:HD11	1.92	0.51
34:1:9:U:O2'	34:1:10:G:O4'	2.29	0.51
34:1:288:C:H2'	34:1:289:A:H8	1.75	0.51
34:1:631:A:O2'	45:L:66:GLY:O	2.28	0.51
34:1:805:G:N2	34:1:828:U:OP2	2.37	0.51
56:5:108:ASN:HD21	56:5:114:LYS:HE3	1.75	0.51
31:c:13:CYS:HB2	31:c:22:ALA:HB3	1.93	0.51
34:1:390:A:H4'	34:1:391:G:H5'	1.92	0.51
34:1:861:A:N3	35:3:79:C:O2'	2.43	0.51
1:2:92:C:N4	1:2:93:G:O6	2.43	0.51
5:j:36:ASP:OD1	5:j:36:ASP:N	2.36	0.51
34:1:674:G:O3'	39:D:63:LYS:NZ	2.43	0.51
34:1:1316:U:H2'	34:1:1317:A:H8	1.76	0.51
34:1:1667:G:O2'	34:1:1991:U:O4	2.23	0.51
45:L:95:VAL:HA	45:L:99:LEU:HD23	1.92	0.51
1:2:718:G:H5'	11:p:117:ASN:HB2	1.92	0.50
1:2:1321:C:O2'	19:x:78:ARG:NH1	2.44	0.50
2:g:58:ILE:O	2:g:62:ALA:CB	2.59	0.50
2:g:62:ALA:HB1	2:g:222:ILE:HG13	1.94	0.50
5:j:10:MET:HA	5:j:32:VAL:HA	1.93	0.50
30:b:12:SER:OG	34:1:2021:C:OP1	2.26	0.50
34:1:2302:G:O2'	40:E:126:ASP:OD2	2.29	0.50
10:o:6:ILE:HG22	10:o:98:ILE:HG23	1.92	0.50
34:1:196:A:H61	34:1:831:G:H21	1.58	0.50
34:1:2293:C:OP1	48:O:92:TYR:OH	2.25	0.50
38:C:92:THR:OG1	38:C:93:VAL:N	2.40	0.50
1:2:375:U:O2'	16:u:6:LEU:O	2.28	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:977:A:O2'	1:2:979:C:OP2	2.29	0.50
1:2:1187:G:O5'	9:n:113:LYS:NZ	2.43	0.50
17:v:11:VAL:HG12	17:v:85:VAL:HG23	1.93	0.50
26:X:76:ARG:NE	34:1:271(R):G:OP1	2.41	0.50
34:1:183:C:O2'	34:1:432:A:N3	2.39	0.50
34:1:193:U:N3	34:1:203:C:O2	2.43	0.50
34:1:641:C:O2'	34:1:2350:C:OP1	2.30	0.50
34:1:1607:C:N4	34:1:1622:G:OP2	2.34	0.50
1:2:1152:A:OP1	10:o:70:ARG:NH2	2.45	0.50
5:j:94:ALA:HB2	5:j:119:LEU:HD23	1.94	0.50
6:k:80:ARG:HA	6:k:85:VAL:HG11	1.93	0.50
9:n:105:ASP:OD2	9:n:107:ARG:NH1	2.42	0.50
34:1:1119:C:H2'	34:1:1120:G:H8	1.75	0.50
34:1:1812:A:H2'	34:1:1813:G:H8	1.76	0.50
34:1:2870:C:OP1	47:N:57:ARG:NH2	2.44	0.50
47:N:79:LEU:HD12	47:N:83:ILE:HB	1.92	0.50
54:U:96:ILE:HD11	54:U:99:CYS:HB3	1.92	0.50
34:1:371:A:N6	34:1:402:A:OP2	2.43	0.50
34:1:882:G:H4'	60:4:329:C:H41	1.75	0.50
36:A:63:SER:OG	36:A:64:LEU:N	2.44	0.50
36:A:66:HIS:NE2	36:A:186:ALA:O	2.45	0.50
39:D:185:ASP:HA	39:D:188:ARG:HD3	1.93	0.50
17:v:15:MET:N	17:v:15:MET:SD	2.85	0.50
18:w:23:LYS:HB2	18:w:58:LEU:HD12	1.93	0.50
43:J:34:LEU:HD11	43:J:120:LEU:HB2	1.93	0.50
17:v:62:SER:OG	17:v:72:ARG:NE	2.37	0.50
34:1:2723:C:OP1	47:N:5:LYS:NZ	2.45	0.50
34:1:2791:C:H4'	34:1:2792:G:H5'	1.93	0.50
60:4:144:C:O2'	60:4:145:C:O4'	2.29	0.50
60:4:295:A:H8	60:4:296:G:H1'	1.76	0.50
1:2:408:A:OP2	4:i:115:ARG:NH2	2.45	0.50
1:2:1512:U:H2'	1:2:1513:A:C8	2.47	0.50
9:n:121:ARG:NH1	9:n:122:ALA:O	2.41	0.50
20:y:45:GLN:HG2	20:y:91:LEU:HD11	1.93	0.50
26:X:51:VAL:HG12	26:X:60:PHE:HB2	1.93	0.50
34:1:52:A:OP2	34:1:117:G:N1	2.40	0.50
44:K:19:ILE:HG22	44:K:43:VAL:HA	1.92	0.50
46:M:104:PHE:HE1	46:M:125:LEU:HD11	1.77	0.50
1:2:18:C:OP1	5:j:127:ASN:ND2	2.45	0.49
1:2:1216:G:H5''	14:s:5:ALA:HB2	1.94	0.49
26:X:16:ASN:OD1	26:X:16:ASN:N	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:578:A:OP1	34:1:1255:U:O2'	2.28	0.49
34:1:1059:G:H3'	34:1:1060:U:H2'	1.93	0.49
34:1:1950:G:N1	34:1:1954:G:O2'	2.39	0.49
48:O:24:LEU:HB3	48:O:85:VAL:HG12	1.94	0.49
49:P:117:ASP:OD2	49:P:120:ARG:NE	2.42	0.49
50:Q:31:SER:HB3	50:Q:34:LYS:HB2	1.94	0.49
56:5:9:ARG:O	56:5:13:ASP:CB	2.60	0.49
1:2:390:C:H4'	16:u:28:ARG:HH21	1.77	0.49
1:2:407:G:OP1	4:i:3:ARG:NH1	2.40	0.49
1:2:934:C:O2'	1:2:1344:C:OP2	2.30	0.49
13:r:57:ARG:HH21	29:a:35:VAL:HG21	1.77	0.49
17:v:55:ASP:HB3	17:v:76:LEU:HD21	1.93	0.49
34:1:443:A:OP2	34:1:614(B):G:N1	2.34	0.49
34:1:467:G:HO2'	34:1:796:C:HO2'	1.48	0.49
34:1:2228:G:OP2	37:B:263:ARG:NH1	2.46	0.49
35:3:103:G:O2'	55:V:73:GLN:NE2	2.44	0.49
39:D:168:ARG:HG3	39:D:175:THR:HG21	1.94	0.49
1:2:189(B):C:N3	1:2:189(J):G:N2	2.44	0.49
1:2:950:U:H2'	1:2:951:G:C8	2.47	0.49
1:2:1010:G:H2'	1:2:1011:G:C8	2.47	0.49
1:2:1095:U:OP1	1:2:1108:G:N2	2.37	0.49
9:n:112:LYS:HA	9:n:119:ALA:HB2	1.94	0.49
11:p:34:ASP:OD1	11:p:38:ASN:N	2.45	0.49
13:r:33:ALA:HA	13:r:36:LYS:HB3	1.94	0.49
25:W:67:VAL:HG22	25:W:81:VAL:HG12	1.93	0.49
34:1:271(H):G:N1	34:1:271(Q):G:O6	2.44	0.49
34:1:1029:A:N6	34:1:1125:G:O2'	2.45	0.49
34:1:2447:G:N2	34:1:2450:A:OP2	2.34	0.49
46:M:42:ILE:HD12	46:M:125:LEU:HD22	1.94	0.49
49:P:29:ARG:HG2	49:P:86:ILE:HG22	1.94	0.49
1:2:559:A:OP1	5:j:126:ARG:NH2	2.46	0.49
1:2:589:C:H5''	8:m:29:SER:HB3	1.94	0.49
34:1:494:G:O5'	52:S:8:ARG:NH1	2.45	0.49
34:1:2064:C:O2'	34:1:2251:G:N2	2.37	0.49
38:C:3:GLY:HA3	38:C:81:ILE:HG21	1.93	0.49
41:F:154:PRO:HA	41:F:161:GLY:HA3	1.94	0.49
1:2:188:C:O4'	20:y:89:ARG:NH2	2.44	0.49
25:W:39:ARG:NH1	25:W:58:THR:OG1	2.45	0.49
33:e:11:LYS:HB2	33:e:60:LEU:HD21	1.95	0.49
34:1:30:G:OP2	50:Q:5:LYS:NZ	2.34	0.49
34:1:863:A:H2'	34:1:864:G:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:1638:C:O2	34:1:2698:U:O2'	2.30	0.49
1:2:15:G:H1	1:2:920:U:H3	1.60	0.49
1:2:975:A:H4'	1:2:976:G:H5''	1.94	0.49
13:r:97:PRO:HB3	13:r:110:ARG:HG3	1.94	0.49
14:s:24:CYS:SG	14:s:25:VAL:N	2.85	0.49
28:Z:30:ARG:NH1	34:1:1159:U:OP2	2.45	0.49
32:d:10:ARG:O	32:d:14:LYS:HB2	2.12	0.49
33:e:28:GLY:N	34:1:2393:A:OP1	2.43	0.49
34:1:265:A:N6	34:1:427:U:O2'	2.44	0.49
34:1:373:U:H2'	34:1:374:A:H8	1.78	0.49
34:1:2392:A:H8	45:L:60:MET:HG2	1.78	0.49
34:1:2848:G:OP1	49:P:96:ARG:NH1	2.45	0.49
35:3:39:A:O2'	35:3:46:A:N1	2.39	0.49
44:K:68:GLU:HG3	44:K:78:ARG:HB2	1.95	0.49
49:P:28:VAL:HA	49:P:45:PHE:O	2.13	0.49
1:2:859:A:OP2	1:2:869:G:N1	2.34	0.49
1:2:1015:A:H2'	1:2:1016:A:C8	2.47	0.49
5:j:19:MET:HE1	5:j:24:ARG:HH21	1.78	0.49
13:r:108:ARG:HD2	13:r:114:ARG:HE	1.78	0.49
17:v:17:LYS:O	17:v:69:LYS:NZ	2.44	0.49
17:v:83:ASP:OD1	17:v:83:ASP:N	2.45	0.49
29:a:15:ILE:HB	29:a:32:TYR:HB3	1.94	0.49
34:1:431:U:H2'	34:1:432:A:H8	1.76	0.49
34:1:665:C:H2'	34:1:666:G:H8	1.77	0.49
34:1:1087:G:H2'	34:1:1088:A:H4'	1.93	0.49
60:4:132:U:O4	60:4:166:C:N4	2.45	0.49
1:2:714:G:H2'	1:2:715:A:C8	2.48	0.49
1:2:811:C:O2'	1:2:901:A:N1	2.45	0.49
4:i:127:THR:HA	4:i:132:ARG:HA	1.95	0.49
34:1:1001:A:H62	34:1:1154:G:H21	1.58	0.49
47:N:78:LYS:O	47:N:82:GLU:HB2	2.11	0.49
60:4:24:G:H2'	60:4:25:G:H8	1.78	0.49
1:2:1418:A:N6	1:2:1482:G:O2'	2.45	0.49
2:g:174:VAL:HG12	2:g:184:VAL:HG11	1.95	0.49
9:n:63:ILE:HD13	9:n:77:ILE:HD12	1.94	0.49
19:x:19:VAL:HG11	19:x:41:VAL:HG21	1.95	0.49
25:W:20:ARG:HD3	34:1:2271:G:H5'	1.93	0.49
33:e:32:LEU:HD13	33:e:34:TRP:HE3	1.78	0.49
34:1:1316:U:H2'	34:1:1317:A:C8	2.48	0.49
34:1:2503:A:O2'	34:1:2505:G:OP2	2.25	0.49
60:4:147:G:O6	60:4:216:A:N6	2.34	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:550:G:O2'	12:q:119:LYS:NZ	2.46	0.49
10:o:51:ARG:HE	10:o:61:GLU:HB2	1.78	0.49
17:v:82:MET:HA	17:v:85:VAL:HG12	1.94	0.49
34:1:675:A:N3	34:1:2443:C:O2'	2.42	0.49
34:1:964:C:O2'	34:1:2273:A:N3	2.34	0.49
52:S:83:LYS:HG2	52:S:97:LYS:HG2	1.95	0.49
1:2:942:G:H21	9:n:124:GLN:HE22	1.61	0.48
1:2:1064:G:N2	1:2:1190:G:H2'	2.28	0.48
1:2:1297:C:OP2	13:r:44:ARG:NH2	2.45	0.48
30:b:41:PRO:HG2	30:b:44:THR:HG21	1.94	0.48
49:P:92:GLY:HA2	49:P:114:LEU:HB3	1.95	0.48
1:2:538:G:H2'	1:2:539:A:H8	1.77	0.48
6:k:14:LEU:HD11	6:k:84:ASN:HB3	1.94	0.48
7:l:6:ARG:O	7:l:6:ARG:NH1	2.37	0.48
34:1:1550:C:OP1	34:1:1720:U:O2'	2.21	0.48
60:4:62:G:H21	60:4:63:C:H5	1.61	0.48
60:4:257:C:N3	60:4:259:A:N6	2.56	0.48
60:4:264:G:N2	60:4:265:G:N3	2.60	0.48
1:2:266:G:O2'	1:2:267:C:OP2	2.30	0.48
1:2:1366:C:O3'	10:o:60:ARG:NH2	2.46	0.48
9:n:32:ASP:HB3	9:n:35:GLU:HB2	1.93	0.48
34:1:1312:U:O2	34:1:1339:G:N2	2.38	0.48
34:1:1363:C:O2'	34:1:1809:A:N3	2.43	0.48
43:J:19:GLU:HG2	43:J:59:LYS:HE2	1.94	0.48
52:S:3:ALA:O	52:S:106:ILE:HA	2.12	0.48
4:i:173:TRP:CD2	4:i:189:PRO:HB3	2.49	0.48
5:j:75:THR:OG1	5:j:76:ILE:N	2.46	0.48
11:p:21:ILE:HB	11:p:84:VAL:HG12	1.94	0.48
34:1:261:G:HO2'	34:1:610:G:HO2'	1.56	0.48
34:1:1181:C:H2'	34:1:1182:A:C8	2.48	0.48
34:1:1571:A:H2'	34:1:1572:A:C8	2.48	0.48
34:1:1749:A:H5''	34:1:1749:A:H8	1.78	0.48
34:1:1972:A:H2'	34:1:1973:G:H8	1.79	0.48
41:F:33:LEU:HD21	41:F:136:ILE:HB	1.95	0.48
59:I:233:UNK:O	59:I:237:UNK:CB	2.61	0.48
60:4:279:C:H2'	60:4:280:G:C4	2.48	0.48
1:2:401:C:OP1	4:i:77:ASN:ND2	2.46	0.48
1:2:833:U:O2	1:2:854:G:N1	2.46	0.48
1:2:1363:C:O2'	1:2:1363(A):A:O5'	2.31	0.48
9:n:4:TYR:HB2	9:n:19:LEU:HB2	1.94	0.48
34:1:463:G:N2	34:1:466:A:OP2	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:1275:A:N1	34:1:1295:C:O2'	2.41	0.48
37:B:134:ARG:N	37:B:187:GLY:O	2.45	0.48
39:D:153:SER:N	39:D:190:GLU:OE1	2.43	0.48
45:L:6:LEU:HG	45:L:8:PRO:HD2	1.95	0.48
52:S:22:ASP:OD1	52:S:25:ARG:NH1	2.37	0.48
1:2:769:G:OP2	1:2:803:G:O2'	2.31	0.48
1:2:1372:U:OP1	9:n:72:GLY:N	2.46	0.48
4:i:98:GLU:HG3	4:i:194:LEU:HD11	1.95	0.48
26:X:26:ARG:NH1	26:X:34:THR:OG1	2.43	0.48
34:1:180:G:N2	34:1:215:G:O6	2.47	0.48
34:1:299:A:N1	34:1:322:A:O2'	2.42	0.48
34:1:2479:G:OP1	34:1:2537:U:O2'	2.25	0.48
34:1:2580:U:H5'	38:C:131:ALA:H	1.79	0.48
34:1:2702:U:O2	34:1:2703:C:N4	2.47	0.48
34:1:2795:G:OP2	34:1:2801(A):A:N6	2.39	0.48
38:C:143:ASN:HB2	38:C:147:PRO:HD2	1.95	0.48
45:L:120:ALA:HB2	45:L:137:LYS:HG3	1.96	0.48
55:V:5:LEU:HD21	55:V:39:VAL:HG21	1.96	0.48
56:5:107:PHE:HA	56:5:112:TYR:O	2.13	0.48
2:g:62:ALA:O	2:g:226:ARG:NH2	2.40	0.48
4:i:3:ARG:HH11	4:i:115:ARG:HB3	1.78	0.48
26:X:41:ARG:NH2	34:1:205:G:H1	2.12	0.48
32:d:3:ARG:NH1	34:1:752:A:OP2	2.46	0.48
34:1:693:C:O2'	34:1:1353:A:N3	2.39	0.48
34:1:1341:U:OP2	34:1:1394:U:O2'	2.21	0.48
34:1:1754:C:H5	49:P:96:ARG:HH21	1.61	0.48
34:1:2124:G:N7	34:1:2125:G:N2	2.62	0.48
34:1:2627:G:O2'	34:1:2781:A:N1	2.37	0.48
42:G:3:VAL:HB	42:G:36:ALA:HB1	1.95	0.48
1:2:79:G:H1	1:2:91:C:H42	1.61	0.48
8:m:100:ILE:O	8:m:125:ARG:NH2	2.47	0.48
21:z:10:ARG:HA	21:z:13:ILE:HG22	1.94	0.48
34:1:851:U:H2'	34:1:852:G:H8	1.78	0.48
39:D:182:ASN:N	39:D:182:ASN:OD1	2.45	0.48
1:2:461:A:O2'	1:2:471:G:OP2	2.31	0.48
1:2:1026:G:H3'	1:2:1027:C:H6	1.77	0.48
11:p:84:VAL:HG23	11:p:110:ASP:HA	1.95	0.48
18:w:59:SER:OG	18:w:60:ALA:N	2.46	0.48
34:1:2291:U:H2'	34:1:2292:C:C6	2.49	0.48
44:K:63:VAL:HG12	44:K:106:LEU:HD11	1.96	0.48
44:K:104:ARG:NH2	49:P:43:GLN:OE1	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:S:10:VAL:HG11	52:S:103:ILE:HD11	1.96	0.48
54:U:50:ARG:NE	54:U:54:LYS:O	2.30	0.48
1:2:10:A:H2'	1:2:11:G:H8	1.78	0.48
5:j:13:ILE:HG13	56:5:141:LEU:HD21	1.96	0.48
26:X:52:ARG:NH1	34:1:2200:C:OP2	2.46	0.48
34:1:536:A:OP1	50:Q:53:ARG:NH1	2.47	0.48
34:1:581:C:H2'	34:1:582:G:C8	2.49	0.48
34:1:1275:A:OP2	34:1:1646:C:N4	2.47	0.48
34:1:2539:C:O2'	58:f:35:ARG:NH1	2.46	0.48
34:1:2863:C:N4	34:1:2864:G:O6	2.46	0.48
37:B:233:HIS:HE2	37:B:246:PRO:HA	1.78	0.48
60:4:182:G:OP2	60:4:215:G:N1	2.42	0.48
1:2:1432:G:OP1	49:P:108:ARG:N	2.47	0.47
1:2:1510:U:H2'	1:2:1511:G:H8	1.79	0.47
5:j:147:ASP:OD1	5:j:147:ASP:N	2.38	0.47
34:1:182:A:N3	34:1:433:C:O2'	2.44	0.47
34:1:271:A:N9	34:1:271:A:N1	2.40	0.47
39:D:148:LEU:HD21	39:D:154:VAL:HG21	1.96	0.47
43:J:128:HIS:O	43:J:130:HIS:N	2.47	0.47
51:R:73:SER:HB2	51:R:88:ARG:HG3	1.96	0.47
52:S:18:ARG:HA	52:S:21:VAL:HG12	1.95	0.47
1:2:343:U:O2'	1:2:346:G:O6	2.24	0.47
1:2:412:A:N3	4:i:35:ARG:NH2	2.61	0.47
1:2:706:A:H1'	11:p:29:ILE:HG21	1.97	0.47
5:j:83:GLU:HA	5:j:88:LYS:HA	1.96	0.47
34:1:335:C:O2	54:U:70:SER:OG	2.31	0.47
34:1:472:A:O2'	34:1:508:G:N1	2.38	0.47
34:1:1001:A:H62	34:1:1154:G:N2	2.12	0.47
34:1:1433:U:H2'	34:1:1434:A:H8	1.78	0.47
34:1:2566:A:N6	44:K:28:SER:O	2.42	0.47
39:D:54:ARG:HD2	39:D:81:PRO:HD3	1.96	0.47
51:R:24:LYS:HA	51:R:94:LEU:HB2	1.94	0.47
58:f:1:MET:HB2	58:f:4:ARG:HE	1.78	0.47
60:4:156:U:O2	60:4:176:A:N6	2.47	0.47
1:2:375:U:H5''	16:u:69:THR:HG21	1.96	0.47
1:2:538:G:H2'	1:2:539:A:C8	2.49	0.47
1:2:686:U:O4	1:2:703:G:O2'	2.29	0.47
1:2:1250:A:H4'	9:n:67:GLY:HA2	1.96	0.47
9:n:126:SER:O	9:n:128:ARG:NH1	2.48	0.47
12:q:32:PHE:HD1	12:q:86:ARG:HA	1.79	0.47
34:1:271(D):G:H1	34:1:271(T):C:H42	1.61	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:271(R):G:H2'	34:1:271(S):G:C8	2.47	0.47
34:1:1791:A:N6	34:1:1828:G:O2'	2.47	0.47
35:3:42:C:O2'	40:E:67:LYS:O	2.26	0.47
37:B:145:VAL:HB	37:B:155:LEU:HB3	1.95	0.47
38:C:181:LEU:HD11	49:P:7:ILE:HG23	1.97	0.47
51:R:19:LYS:HD2	51:R:19:LYS:HA	1.63	0.47
1:2:125:U:O3'	1:2:633:G:N2	2.47	0.47
2:g:43:ASP:O	2:g:47:THR:OG1	2.27	0.47
3:h:22:TRP:NE1	3:h:36:ASP:OD2	2.45	0.47
3:h:189:ALA:HB3	3:h:196:LEU:HB2	1.95	0.47
7:l:115:ARG:HH12	7:l:117:ALA:HB3	1.79	0.47
16:u:53:VAL:HG23	16:u:79:VAL:HG22	1.97	0.47
22:7:17(A):U:H1'	22:7:18:G:H8	1.79	0.47
25:W:72:ARG:NH2	35:3:11:C:OP2	2.39	0.47
34:1:745:G:O6	34:1:746:A:N6	2.48	0.47
34:1:952:G:OP2	46:M:16:ARG:NH1	2.45	0.47
34:1:1007:C:OP1	43:J:35:ARG:NH1	2.41	0.47
37:B:62:TYR:HE1	37:B:88:ARG:HH22	1.62	0.47
60:4:292:C:H2'	60:4:293:G:H8	1.79	0.47
1:2:114:U:H2'	1:2:115:G:C8	2.48	0.47
2:g:168:THR:OG1	2:g:191:ASP:O	2.29	0.47
4:i:101:LEU:HD22	4:i:138:TYR:HD2	1.79	0.47
34:1:517:C:O2'	52:S:18:ARG:NH2	2.48	0.47
34:1:1858:G:H2'	34:1:1883:G:H22	1.78	0.47
34:1:2319:G:N2	34:1:2334:G:OP1	2.38	0.47
34:1:2683:C:H5''	49:P:53:ARG:NH2	2.29	0.47
35:3:87:G:O2'	35:3:89:G:N7	2.42	0.47
37:B:22:SER:OG	37:B:23:GLU:OE2	2.30	0.47
60:4:135:C:N4	60:4:165:G:O6	2.46	0.47
60:4:156:U:O2'	60:4:157:C:O4'	2.22	0.47
60:4:203:C:N4	60:4:225:G:C6	2.82	0.47
60:4:290:C:N4	60:4:291:G:O6	2.47	0.47
1:2:946:A:O2'	1:2:1333:A:N3	2.45	0.47
1:2:950:U:H2'	1:2:951:G:H8	1.80	0.47
2:g:178:ARG:HG3	2:g:196:LEU:HB2	1.97	0.47
4:i:47:ARG:NH1	56:5:142:GLU:OE2	2.47	0.47
6:k:25:ILE:HG12	6:k:82:ARG:HH21	1.80	0.47
26:X:19:GLN:HE21	34:1:379:G:H21	1.63	0.47
34:1:372:G:N1	34:1:401:A:OP2	2.39	0.47
34:1:639:U:O4	34:1:649:G:O6	2.33	0.47
34:1:1718:G:H5'	34:1:1718:G:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:2241:A:H2'	34:1:2242:G:C8	2.49	0.47
34:1:2845:G:H2'	34:1:2846:G:H8	1.79	0.47
40:E:34:LEU:HD12	40:E:34:LEU:HA	1.73	0.47
40:E:68:PRO:HB3	40:E:92:VAL:HB	1.97	0.47
47:N:36:THR:OG1	47:N:37:THR:O	2.30	0.47
49:P:118:ARG:HA	49:P:121:ILE:HG22	1.97	0.47
51:R:21:ARG:HH22	51:R:71:LEU:HD11	1.79	0.47
56:5:108:ASN:ND2	60:4:17:C:O4'	2.47	0.47
1:2:17:U:H2'	1:2:18:C:C6	2.50	0.47
1:2:165:C:H2'	1:2:166:G:C8	2.48	0.47
17:v:13:ASP:OD1	17:v:13:ASP:N	2.47	0.47
27:Y:47:ASN:HA	27:Y:51:ARG:HB3	1.96	0.47
28:Z:24:LYS:HE2	28:Z:24:LYS:HB3	1.74	0.47
30:b:30:LEU:HB3	30:b:39:MET:HB3	1.96	0.47
34:1:569:U:O2'	34:1:983:A:N1	2.45	0.47
34:1:806:C:O2	34:1:2444:G:O2'	2.32	0.47
34:1:1230:C:H2'	34:1:1231:G:H8	1.80	0.47
34:1:2490:G:H5''	34:1:2490:G:H8	1.79	0.47
34:1:2587:A:N6	34:1:2608:G:O2'	2.48	0.47
44:K:19:ILE:HD11	44:K:84:ALA:HB3	1.97	0.47
54:U:46:LYS:HG3	54:U:62:GLU:HB3	1.96	0.47
1:2:433:C:H2'	1:2:434:U:H6	1.80	0.47
1:2:1181:G:H2'	1:2:1182:G:C8	2.49	0.47
8:m:4:ASP:HB3	8:m:7:ALA:HB3	1.97	0.47
14:s:47:LEU:HD22	14:s:52:GLN:HB2	1.97	0.47
19:x:51:VAL:HG23	19:x:58:VAL:HG23	1.96	0.47
32:d:39:ARG:NH2	34:1:467:G:N7	2.63	0.47
34:1:688:U:H2'	34:1:689:A:H8	1.78	0.47
34:1:1538:G:H2'	34:1:1539:G:C8	2.50	0.47
34:1:2266:A:N6	34:1:2273:A:OP2	2.46	0.47
35:3:88:C:H41	35:3:89:G:N2	2.13	0.47
47:N:76:VAL:HG13	47:N:79:LEU:HD23	1.97	0.47
49:P:28:VAL:HG13	49:P:46:GLU:HA	1.95	0.47
53:T:51:VAL:HA	53:T:81:VAL:HA	1.97	0.47
1:2:978:A:OP1	1:2:1361:G:N1	2.31	0.47
9:n:17:VAL:HG21	9:n:81:ILE:HD13	1.97	0.47
30:b:27:PRO:HA	52:S:23:LEU:HD21	1.97	0.47
31:c:25:LYS:HE3	34:1:2285:C:H41	1.80	0.47
34:1:576:U:H2'	34:1:577:G:C8	2.50	0.47
34:1:848:G:OP2	34:1:928:G:N1	2.38	0.47
34:1:1980:G:O2'	34:1:1982:C:OP2	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:3:76:G:H2'	35:3:77:U:H6	1.79	0.47
40:E:165:THR:OG1	40:E:166:ASP:N	2.47	0.47
60:4:332:C:H1'	60:4:335:C:H41	1.79	0.47
1:2:501:C:H2'	1:2:502:G:C8	2.50	0.47
1:2:738:C:OP1	6:k:2:ARG:NH1	2.47	0.47
1:2:902:G:H2'	1:2:903:G:H8	1.80	0.47
1:2:1172:C:H2'	1:2:1173:G:H8	1.79	0.47
1:2:1427:U:H2'	1:2:1428:A:C8	2.50	0.47
2:g:170:GLU:HB3	2:g:173:ALA:HB3	1.96	0.47
28:Z:26:LEU:O	28:Z:35:ARG:NH2	2.48	0.47
29:a:28:LYS:HB3	29:a:28:LYS:HE2	1.79	0.47
34:1:218:A:H2	34:1:235:U:H4'	1.80	0.47
34:1:271(P):C:H5'	42:G:45:LYS:HE3	1.97	0.47
34:1:1528(A):A:H62	34:1:1541:G:N2	2.13	0.47
34:1:2482:G:HO2'	60:4:337:C:HO2'	1.63	0.47
34:1:2522:U:O2'	34:1:2647:U:OP1	2.28	0.47
34:1:2637:U:O4	34:1:2776:A:N7	2.48	0.47
34:1:2730:C:O2'	38:C:168:MET:O	2.27	0.47
44:K:81:ASP:OD1	44:K:81:ASP:N	2.47	0.47
52:S:76:VAL:HG12	52:S:103:ILE:HG23	1.97	0.47
1:2:54:C:OP1	1:2:351:G:N2	2.48	0.46
1:2:527:G:O2'	1:2:535:A:N1	2.46	0.46
1:2:1054:C:H6	56:5:128:LYS:HZ3	1.62	0.46
1:2:1118:C:H1'	1:2:1179:A:C4	2.51	0.46
1:2:1304:G:OP1	21:z:2:GLY:N	2.48	0.46
11:p:43:SER:OG	11:p:44:SER:N	2.48	0.46
11:p:83:ILE:HG12	11:p:109:VAL:HB	1.96	0.46
12:q:22:SER:OG	12:q:23:LYS:N	2.47	0.46
34:1:840:C:H2'	34:1:841:A:C8	2.50	0.46
34:1:1384:A:H1'	34:1:1405:U:H1'	1.97	0.46
40:E:41:GLN:HB3	40:E:43:LEU:HD13	1.97	0.46
56:5:32:LYS:HA	56:5:35:ARG:HB2	1.97	0.46
60:4:24:G:H2'	60:4:25:G:C8	2.50	0.46
60:4:227:G:O6	60:4:228:G:N2	2.48	0.46
14:s:60:SER:O	14:s:60:SER:OG	2.32	0.46
29:a:14:ILE:O	29:a:21:VAL:HA	2.15	0.46
34:1:389:G:H1	45:L:71:VAL:H	1.63	0.46
34:1:852:G:H2'	34:1:853:G:H8	1.79	0.46
35:3:29:A:OP2	48:O:31:SER:OG	2.32	0.46
39:D:68:LYS:HG3	39:D:69:HIS:ND1	2.31	0.46
49:P:107:ASP:OD1	49:P:107:ASP:N	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:R:19:LYS:HZ3	51:R:20:LEU:H	1.63	0.46
1:2:335:C:O2'	1:2:1433:A:N3	2.41	0.46
10:o:30:SER:OG	10:o:30:SER:O	2.33	0.46
12:q:33:ARG:HA	12:q:33:ARG:HD3	1.78	0.46
34:1:385:C:O2'	34:1:388:G:N2	2.48	0.46
34:1:557:U:H5'	43:J:111:PRO:HB2	1.96	0.46
34:1:1254:A:H5''	34:1:1255:U:H5'	1.97	0.46
34:1:1332:G:H22	34:1:1610:A:H5'	1.81	0.46
34:1:2741:A:OP1	58:f:22:ARG:NH1	2.48	0.46
44:K:80:ASP:OD2	49:P:64:ARG:NH2	2.42	0.46
56:5:59:TYR:HB2	56:5:74:ARG:HE	1.81	0.46
1:2:559:A:H4'	1:2:560:U:H3'	1.98	0.46
2:g:185:ILE:HA	2:g:199:TYR:O	2.16	0.46
9:n:60:ASP:OD1	9:n:61:ALA:N	2.48	0.46
10:o:34:VAL:HG23	10:o:74:ILE:HA	1.96	0.46
16:u:1:MET:HG3	16:u:3:LYS:HG3	1.98	0.46
28:Z:8:LEU:HB2	28:Z:28:LEU:HD13	1.98	0.46
34:1:241:A:H61	34:1:255:A:H5''	1.80	0.46
34:1:684:G:N2	34:1:788:A:OP2	2.44	0.46
34:1:1509(B):A:H2'	34:1:1510:G:H8	1.80	0.46
34:1:2632:A:O2'	38:C:61:ARG:NH2	2.48	0.46
34:1:2845:G:H2'	34:1:2846:G:C8	2.50	0.46
47:N:28:LEU:HD23	47:N:48:VAL:HG21	1.97	0.46
52:S:76:VAL:HA	52:S:102:HIS:O	2.16	0.46
1:2:222:U:H2'	1:2:223:U:C6	2.50	0.46
1:2:501:C:H2'	1:2:502:G:H8	1.81	0.46
1:2:973:G:H3'	1:2:974:A:H5''	1.98	0.46
1:2:1342:C:H2'	1:2:1343:G:C8	2.50	0.46
1:2:1407:C:H2'	1:2:1408:A:H8	1.80	0.46
6:k:76:ALA:O	6:k:80:ARG:NE	2.49	0.46
15:t:43:LEU:HD11	15:t:53:HIS:HA	1.96	0.46
34:1:261:G:O2'	34:1:610:G:O2'	2.29	0.46
34:1:271:A:C1'	34:1:271:A:C6	2.96	0.46
34:1:442:G:N2	39:D:48:THR:OG1	2.48	0.46
34:1:572:A:H61	34:1:2029:G:H21	1.63	0.46
34:1:2086:U:H2'	34:1:2087:G:C8	2.50	0.46
34:1:2515:C:H2'	34:1:2516:G:H8	1.80	0.46
35:3:75:G:H21	55:V:85:HIS:CE1	2.34	0.46
37:B:108:PRO:HG2	37:B:111:LEU:HG	1.98	0.46
38:C:47:VAL:HG21	38:C:86:PRO:HD3	1.97	0.46
48:O:82:ILE:HD13	48:O:82:ILE:HA	1.84	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1351:U:H3	1:2:1371:G:H1	1.62	0.46
28:Z:6:VAL:HG22	28:Z:28:LEU:HD11	1.98	0.46
34:1:407:G:H2'	34:1:408:G:H8	1.81	0.46
34:1:1418:G:N2	34:1:1579:A:N7	2.64	0.46
34:1:1614:A:N1	52:S:91:GLY:HA2	2.31	0.46
34:1:2408:U:H2'	34:1:2409:G:C8	2.50	0.46
36:A:43:VAL:O	36:A:175:VAL:HA	2.15	0.46
38:C:32:PRO:HA	38:C:90:THR:HA	1.97	0.46
60:4:228:G:H2'	60:4:229:G:C8	2.51	0.46
1:2:356:A:N3	1:2:368:U:O2'	2.38	0.46
1:2:369:C:OP2	1:2:388:G:N1	2.35	0.46
1:2:580:U:H3	1:2:761:G:H1	1.64	0.46
1:2:592:G:H2'	1:2:593:G:C8	2.50	0.46
3:h:40:ARG:NH2	3:h:55:VAL:O	2.49	0.46
28:Z:5:LYS:HB3	28:Z:57:GLU:HG2	1.98	0.46
34:1:782:A:O2'	37:B:225:ALA:O	2.34	0.46
34:1:2683:C:OP1	49:P:53:ARG:NH1	2.47	0.46
38:C:105:THR:HG21	38:C:164:ARG:HH21	1.81	0.46
49:P:29:ARG:HB2	49:P:85:LYS:HA	1.96	0.46
1:2:406:G:N3	4:i:119:GLN:NE2	2.52	0.46
1:2:744:C:H2'	1:2:745:C:H6	1.80	0.46
1:2:1031:G:H2'	1:2:1032:G:C8	2.51	0.46
1:2:1355:G:H2'	1:2:1356:G:C8	2.51	0.46
2:g:149:LEU:HD12	2:g:149:LEU:HA	1.81	0.46
19:x:11:VAL:HG11	19:x:16:LEU:HD13	1.98	0.46
27:Y:26:ARG:HH21	53:T:9:LEU:HA	1.80	0.46
34:1:137:C:H2'	34:1:139(A):G:C8	2.51	0.46
34:1:186:G:H2'	34:1:187:G:H8	1.81	0.46
34:1:822:U:H2'	34:1:823:G:H8	1.80	0.46
34:1:1301:A:H62	34:1:1641:A:H61	1.64	0.46
34:1:1791:A:H3'	34:1:1792:G:H8	1.80	0.46
37:B:75:ILE:HG21	37:B:99:ASP:HB2	1.97	0.46
46:M:71:ASP:N	46:M:71:ASP:OD1	2.49	0.46
49:P:30:VAL:HG21	49:P:83:ILE:HB	1.97	0.46
56:5:23:GLY:O	56:5:80:LEU:N	2.43	0.46
60:4:311:G:H2'	60:4:312:A:C8	2.51	0.46
9:n:65:VAL:HG22	9:n:73:GLN:HG2	1.97	0.46
26:X:64:ALA:HA	26:X:67:ILE:HG13	1.97	0.46
34:1:271:A:N6	34:1:271:A:C8	2.54	0.46
34:1:363:G:OP2	34:1:363(E):U:O2'	2.32	0.46
34:1:407:G:H2'	34:1:408:G:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:999:U:H2'	34:1:1000:A:H8	1.81	0.46
34:1:1088:A:O2'	34:1:1089:G:N7	2.44	0.46
34:1:2579:C:H1'	38:C:134:ILE:HD13	1.97	0.46
34:1:2809:A:OP2	34:1:2891:G:N1	2.46	0.46
46:M:63:LYS:HB2	46:M:107:ALA:HB3	1.98	0.46
51:R:71:LEU:O	51:R:73:SER:OG	2.28	0.46
60:4:318:G:H2'	60:4:319:G:H8	1.81	0.46
1:2:51:A:N7	1:2:114:U:O2'	2.46	0.46
1:2:374:A:O2'	1:2:451:A:OP2	2.34	0.46
1:2:693:G:C8	24:9:13:U:C4	3.04	0.46
12:q:78:GLN:N	12:q:81:SER:OG	2.48	0.46
30:b:45:VAL:HG11	47:N:98:LEU:HD13	1.96	0.46
34:1:892:G:H21	34:1:893:C:H5''	1.81	0.46
34:1:1071:G:N2	34:1:1089:G:H1	2.14	0.46
34:1:1622:G:H2'	34:1:1623:G:H8	1.81	0.46
34:1:2011:U:OP2	52:S:16:LYS:NZ	2.41	0.46
34:1:2377:A:H2'	34:1:2378:A:C8	2.51	0.46
34:1:2742:C:OP2	58:f:24:TYR:OH	2.26	0.46
34:1:2864:G:H5'	49:P:119:LYS:HE2	1.98	0.46
36:A:45:ALA:HA	36:A:209:LEU:O	2.16	0.46
37:B:124:PRO:O	37:B:129:ASN:ND2	2.39	0.46
46:M:12:GLN:HG2	46:M:73:PRO:HD2	1.98	0.46
1:2:45:U:H2'	1:2:46:G:H8	1.80	0.45
1:2:514:C:H2'	1:2:515:G:C8	2.51	0.45
5:j:33:VAL:HG23	5:j:112:LEU:HD12	1.97	0.45
8:m:1:MET:HE3	8:m:1:MET:HB3	1.74	0.45
34:1:106:C:O4'	54:U:2:ARG:NH2	2.46	0.45
34:1:975:C:H42	34:1:984:A:H5'	1.82	0.45
34:1:1636:C:H2'	34:1:1637:A:C8	2.51	0.45
34:1:1801:G:OP2	37:B:154:LYS:NZ	2.41	0.45
34:1:2033:A:O2'	34:1:2035:G:OP2	2.33	0.45
35:3:36:C:O2	35:3:49:C:O2'	2.32	0.45
35:3:75:G:O2'	55:V:10:ARG:NH2	2.48	0.45
38:C:51:PHE:HB3	38:C:76:ARG:HB2	1.98	0.45
43:J:21:LYS:HD3	43:J:21:LYS:HA	1.81	0.45
44:K:12:ASP:N	44:K:12:ASP:OD1	2.48	0.45
1:2:413:G:O6	4:i:35:ARG:NE	2.49	0.45
1:2:547:A:OP2	4:i:2:GLY:N	2.49	0.45
1:2:736:C:H2'	1:2:737:A:C8	2.52	0.45
1:2:1240:U:H3'	1:2:1241:G:H8	1.82	0.45
4:i:208:SER:O	4:i:208:SER:OG	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:v:46:ASP:OD1	17:v:46:ASP:N	2.46	0.45
34:1:607:U:H4'	39:D:100:THR:HG21	1.98	0.45
34:1:714:U:N3	34:1:717:G:OP2	2.44	0.45
34:1:2853:C:H2'	34:1:2854:G:H8	1.81	0.45
36:A:40:THR:OG1	36:A:214:VAL:O	2.28	0.45
37:B:50:THR:OG1	37:B:51:VAL:N	2.49	0.45
38:C:23:VAL:HG11	38:C:173:VAL:HG11	1.98	0.45
38:C:34:VAL:HG21	38:C:78:LEU:HD22	1.98	0.45
52:S:87:PRO:HA	52:S:93:ALA:HA	1.98	0.45
60:4:133:C:H2'	60:4:134:G:C8	2.51	0.45
1:2:1226:C:O2'	13:r:111:LYS:NZ	2.44	0.45
3:h:180:ALA:HA	3:h:206:GLU:HG3	1.98	0.45
4:i:190:ASP:H	4:i:193:ASP:HB2	1.80	0.45
5:j:11:ILE:HG21	5:j:105:VAL:HG13	1.97	0.45
15:t:35:ARG:NE	15:t:59:MET:SD	2.77	0.45
34:1:1901:A:OP2	37:B:255:LYS:NZ	2.39	0.45
34:1:2716:U:H2'	34:1:2717:G:H8	1.81	0.45
34:1:2755:C:H3'	58:f:19:ARG:HH21	1.81	0.45
43:J:58:ASP:OD1	43:J:58:ASP:N	2.50	0.45
55:V:6:LYS:NZ	55:V:61:LEU:O	2.49	0.45
1:2:473:G:H2'	1:2:474:G:H8	1.81	0.45
5:j:76:ILE:HG23	5:j:142:LEU:HD21	1.98	0.45
8:m:86:ILE:HG13	8:m:136:GLU:HG3	1.99	0.45
23:8:19:G:O4'	23:8:57:G:N2	2.46	0.45
28:Z:16:PRO:HA	34:1:969:U:H5'	1.98	0.45
29:a:24:THR:OG1	29:a:25:TYR:N	2.48	0.45
34:1:919:G:N2	34:1:2269:A:OP2	2.49	0.45
34:1:1094:U:H5'	34:1:1098:A:H62	1.81	0.45
34:1:1802:A:H2'	34:1:1803:A:C8	2.50	0.45
35:3:60:C:H2'	35:3:61:G:H8	1.82	0.45
1:2:269:C:H2'	1:2:270:A:C8	2.51	0.45
1:2:674:G:H2'	1:2:675:A:C8	2.50	0.45
1:2:1397:C:OP2	5:j:24:ARG:NH2	2.46	0.45
8:m:66:GLY:H	8:m:76:PRO:HB2	1.81	0.45
23:8:63:G:H2'	23:8:64:A:H8	1.81	0.45
26:X:36:GLY:O	34:1:2432:A:N6	2.50	0.45
33:e:15:LYS:HE2	33:e:15:LYS:HB2	1.84	0.45
34:1:92:A:H2'	34:1:93:G:H8	1.82	0.45
34:1:1358:G:N1	34:1:1372:U:OP2	2.33	0.45
34:1:1479:G:O2'	34:1:1559:G:O2'	2.27	0.45
34:1:1657:C:OP1	38:C:136:ARG:N	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:2591:C:H2'	34:1:2592:G:C8	2.51	0.45
34:1:2676:C:H2'	34:1:2677:G:H8	1.81	0.45
41:F:70:THR:O	41:F:74:ASN:ND2	2.50	0.45
49:P:50:ILE:HD11	49:P:64:ARG:HD2	1.97	0.45
1:2:707:C:H1'	11:p:39:PRO:HG3	1.98	0.45
3:h:73:PRO:HA	3:h:76:VAL:HG12	1.98	0.45
4:i:190:ASP:OD1	4:i:191:ARG:N	2.45	0.45
4:i:196:LEU:HD23	4:i:196:LEU:HA	1.85	0.45
34:1:272(D):G:H2'	34:1:272(E):G:C8	2.52	0.45
34:1:2539:C:H4'	58:f:3:VAL:HG21	1.98	0.45
1:2:79:G:C8	1:2:84:U:H5''	2.51	0.45
1:2:1358:U:H5''	14:s:34:TYR:HA	1.99	0.45
1:2:1427:U:H2'	1:2:1428:A:H8	1.82	0.45
5:j:95:ALA:O	5:j:98:THR:OG1	2.31	0.45
25:W:30:VAL:HG22	25:W:66:VAL:HG12	1.99	0.45
34:1:1009:A:N3	34:1:1153:C:O2'	2.37	0.45
34:1:1019:U:H3	34:1:1142(A):A:H62	1.64	0.45
34:1:1516:C:H2'	34:1:1517:G:H8	1.82	0.45
34:1:1638:C:O3'	34:1:2709:G:N2	2.50	0.45
34:1:2714:G:C8	34:1:2714:G:H5''	2.52	0.45
34:1:2786:U:H2'	34:1:2787:C:H6	1.81	0.45
35:3:88:C:N4	35:3:89:G:N3	2.64	0.45
39:D:68:LYS:HA	39:D:68:LYS:HD3	1.77	0.45
47:N:2:ARG:HG3	47:N:5:LYS:HE3	1.97	0.45
49:P:85:LYS:HA	49:P:85:LYS:HD3	1.66	0.45
1:2:1030(C):G:H2'	1:2:1030(D):A:C8	2.52	0.45
2:g:56:ARG:HA	2:g:56:ARG:HD3	1.74	0.45
2:g:205:ASP:OD1	2:g:205:ASP:N	2.50	0.45
4:i:169:LYS:HA	4:i:169:LYS:HD2	1.66	0.45
6:k:79:LEU:HD23	6:k:79:LEU:HA	1.85	0.45
9:n:53:VAL:HG22	9:n:95:LYS:HD3	1.99	0.45
23:8:62:C:H2'	23:8:63:G:C8	2.52	0.45
34:1:597:U:H2'	34:1:598:G:H8	1.81	0.45
34:1:995:C:O2	43:J:4:TYR:OH	2.32	0.45
34:1:1636:C:H2'	34:1:1637:A:H8	1.82	0.45
34:1:1921:G:H2'	34:1:1922:G:H8	1.82	0.45
34:1:2648:C:H2'	34:1:2649:U:C6	2.51	0.45
40:E:39:ILE:HB	40:E:92:VAL:HG12	1.99	0.45
41:F:84:SER:OG	41:F:86:GLU:OE2	2.35	0.45
43:J:47:ALA:O	43:J:119:ARG:NH2	2.47	0.45
45:L:23:PRO:O	45:L:33:ARG:NH1	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:4:280:G:C5	60:4:296:G:N2	2.85	0.45
3:h:112:SER:O	3:h:112:SER:OG	2.31	0.45
8:m:87:SER:HB2	8:m:93:VAL:HG12	1.98	0.45
14:s:15:LYS:HA	14:s:15:LYS:HD2	1.67	0.45
19:x:51:VAL:O	19:x:57:HIS:HA	2.17	0.45
27:Y:19:VAL:HG13	53:T:5:TYR:HE2	1.82	0.45
34:1:573:G:H5'	34:1:575:A:N7	2.32	0.45
54:U:13:VAL:HG11	54:U:72:VAL:HB	1.98	0.45
1:2:770:C:H2'	1:2:771:G:H8	1.82	0.45
1:2:1151:A:O2'	1:2:1152:A:O5'	2.34	0.45
1:2:1507:A:H2'	1:2:1508:G:C8	2.52	0.45
9:n:20:ARG:N	9:n:60:ASP:O	2.47	0.45
13:r:85:GLY:HA2	13:r:90:LEU:HG	1.99	0.45
26:X:24:ALA:HB1	26:X:26:ARG:HD3	1.97	0.45
29:a:16:CYS:SG	29:a:17:GLY:N	2.90	0.45
34:1:805:G:O2'	34:1:2068:U:OP2	2.32	0.45
34:1:2831:G:O2'	34:1:2884:U:OP1	2.32	0.45
38:C:5:LEU:HD11	38:C:79:ARG:HB2	1.99	0.45
60:4:293:G:O2'	60:4:294:U:O4'	2.33	0.45
1:2:420:U:O2'	1:2:423:G:O6	2.35	0.44
1:2:573:A:N3	1:2:883:C:O2'	2.47	0.44
2:g:19:HIS:HD2	2:g:20:GLU:HG2	1.82	0.44
3:h:132:ARG:NH2	56:5:144:LEU:OXT	2.50	0.44
6:k:5:GLU:HG2	6:k:62:TRP:CZ2	2.52	0.44
6:k:39:LYS:HA	6:k:39:LYS:HD3	1.85	0.44
13:r:17:VAL:O	13:r:20:THR:OG1	2.27	0.44
15:t:63:ARG:HH22	34:1:715:G:H4'	1.82	0.44
16:u:55:ARG:HD2	16:u:55:ARG:HA	1.71	0.44
34:1:1604:C:O2'	34:1:1610:A:N1	2.39	0.44
34:1:2593:U:H2'	34:1:2594:C:C6	2.52	0.44
36:A:211:SER:HA	36:A:220:PRO:HA	1.99	0.44
48:O:83:LYS:HG2	48:O:105:ALA:HB3	1.98	0.44
1:2:1350:A:O2'	7:l:33:ASP:OD1	2.35	0.44
1:2:1376:U:H2'	1:2:1377:A:C8	2.53	0.44
2:g:133:LYS:HD2	2:g:133:LYS:HA	1.76	0.44
3:h:3:ASN:N	3:h:3:ASN:OD1	2.46	0.44
5:j:91:LEU:HB3	5:j:118:ILE:HD11	1.98	0.44
6:k:11:ASN:HB2	6:k:14:LEU:HG	1.99	0.44
15:t:70:LEU:HA	15:t:70:LEU:HD12	1.78	0.44
20:y:42:GLN:NE2	20:y:46:GLU:OE2	2.47	0.44
31:c:35:GLU:N	31:c:51:GLU:OE1	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:679:C:H2'	34:1:680:G:C8	2.50	0.44
34:1:2635:C:OP1	38:C:79:ARG:NH1	2.38	0.44
43:J:30:ILE:HG23	43:J:52:VAL:HG11	1.99	0.44
45:L:21:ARG:HD2	45:L:29:LYS:HE2	1.99	0.44
47:N:96:ARG:O	47:N:114:VAL:HA	2.18	0.44
51:R:62:LEU:HD22	51:R:96:ILE:HG21	1.99	0.44
51:R:80:GLN:O	51:R:81:TYR:N	2.51	0.44
59:H:106:UNK:O	59:H:108:UNK:N	2.49	0.44
1:2:127:G:O2'	17:v:2:PRO:O	2.36	0.44
20:y:41:ILE:O	20:y:45:GLN:HB2	2.17	0.44
25:W:6:GLY:HA3	46:M:80:GLU:HG3	1.98	0.44
25:W:19:LYS:HD3	25:W:19:LYS:HA	1.81	0.44
34:1:749:C:H5'	34:1:1271:G:H1'	1.99	0.44
34:1:2100:G:H2'	34:1:2101:G:C8	2.52	0.44
34:1:2631:G:N2	38:C:61:ARG:HH12	2.16	0.44
34:1:2647:U:H2'	34:1:2648:C:H6	1.83	0.44
35:3:5:C:O2'	35:3:27:C:O2	2.31	0.44
37:B:80:ALA:HA	37:B:113:VAL:HG13	1.99	0.44
41:F:113:VAL:HG11	41:F:151:ILE:HD12	1.99	0.44
51:R:22:VAL:HG12	51:R:94:LEU:HB3	1.99	0.44
52:S:5:ALA:HB2	52:S:54:ALA:HB2	1.98	0.44
56:5:35:ARG:NH2	56:5:111:GLY:O	2.50	0.44
1:2:662:G:O2'	1:2:836:G:OP1	2.35	0.44
1:2:920:U:H2'	1:2:921:U:C6	2.52	0.44
1:2:1163:C:H2'	1:2:1164:G:H8	1.82	0.44
1:2:1295:G:O3'	13:r:14:ARG:NH2	2.50	0.44
1:2:1355:G:H2'	1:2:1356:G:H8	1.82	0.44
19:x:39:THR:HA	19:x:70:LYS:HA	1.99	0.44
34:1:414:C:H2'	34:1:415:A:C8	2.52	0.44
34:1:2471:C:H3'	34:1:2472:G:H8	1.82	0.44
34:1:2619:C:H5''	38:C:152:LYS:HG3	1.99	0.44
38:C:105:THR:HB	38:C:197:ILE:HG12	2.00	0.44
38:C:132:HIS:HA	38:C:135:HIS:CE1	2.53	0.44
39:D:75:HIS:HE1	39:D:82:ILE:HD11	1.82	0.44
47:N:33:ARG:HH21	47:N:113:LEU:HD11	1.82	0.44
48:O:57:LYS:HD3	48:O:68:GLN:HB3	1.99	0.44
1:2:1150:U:O4	1:2:1151:A:N6	2.50	0.44
34:1:185:U:H2'	34:1:186:G:C8	2.53	0.44
34:1:783:A:H8	34:1:784:A:H4'	1.83	0.44
34:1:1049:C:H2'	34:1:1050:A:C8	2.53	0.44
34:1:1718:G:H5'	34:1:1718:G:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:2296:U:OP2	48:O:13:ARG:NH1	2.50	0.44
34:1:2505:G:H3'	34:1:2576:G:H22	1.82	0.44
41:F:70:THR:HG22	41:F:74:ASN:HD21	1.82	0.44
51:R:19:LYS:NZ	51:R:20:LEU:H	2.16	0.44
53:T:65:ARG:HH21	53:T:66:LEU:HD13	1.83	0.44
1:2:971:G:H4'	1:2:972:C:H5''	1.98	0.44
1:2:1268:A:N3	1:2:1326:C:O2'	2.37	0.44
2:g:111:ARG:HB3	2:g:145:LEU:HD11	1.98	0.44
33:e:61:LEU:HD13	34:1:593:G:H4'	1.99	0.44
34:1:251:A:N6	34:1:386:G:O6	2.44	0.44
34:1:587:C:H41	45:L:33:ARG:HG3	1.82	0.44
34:1:1141:U:OP1	43:J:25:ARG:NH1	2.49	0.44
34:1:1278:A:H4'	47:N:34:ILE:HG23	2.00	0.44
34:1:1809:A:H2'	34:1:1810:A:C8	2.53	0.44
34:1:2439:A:O2'	34:1:2600:A:OP1	2.26	0.44
34:1:2653:U:H3'	34:1:2654:A:C8	2.53	0.44
5:j:50:GLU:HB2	5:j:53:LEU:HD12	1.99	0.44
7:l:107:ALA:O	7:l:111:ARG:HB2	2.18	0.44
17:v:4:LYS:HB3	17:v:61:GLU:HB2	1.99	0.44
34:1:172:C:H2'	34:1:173:G:C8	2.53	0.44
37:B:45:ASN:N	37:B:45:ASN:OD1	2.51	0.44
45:L:91:PHE:HE1	45:L:95:VAL:HB	1.82	0.44
47:N:76:VAL:HA	47:N:79:LEU:HB3	2.00	0.44
1:2:12:U:O2'	1:2:914:A:OP1	2.35	0.44
1:2:246:A:N1	1:2:278:G:O2'	2.46	0.44
1:2:310:G:OP1	16:u:27:LYS:NZ	2.40	0.44
1:2:626:U:H2'	1:2:627:G:H8	1.83	0.44
1:2:916:G:H2'	1:2:917:G:H8	1.83	0.44
1:2:1287:A:H2'	1:2:1288:A:C8	2.53	0.44
2:g:114:ARG:HD3	2:g:114:ARG:HA	1.85	0.44
7:l:84:ASN:HD21	23:8:33:U:H4'	1.83	0.44
12:q:54:LYS:HD3	12:q:75:HIS:CE1	2.53	0.44
34:1:59:U:O2'	34:1:74:A:OP2	2.32	0.44
34:1:740:U:H2'	34:1:741:G:C8	2.53	0.44
34:1:922:U:H2'	34:1:923:C:C6	2.53	0.44
34:1:992:C:H2'	34:1:993:G:H8	1.83	0.44
34:1:1055:G:H21	34:1:1085:A:H2	1.66	0.44
34:1:1071:G:N3	34:1:1089:G:N1	2.66	0.44
1:2:309:G:H2'	1:2:310:G:H8	1.83	0.44
1:2:475:G:H2'	1:2:476:G:H8	1.82	0.44
1:2:948:C:H2'	1:2:949:A:H8	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1327:C:H5''	21:z:20:LYS:HB3	2.00	0.44
3:h:156:ARG:NH1	3:h:160:ALA:O	2.51	0.44
4:i:43:HIS:O	4:i:45:GLN:N	2.51	0.44
9:n:86:VAL:HG22	9:n:93:ARG:HA	2.00	0.44
11:p:32:ILE:HD11	11:p:68:ALA:HB1	1.99	0.44
18:w:40:LEU:HB3	18:w:79:LEU:HD11	2.00	0.44
27:Y:26:ARG:NE	53:T:9:LEU:O	2.51	0.44
34:1:589:C:H2'	34:1:590:A:C8	2.53	0.44
34:1:1119:C:H2'	34:1:1120:G:C8	2.53	0.44
34:1:2632:A:O2'	34:1:2811:G:O2'	2.34	0.44
40:E:4:ASP:OD1	40:E:4:ASP:N	2.46	0.44
45:L:13:ASN:OD1	45:L:13:ASN:N	2.49	0.44
1:2:184:G:H2'	1:2:185:A:H8	1.83	0.43
1:2:266:G:H5'	1:2:268:C:H5	1.83	0.43
1:2:1286:A:N6	1:2:1354:C:O3'	2.51	0.43
3:h:120:VAL:HB	3:h:198:VAL:HG11	1.99	0.43
6:k:51:PRO:HB2	6:k:54:LYS:HA	2.00	0.43
7:l:27:ILE:HD12	7:l:40:ALA:HA	1.99	0.43
8:m:23:SER:HA	8:m:61:VAL:O	2.18	0.43
11:p:80:VAL:HG13	11:p:103:LEU:HD12	1.99	0.43
15:t:29:VAL:O	15:t:33:THR:OG1	2.32	0.43
25:W:45:PHE:HZ	34:1:857:C:H5'	1.83	0.43
34:1:1083:U:N3	34:1:1086:A:OP2	2.51	0.43
35:3:8:U:O2	35:3:113:G:O6	2.36	0.43
1:2:413:G:H1'	1:2:428:G:N2	2.33	0.43
1:2:728:A:H2'	1:2:729:A:H8	1.83	0.43
1:2:1058:G:OP1	3:h:199:LYS:NZ	2.32	0.43
1:2:1479:C:H2'	1:2:1480:G:C8	2.52	0.43
3:h:29:TYR:OH	14:s:54:PRO:O	2.35	0.43
23:8:28:G:H2'	23:8:29:G:C8	2.53	0.43
34:1:479:A:H4'	34:1:480:A:H5'	2.00	0.43
34:1:2776:A:H4'	34:1:2777:G:H5''	2.00	0.43
34:1:2822:G:OP1	38:C:159:HIS:NE2	2.50	0.43
37:B:108:PRO:HB3	37:B:143:HIS:CE1	2.53	0.43
38:C:92:THR:HB	38:C:180:ASN:HD21	1.83	0.43
39:D:135:LYS:HB3	39:D:138:GLU:HG3	2.00	0.43
39:D:157:VAL:HB	39:D:194:MET:HB3	2.00	0.43
46:M:47:ILE:HD13	46:M:47:ILE:HA	1.79	0.43
50:Q:88:ILE:HB	50:Q:90:VAL:HG22	2.00	0.43
51:R:3:ALA:HB3	51:R:14:VAL:HG23	2.00	0.43
54:U:15:VAL:HG21	54:U:67:LEU:HD21	1.98	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:4:189:C:H2'	60:4:190:G:C8	2.53	0.43
60:4:218:G:OP2	60:4:218:G:N2	2.44	0.43
1:2:836:G:H2'	1:2:837:G:H8	1.83	0.43
1:2:1129:C:H4'	1:2:1130:A:H5'	2.01	0.43
1:2:1512:U:H2'	1:2:1513:A:H8	1.83	0.43
2:g:16:HIS:CD2	2:g:210:SER:HA	2.54	0.43
5:j:10:MET:HB3	5:j:32:VAL:HG12	2.00	0.43
8:m:116:LYS:HD3	8:m:127:LEU:HD23	2.01	0.43
15:t:82:ILE:HD12	15:t:87:ILE:HB	2.01	0.43
23:8:28:G:H2'	23:8:29:G:H8	1.83	0.43
33:e:46:ARG:NH1	34:1:630:G:OP1	2.51	0.43
34:1:513:A:H2	34:1:582:G:H4'	1.82	0.43
34:1:815:C:OP1	51:R:87:HIS:NE2	2.49	0.43
34:1:918:A:OP2	34:1:2268:A:N6	2.50	0.43
43:J:4:TYR:OH	50:Q:94:ASN:OD1	2.36	0.43
46:M:59:ARG:H	46:M:59:ARG:HG2	1.68	0.43
56:5:24:ILE:HD12	56:5:26:LEU:HD21	2.00	0.43
1:2:34:C:H2'	1:2:35:G:C8	2.53	0.43
1:2:439:A:OP2	1:2:493:G:N1	2.45	0.43
1:2:626:U:OP1	16:u:18:ARG:NH2	2.50	0.43
1:2:877:C:H2'	1:2:878:G:H8	1.83	0.43
2:g:24:TRP:HZ3	2:g:29:ALA:HB2	1.84	0.43
4:i:14:ARG:HB2	4:i:40:PRO:HD2	1.99	0.43
15:t:42:HIS:NE2	15:t:49:ASP:OD2	2.48	0.43
22:7:54:5MU:H2'	22:7:55:U:O4'	2.18	0.43
34:1:271(L):U:H4'	34:1:271(M):G:C5	2.53	0.43
34:1:500:G:N2	34:1:503:A:O5'	2.41	0.43
34:1:629:G:O2'	34:1:639:U:O2	2.36	0.43
34:1:1215:G:N2	34:1:1234:U:O2	2.46	0.43
34:1:1528:A:N6	34:1:1544:A:N1	2.67	0.43
34:1:1542:A:N7	34:1:1544:A:H5''	2.33	0.43
38:C:120:TRP:CD1	38:C:155:LYS:HB3	2.54	0.43
41:F:137:ASP:HB3	41:F:141:VAL:HG23	2.01	0.43
46:M:129:THR:OG1	46:M:130:LYS:O	2.36	0.43
49:P:35:LYS:NZ	49:P:41:ARG:HE	2.15	0.43
1:2:325:A:OP2	20:y:70:SER:OG	2.31	0.43
1:2:1238:A:N7	1:2:1299:A:N6	2.66	0.43
4:i:112:VAL:HG13	4:i:161:ASN:HD21	1.84	0.43
9:n:35:GLU:OE2	9:n:38:GLN:NE2	2.46	0.43
9:n:46:ALA:HB2	9:n:74:ILE:HG23	2.00	0.43
12:q:87:GLY:HA2	12:q:98:TYR:HD1	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:x:10:PHE:CE2	19:x:39:THR:HB	2.52	0.43
26:X:81:LYS:HA	26:X:81:LYS:HD3	1.77	0.43
34:1:534:U:H2'	34:1:535:C:C6	2.53	0.43
34:1:1794:U:H2'	34:1:1795:C:H6	1.82	0.43
38:C:59:VAL:HG11	38:C:72:VAL:HG12	2.00	0.43
45:L:61:ARG:H	45:L:61:ARG:HG2	1.63	0.43
46:M:110:THR:OG1	46:M:111:GLU:N	2.51	0.43
47:N:13:HIS:CE1	47:N:16:HIS:HB2	2.53	0.43
50:Q:27:LEU:HA	50:Q:27:LEU:HD23	1.81	0.43
1:2:1313:U:H2'	1:2:1314:C:C6	2.53	0.43
5:j:78:HIS:HB2	8:m:104:ARG:HB2	2.01	0.43
13:r:91:ARG:HG3	13:r:98:VAL:HG12	2.00	0.43
23:8:68:C:H2'	23:8:69:G:C8	2.52	0.43
25:W:55:ARG:HB3	34:1:2364:C:H5''	2.00	0.43
34:1:347:A:H2'	34:1:348:G:C8	2.54	0.43
34:1:631:A:H4'	45:L:65:ARG:HA	2.00	0.43
34:1:918:A:N3	35:3:80:U:O2'	2.41	0.43
34:1:1837:C:N4	34:1:1899:G:N7	2.67	0.43
34:1:2448:A:H3'	34:1:2449:U:H2'	2.01	0.43
34:1:2647:U:H2'	34:1:2648:C:C6	2.53	0.43
36:A:59:ARG:NH1	36:A:60:GLY:O	2.51	0.43
40:E:67:LYS:HE2	40:E:67:LYS:HB2	1.82	0.43
45:L:120:ALA:H	45:L:137:LYS:NZ	2.16	0.43
48:O:35:ILE:HG23	48:O:53:SER:HB2	2.01	0.43
50:Q:28:ARG:HA	50:Q:28:ARG:HD3	1.86	0.43
1:2:626:U:H2'	1:2:627:G:C8	2.54	0.43
1:2:647:C:H2'	1:2:648:A:H8	1.83	0.43
1:2:991:U:O4	1:2:1212:U:O2'	2.29	0.43
12:q:60:LEU:HD11	12:q:85:ILE:HG13	2.00	0.43
16:u:1:MET:SD	16:u:65:GLN:NE2	2.77	0.43
17:v:52:LYS:N	17:v:55:ASP:OD2	2.51	0.43
19:x:67:VAL:HG11	29:a:50:VAL:HG12	2.00	0.43
25:W:53:MET:HG2	25:W:57:PHE:HA	2.01	0.43
27:Y:28:LYS:HD3	27:Y:28:LYS:HA	1.82	0.43
30:b:45:VAL:HA	30:b:50:GLY:HA2	2.00	0.43
33:e:6:THR:HG21	33:e:63:PRO:HD3	2.00	0.43
34:1:881:G:H2'	34:1:882:G:H8	1.84	0.43
34:1:960:A:H61	46:M:82:ARG:NH2	2.16	0.43
34:1:1448:G:H1'	34:1:1528:A:H61	1.83	0.43
34:1:2002:G:H2'	34:1:2003:G:C8	2.54	0.43
34:1:2443:C:H2'	34:1:2444:G:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:J:136:GLU:HG2	43:J:138:LEU:HD21	2.00	0.43
1:2:41:G:H2'	1:2:42:G:H8	1.84	0.43
4:i:194:LEU:HD23	4:i:194:LEU:HA	1.84	0.43
7:l:29:LYS:HD2	7:l:29:LYS:HA	1.77	0.43
32:d:11:LYS:NZ	34:1:686:G:H5''	2.34	0.43
34:1:184:C:H2'	34:1:185:U:C6	2.54	0.43
34:1:345:A:N3	34:1:347:A:N6	2.67	0.43
34:1:642:G:N2	34:1:645:C:OP2	2.52	0.43
34:1:1423:G:H2'	34:1:1424:G:H8	1.83	0.43
34:1:1476:C:H2'	34:1:1477:A:H8	1.83	0.43
34:1:2790:A:N3	34:1:2791:C:H5''	2.33	0.43
37:B:233:HIS:CE1	37:B:247:ALA:H	2.37	0.43
49:P:28:VAL:HG22	49:P:46:GLU:HA	2.00	0.43
60:4:23:G:O6	60:4:315:U:O4	2.37	0.43
1:2:665:A:N7	1:2:724:G:O6	2.52	0.43
9:n:29:ASN:OD1	9:n:65:VAL:N	2.41	0.43
11:p:33:THR:HA	11:p:40:ILE:H	1.84	0.43
13:r:57:ARG:O	13:r:61:GLU:HG3	2.18	0.43
20:y:38:LYS:HD3	20:y:38:LYS:HA	1.77	0.43
34:1:1651:G:H4'	47:N:39:PRO:HG2	2.01	0.43
34:1:1749:A:H5''	34:1:1749:A:C8	2.54	0.43
34:1:1818:U:H4'	34:1:1821:A:H1'	2.01	0.43
34:1:2532:G:O2'	34:1:2657:A:N6	2.45	0.43
34:1:2816:C:H2'	34:1:2817:G:H8	1.84	0.43
34:1:2836:U:H2'	34:1:2837:G:C8	2.53	0.43
47:N:2:ARG:HA	47:N:2:ARG:HD2	1.89	0.43
48:O:34:HIS:CE1	48:O:54:LEU:HB3	2.54	0.43
50:Q:110:VAL:HG22	50:Q:114:LYS:HE3	2.00	0.43
52:S:5:ALA:HB3	52:S:105:VAL:H	1.82	0.43
1:2:709:G:H2'	1:2:710:G:H8	1.84	0.43
1:2:1172:C:H2'	1:2:1173:G:C8	2.53	0.43
1:2:1404:C:H2'	1:2:1405:G:C8	2.54	0.43
2:g:212:GLN:NE2	2:g:233:SER:O	2.49	0.43
4:i:105:VAL:HG13	4:i:110:PHE:HB2	2.01	0.43
4:i:108:LEU:HD11	4:i:183:GLY:HA3	2.01	0.43
15:t:56:LEU:HD12	15:t:56:LEU:HA	1.83	0.43
26:X:75:GLU:O	26:X:76:ARG:NH1	2.43	0.43
27:Y:52:ASP:HA	27:Y:55:ARG:HB3	2.00	0.43
30:b:56:LYS:HB3	30:b:59:GLU:HG2	2.01	0.43
34:1:861:A:N6	34:1:916:G:O2'	2.52	0.43
34:1:1039:G:H2'	34:1:1040:C:H4'	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:1399:C:H2'	34:1:1400:G:H8	1.83	0.43
34:1:1792:G:O2'	34:1:1830:C:OP1	2.36	0.43
34:1:2676:C:H2'	34:1:2677:G:C8	2.54	0.43
38:C:64:LYS:HG2	38:C:66:HIS:HD2	1.84	0.43
39:D:102:PRO:HB2	39:D:105:VAL:HG23	2.00	0.43
52:S:58:ALA:HB1	52:S:64:MET:HB2	2.01	0.43
60:4:14:U:H6	60:4:14:U:H2'	1.60	0.43
1:2:409:G:OP1	4:i:24:GLU:N	2.52	0.42
1:2:1058:G:O6	1:2:1199:U:O4	2.37	0.42
1:2:1117:G:H21	1:2:1180:A:H1'	1.84	0.42
1:2:1141:C:H2'	1:2:1142:G:C8	2.54	0.42
8:m:119:LEU:HB3	8:m:123:GLU:HB2	2.01	0.42
9:n:50:LEU:HA	9:n:50:LEU:HD23	1.84	0.42
13:r:102:ARG:HE	13:r:102:ARG:HB2	1.53	0.42
16:u:66:PRO:HG2	16:u:71:ARG:HD3	2.01	0.42
34:1:347:A:H2'	34:1:348:G:H8	1.84	0.42
34:1:1296:G:OP1	34:1:2709:G:O2'	2.26	0.42
34:1:2392:A:C8	45:L:60:MET:HG2	2.54	0.42
47:N:65:LEU:HD23	47:N:68:ARG:HD2	2.01	0.42
50:Q:27:LEU:HD22	50:Q:31:SER:HB2	2.01	0.42
1:2:224:C:H2'	1:2:225:C:C6	2.54	0.42
1:2:985:C:H2'	1:2:986:A:H8	1.83	0.42
1:2:1513:A:H2'	1:2:1514:C:C6	2.54	0.42
13:r:38:GLY:O	13:r:55:ARG:NH1	2.52	0.42
17:v:4:LYS:HG3	17:v:6:LEU:HG	2.02	0.42
17:v:17:LYS:HB3	17:v:45:HIS:CE1	2.54	0.42
20:y:30:LYS:HE3	20:y:30:LYS:HB2	1.82	0.42
23:8:6:G:H2'	23:8:7:A:C8	2.54	0.42
26:X:26:ARG:HB2	26:X:34:THR:HA	2.01	0.42
30:b:33:CYS:SG	30:b:40:LYS:HE3	2.58	0.42
34:1:1165:U:H2'	34:1:1166:C:C6	2.54	0.42
34:1:1196:C:O2'	34:1:1227:G:O2'	2.21	0.42
34:1:1949:G:H2'	34:1:1950:G:C8	2.54	0.42
46:M:58:PHE:HD2	46:M:61:GLY:HA3	1.84	0.42
49:P:28:VAL:O	49:P:29:ARG:NE	2.53	0.42
56:5:26:LEU:HD13	56:5:26:LEU:HA	1.92	0.42
1:2:56:U:H2'	1:2:57:G:C8	2.55	0.42
1:2:582:U:OP2	1:2:758:G:N1	2.42	0.42
1:2:695:A:H2	1:2:787:A:H1'	1.84	0.42
1:2:711:G:H2'	1:2:712:A:H8	1.84	0.42
1:2:1286:A:N3	21:z:18:TYR:OH	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1479:C:H2'	1:2:1480:G:H8	1.83	0.42
1:2:1522:U:H2'	1:2:1523:G:C8	2.52	0.42
3:h:11:ARG:NH2	3:h:177:THR:O	2.48	0.42
3:h:70:VAL:O	3:h:105:GLU:HA	2.19	0.42
3:h:157:ILE:HA	3:h:196:LEU:HD11	2.01	0.42
4:i:36:ARG:HE	4:i:36:ARG:HB2	1.68	0.42
5:j:64:ARG:HA	5:j:64:ARG:HD3	1.86	0.42
12:q:17:LYS:HA	12:q:17:LYS:HD3	1.84	0.42
33:e:11:LYS:HA	33:e:60:LEU:HD11	2.01	0.42
33:e:52:LYS:HA	33:e:52:LYS:HD3	1.65	0.42
34:1:459:U:H2'	34:1:460:A:H8	1.84	0.42
34:1:526:A:O2'	34:1:2043:C:O2	2.34	0.42
34:1:663:G:O3'	45:L:21:ARG:NH2	2.52	0.42
34:1:673:C:N4	34:1:674:G:O6	2.52	0.42
34:1:1718:G:H2'	34:1:1719:G:H8	1.84	0.42
34:1:2581:G:N1	34:1:2610:C:O2'	2.51	0.42
34:1:2801:A:O2'	34:1:2894:G:OP1	2.33	0.42
40:E:128:ARG:HA	40:E:128:ARG:HD3	1.83	0.42
60:4:249:C:H2'	60:4:250:C:H5	1.85	0.42
60:4:332:C:HO2'	60:4:334:C:H41	1.62	0.42
1:2:166:G:H2'	1:2:167:G:H8	1.84	0.42
13:r:23:TYR:HB3	13:r:67:GLU:HB3	2.02	0.42
22:7:58:A:O2'	22:7:60:U:OP2	2.33	0.42
34:1:309:G:N3	34:1:329:G:O2'	2.51	0.42
34:1:391:G:O2'	34:1:410:G:OP1	2.35	0.42
34:1:1297:C:H2'	34:1:1298:C:C6	2.55	0.42
34:1:1952:A:C5	44:K:22:ILE:HD12	2.54	0.42
34:1:2853:C:H2'	34:1:2854:G:C8	2.55	0.42
38:C:111:ARG:HD2	38:C:160:TYR:CD2	2.54	0.42
39:D:187:VAL:HG11	45:L:7:ARG:HH21	1.84	0.42
54:U:68:HIS:O	54:U:71:LYS:NZ	2.40	0.42
1:2:663:A:O3'	18:w:64:ARG:NH2	2.48	0.42
1:2:709:G:H2'	1:2:710:G:C8	2.55	0.42
1:2:1095:U:P	1:2:1108:G:H1	2.42	0.42
1:2:1376:U:OP1	7:l:98:SER:OG	2.34	0.42
2:g:58:ILE:O	2:g:62:ALA:HB2	2.19	0.42
4:i:156:GLU:HA	4:i:159:ARG:HH11	1.84	0.42
7:l:70:LYS:HG3	7:l:96:GLN:HB3	2.01	0.42
8:m:83:ILE:HG13	8:m:137:VAL:HG22	2.00	0.42
10:o:87:THR:OG1	10:o:88:LEU:N	2.53	0.42
13:r:121:LYS:H	13:r:121:LYS:HG2	1.70	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:t:67:LEU:HD23	15:t:67:LEU:HA	1.82	0.42
17:v:74:LEU:HD12	17:v:74:LEU:HA	1.84	0.42
33:e:42:ARG:NH1	34:1:2382:G:H21	2.18	0.42
34:1:687:C:O2'	34:1:1780:A:N1	2.50	0.42
34:1:1265:A:H61	34:1:2013:A:H5''	1.83	0.42
34:1:1479:G:O6	34:1:1512:U:O2	2.38	0.42
34:1:1539:G:C2	34:1:1540:U:H1'	2.54	0.42
34:1:2247:A:H2'	34:1:2248:C:C6	2.55	0.42
40:E:18:GLU:O	40:E:22:ARG:HB2	2.20	0.42
40:E:124:SER:HB2	40:E:131:TYR:CE1	2.53	0.42
42:G:2:LYS:HB2	42:G:39:ALA:HB3	2.01	0.42
42:G:20:ASP:OD1	42:G:20:ASP:N	2.49	0.42
1:2:337:C:H2'	1:2:338:A:H8	1.85	0.42
1:2:1314:C:H2'	1:2:1315:U:C6	2.54	0.42
1:2:1356:G:H2'	1:2:1357:A:H8	1.83	0.42
3:h:62:ASP:HA	3:h:97:LYS:HD3	2.00	0.42
11:p:27:ASN:OD1	11:p:28:THR:N	2.48	0.42
11:p:38:ASN:HA	11:p:39:PRO:HD3	1.90	0.42
13:r:66:LEU:O	13:r:70:LEU:HB3	2.20	0.42
27:Y:51:ARG:NH1	27:Y:52:ASP:OD1	2.52	0.42
30:b:20:ARG:HA	30:b:23:HIS:CD2	2.54	0.42
33:e:6:THR:OG1	34:1:243:U:OP1	2.29	0.42
33:e:25:MET:HG3	45:L:64:LYS:HD2	2.01	0.42
34:1:94:C:H6	34:1:94:C:H2'	1.66	0.42
34:1:632:A:H2'	34:1:633:A:C8	2.55	0.42
34:1:676:A:H2	34:1:802:A:H61	1.68	0.42
34:1:1403:C:H5'	34:1:1471:A:H1'	2.01	0.42
34:1:2698:U:H2'	34:1:2699:C:C6	2.55	0.42
39:D:31:HIS:ND1	45:L:13:ASN:OD1	2.53	0.42
39:D:34:TRP:CD1	45:L:11:GLY:HA2	2.54	0.42
39:D:36:VAL:HG13	39:D:183:VAL:HG11	2.02	0.42
40:E:47:LYS:HA	40:E:47:LYS:HD3	1.83	0.42
50:Q:24:TYR:HB2	50:Q:29:SER:HB2	2.02	0.42
50:Q:27:LEU:O	50:Q:31:SER:CB	2.66	0.42
1:2:262:A:H5''	20:y:76:ALA:HB2	2.02	0.42
1:2:685:G:N2	1:2:704:A:OP2	2.50	0.42
1:2:769:G:H4'	1:2:1513:A:H4'	2.01	0.42
1:2:971:G:N1	1:2:1363(A):A:OP2	2.42	0.42
1:2:1014:A:H2'	1:2:1015:A:C8	2.55	0.42
1:2:1251:A:N3	1:2:1369:C:O2'	2.43	0.42
2:g:185:ILE:HD13	2:g:185:ILE:HG21	1.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:h:43:LEU:HB3	3:h:47:LEU:HD22	2.02	0.42
4:i:2:GLY:C	4:i:4:TYR:H	2.28	0.42
13:r:68:GLY:O	13:r:70:LEU:N	2.53	0.42
34:1:1854:A:H3'	34:1:1855:G:H8	1.84	0.42
34:1:1935:G:H3'	34:1:1962:C:H42	1.84	0.42
36:A:75:LEU:HD13	36:A:120:MET:HA	2.01	0.42
50:Q:92:ARG:O	50:Q:94:ASN:N	2.52	0.42
52:S:5:ALA:HB1	52:S:50:VAL:HG22	2.01	0.42
55:V:28:MET:HG3	55:V:37:VAL:HG11	2.01	0.42
60:4:192:G:H2'	60:4:193:G:C8	2.55	0.42
1:2:59:A:H5''	1:2:387:U:H5''	2.02	0.42
1:2:188:C:N4	1:2:189(L):G:H1	2.17	0.42
1:2:377:G:H2'	1:2:378:G:H8	1.85	0.42
1:2:438:G:N1	1:2:495:A:OP2	2.48	0.42
4:i:111:ALA:HB1	4:i:116:GLN:HB3	2.02	0.42
11:p:48:ILE:HD11	11:p:67:ASP:HB2	2.02	0.42
34:1:1130:U:H3	34:1:2025:C:H5''	1.84	0.42
34:1:1353:A:OP2	34:1:1377:G:N1	2.38	0.42
38:C:2:LYS:NZ	38:C:95:ILE:O	2.43	0.42
1:2:390:C:H2'	1:2:391:G:C8	2.55	0.42
1:2:552:U:O4	1:2:553:A:N6	2.53	0.42
1:2:643:C:O2'	8:m:132:GLU:OE1	2.36	0.42
2:g:180:LEU:HD23	2:g:180:LEU:HA	1.87	0.42
3:h:16:ARG:HE	3:h:16:ARG:HB2	1.72	0.42
10:o:13:HIS:HA	10:o:16:LEU:HB3	2.02	0.42
11:p:29:ILE:HA	11:p:44:SER:HA	2.01	0.42
12:q:124:LYS:HA	12:q:125:PRO:HD3	1.88	0.42
25:W:41:ARG:HD3	25:W:41:ARG:HA	1.84	0.42
34:1:1476:C:H2'	34:1:1477:A:C8	2.54	0.42
34:1:1569:A:H2'	34:1:1570:A:C8	2.54	0.42
34:1:1811:G:H2'	34:1:1812:A:C8	2.55	0.42
34:1:1923:U:H2'	34:1:1924:C:C6	2.54	0.42
34:1:2250:G:N2	34:1:2276:G:OP1	2.45	0.42
34:1:2732:G:H3'	34:1:2733:A:O4'	2.19	0.42
49:P:60:THR:HG23	49:P:77:PRO:HA	2.01	0.42
50:Q:58:ARG:O	50:Q:62:ILE:HG12	2.19	0.42
54:U:8:LYS:HG3	54:U:74:PRO:HB3	2.02	0.42
60:4:241:C:OP2	60:4:257:C:N4	2.53	0.42
1:2:728:A:H2'	1:2:729:A:C8	2.55	0.42
1:2:835:U:H5'	18:w:61:LYS:HZ1	1.83	0.42
2:g:68:ILE:HA	2:g:161:ALA:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:g:164:VAL:O	2:g:186:ALA:HA	2.19	0.42
6:k:4:TYR:HD1	6:k:92:LYS:HA	1.83	0.42
11:p:48:ILE:O	11:p:50:TYR:N	2.53	0.42
11:p:58:PRO:HA	11:p:61:ALA:HB3	2.01	0.42
14:s:47:LEU:HD23	14:s:47:LEU:HA	1.87	0.42
18:w:88:LYS:HB3	18:w:88:LYS:HE2	1.90	0.42
21:z:3:LYS:HA	21:z:11:GLY:HA2	2.02	0.42
26:X:41:ARG:NH2	34:1:190:A:OP2	2.52	0.42
34:1:298:G:OP1	54:U:85:VAL:N	2.41	0.42
34:1:2250:G:O2'	34:1:2496:C:OP1	2.29	0.42
38:C:203:LYS:HE3	38:C:203:LYS:HB3	1.91	0.42
50:Q:116:ALA:O	50:Q:117:GLN:NE2	2.53	0.42
53:T:77:LYS:HA	53:T:77:LYS:HD3	1.79	0.42
1:2:21:G:H2'	1:2:22:G:C8	2.55	0.41
1:2:489:C:H2'	1:2:490:G:H8	1.84	0.41
1:2:766:A:H61	1:2:1511:G:H1'	1.84	0.41
1:2:1265:G:H2'	1:2:1266:G:C8	2.55	0.41
5:j:69:VAL:HG11	5:j:113:ALA:HB1	2.01	0.41
12:q:27:LEU:O	12:q:29:GLY:N	2.53	0.41
20:y:54:LYS:HB2	20:y:54:LYS:HE3	1.87	0.41
34:1:709:U:H2'	34:1:710:G:C8	2.55	0.41
34:1:1125:G:O6	34:1:1126:A:N6	2.54	0.41
38:C:47:VAL:HG12	38:C:49:LEU:HD22	2.02	0.41
38:C:106:GLY:HA3	38:C:196:VAL:HG12	2.02	0.41
38:C:110:GLY:HA2	38:C:161:GLY:HA3	2.00	0.41
50:Q:112:ARG:HE	51:R:50:PRO:HG2	1.85	0.41
54:U:17:SER:HB2	54:U:71:LYS:HD3	2.02	0.41
56:5:56:GLU:HA	56:5:76:LYS:HG2	2.02	0.41
1:2:398:C:H2'	1:2:399:G:C8	2.55	0.41
1:2:740:U:H2'	1:2:741:G:H8	1.85	0.41
7:l:50:ILE:HD13	7:l:50:ILE:HA	1.93	0.41
23:8:70:G:H2'	23:8:71:G:H8	1.84	0.41
31:c:51:GLU:HG2	31:c:52:VAL:HG23	2.02	0.41
34:1:272(D):G:H2'	34:1:272(E):G:H8	1.84	0.41
34:1:451:C:N4	34:1:454:A:OP2	2.32	0.41
34:1:627:A:O2'	34:1:636:G:N2	2.49	0.41
34:1:805:G:OP2	45:L:42:SER:OG	2.38	0.41
35:3:20:C:H2'	35:3:21:G:H5''	2.02	0.41
38:C:24:THR:OG1	38:C:25:VAL:N	2.54	0.41
39:D:8:GLN:HG3	39:D:9:ILE:H	1.84	0.41
41:F:88:LEU:N	41:F:163:TYR:O	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:G:40:THR:HG23	42:G:43:ASN:H	1.85	0.41
60:4:189:C:H2'	60:4:190:G:H8	1.85	0.41
60:4:236:C:OP2	60:4:237:C:N4	2.53	0.41
1:2:696:A:N3	1:2:786:G:O2'	2.40	0.41
1:2:1026:G:H3'	1:2:1027:C:C6	2.54	0.41
6:k:6:VAL:HG12	6:k:90:VAL:HG22	2.02	0.41
6:k:48:LEU:HD23	6:k:48:LEU:HA	1.91	0.41
11:p:95:ILE:HD13	11:p:95:ILE:HA	1.92	0.41
29:a:4:GLY:O	29:a:6:HIS:ND1	2.41	0.41
34:1:1028:A:H4'	35:3:89:G:H22	1.85	0.41
34:1:1437:C:O2'	34:1:1516:C:O2'	2.35	0.41
34:1:1769:G:H2'	34:1:1770:G:H8	1.85	0.41
34:1:2055:C:H2'	34:1:2504:U:H4'	2.02	0.41
35:3:115:G:HO2'	48:O:50:SER:HG	1.60	0.41
38:C:5:LEU:HD12	38:C:195:LEU:HD11	2.02	0.41
42:G:50:ARG:HA	42:G:50:ARG:HD2	1.76	0.41
49:P:91:ARG:HG3	49:P:116:ALA:HA	2.02	0.41
60:4:35:G:N2	60:4:36:C:H41	2.15	0.41
2:g:30:ARG:HH21	2:g:194:PRO:HG2	1.85	0.41
3:h:11:ARG:NH2	3:h:175:LEU:O	2.44	0.41
3:h:14:ILE:HD11	3:h:178:LEU:HB3	2.02	0.41
3:h:55:VAL:HG13	3:h:68:VAL:HG12	2.00	0.41
6:k:15:ASP:OD1	6:k:15:ASP:N	2.52	0.41
34:1:494:G:H21	52:S:57:ASN:HD21	1.69	0.41
34:1:1186:G:H2'	34:1:1187:G:O4'	2.20	0.41
34:1:2599:G:OP2	37:B:236:GLY:N	2.46	0.41
34:1:2795:G:H1	34:1:2802:G:H1	1.68	0.41
38:C:120:TRP:CG	38:C:155:LYS:HB3	2.55	0.41
39:D:134:GLY:HA2	39:D:166:ALA:HB2	2.02	0.41
39:D:176:LEU:HD12	39:D:176:LEU:HA	1.87	0.41
46:M:64:ILE:HG23	46:M:106:VAL:HG12	2.01	0.41
47:N:38:VAL:HG12	47:N:42:LYS:HD2	2.02	0.41
48:O:61:ASN:ND2	48:O:64:GLU:OE2	2.54	0.41
48:O:92:TYR:HD2	48:O:94:TYR:H	1.68	0.41
1:2:812:C:OP1	1:2:902:G:N2	2.51	0.41
1:2:987:G:H2'	1:2:988:G:H8	1.85	0.41
1:2:1302:U:OP2	13:r:21:TYR:OH	2.29	0.41
1:2:1352:C:OP1	21:z:3:LYS:NZ	2.39	0.41
1:2:1520:G:H2'	1:2:1521:G:C8	2.56	0.41
2:g:216:SER:HA	2:g:219:VAL:HG12	2.02	0.41
5:j:106:PRO:HA	5:j:109:ILE:HD12	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:y:15:ARG:HE	20:y:15:ARG:HB3	1.53	0.41
20:y:50:GLU:HG3	20:y:100:ILE:HG12	2.02	0.41
22:7:23:C:H2'	22:7:24:U:C6	2.56	0.41
23:8:63:G:H2'	23:8:64:A:C8	2.55	0.41
34:1:1206:G:O6	34:1:1240:U:C4	2.73	0.41
34:1:1231:G:H2'	34:1:1232:G:H8	1.85	0.41
34:1:1541:G:H1'	34:1:1542:A:C5	2.56	0.41
34:1:1791:A:H4'	37:B:206:LEU:HB2	2.02	0.41
34:1:2415:G:H4'	45:L:66:GLY:HA3	2.01	0.41
45:L:64:LYS:O	45:L:66:GLY:N	2.53	0.41
47:N:9:LYS:HB3	47:N:9:LYS:HE2	1.81	0.41
56:5:5:LEU:HD13	56:5:5:LEU:HA	1.92	0.41
1:2:898:G:N2	1:2:901:A:OP2	2.45	0.41
23:8:16:U:H3'	23:8:17:C:H5'	2.02	0.41
27:Y:26:ARG:HD3	27:Y:26:ARG:HA	1.67	0.41
29:a:26:SER:HB3	40:E:105:LYS:HD3	2.02	0.41
34:1:852:G:H2'	34:1:853:G:C8	2.56	0.41
34:1:1388:G:H2'	34:1:1389:G:C8	2.56	0.41
34:1:1438:U:H2'	34:1:1439:A:C8	2.54	0.41
34:1:2098:U:O2	34:1:2191:G:C2	2.73	0.41
34:1:2100:G:O6	34:1:2189:U:C2	2.74	0.41
34:1:2345:G:O2'	34:1:2381:C:O2	2.34	0.41
34:1:2577:A:H2'	34:1:2614:A:H62	1.84	0.41
35:3:56:G:H4'	35:3:57:A:H5'	2.01	0.41
40:E:18:GLU:HA	40:E:21:ARG:HG2	2.03	0.41
43:J:34:LEU:HD23	43:J:34:LEU:HA	1.86	0.41
51:R:44:LYS:H	51:R:47:VAL:HG23	1.85	0.41
1:2:778:G:H1'	11:p:119:CYS:HB3	2.03	0.41
1:2:986:A:N3	19:x:52:TYR:OH	2.51	0.41
1:2:1016:A:H2'	1:2:1017:G:O4'	2.20	0.41
3:h:134:ILE:HG23	3:h:151:VAL:HB	2.02	0.41
4:i:122:ARG:NH1	4:i:134:ASP:O	2.51	0.41
5:j:151:LEU:HA	5:j:151:LEU:HD23	1.84	0.41
27:Y:14:ARG:HH21	27:Y:57:ILE:HG22	1.84	0.41
33:e:29:LYS:O	33:e:31:HIS:N	2.54	0.41
34:1:61:G:H22	34:1:94:C:H1'	1.84	0.41
34:1:532:A:N7	34:1:2021:C:O2'	2.53	0.41
34:1:586:A:N1	34:1:809:G:O2'	2.53	0.41
34:1:947:G:H2'	34:1:948:G:H8	1.86	0.41
34:1:2688:U:OP1	34:1:2713:A:N6	2.54	0.41
39:D:75:HIS:CE1	39:D:82:ILE:HD11	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:D:108:LYS:HE3	39:D:112:MET:HE3	2.02	0.41
46:M:32:TYR:O	46:M:105:GLU:HA	2.20	0.41
1:2:372:C:N4	1:2:388:G:OP2	2.39	0.41
1:2:974:A:P	14:s:29:ARG:HH21	2.44	0.41
4:i:208:SER:HB3	5:j:101:ILE:HD12	2.03	0.41
7:l:16:LEU:HD21	9:n:42:ARG:HA	2.02	0.41
8:m:14:ARG:HA	8:m:17:THR:HG22	2.02	0.41
12:q:23:LYS:HA	12:q:23:LYS:HD2	1.94	0.41
15:t:33:THR:HG21	15:t:85:LEU:HD22	2.02	0.41
26:X:13:ILE:HD11	26:X:46:LEU:HD13	2.03	0.41
32:d:7:PRO:HA	34:1:686:G:H8	1.85	0.41
33:e:4:MET:HE2	33:e:61:LEU:HD11	2.02	0.41
34:1:203:C:H3'	34:1:204:A:H5''	2.02	0.41
34:1:380:U:H2'	34:1:381:G:H8	1.86	0.41
34:1:477:A:N6	34:1:500:G:O3'	2.54	0.41
34:1:480:A:N3	34:1:499:U:O2'	2.48	0.41
34:1:810:U:C2	45:L:33:ARG:HD3	2.56	0.41
34:1:1032:A:H2	34:1:1122:G:H22	1.67	0.41
34:1:1227:G:H5''	50:Q:16:LYS:NZ	2.36	0.41
34:1:1550:C:H2'	34:1:1551:C:H6	1.85	0.41
34:1:2009:G:N3	47:N:107:ASP:HA	2.35	0.41
34:1:2199:A:H3'	34:1:2200:C:H6	1.86	0.41
39:D:37:VAL:HG11	45:L:7:ARG:NH1	2.36	0.41
50:Q:81:HIS:CD2	50:Q:117:GLN:HG3	2.56	0.41
1:2:10:A:H2'	1:2:11:G:C8	2.55	0.41
1:2:45:U:OP1	1:2:307:C:O2'	2.39	0.41
1:2:266:G:OP2	1:2:267:C:N4	2.54	0.41
1:2:301:G:H2'	1:2:302:G:H8	1.86	0.41
1:2:473:G:H2'	1:2:474:G:C8	2.55	0.41
1:2:877:C:H2'	1:2:878:G:C8	2.56	0.41
1:2:1071:C:H2'	1:2:1072:G:C8	2.54	0.41
4:i:61:LYS:HA	4:i:203:VAL:HG22	2.02	0.41
6:k:71:ARG:HE	6:k:71:ARG:HB2	1.70	0.41
7:l:86:GLN:HB3	7:l:148:ASN:HD21	1.85	0.41
12:q:33:ARG:O	12:q:85:ILE:HB	2.21	0.41
19:x:18:LYS:HE3	19:x:18:LYS:HB2	1.87	0.41
20:y:26:ASN:HA	20:y:29:LYS:HG2	2.03	0.41
20:y:86:ARG:HG3	20:y:90:GLN:HE22	1.85	0.41
34:1:144:C:H2'	34:1:145:G:C8	2.56	0.41
34:1:185:U:H2'	34:1:186:G:H8	1.84	0.41
34:1:307:G:O2'	34:1:309:G:N7	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:320:A:O2'	34:1:322:A:OP2	2.29	0.41
34:1:514:A:N3	34:1:581:C:O2'	2.42	0.41
34:1:796:C:H2'	34:1:797:C:C6	2.56	0.41
34:1:840:C:H2'	34:1:841:A:H8	1.85	0.41
34:1:959:A:H2'	34:1:960:A:C8	2.56	0.41
34:1:1604:C:H2'	34:1:1605:C:C6	2.56	0.41
34:1:1645:G:H5''	34:1:1646:C:H5'	2.02	0.41
34:1:2619:C:H2'	34:1:2620:C:C6	2.56	0.41
37:B:134:ARG:NH1	37:B:170:GLY:O	2.54	0.41
40:E:39:ILE:HG21	40:E:60:LEU:HD11	2.02	0.41
41:F:125:VAL:HG22	41:F:131:VAL:HG23	2.02	0.41
47:N:35:THR:HA	47:N:112:ALA:O	2.21	0.41
49:P:49:VAL:HA	49:P:63:VAL:HA	2.03	0.41
56:5:112:TYR:OH	60:4:16:U:O2	2.38	0.41
60:4:125:C:H2'	60:4:126:G:C8	2.56	0.41
1:2:629:G:H2'	1:2:630:G:H8	1.86	0.41
1:2:745:C:OP1	1:2:851:G:O2'	2.39	0.41
1:2:835:U:OP1	18:w:64:ARG:NH1	2.47	0.41
1:2:1057:G:H5''	3:h:154:SER:HB3	2.02	0.41
1:2:1141:C:H2'	1:2:1142:G:H8	1.85	0.41
2:g:74:LYS:HG3	2:g:77:ALA:H	1.85	0.41
3:h:18:TRP:O	3:h:21:ARG:NH2	2.53	0.41
4:i:128:VAL:HG11	4:i:138:TYR:HE2	1.85	0.41
16:u:4:ILE:HA	16:u:20:VAL:O	2.21	0.41
34:1:236:C:H2'	34:1:237:C:H6	1.86	0.41
34:1:2415:G:H4'	45:L:67:MET:H	1.87	0.41
34:1:2681:C:OP2	38:C:109:LYS:NZ	2.32	0.41
35:3:28:C:H2'	35:3:29:A:H8	1.86	0.41
37:B:49:ILE:HD12	37:B:52:ARG:HB3	2.03	0.41
38:C:76:ARG:H	38:C:76:ARG:HG2	1.77	0.41
45:L:83:VAL:HG22	45:L:112:LEU:HD11	2.03	0.41
49:P:29:ARG:HB3	49:P:30:VAL:H	1.48	0.41
51:R:27:ALA:O	51:R:64:HIS:NE2	2.51	0.41
54:U:21:LYS:HE3	54:U:21:LYS:HB3	1.92	0.41
1:2:189:G:H2'	1:2:189(L):G:N2	2.33	0.40
1:2:744:C:H2'	1:2:745:C:C6	2.56	0.40
1:2:831:U:C4	1:2:832:C:N4	2.90	0.40
1:2:900:A:H2'	1:2:901:A:C8	2.56	0.40
4:i:147:ALA:HA	4:i:182:LYS:HA	2.03	0.40
7:l:111:ARG:HG2	7:l:112:PRO:HD2	2.02	0.40
19:x:71:LEU:HD13	19:x:71:LEU:HA	1.91	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:e:26:LYS:HE2	33:e:26:LYS:HB3	1.90	0.40
34:1:151:C:H2'	34:1:152:G:H8	1.85	0.40
34:1:269:U:H3'	34:1:271(X):G:H1	1.85	0.40
34:1:859:G:O2'	34:1:916:G:O6	2.31	0.40
34:1:1297:C:O2'	34:1:1302:A:N1	2.45	0.40
34:1:1668:A:N6	34:1:1676:A:H61	2.19	0.40
34:1:2314:C:H2'	34:1:2315:G:C8	2.57	0.40
38:C:52:LEU:HA	38:C:53:PRO:HD3	1.92	0.40
39:D:3:GLU:HB2	39:D:20:LEU:O	2.21	0.40
44:K:13:ASN:ND2	44:K:96:THR:OG1	2.34	0.40
53:T:64:LYS:HG3	53:T:65:ARG:H	1.86	0.40
54:U:47:LYS:HA	54:U:47:LYS:HD2	1.92	0.40
55:V:45:ASP:OD1	55:V:45:ASP:N	2.53	0.40
60:4:180:C:N4	60:4:181:G:O6	2.53	0.40
1:2:22:G:H4'	1:2:885:G:C8	2.56	0.40
1:2:664:G:P	18:w:64:ARG:HH21	2.44	0.40
1:2:711:G:H2'	1:2:712:A:C8	2.57	0.40
17:v:58:GLU:OE1	17:v:75:ARG:NE	2.54	0.40
18:w:78:LEU:HA	18:w:78:LEU:HD23	1.82	0.40
33:e:47:LYS:HE2	34:1:2360:A:H5''	2.03	0.40
34:1:122:G:OP1	34:1:149:A:O2'	2.32	0.40
34:1:1803:A:N6	34:1:1814:G:O2'	2.35	0.40
34:1:2657:A:H5''	34:1:2658:C:C5	2.57	0.40
34:1:2693:A:H2'	34:1:2694:G:C8	2.56	0.40
34:1:2804:C:H2'	34:1:2805:G:C8	2.55	0.40
37:B:6:PHE:HE2	37:B:18:VAL:HG23	1.86	0.40
37:B:77:ALA:O	37:B:116:GLN:HA	2.21	0.40
38:C:19:ARG:HA	44:K:73:ASP:HA	2.02	0.40
39:D:8:GLN:N	39:D:125:LEU:O	2.52	0.40
39:D:9:ILE:HA	39:D:10:PRO:HD2	1.97	0.40
43:J:55:VAL:HG11	43:J:128:HIS:ND1	2.35	0.40
46:M:77:LYS:HE3	46:M:82:ARG:HA	2.03	0.40
49:P:64:ARG:HB2	49:P:73:GLU:HG2	2.03	0.40
50:Q:90:VAL:HB	51:R:40:LEU:HD22	2.02	0.40
52:S:84:ARG:HA	52:S:84:ARG:HD3	1.87	0.40
1:2:191:G:N3	20:y:105:SER:HB2	2.36	0.40
1:2:580:U:O4	1:2:761:G:O6	2.39	0.40
1:2:868:C:H2'	1:2:869:G:O4'	2.22	0.40
2:g:23:ARG:HD2	2:g:23:ARG:HA	1.91	0.40
4:i:174:LEU:HD23	4:i:185:PHE:HA	2.02	0.40
17:v:29:HIS:HB3	17:v:33:GLY:H	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:23:G:P	34:1:504:U:H3	2.44	0.40
34:1:255:A:O2'	34:1:384:U:OP1	2.31	0.40
34:1:1028:A:N3	34:1:2486:G:O2'	2.39	0.40
34:1:2508:G:H1	34:1:2580:U:H3	1.67	0.40
34:1:2511:U:H5''	38:C:123:ALA:HB3	2.02	0.40
37:B:155:LEU:HD11	37:B:177:LEU:HD22	2.04	0.40
45:L:23:PRO:HB2	45:L:33:ARG:CZ	2.51	0.40
52:S:64:MET:HE2	52:S:64:MET:HB3	1.92	0.40
52:S:68:ARG:HH12	52:S:113:LYS:H	1.68	0.40
55:V:61:LEU:HD13	55:V:61:LEU:HA	1.90	0.40
55:V:87:ASP:N	55:V:87:ASP:OD1	2.55	0.40
56:5:133:LYS:H	56:5:133:LYS:HG2	1.73	0.40
60:4:246:C:H41	60:4:279:C:H6	1.68	0.40
1:2:1032:G:O2'	1:2:1033:G:O4'	2.38	0.40
1:2:1391:U:H2'	1:2:1392:G:C8	2.56	0.40
2:g:201:ILE:HG21	2:g:214:ILE:HG21	2.03	0.40
4:i:181:MET:HE2	4:i:181:MET:HB3	1.97	0.40
5:j:103:GLY:O	5:j:107:ARG:HB2	2.21	0.40
5:j:123:LEU:HD23	5:j:123:LEU:HA	1.91	0.40
12:q:42:THR:O	12:q:42:THR:OG1	2.31	0.40
23:8:71:G:H4'	34:1:1851:U:H4'	2.03	0.40
25:W:22:GLY:N	25:W:39:ARG:O	2.53	0.40
26:X:25:LYS:HB3	26:X:25:LYS:HE2	1.88	0.40
27:Y:51:ARG:C	27:Y:51:ARG:HH11	2.29	0.40
28:Z:23:LEU:HD13	28:Z:23:LEU:HA	1.83	0.40
34:1:824:A:H1'	34:1:2358:G:N7	2.37	0.40
34:1:2714:G:H5''	34:1:2714:G:H8	1.87	0.40
34:1:2880:C:O3'	47:N:90:ARG:NH1	2.53	0.40
37:B:231:HIS:CD2	37:B:249:PRO:HG3	2.56	0.40
38:C:11:MET:HA	38:C:24:THR:HA	2.03	0.40
39:D:135:LYS:HA	39:D:135:LYS:HD3	1.87	0.40
43:J:41:ASP:HB2	43:J:48:MET:HE3	2.04	0.40
43:J:74:ARG:NH2	43:J:101:HIS:HB3	2.37	0.40
44:K:10:VAL:HG22	44:K:19:ILE:HG12	2.04	0.40
1:2:41:G:H2'	1:2:42:G:C8	2.56	0.40
1:2:783:C:OP1	1:2:1515:C:O2'	2.38	0.40
1:2:1002:G:H2'	1:2:1003:G:C8	2.57	0.40
1:2:1030(A):G:O2'	1:2:1030(C):G:N7	2.48	0.40
1:2:1139:G:H22	1:2:1144:G:H1	1.69	0.40
13:r:14:ARG:O	13:r:18:ALA:HB2	2.22	0.40
15:t:26:GLU:OE2	15:t:77:ARG:NH1	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:u:43:LYS:HG2	16:u:48:TRP:CD2	2.56	0.40
32:d:14:LYS:HB2	32:d:14:LYS:HE3	1.90	0.40
33:e:7:HIS:HD2	33:e:9:GLY:H	1.70	0.40
34:1:536:A:H5'	50:Q:53:ARG:HD3	2.04	0.40
34:1:947:G:H2'	34:1:948:G:C8	2.57	0.40
34:1:971:C:O2'	34:1:983:A:N3	2.40	0.40
34:1:2847:U:O2	34:1:2869:G:O6	2.39	0.40
35:3:28:C:H2'	35:3:29:A:C8	2.57	0.40
36:A:50:ASP:HA	36:A:51:PRO:HD3	1.88	0.40
38:C:8:LYS:O	38:C:193:GLY:N	2.54	0.40
39:D:192:LEU:HD21	39:D:194:MET:HE3	2.03	0.40
42:G:45:LYS:HA	42:G:48:GLU:HB3	2.02	0.40
49:P:24:PRO:HA	49:P:49:VAL:HG13	2.04	0.40
50:Q:5:LYS:HB3	50:Q:5:LYS:HE2	2.00	0.40
60:4:247:G:OP1	60:4:297:A:N6	2.42	0.40
60:4:328:U:N3	60:4:331:A:OP1	2.35	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	g	232/235 (99%)	206 (89%)	26 (11%)	0	100	100
3	h	205/207 (99%)	182 (89%)	22 (11%)	1 (0%)	24	56
4	i	206/208 (99%)	189 (92%)	16 (8%)	1 (0%)	24	56
5	j	149/151 (99%)	137 (92%)	12 (8%)	0	100	100
6	k	99/101 (98%)	91 (92%)	8 (8%)	0	100	100
7	l	153/155 (99%)	143 (94%)	10 (6%)	0	100	100
8	m	136/138 (99%)	124 (91%)	12 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	n	125/127 (98%)	103 (82%)	22 (18%)	0	100	100
10	o	97/99 (98%)	85 (88%)	12 (12%)	0	100	100
11	p	117/119 (98%)	104 (89%)	12 (10%)	1 (1%)	14	45
12	q	123/125 (98%)	89 (72%)	33 (27%)	1 (1%)	16	48
13	r	114/120 (95%)	91 (80%)	21 (18%)	2 (2%)	6	34
14	s	58/60 (97%)	50 (86%)	6 (10%)	2 (3%)	3	25
15	t	86/88 (98%)	81 (94%)	5 (6%)	0	100	100
16	u	82/84 (98%)	76 (93%)	6 (7%)	0	100	100
17	v	98/100 (98%)	85 (87%)	13 (13%)	0	100	100
18	w	68/70 (97%)	66 (97%)	2 (3%)	0	100	100
19	x	77/79 (98%)	64 (83%)	13 (17%)	0	100	100
20	y	97/99 (98%)	87 (90%)	10 (10%)	0	100	100
21	z	23/25 (92%)	19 (83%)	4 (17%)	0	100	100
25	W	83/85 (98%)	72 (87%)	11 (13%)	0	100	100
26	X	87/89 (98%)	61 (70%)	26 (30%)	0	100	100
27	Y	49/51 (96%)	40 (82%)	9 (18%)	0	100	100
28	Z	58/60 (97%)	52 (90%)	6 (10%)	0	100	100
29	a	56/58 (97%)	41 (73%)	14 (25%)	1 (2%)	6	34
30	b	57/59 (97%)	42 (74%)	14 (25%)	1 (2%)	6	34
31	c	43/45 (96%)	27 (63%)	12 (28%)	4 (9%)	0	7
32	d	47/49 (96%)	46 (98%)	1 (2%)	0	100	100
33	e	62/64 (97%)	42 (68%)	20 (32%)	0	100	100
36	A	183/229 (80%)	120 (66%)	62 (34%)	1 (0%)	24	56
37	B	270/272 (99%)	227 (84%)	41 (15%)	2 (1%)	18	50
38	C	203/205 (99%)	168 (83%)	33 (16%)	2 (1%)	12	43
39	D	206/208 (99%)	184 (89%)	20 (10%)	2 (1%)	12	43
40	E	177/181 (98%)	145 (82%)	30 (17%)	2 (1%)	11	42
41	F	158/160 (99%)	131 (83%)	25 (16%)	2 (1%)	9	38
42	G	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
43	J	137/139 (99%)	104 (76%)	28 (20%)	5 (4%)	2	23
44	K	120/122 (98%)	103 (86%)	17 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	L	144/146 (99%)	88 (61%)	51 (35%)	5 (4%)	3	24
46	M	134/136 (98%)	111 (83%)	21 (16%)	2 (2%)	8	36
47	N	115/117 (98%)	92 (80%)	22 (19%)	1 (1%)	14	45
48	O	97/99 (98%)	64 (66%)	29 (30%)	4 (4%)	2	20
49	P	136/138 (99%)	95 (70%)	40 (29%)	1 (1%)	18	50
50	Q	115/117 (98%)	102 (89%)	11 (10%)	2 (2%)	7	34
51	R	97/101 (96%)	67 (69%)	30 (31%)	0	100	100
52	S	111/113 (98%)	97 (87%)	14 (13%)	0	100	100
53	T	91/93 (98%)	58 (64%)	31 (34%)	2 (2%)	5	31
54	U	99/101 (98%)	55 (56%)	39 (39%)	5 (5%)	1	17
55	V	89/92 (97%)	75 (84%)	14 (16%)	0	100	100
56	5	142/144 (99%)	121 (85%)	21 (15%)	0	100	100
58	f	35/37 (95%)	24 (69%)	11 (31%)	0	100	100
All	All	5803/5960 (97%)	4781 (82%)	970 (17%)	52 (1%)	16	45

All (52) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	i	5	ILE
13	r	69	GLU
13	r	70	LEU
40	E	96	ARG
41	F	170	ARG
43	J	78	TYR
43	J	79	PRO
43	J	96	GLU
48	O	17	ARG
48	O	18	ILE
53	T	89	ILE
53	T	90	GLU
14	s	37	PHE
40	E	97	ASP
41	F	158	HIS
43	J	57	ALA
45	L	101	VAL
50	Q	93	LYS
54	U	38	ILE

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Mol	Chain	Res	Type
12	q	91	LYS
14	s	36	PHE
31	c	28	ARG
31	c	52	VAL
39	D	22	ALA
45	L	35	HIS
45	L	100	LEU
11	p	49	GLY
31	c	44	ARG
38	C	145	LYS
47	N	107	ASP
29	a	41	PRO
31	c	46	HIS
39	D	21	ALA
45	L	47	ASP
46	M	8	LYS
48	O	58	LEU
50	Q	92	ARG
49	P	69	GLY
3	h	207	VAL
36	A	174	PRO
43	J	95	PRO
45	L	34	GLY
46	M	81	VAL
54	U	39	VAL
37	B	36	PRO
48	O	90	GLY
54	U	37	VAL
37	B	244	ARG
54	U	81	LYS
30	b	33	CYS
54	U	49	VAL
38	C	93	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	g	202/203 (100%)	199 (98%)	3 (2%)	57	68
3	h	160/161 (99%)	160 (100%)	0	100	100
4	i	180/180 (100%)	179 (99%)	1 (1%)	78	79
5	j	115/116 (99%)	115 (100%)	0	100	100
6	k	90/90 (100%)	90 (100%)	0	100	100
7	l	126/126 (100%)	125 (99%)	1 (1%)	73	76
8	m	119/119 (100%)	118 (99%)	1 (1%)	73	76
9	n	98/98 (100%)	97 (99%)	1 (1%)	68	74
10	o	88/89 (99%)	87 (99%)	1 (1%)	65	73
11	p	90/90 (100%)	89 (99%)	1 (1%)	65	73
12	q	104/104 (100%)	103 (99%)	1 (1%)	68	74
13	r	96/96 (100%)	95 (99%)	1 (1%)	68	74
14	s	49/49 (100%)	49 (100%)	0	100	100
15	t	79/79 (100%)	79 (100%)	0	100	100
16	u	72/72 (100%)	71 (99%)	1 (1%)	59	70
17	v	94/95 (99%)	93 (99%)	1 (1%)	65	73
18	w	61/61 (100%)	61 (100%)	0	100	100
19	x	69/69 (100%)	69 (100%)	0	100	100
20	y	76/76 (100%)	75 (99%)	1 (1%)	61	71
21	z	19/20 (95%)	19 (100%)	0	100	100
25	W	61/67 (91%)	61 (100%)	0	100	100
26	X	73/74 (99%)	73 (100%)	0	100	100
27	Y	46/47 (98%)	45 (98%)	1 (2%)	45	63
28	Z	51/52 (98%)	50 (98%)	1 (2%)	48	64
29	a	52/52 (100%)	52 (100%)	0	100	100
30	b	51/51 (100%)	50 (98%)	1 (2%)	48	64
31	c	43/44 (98%)	39 (91%)	4 (9%)	8	32
32	d	41/42 (98%)	41 (100%)	0	100	100
33	e	53/54 (98%)	52 (98%)	1 (2%)	50	65
36	A	61/181 (34%)	61 (100%)	0	100	100
37	B	213/214 (100%)	211 (99%)	2 (1%)	70	75
38	C	165/165 (100%)	164 (99%)	1 (1%)	78	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	D	165/165 (100%)	162 (98%)	3 (2%)	51	67
40	E	155/155 (100%)	155 (100%)	0	100	100
41	F	132/133 (99%)	130 (98%)	2 (2%)	57	68
42	G	47/47 (100%)	46 (98%)	1 (2%)	47	64
43	J	117/118 (99%)	115 (98%)	2 (2%)	53	67
44	K	100/100 (100%)	99 (99%)	1 (1%)	68	74
45	L	112/112 (100%)	111 (99%)	1 (1%)	70	75
46	M	106/106 (100%)	103 (97%)	3 (3%)	38	58
47	N	100/100 (100%)	97 (97%)	3 (3%)	36	57
48	O	77/77 (100%)	76 (99%)	1 (1%)	61	71
49	P	120/120 (100%)	116 (97%)	4 (3%)	33	55
50	Q	92/93 (99%)	92 (100%)	0	100	100
51	R	82/82 (100%)	82 (100%)	0	100	100
52	S	91/92 (99%)	91 (100%)	0	100	100
53	T	74/75 (99%)	72 (97%)	2 (3%)	39	59
54	U	84/85 (99%)	83 (99%)	1 (1%)	63	72
55	V	83/84 (99%)	81 (98%)	2 (2%)	43	61
56	5	120/120 (100%)	118 (98%)	2 (2%)	53	67
57	6	1/1 (100%)	1 (100%)	0	100	100
58	f	34/34 (100%)	33 (97%)	1 (3%)	37	57
All	All	4789/4935 (97%)	4735 (99%)	54 (1%)	63	73

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	g	19	HIS
2	g	185	ILE
2	g	187	LEU
4	i	88	VAL
7	l	120	ILE
8	m	51	VAL
9	n	53	VAL
10	o	49	VAL
11	p	127	LYS
12	q	39	VAL

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Mol	Chain	Res	Type
13	r	70	LEU
16	u	73	LEU
17	v	35	VAL
20	y	84	LEU
27	Y	35	LEU
28	Z	56	VAL
30	b	57	VAL
31	c	44	ARG
31	c	45	LYS
31	c	46	HIS
31	c	47	THR
33	e	14	VAL
37	B	10	THR
37	B	192	THR
38	C	77	ILE
39	D	20	LEU
39	D	23	ASP
39	D	84	VAL
41	F	107	VAL
41	F	114	VAL
42	G	12	LEU
43	J	43	THR
43	J	62	VAL
44	K	65	THR
45	L	95	VAL
46	M	27	VAL
46	M	90	VAL
46	M	96	VAL
47	N	4	LEU
47	N	97	VAL
47	N	117	VAL
48	O	35	ILE
49	P	42	ILE
49	P	49	VAL
49	P	63	VAL
49	P	72	VAL
53	T	26	TYR
53	T	77	LYS
54	U	38	ILE
55	V	63	ASP
55	V	71	VAL
56	5	24	ILE

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Mol	Chain	Res	Type
56	5	72	ASP
58	f	16	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (72) such sidechains are listed below:

Mol	Chain	Res	Type
2	g	135	GLN
3	h	6	HIS
3	h	37	GLN
3	h	110	ASN
3	h	118	GLN
3	h	181	ASN
4	i	161	ASN
5	j	78	HIS
6	k	27	GLN
6	k	73	ASN
7	l	28	ASN
7	l	51	GLN
7	l	86	GLN
7	l	148	ASN
8	m	70	GLN
9	n	23	ASN
9	n	34	ASN
9	n	124	GLN
11	p	13	GLN
11	p	116	HIS
11	p	117	ASN
12	q	75	HIS
15	t	9	GLN
15	t	62	GLN
17	v	94	ASN
25	W	80	HIS
26	X	19	GLN
26	X	45	ASN
26	X	56	GLN
26	X	66	HIS
30	b	23	HIS
30	b	43	HIS
36	A	56	GLN
36	A	71	GLN
37	B	87	ASN
37	B	116	GLN

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Mol	Chain	Res	Type
38	C	55	ASN
38	C	66	HIS
38	C	121	ASN
38	C	169	ASN
38	C	180	ASN
39	D	40	GLN
39	D	67	GLN
39	D	182	ASN
39	D	203	GLN
39	D	204	ASN
40	E	108	ASN
40	E	121	ASN
40	E	130	ASN
41	F	74	ASN
41	F	147	ASN
42	G	28	ASN
44	K	82	ASN
44	K	88	ASN
45	L	38	GLN
45	L	70	GLN
46	M	12	GLN
46	M	113	GLN
47	N	24	GLN
49	P	90	GLN
50	Q	66	ASN
52	S	34	ASN
52	S	57	ASN
52	S	61	ASN
52	S	102	HIS
53	T	87	GLN
54	U	43	ASN
54	U	92	ASN
55	V	34	ASN
55	V	65	GLN
55	V	73	GLN
58	f	34	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1497/1522 (98%)	356 (23%)	29 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
22	7	76/77 (98%)	32 (42%)	1 (1%)
23	8	75/76 (98%)	16 (21%)	2 (2%)
24	9	6/6 (100%)	3 (50%)	1 (16%)
34	1	2809/2915 (96%)	953 (33%)	35 (1%)
35	3	118/119 (99%)	39 (33%)	1 (0%)
60	4	317/349 (90%)	203 (64%)	11 (3%)
All	All	4898/5064 (96%)	1602 (32%)	80 (1%)

All (1602) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	8	A
1	2	9	G
1	2	31	G
1	2	32	A
1	2	39	G
1	2	44	G
1	2	47	C
1	2	48	C
1	2	50	A
1	2	51	A
1	2	61	G
1	2	64	G
1	2	65	U
1	2	73	G
1	2	77	G
1	2	80	G
1	2	81	U
1	2	89	C
1	2	90	U
1	2	92	C
1	2	96	U
1	2	97	G
1	2	101	A
1	2	116	A
1	2	120	A
1	2	121	C
1	2	122	G
1	2	129	U
1	2	129(A)	G
1	2	130	A
1	2	131	C

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Mol	Chain	Res	Type
1	2	147	G
1	2	149	A
1	2	150	C
1	2	153	C
1	2	163	C
1	2	169	C
1	2	170	U
1	2	172	A
1	2	173	U
1	2	181	G
1	2	182	U
1	2	187	C
1	2	188	C
1	2	189(E)	U
1	2	189(F)	U
1	2	189(G)	G
1	2	189(H)	G
1	2	189(K)	U
1	2	189(L)	G
1	2	195	A
1	2	196	A
1	2	197	A
1	2	202	U
1	2	203	U
1	2	204	U
1	2	216	G
1	2	220	G
1	2	244	U
1	2	245	C
1	2	247	G
1	2	251	G
1	2	263	A
1	2	267	C
1	2	274	A
1	2	279	A
1	2	281	G
1	2	289	G
1	2	298	A
1	2	299	G
1	2	301	G
1	2	306	G
1	2	321	A

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Mol	Chain	Res	Type
1	2	328	C
1	2	329	A
1	2	330	C
1	2	332	G
1	2	344	A
1	2	345	C
1	2	347	G
1	2	351	G
1	2	352	C
1	2	353	A
1	2	354	G
1	2	366	C
1	2	367	U
1	2	372	C
1	2	373	A
1	2	381	C
1	2	382	A
1	2	385	C
1	2	388	G
1	2	389	A
1	2	390	C
1	2	397	A
1	2	398	C
1	2	406	G
1	2	409	G
1	2	411	A
1	2	412	A
1	2	421	U
1	2	424	G
1	2	429	U
1	2	435	C
1	2	436	C
1	2	437	U
1	2	438	G
1	2	439	A
1	2	450	G
1	2	452	A
1	2	461	A
1	2	471	G
1	2	472	A
1	2	473	G
1	2	479	C

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Mol	Chain	Res	Type
1	2	484	G
1	2	485	G
1	2	495	A
1	2	496	A
1	2	498	U
1	2	503	C
1	2	509	A
1	2	510	A
1	2	511	C
1	2	518	C
1	2	521	G
1	2	524	G
1	2	527	G
1	2	531	U
1	2	532	A
1	2	533	A
1	2	547	A
1	2	558	G
1	2	559	A
1	2	562	C
1	2	564	C
1	2	567	G
1	2	570	G
1	2	572	A
1	2	573	A
1	2	574	A
1	2	575	G
1	2	576	G
1	2	577	G
1	2	588	G
1	2	603	U
1	2	607	A
1	2	615	C
1	2	630	G
1	2	632	A
1	2	633	G
1	2	641	U
1	2	653	A
1	2	661	G
1	2	665	A
1	2	671	G
1	2	686	U

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Mol	Chain	Res	Type
1	2	688	G
1	2	693	G
1	2	702	A
1	2	704	A
1	2	717	C
1	2	723	U
1	2	724	G
1	2	731	G
1	2	734	G
1	2	749	C
1	2	752	G
1	2	755	G
1	2	756	C
1	2	758	G
1	2	759	A
1	2	761	G
1	2	773	G
1	2	784	C
1	2	787	A
1	2	789	U
1	2	790	A
1	2	793	U
1	2	794	A
1	2	799	G
1	2	815	A
1	2	816	A
1	2	817	C
1	2	821	G
1	2	828	A
1	2	832	C
1	2	833	U
1	2	839	U
1	2	840	C
1	2	841	U
1	2	848	C
1	2	855	G
1	2	869	G
1	2	876	G
1	2	889	A
1	2	891	U
1	2	902	G
1	2	914	A

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Mol	Chain	Res	Type
1	2	926	G
1	2	927	G
1	2	932	C
1	2	934	C
1	2	935	A
1	2	958	A
1	2	960	U
1	2	961	U
1	2	966	G
1	2	968	A
1	2	969	A
1	2	974	A
1	2	975	A
1	2	976	G
1	2	977	A
1	2	978	A
1	2	981	U
1	2	982	U
1	2	989	C
1	2	991	U
1	2	992	U
1	2	993	G
1	2	995	C
1	2	997	U
1	2	998	G
1	2	1009	G
1	2	1026	G
1	2	1029	C
1	2	1030(A)	G
1	2	1030(C)	G
1	2	1031	G
1	2	1033	G
1	2	1042	G
1	2	1044	A
1	2	1045	C
1	2	1046	A
1	2	1054	C
1	2	1055	A
1	2	1064	G
1	2	1065	U
1	2	1066	C
1	2	1068	G

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Mol	Chain	Res	Type
1	2	1070	U
1	2	1081	G
1	2	1085	U
1	2	1094	G
1	2	1095	U
1	2	1100	C
1	2	1101	A
1	2	1108	G
1	2	1117	G
1	2	1118	C
1	2	1124	G
1	2	1125	U
1	2	1126	U
1	2	1129	C
1	2	1136	U
1	2	1137	C
1	2	1138	G
1	2	1140	C
1	2	1141	C
1	2	1145	C
1	2	1147	C
1	2	1152	A
1	2	1154	G
1	2	1159	U
1	2	1171	G
1	2	1179	A
1	2	1181	G
1	2	1183	A
1	2	1184	G
1	2	1186	G
1	2	1190	G
1	2	1196	U
1	2	1197	G
1	2	1202	G
1	2	1211	U
1	2	1212	U
1	2	1213	A
1	2	1214	C
1	2	1225	A
1	2	1226	C
1	2	1227	A
1	2	1228	C

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Mol	Chain	Res	Type
1	2	1236	A
1	2	1238	A
1	2	1239	A
1	2	1240	U
1	2	1241	G
1	2	1253	G
1	2	1255	G
1	2	1256	A
1	2	1257	U
1	2	1260	C
1	2	1268	A
1	2	1270	C
1	2	1279	A
1	2	1280	A
1	2	1281	U
1	2	1285	A
1	2	1286	A
1	2	1287	A
1	2	1293	G
1	2	1294	G
1	2	1297	C
1	2	1300	G
1	2	1301	U
1	2	1302	U
1	2	1303	C
1	2	1305	G
1	2	1312	G
1	2	1313	U
1	2	1317	C
1	2	1320	C
1	2	1322	C
1	2	1323	G
1	2	1325	C
1	2	1326	C
1	2	1331	G
1	2	1336	C
1	2	1346	A
1	2	1347	G
1	2	1353	G
1	2	1359	C
1	2	1360	A
1	2	1364	U

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Mol	Chain	Res	Type
1	2	1370	G
1	2	1387	G
1	2	1394	A
1	2	1399	C
1	2	1402	C
1	2	1404	C
1	2	1414	U
1	2	1419	G
1	2	1442(B)	A
1	2	1443	G
1	2	1452	C
1	2	1456	G
1	2	1476	G
1	2	1487	G
1	2	1491	G
1	2	1492	A
1	2	1493	A
1	2	1497	G
1	2	1498	U
1	2	1499	A
1	2	1502	A
1	2	1503	A
1	2	1504	G
1	2	1505	G
1	2	1517	G
1	2	1519	A
1	2	1520	G
1	2	1524	C
1	2	1529	G
1	2	1530	G
1	2	1531	A
22	7	4	G
22	7	5	G
22	7	6	G
22	7	7	G
22	7	8	U
22	7	9	G
22	7	14	A
22	7	15	G
22	7	17	C
22	7	17(A)	U
22	7	18	G

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Mol	Chain	Res	Type
22	7	19	G
22	7	20	U
22	7	21	A
22	7	37	A
22	7	43	A
22	7	45	G
22	7	47	U
22	7	48	C
22	7	50	U
22	7	52	G
22	7	53	G
22	7	54	5MU
22	7	59	A
22	7	63	G
22	7	64	G
22	7	65	C
22	7	67	C
22	7	71	C
22	7	72	A
22	7	75	C
22	7	76	A
23	8	10	G
23	8	16	U
23	8	17	C
23	8	18	G
23	8	19	G
23	8	20	U
23	8	21	A
23	8	33	U
23	8	46	G
23	8	47	U
23	8	48	C
23	8	51	U
23	8	67	C
23	8	70	G
23	8	71	G
23	8	74	C
24	9	14	U
24	9	15	C
24	9	18	G
34	1	8	A
34	1	9	U

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Mol	Chain	Res	Type
34	1	10	G
34	1	18	C
34	1	33	U
34	1	34	C
34	1	35	G
34	1	44	G
34	1	45	C
34	1	50	U
34	1	55	G
34	1	59	U
34	1	61	G
34	1	63	U
34	1	68	G
34	1	69	C
34	1	71	A
34	1	72	U
34	1	74	A
34	1	75	G
34	1	82	G
34	1	88	G
34	1	90	U
34	1	92	A
34	1	93	G
34	1	95	G
34	1	96	G
34	1	100	G
34	1	102	G
34	1	110	G
34	1	112	U
34	1	114	U
34	1	118	A
34	1	119	A
34	1	120	U
34	1	121	G
34	1	125	G
34	1	129	C
34	1	131	G
34	1	137	C
34	1	141	A
34	1	142(A)	C
34	1	143	G
34	1	145	G

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Mol	Chain	Res	Type
34	1	149	A
34	1	153	C
34	1	154	G
34	1	172	C
34	1	173	G
34	1	174	C
34	1	182	A
34	1	188	G
34	1	194	G
34	1	196	A
34	1	197	A
34	1	198	C
34	1	199	A
34	1	204	A
34	1	205	G
34	1	213	A
34	1	214	G
34	1	216	A
34	1	221	A
34	1	222	A
34	1	224	G
34	1	227	A
34	1	229	A
34	1	230	U
34	1	232	G
34	1	233	A
34	1	241	A
34	1	243	U
34	1	245	G
34	1	248	G
34	1	250	G
34	1	252	G
34	1	259	G
34	1	261	G
34	1	264	C
34	1	265	A
34	1	266	G
34	1	267	C
34	1	268	C
34	1	271(D)	G
34	1	271(H)	G
34	1	271(I)	G

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Mol	Chain	Res	Type
34	1	271(J)	C
34	1	271(K)	U
34	1	271(L)	U
34	1	271(M)	G
34	1	271(O)	C
34	1	271(P)	C
34	1	271(R)	G
34	1	271(T)	C
34	1	271(W)	G
34	1	271(X)	G
34	1	271(Y)	U
34	1	271(Z)	C
34	1	272(E)	G
34	1	272(H)	C
34	1	274	G
34	1	275	G
34	1	279	C
34	1	280	C
34	1	284	U
34	1	286	C
34	1	287	C
34	1	292	C
34	1	295	G
34	1	298	G
34	1	299	A
34	1	308	G
34	1	311	A
34	1	316	C
34	1	317	G
34	1	322	A
34	1	324	A
34	1	329	G
34	1	330	A
34	1	332	A
34	1	335	C
34	1	338	G
34	1	345	A
34	1	349	G
34	1	352	G
34	1	353	G
34	1	355	G
34	1	358	U

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Mol	Chain	Res	Type
34	1	359	A
34	1	362	U
34	1	363(B)	G
34	1	363(E)	U
34	1	363(F)	A
34	1	364	C
34	1	380	U
34	1	386	G
34	1	387	U
34	1	388	G
34	1	396	G
34	1	405	U
34	1	406	G
34	1	411	G
34	1	412	A
34	1	416	C
34	1	418	G
34	1	428	A
34	1	431	U
34	1	436	C
34	1	441	U
34	1	442	G
34	1	444	C
34	1	448	U
34	1	449	A
34	1	454	A
34	1	456	C
34	1	457	A
34	1	464	U
34	1	467	G
34	1	470	A
34	1	475	U
34	1	479	A
34	1	481	G
34	1	486	C
34	1	491	G
34	1	494	G
34	1	496	G
34	1	500	G
34	1	504	U
34	1	505	A
34	1	508	G

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Mol	Chain	Res	Type
34	1	509	C
34	1	518	G
34	1	525	U
34	1	526	A
34	1	529	A
34	1	530	G
34	1	531	C
34	1	532	A
34	1	533	G
34	1	537	C
34	1	541	C
34	1	542	C
34	1	543	C
34	1	547	A
34	1	548	A
34	1	549	G
34	1	551	G
34	1	552	G
34	1	556	G
34	1	557	U
34	1	559	G
34	1	562	U
34	1	563	G
34	1	569	U
34	1	571	A
34	1	573	G
34	1	574	C
34	1	575	A
34	1	583	G
34	1	588	U
34	1	599	G
34	1	602	G
34	1	603	A
34	1	604	G
34	1	607	U
34	1	614	U
34	1	614(A)	U
34	1	614(B)	G
34	1	614(C)	A
34	1	615	G
34	1	620	G
34	1	621	A

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Mol	Chain	Res	Type
34	1	622	G
34	1	624	C
34	1	627	A
34	1	628	G
34	1	634	C
34	1	637	A
34	1	645	C
34	1	646	A
34	1	650	C
34	1	651	G
34	1	652	C
34	1	656	G
34	1	669	G
34	1	673	C
34	1	686	G
34	1	696	G
34	1	701	G
34	1	705	A
34	1	707	G
34	1	722	A
34	1	726	G
34	1	730	C
34	1	734	A
34	1	740	U
34	1	748	G
34	1	749	C
34	1	752	A
34	1	753	C
34	1	759	G
34	1	762	U
34	1	764	A
34	1	765	G
34	1	771	G
34	1	775	G
34	1	776	G
34	1	782	A
34	1	783	A
34	1	784	A
34	1	785	G
34	1	788	A
34	1	789	A
34	1	800	A

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Mol	Chain	Res	Type
34	1	805	G
34	1	811	U
34	1	812	C
34	1	819	A
34	1	826	U
34	1	827	U
34	1	828	U
34	1	830	G
34	1	845	G
34	1	846	C
34	1	854	G
34	1	856	C
34	1	857	C
34	1	858	U
34	1	859	G
34	1	863	A
34	1	866	A
34	1	867	C
34	1	872	A
34	1	877	U
34	1	879	G
34	1	881	G
34	1	883	G
34	1	884	C
34	1	892	G
34	1	893	C
34	1	894	C
34	1	895	U
34	1	897	C
34	1	898	C
34	1	899	A
34	1	900	A
34	1	904	C
34	1	907	U
34	1	910	A
34	1	914	C
34	1	915	C
34	1	917	A
34	1	919	G
34	1	932	G
34	1	933	A
34	1	941	A

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Mol	Chain	Res	Type
34	1	945	A
34	1	946	G
34	1	953	A
34	1	959	A
34	1	961	C
34	1	964	C
34	1	965	C
34	1	973	A
34	1	974	G
34	1	980	A
34	1	983	A
34	1	985	C
34	1	989	G
34	1	990	A
34	1	996	A
34	1	999	U
34	1	1000	A
34	1	1004	C
34	1	1005	C
34	1	1008	C
34	1	1011	G
34	1	1012	U
34	1	1013	C
34	1	1015	G
34	1	1017	G
34	1	1020	A
34	1	1022	G
34	1	1023	U
34	1	1025	G
34	1	1026	U
34	1	1033	U
34	1	1035	U
34	1	1040	C
34	1	1042	G
34	1	1043	C
34	1	1044	G
34	1	1045	A
34	1	1046	A
34	1	1047	G
34	1	1048	A
34	1	1049	C
34	1	1050	A

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Mol	Chain	Res	Type
34	1	1051	G
34	1	1052	C
34	1	1053	C
34	1	1059	G
34	1	1060	U
34	1	1061	U
34	1	1062	G
34	1	1065	U
34	1	1066	U
34	1	1067	A
34	1	1068	G
34	1	1069	A
34	1	1070	A
34	1	1071	G
34	1	1072	C
34	1	1073	A
34	1	1075	C
34	1	1076	C
34	1	1077	A
34	1	1078	U
34	1	1079	C
34	1	1080	C
34	1	1083	U
34	1	1084	A
34	1	1085	A
34	1	1086	A
34	1	1087	G
34	1	1088	A
34	1	1089	G
34	1	1093	G
34	1	1094	U
34	1	1096	A
34	1	1101	U
34	1	1102	C
34	1	1104	C
34	1	1108	U
34	1	1110	G
34	1	1111	A
34	1	1112	G
34	1	1113	U
34	1	1115	G
34	1	1116	C

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Mol	Chain	Res	Type
34	1	1126	A
34	1	1128	A
34	1	1129	A
34	1	1130	U
34	1	1131	G
34	1	1135	C
34	1	1136	G
34	1	1139	G
34	1	1141	U
34	1	1148	A
34	1	1149	G
34	1	1152	C
34	1	1155	A
34	1	1156	A
34	1	1169	G
34	1	1170	G
34	1	1171	G
34	1	1173	G
34	1	1174	A
34	1	1175	U
34	1	1176	G
34	1	1177	A
34	1	1178	C
34	1	1179	C
34	1	1180	C
34	1	1190	G
34	1	1191	G
34	1	1195	G
34	1	1196	C
34	1	1204	A
34	1	1205	U
34	1	1210	A
34	1	1211	U
34	1	1212	G
34	1	1218	C
34	1	1220	A
34	1	1221	C
34	1	1221(A)	C
34	1	1222	C
34	1	1227	G
34	1	1233	C
34	1	1236	G

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Mol	Chain	Res	Type
34	1	1240	U
34	1	1241	A
34	1	1244	G
34	1	1246	A
34	1	1247	A
34	1	1250	G
34	1	1251	C
34	1	1252	G
34	1	1253	A
34	1	1255	U
34	1	1256	G
34	1	1263	U
34	1	1265	A
34	1	1267	U
34	1	1270	C
34	1	1271	G
34	1	1272	A
34	1	1274	A
34	1	1275	A
34	1	1281	G
34	1	1282	U
34	1	1293	C
34	1	1300	U
34	1	1301	A
34	1	1311	G
34	1	1312	U
34	1	1314	C
34	1	1318	C
34	1	1319	G
34	1	1321	A
34	1	1323	U
34	1	1324	G
34	1	1325	G
34	1	1326	U
34	1	1329	U
34	1	1330	C
34	1	1332	G
34	1	1333	C
34	1	1340	U
34	1	1341	U
34	1	1347	G
34	1	1349	A

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Mol	Chain	Res	Type
34	1	1352	U
34	1	1359	A
34	1	1360	A
34	1	1368	G
34	1	1372	U
34	1	1378	A
34	1	1379	A
34	1	1380	G
34	1	1384	A
34	1	1385	G
34	1	1386	C
34	1	1388	G
34	1	1389	G
34	1	1390	U
34	1	1392	A
34	1	1394	U
34	1	1395	A
34	1	1406	U
34	1	1407	C
34	1	1415	U
34	1	1416	G
34	1	1417	C
34	1	1419	A
34	1	1420	U
34	1	1421	G
34	1	1428	C
34	1	1433	U
34	1	1436	G
34	1	1437	C
34	1	1444	G
34	1	1445	A
34	1	1448	G
34	1	1451	C
34	1	1455	G
34	1	1458	C
34	1	1459	G
34	1	1460	A
34	1	1461	G
34	1	1465	G
34	1	1466	G
34	1	1467	C
34	1	1471	A

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Mol	Chain	Res	Type
34	1	1475	G
34	1	1476	C
34	1	1478	G
34	1	1480	G
34	1	1481	U
34	1	1482	G
34	1	1488	G
34	1	1490	A
34	1	1493	C
34	1	1494	A
34	1	1495	A
34	1	1497	U
34	1	1498	C
34	1	1501	C
34	1	1502	C
34	1	1504	C
34	1	1505	C
34	1	1507	A
34	1	1508	A
34	1	1509	C
34	1	1509(A)	A
34	1	1509(B)	A
34	1	1513	C
34	1	1515	G
34	1	1517	G
34	1	1520	G
34	1	1528	A
34	1	1528(A)	A
34	1	1541	G
34	1	1542	A
34	1	1543	C
34	1	1544	A
34	1	1545	A
34	1	1554	A
34	1	1558	A
34	1	1559	G
34	1	1566	A
34	1	1569	A
34	1	1578	U
34	1	1579	A
34	1	1580	A
34	1	1581	G

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Mol	Chain	Res	Type
34	1	1583	A
34	1	1584	C
34	1	1586	A
34	1	1588	C
34	1	1594	G
34	1	1595	G
34	1	1598	C
34	1	1603	A
34	1	1608	A
34	1	1617	C
34	1	1618	A
34	1	1622	G
34	1	1634	A
34	1	1635	G
34	1	1640	C
34	1	1647	G
34	1	1648	C
34	1	1649	G
34	1	1652	A
34	1	1653	G
34	1	1654	A
34	1	1658	C
34	1	1660	C
34	1	1664	A
34	1	1665	A
34	1	1667	G
34	1	1668	A
34	1	1669	A
34	1	1670	C
34	1	1672	C
34	1	1674	G
34	1	1691	C
34	1	1693	U
34	1	1694	C
34	1	1695	G
34	1	1696	G
34	1	1698	A
34	1	1699	G
34	1	1706	U
34	1	1707	G
34	1	1709	U
34	1	1718	G

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Mol	Chain	Res	Type
34	1	1721	G
34	1	1722	A
34	1	1739	U
34	1	1740	G
34	1	1744	C
34	1	1748	G
34	1	1751	C
34	1	1753	G
34	1	1754	C
34	1	1757	U
34	1	1763	G
34	1	1764	G
34	1	1773	A
34	1	1779	U
34	1	1780	A
34	1	1781	C
34	1	1782	C
34	1	1791	A
34	1	1792	G
34	1	1799	G
34	1	1800	C
34	1	1801	G
34	1	1809	A
34	1	1815	A
34	1	1816	G
34	1	1820	U
34	1	1822	G
34	1	1833	U
34	1	1835	G
34	1	1837	C
34	1	1838	C
34	1	1846	G
34	1	1847	A
34	1	1848	A
34	1	1853	A
34	1	1858	G
34	1	1864	U
34	1	1865	G
34	1	1876	A
34	1	1878	G
34	1	1881	C
34	1	1885	A

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Mol	Chain	Res	Type
34	1	1888	G
34	1	1889	A
34	1	1901	A
34	1	1903	G
34	1	1906	G
34	1	1912	A
34	1	1913	A
34	1	1927	A
34	1	1929	G
34	1	1930	G
34	1	1931	U
34	1	1936	A
34	1	1937	A
34	1	1938	A
34	1	1946	U
34	1	1948	G
34	1	1949	G
34	1	1955	U
34	1	1960	A
34	1	1962	C
34	1	1963	U
34	1	1964	G
34	1	1967	C
34	1	1969	A
34	1	1970	A
34	1	1971	A
34	1	1972	A
34	1	1982	C
34	1	1987	G
34	1	1992	G
34	1	1993	U
34	1	1997	G
34	1	2013	A
34	1	2020	A
34	1	2021	C
34	1	2023	G
34	1	2026	C
34	1	2027	G
34	1	2031	A
34	1	2032	G
34	1	2033	A
34	1	2034	U

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Mol	Chain	Res	Type
34	1	2036	C
34	1	2043	C
34	1	2046	G
34	1	2049	G
34	1	2051	A
34	1	2052	G
34	1	2055	C
34	1	2056	G
34	1	2057	A
34	1	2059	A
34	1	2060	A
34	1	2061	G
34	1	2062	A
34	1	2069	G
34	1	2076	U
34	1	2077	A
34	1	2089	U
34	1	2093	G
34	1	2099	U
34	1	2100	G
34	1	2102	U
34	1	2103	C
34	1	2104	G
34	1	2108	C
34	1	2110	G
34	1	2111	C
34	1	2112	G
34	1	2113	U
34	1	2114	A
34	1	2116	G
34	1	2117	A
34	1	2118	U
34	1	2119	A
34	1	2120	G
34	1	2125	G
34	1	2127	G
34	1	2128	C
34	1	2130	U
34	1	2159	G
34	1	2160	G
34	1	2161	C
34	1	2162	G

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Mol	Chain	Res	Type
34	1	2163	C
34	1	2164	C
34	1	2165	G
34	1	2166	G
34	1	2170	A
34	1	2171	A
34	1	2172	U
34	1	2176	A
34	1	2178	C
34	1	2184	G
34	1	2185	C
34	1	2186	G
34	1	2187	G
34	1	2188	C
34	1	2189	U
34	1	2190	G
34	1	2192	G
34	1	2198	A
34	1	2199	A
34	1	2206	G
34	1	2207	G
34	1	2208	A
34	1	2218	U
34	1	2219	G
34	1	2221	G
34	1	2225	A
34	1	2238	G
34	1	2239	G
34	1	2246	G
34	1	2249	U
34	1	2263	C
34	1	2266	A
34	1	2273	A
34	1	2275	C
34	1	2283	C
34	1	2286	A
34	1	2287	A
34	1	2297	C
34	1	2302	G
34	1	2303	G
34	1	2304	G
34	1	2305	A

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Mol	Chain	Res	Type
34	1	2306	C
34	1	2307	G
34	1	2308	G
34	1	2310	A
34	1	2311	A
34	1	2312	U
34	1	2319	G
34	1	2320	A
34	1	2322	A
34	1	2325	G
34	1	2329	G
34	1	2333	A
34	1	2334	G
34	1	2336	A
34	1	2345	G
34	1	2346	A
34	1	2347	C
34	1	2349	G
34	1	2350	C
34	1	2354	G
34	1	2358	G
34	1	2359	C
34	1	2379	G
34	1	2383	G
34	1	2384	G
34	1	2385	C
34	1	2387	U
34	1	2388	A
34	1	2391	G
34	1	2392	A
34	1	2394	C
34	1	2402	C
34	1	2405	G
34	1	2406	U
34	1	2411	A
34	1	2423	U
34	1	2425	A
34	1	2427	C
34	1	2428	G
34	1	2429	G
34	1	2430	A
34	1	2432	A

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Mol	Chain	Res	Type
34	1	2433	A
34	1	2435	A
34	1	2439	A
34	1	2440	C
34	1	2441	C
34	1	2447	G
34	1	2448	A
34	1	2465	C
34	1	2469	A
34	1	2470	G
34	1	2471	C
34	1	2474	C
34	1	2476	A
34	1	2477	C
34	1	2478	A
34	1	2480	C
34	1	2481	G
34	1	2484	G
34	1	2490	G
34	1	2494	G
34	1	2498	C
34	1	2502	G
34	1	2503	A
34	1	2504	U
34	1	2505	G
34	1	2506	U
34	1	2507	C
34	1	2513	G
34	1	2518	A
34	1	2520	C
34	1	2524	G
34	1	2529	G
34	1	2530	A
34	1	2531	A
34	1	2534	A
34	1	2535	G
34	1	2540	C
34	1	2542	A
34	1	2543	G
34	1	2545	G
34	1	2549	G
34	1	2554	U

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Mol	Chain	Res	Type
34	1	2556	C
34	1	2559	C
34	1	2562	U
34	1	2564	A
34	1	2566	A
34	1	2567	G
34	1	2569	G
34	1	2571	C
34	1	2572	A
34	1	2578	G
34	1	2581	G
34	1	2582	G
34	1	2585	U
34	1	2586	C
34	1	2602	A
34	1	2612	C
34	1	2615	U
34	1	2621	A
34	1	2623	G
34	1	2629	A
34	1	2630	G
34	1	2641	G
34	1	2646	C
34	1	2654	A
34	1	2655	G
34	1	2656	U
34	1	2657	A
34	1	2659	G
34	1	2660	A
34	1	2661	G
34	1	2662	A
34	1	2663	G
34	1	2668	G
34	1	2672	G
34	1	2673	G
34	1	2675	A
34	1	2681	C
34	1	2686	G
34	1	2689	U
34	1	2690	C
34	1	2691	C
34	1	2697	G

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Mol	Chain	Res	Type
34	1	2702	U
34	1	2713	A
34	1	2718	G
34	1	2720	U
34	1	2721	A
34	1	2726	U
34	1	2731	G
34	1	2732	G
34	1	2733	A
34	1	2736	G
34	1	2737	G
34	1	2739	U
34	1	2744	G
34	1	2748	A
34	1	2750	A
34	1	2751	G
34	1	2752	C
34	1	2753	A
34	1	2754	U
34	1	2757	A
34	1	2758	A
34	1	2759	G
34	1	2761	G
34	1	2763	G
34	1	2764	A
34	1	2765	A
34	1	2766	G
34	1	2777	G
34	1	2778	A
34	1	2779	U
34	1	2780	G
34	1	2781	A
34	1	2790	A
34	1	2791	C
34	1	2792	G
34	1	2794	C
34	1	2796	U
34	1	2799	C
34	1	2802	G
34	1	2803	C
34	1	2804	C
34	1	2805	G

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Mol	Chain	Res	Type
34	1	2808	U
34	1	2813	A
34	1	2818	G
34	1	2820	A
34	1	2821	A
34	1	2824	C
34	1	2830	G
34	1	2833	G
34	1	2834	G
34	1	2835	A
34	1	2844	G
34	1	2849	U
34	1	2860	A
34	1	2863	C
34	1	2864	G
34	1	2866	U
34	1	2872	G
34	1	2876	G
34	1	2880	C
34	1	2883	A
34	1	2886	G
34	1	2892	A
34	1	2893	G
34	1	2894	G
34	1	2895	U
34	1	2896	C
34	1	2897	U
35	3	3	C
35	3	7	G
35	3	8	U
35	3	9	G
35	3	12	C
35	3	13	A
35	3	15	A
35	3	16	G
35	3	19	G
35	3	22	U
35	3	24	G
35	3	27	C
35	3	28	C
35	3	32	C
35	3	34	U

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Mol	Chain	Res	Type
35	3	35	U
35	3	39	A
35	3	42	C
35	3	45	A
35	3	51	G
35	3	52	A
35	3	56	G
35	3	57	A
35	3	58	A
35	3	66	A
35	3	67	G
35	3	73	A
35	3	75	G
35	3	81	G
35	3	89	G
35	3	91	C
35	3	97	G
35	3	98	G
35	3	106	G
35	3	107	G
35	3	109	C
35	3	110	G
35	3	113	G
35	3	119	G
60	4	7	G
60	4	8	A
60	4	9	A
60	4	10	A
60	4	11	C
60	4	12	G
60	4	13	G
60	4	14	U
60	4	15	C
60	4	16	U
60	4	17	C
60	4	18	G
60	4	19	A
60	4	20	C
60	4	21	G
60	4	29	C
60	4	30	C
60	4	31	G

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Mol	Chain	Res	Type
60	4	33	G
60	4	34	G
60	4	37	G
60	4	38	U
60	4	39	G
60	4	41	C
60	4	42	U
60	4	44	C
60	4	45	G
60	4	47	G
60	4	48	C
60	4	49	C
60	4	50	G
60	4	53	G
60	4	54	U
60	4	55	G
60	4	56	C
60	4	57	G
60	4	58	G
60	4	61	G
60	4	62	G
60	4	63	C
60	4	64	C
60	4	66	C
60	4	67	G
60	4	68	U
60	4	69	A
60	4	70	A
60	4	71	A
60	4	72	A
60	4	73	A
60	4	76	C
60	4	77	G
60	4	78	C
60	4	79	A
60	4	111	C
60	4	112	G
60	4	115	G
60	4	118	U
60	4	119	A
60	4	120	A
60	4	121	U

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Mol	Chain	Res	Type
60	4	122	G
60	4	123	A
60	4	124	C
60	4	126	G
60	4	129	A
60	4	130	C
60	4	133	C
60	4	134	G
60	4	136	C
60	4	142	G
60	4	144	C
60	4	145	C
60	4	148	C
60	4	149	C
60	4	151	G
60	4	152	G
60	4	153	G
60	4	155	C
60	4	156	U
60	4	157	C
60	4	158	A
60	4	159	C
60	4	161	G
60	4	164	A
60	4	165	G
60	4	166	C
60	4	167	G
60	4	168	G
60	4	169	G
60	4	171	A
60	4	172	C
60	4	173	A
60	4	174	C
60	4	175	A
60	4	176	A
60	4	178	C
60	4	182	G
60	4	183	C
60	4	184	U
60	4	185	A
60	4	186	G
60	4	188	C

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Mol	Chain	Res	Type
60	4	189	C
60	4	191	G
60	4	195	C
60	4	197	C
60	4	198	G
60	4	199	C
60	4	201	C
60	4	203	C
60	4	204	U
60	4	205	A
60	4	207	C
60	4	208	C
60	4	209	C
60	4	212	G
60	4	213	G
60	4	214	C
60	4	215	G
60	4	216	A
60	4	217	A
60	4	218	G
60	4	220	U
60	4	221	U
60	4	224	A
60	4	225	G
60	4	226	G
60	4	228	G
60	4	229	G
60	4	230	C
60	4	232	C
60	4	233	G
60	4	236	C
60	4	237	C
60	4	239	G
60	4	242	C
60	4	243	G
60	4	246	C
60	4	247	G
60	4	249	C
60	4	250	C
60	4	251	G
60	4	259	A
60	4	261	C

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Mol	Chain	Res	Type
60	4	262	C
60	4	265	G
60	4	266	A
60	4	267	G
60	4	268	G
60	4	269	A
60	4	270	C
60	4	271	A
60	4	272	C
60	4	273	G
60	4	274	C
60	4	277	A
60	4	279	C
60	4	281	C
60	4	282	G
60	4	283	G
60	4	284	A
60	4	285	C
60	4	287	A
60	4	288	C
60	4	289	G
60	4	291	G
60	4	292	C
60	4	294	U
60	4	295	A
60	4	296	G
60	4	297	A
60	4	298	G
60	4	299	G
60	4	301	C
60	4	304	C
60	4	305	C
60	4	306	G
60	4	307	U
60	4	308	A
60	4	309	G
60	4	310	G
60	4	311	G
60	4	312	A
60	4	315	U
60	4	319	G
60	4	320	A

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Mol	Chain	Res	Type
60	4	321	C
60	4	322	G
60	4	324	G
60	4	325	G
60	4	326	G
60	4	329	C
60	4	331	A
60	4	332	C
60	4	333	U
60	4	334	C
60	4	338	C
60	4	339	C
60	4	341	C
60	4	342	C
60	4	343	U
60	4	347	C
60	4	348	C

All (80) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	60	A
1	2	79	G
1	2	115	G
1	2	119	A
1	2	243	A
1	2	244	U
1	2	266	G
1	2	328	C
1	2	352	C
1	2	366	C
1	2	410	G
1	2	428	G
1	2	484	G
1	2	509	A
1	2	575	G
1	2	687	A
1	2	748	C
1	2	913	A
1	2	997	U
1	2	1044	A
1	2	1064	G

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Mol	Chain	Res	Type
1	2	1065	U
1	2	1067	A
1	2	1201	A
1	2	1285	A
1	2	1300	G
1	2	1491	G
1	2	1498	U
1	2	1504	G
22	7	17(A)	U
23	8	15	G
23	8	70	G
24	9	13	U
34	1	49	A
34	1	71	A
34	1	74	A
34	1	128	C
34	1	140	G
34	1	221	A
34	1	275	G
34	1	387	U
34	1	562	U
34	1	573	G
34	1	587	C
34	1	627	A
34	1	752	A
34	1	856	C
34	1	1052	C
34	1	1058	G
34	1	1060	U
34	1	1069	A
34	1	1221(A)	C
34	1	1300	U
34	1	1427	A
34	1	1509	C
34	1	1541	G
34	1	1544	A
34	1	1558	A
34	1	1652	A
34	1	1653	G
34	1	1819	A
34	1	1992	G
34	1	2126	A

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Mol	Chain	Res	Type
34	1	2191	G
34	1	2422	A
34	1	2506	U
34	1	2689	U
34	1	2859	G
35	3	66	A
60	4	6	U
60	4	9	A
60	4	29	C
60	4	33	G
60	4	128	G
60	4	143	C
60	4	183	C
60	4	245	C
60	4	280	G
60	4	321	C
60	4	333	U

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
22	5MU	7	54	22	19,22,23	1.44	6 (31%)	27,32,35	2.25	6 (22%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	5MU	7	54	22	-	2/7/25/26	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	7	54	5MU	C4-N3	-2.73	1.33	1.38
22	7	54	5MU	C6-C5	2.68	1.39	1.34
22	7	54	5MU	C4-C5	2.39	1.48	1.44
22	7	54	5MU	C6-N1	-2.24	1.34	1.38
22	7	54	5MU	C2-N3	-2.23	1.34	1.38
22	7	54	5MU	C2-N1	2.12	1.41	1.38

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	7	54	5MU	C4-N3-C2	-5.39	120.27	127.34
22	7	54	5MU	C5-C4-N3	5.03	119.69	115.32
22	7	54	5MU	N3-C2-N1	4.90	121.26	114.89
22	7	54	5MU	C5-C6-N1	-4.01	118.96	123.31
22	7	54	5MU	O4-C4-C5	-3.91	120.44	124.92
22	7	54	5MU	O2-C2-N1	-2.49	119.55	122.80

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
22	7	54	5MU	C3'-C4'-C5'-O5'
22	7	54	5MU	O4'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
22	7	54	5MU	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 640 ligands modelled in this entry, 640 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
34	1	20
1	2	7
13	r	2
55	V	1
42	G	1
2	g	1
40	E	1
51	R	1
18	w	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	V	93:ASP	C	179:ASP	N	55.01
1	G	59:ALA	C	146:ALA	N	44.80
1	1	271(Z):C	O3'	272:G	P	25.34
1	1	362:U	O3'	363:G	P	24.58
1	1	363:G	O3'	363(A):A	P	17.94
1	1	270:A	O3'	271:A	P	16.34
1	1	271:A	O3'	271(A):A	P	15.88
1	2	188:C	O3'	189:G	P	14.24
1	1	139:G	O3'	139(A):G	P	11.54
1	1	94:C	O3'	94(A):G	P	9.41
1	1	2801:A	O3'	2801(A):A	P	8.98
1	2	189:G	O3'	189(A):C	P	8.72
1	1	139(A):G	O3'	140:G	P	8.56

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	974:G	O3'	975:C	P	7.93
1	1	1450:G	O3'	1450(A):C	P	7.86
1	1	1141:U	O3'	1142:U	P	6.98
1	1	137:C	O3'	139:G	P	6.74
1	2	1362:C	O3'	1363:C	P	6.46
1	g	240:GLN	C	241:GLU	N	6.42
1	1	2712:U	O3'	2712(A):A	P	6.17
1	1	93:G	O3'	94:C	P	5.39
1	2	1363:C	O3'	1363(A):A	P	5.11
1	1	2799:C	O3'	2801:A	P	4.82
1	1	2711:A	O3'	2712:U	P	4.65
1	1	975:C	O3'	975(A):G	P	4.60
1	1	1449:A	O3'	1450:G	P	4.48
1	2	1441:G	O3'	1442:G	P	4.32
1	E	112:PRO	C	113:ARG	N	3.75
1	r	97:PRO	C	98:VAL	N	3.67
1	1	1142:U	O3'	1142(A):A	P	3.62
1	2	1442:G	O3'	1442(A):G	P	3.51
1	r	112:GLY	C	113:PRO	N	3.30
1	R	80:GLN	C	81:TYR	N	3.26
1	2	1363(A):A	O3'	1364:U	P	3.22
1	w	78:LEU	C	79:LEU	N	1.19

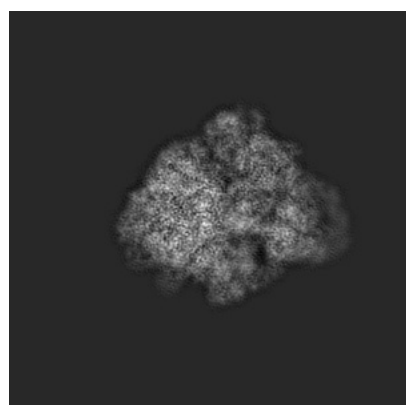
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4475. These allow visual inspection of the internal detail of the map and identification of artifacts.

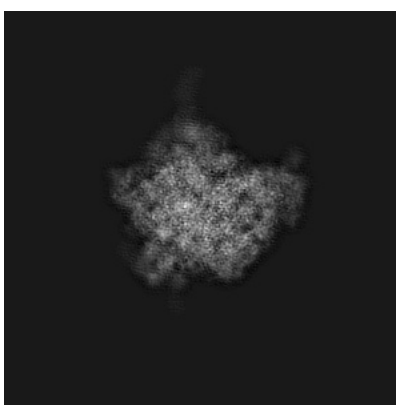
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

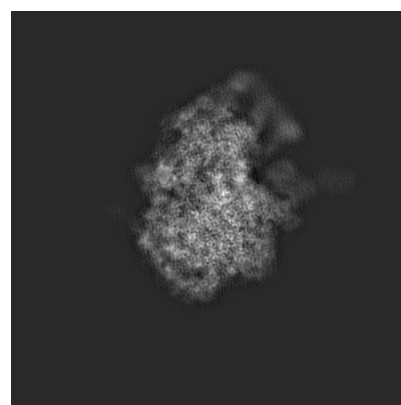
6.1.1 Primary map



X



Y

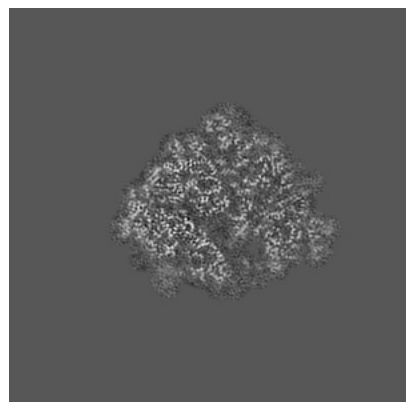


Z

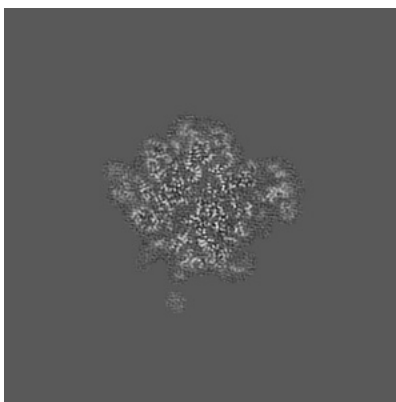
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

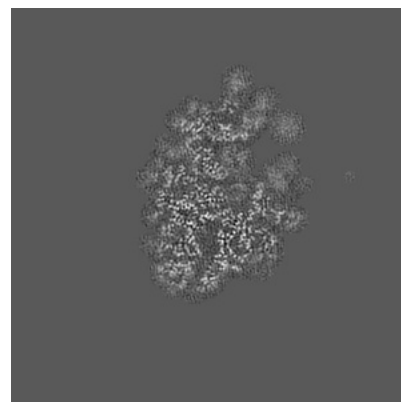
6.2.1 Primary map



X Index: 180



Y Index: 180

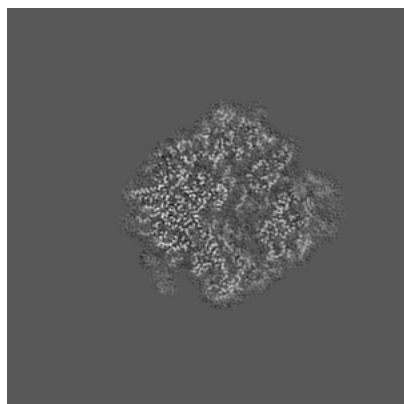


Z Index: 180

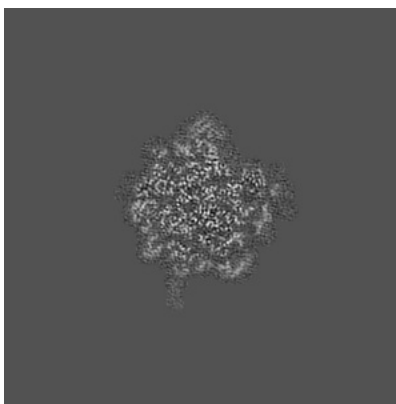
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

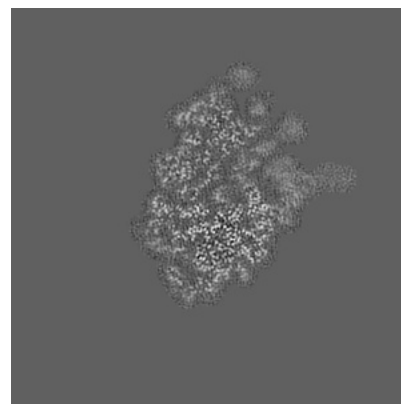
6.3.1 Primary map



X Index: 191



Y Index: 173

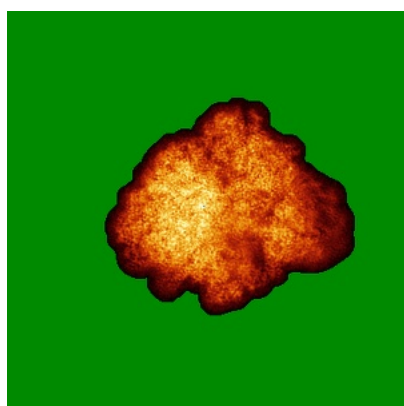


Z Index: 167

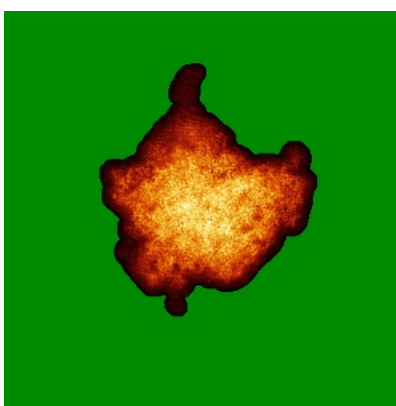
The images above show the largest variance slices of the map in three orthogonal directions.

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

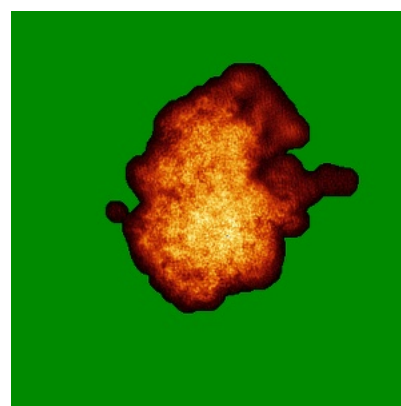
6.4.1 Primary map



X



Y

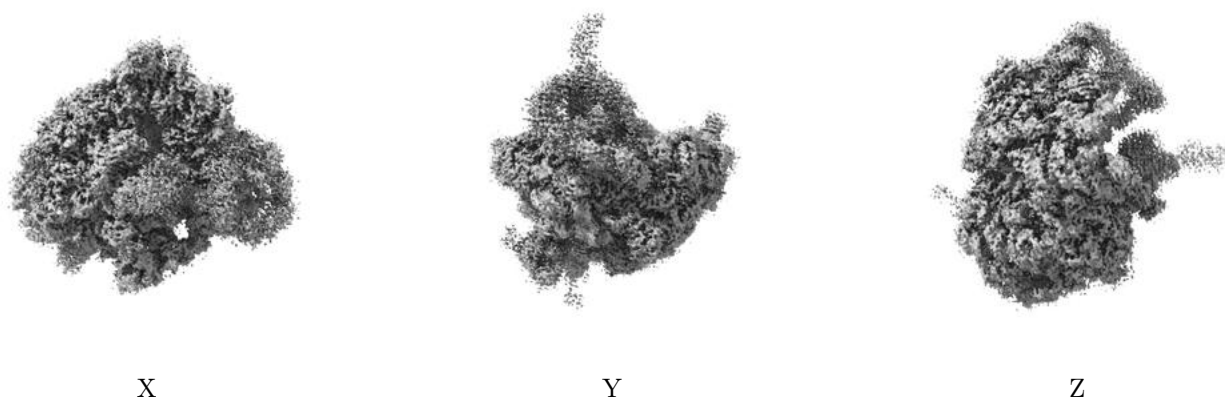


Z

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 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

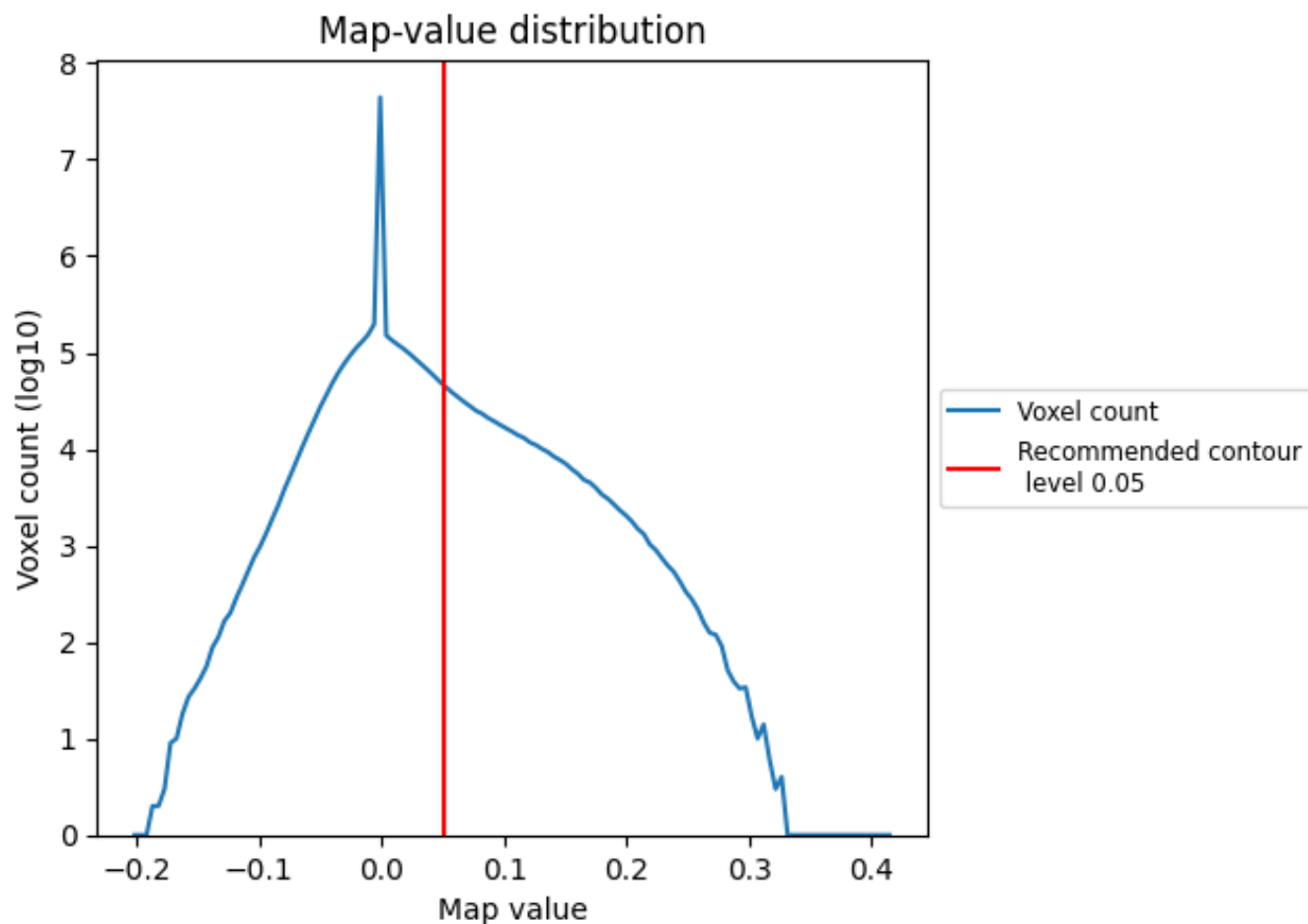
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

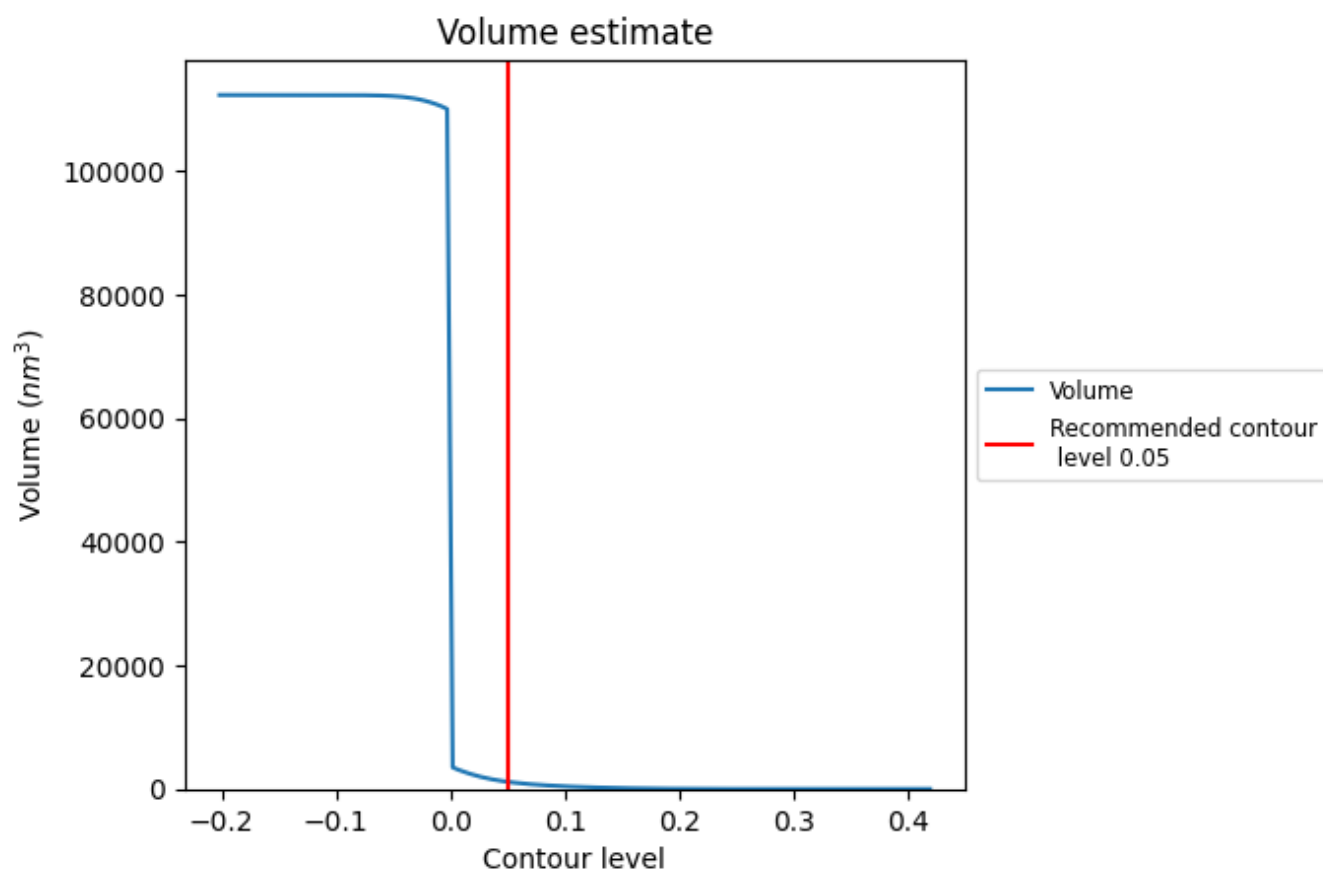
This section contains the results of statistical analysis of the map.

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.

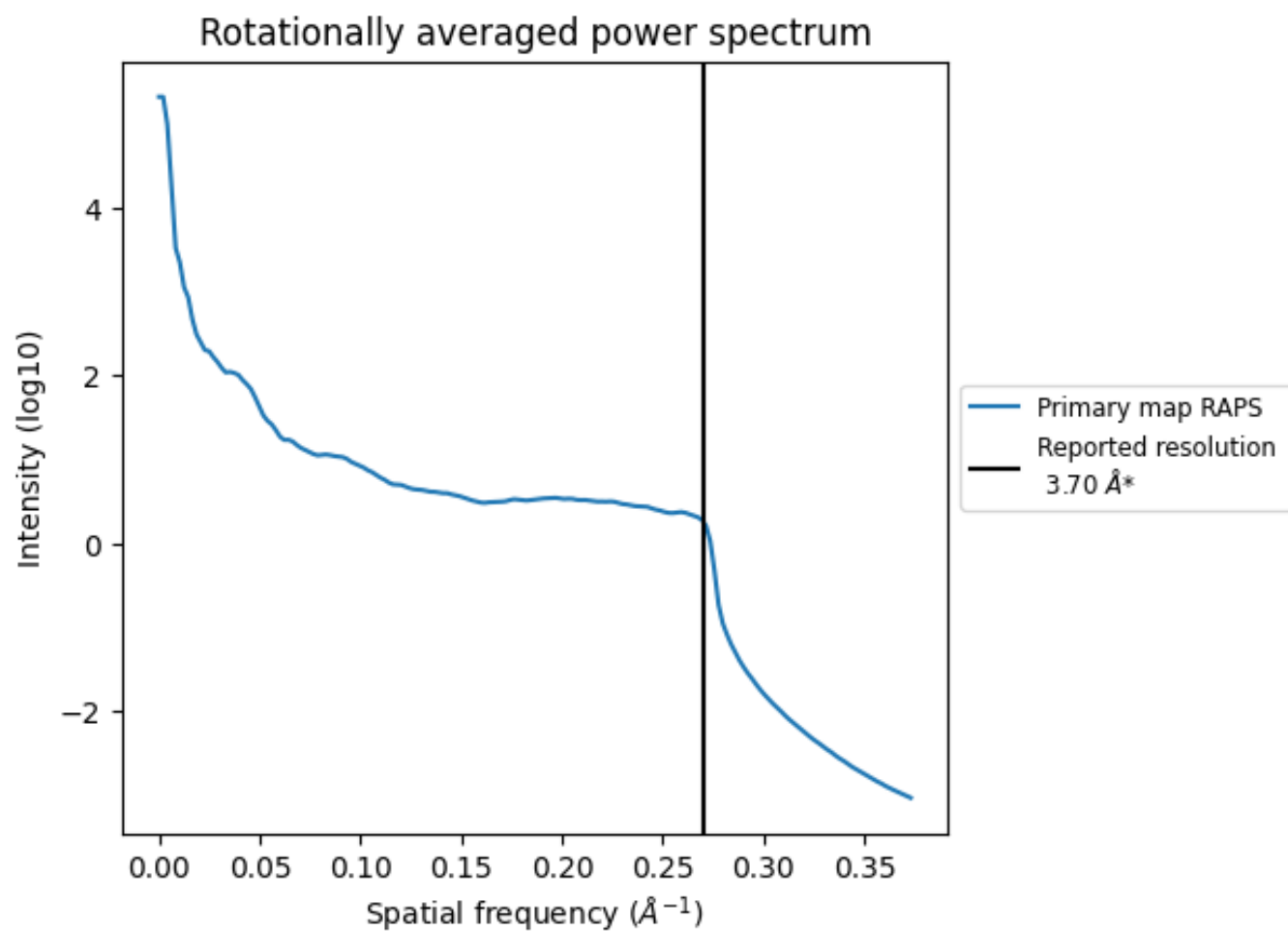
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1158 nm³; this corresponds to an approximate mass of 1046 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 0.270 Å⁻¹

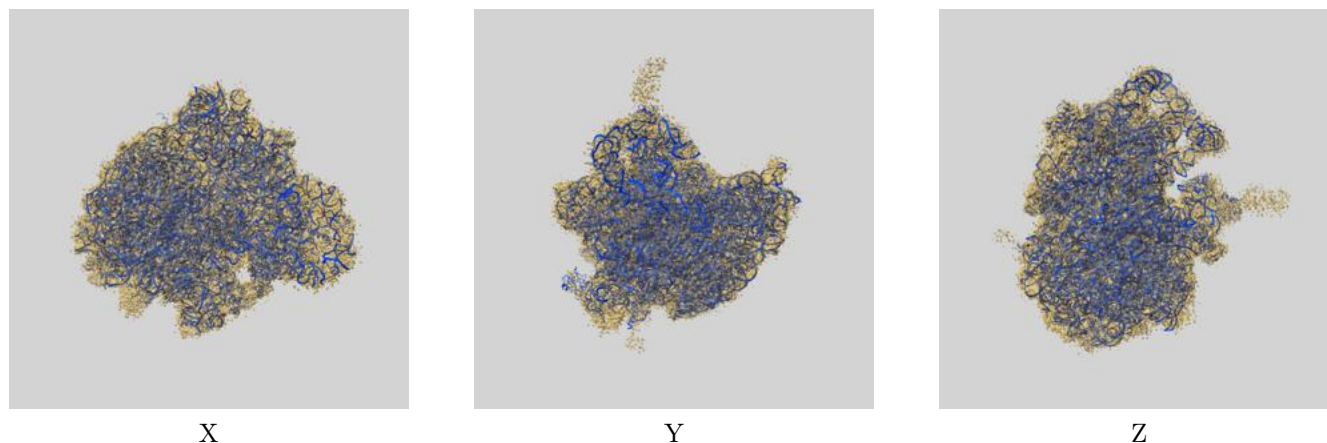
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

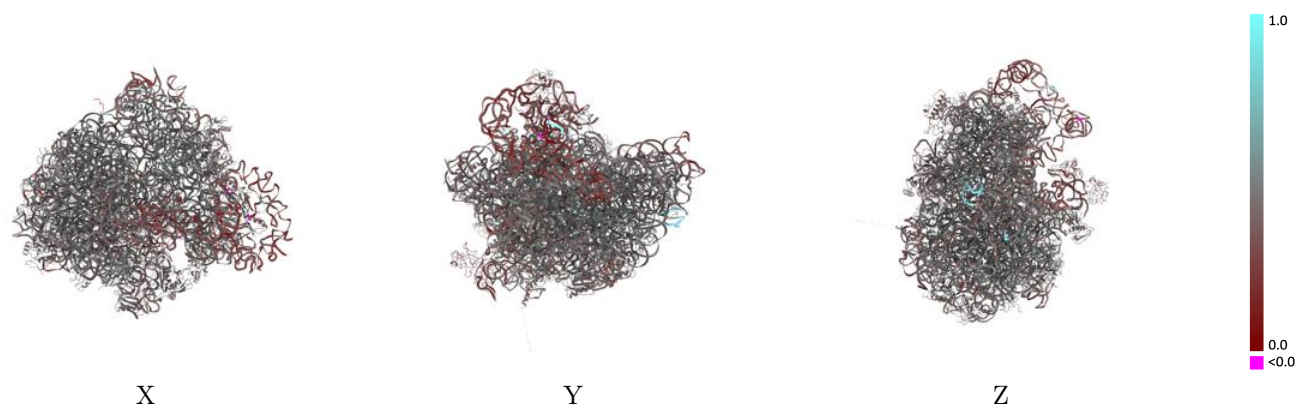
This section contains information regarding the fit between EMDB map EMD-4475 and PDB model 6Q95. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

9.1 Map-model overlay [i](#)



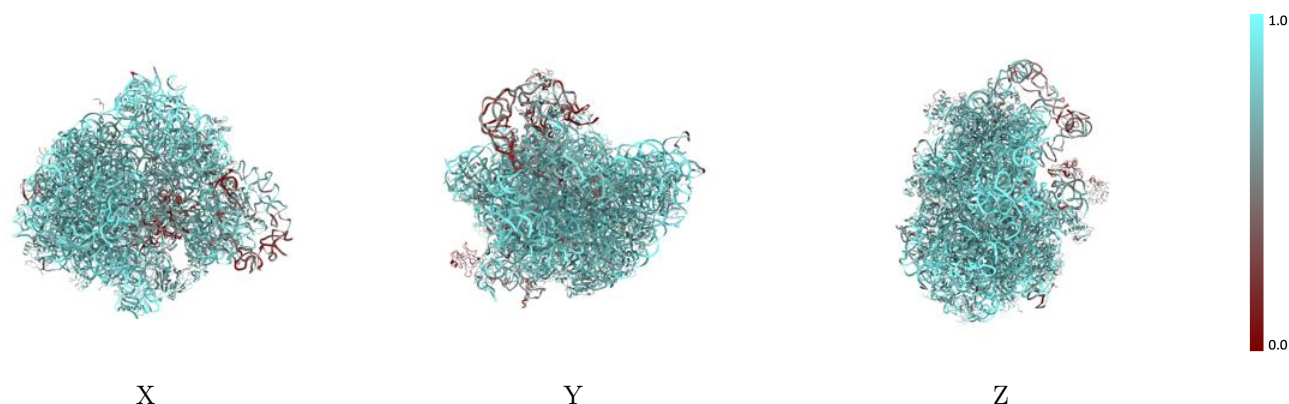
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



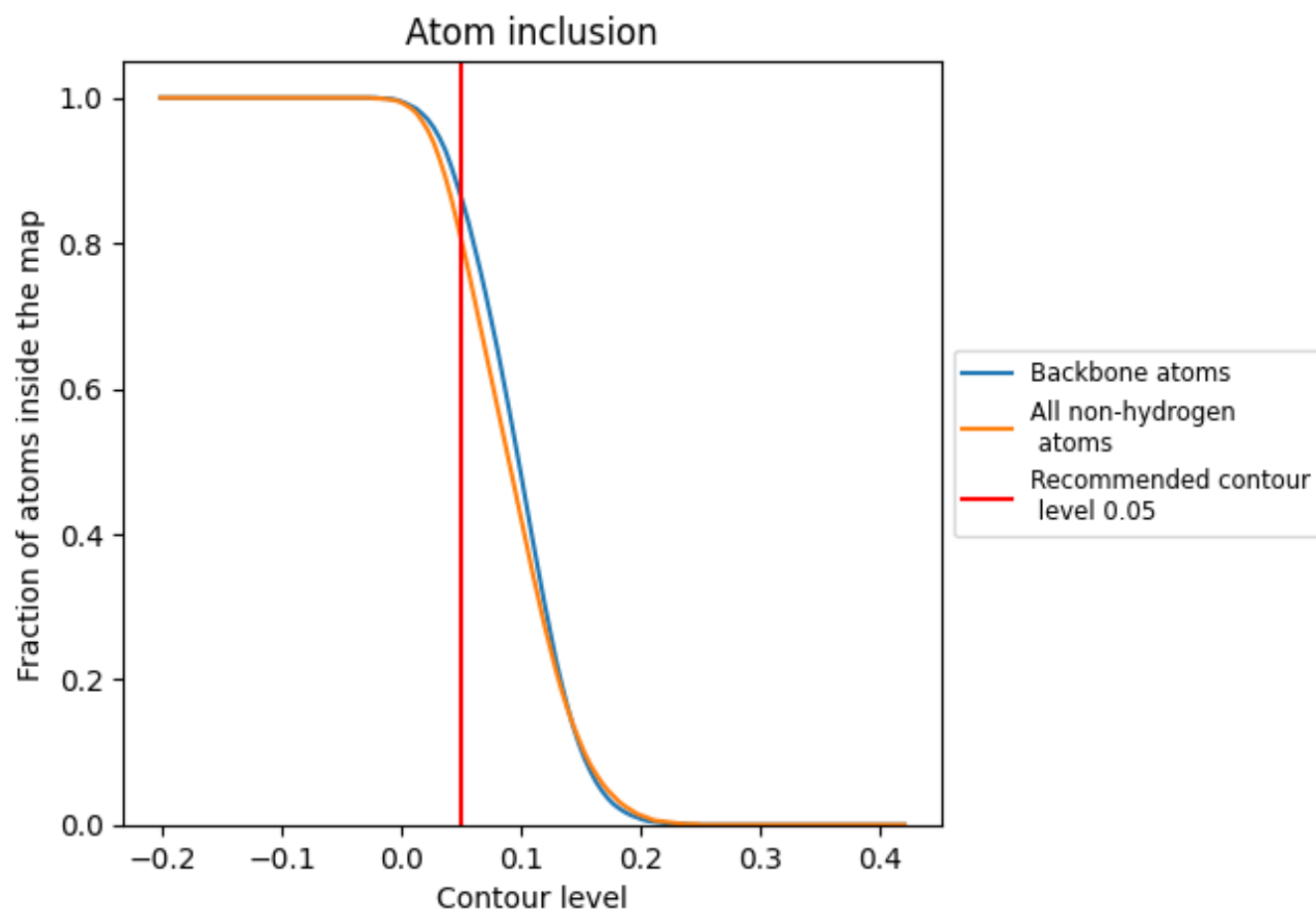
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 80% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8010	 0.4320
1	 0.8790	 0.4400
2	 0.8810	 0.4310
3	 0.9080	 0.4240
4	 0.4760	 0.2810
5	 0.4960	 0.4210
6	 0.7690	 0.4930
7	 0.7630	 0.4040
8	 0.6870	 0.3670
9	 0.7110	 0.4260
A	 0.3110	 0.3390
B	 0.7570	 0.4920
C	 0.7540	 0.4760
D	 0.7240	 0.4520
E	 0.6670	 0.4240
F	 0.7040	 0.4140
G	 0.5660	 0.4080
H	 0.4080	 0.3540
I	 0.1900	 0.3310
J	 0.7230	 0.4650
K	 0.7130	 0.5040
L	 0.6850	 0.4330
M	 0.6960	 0.4600
N	 0.7800	 0.4860
O	 0.7530	 0.4240
P	 0.6850	 0.4370
Q	 0.7770	 0.4760
R	 0.6780	 0.4370
S	 0.7610	 0.4960
T	 0.6930	 0.4180
U	 0.6820	 0.4150
V	 0.7440	 0.4630
W	 0.7600	 0.4990
X	 0.6870	 0.4520
Y	 0.6980	 0.3870



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Chain	Atom inclusion	Q-score
Z	 0.7210	 0.4800
a	 0.7170	 0.4120
b	 0.7400	 0.4690
c	 0.7270	 0.4290
d	 0.7810	 0.5110
e	 0.7100	 0.4620
f	 0.7860	 0.4860
g	 0.6310	 0.4190
h	 0.6950	 0.4640
i	 0.7300	 0.4470
j	 0.7370	 0.4730
k	 0.6840	 0.4320
l	 0.7340	 0.4470
m	 0.7390	 0.4670
n	 0.7360	 0.4290
o	 0.6990	 0.4390
p	 0.7050	 0.4520
q	 0.7220	 0.5000
r	 0.7000	 0.4360
s	 0.7390	 0.4700
t	 0.7160	 0.4510
u	 0.7740	 0.4730
v	 0.7130	 0.4840
w	 0.7030	 0.4500
x	 0.6880	 0.4330
y	 0.7150	 0.4430
z	 0.7810	 0.4670