



Full wwPDB EM Validation Report ⓘ

Mar 17, 2026 – 09:33 PM UTC

PDB ID : 6WD0 / pdb_00006wd0
EMDB ID : EMD-21619
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Cognate Structure I-A)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 3.00 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

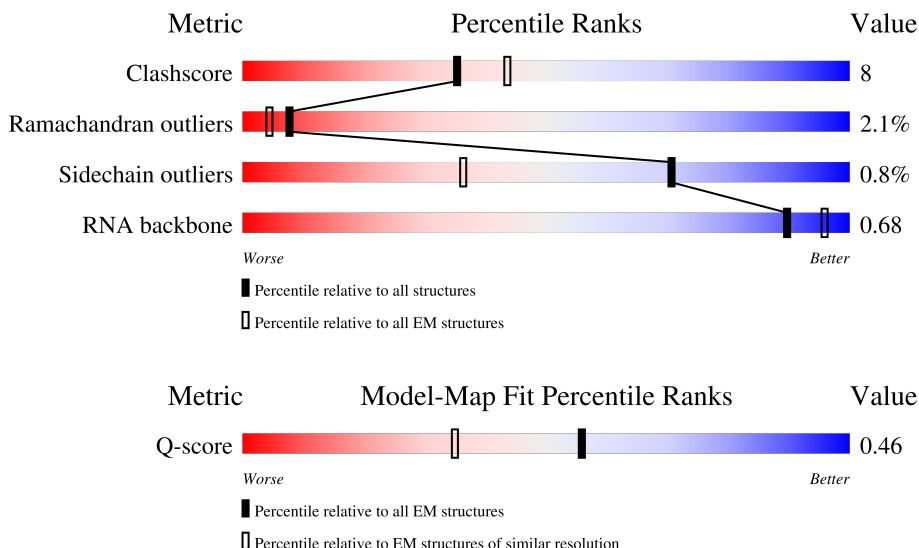
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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.



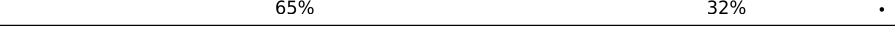
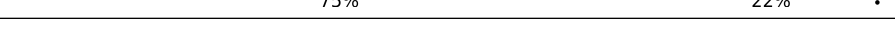
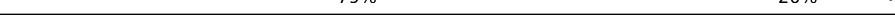
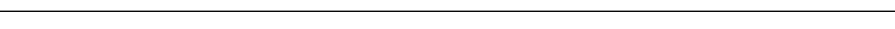
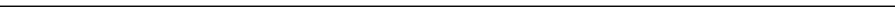
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	b	271	
2	c	209	
3	d	201	

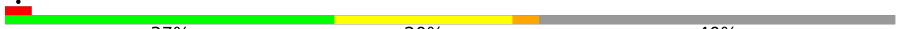
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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	B	56	
27	C	50	
28	D	46	

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Mol	Chain	Length	Quality of chain
29	E	64	 80% 19% .
30	F	38	 74% 24% .
31	G	225	 78% 21%
32	H	206	 68% 30% .
33	I	205	 65% 32% .
34	J	157	 62% 35% ..
35	K	100	 49% 48% .
36	L	151	 77% 21% .
37	M	129	 67% 32% .
38	N	127	 59% 37% ..
39	O	98	 56% 38% 5% .
40	P	116	 63% 34% .
41	Q	123	 63% 31% 5% .
42	R	114	 66% 29% 5%
43	S	100	 66% 31% .
44	T	88	 81% 18% .
45	U	82	 66% 33% .
46	V	80	 75% 22% ..
47	W	65	 80% 18% .
48	X	79	 59% 39% .
49	Y	85	 65% 32% .
50	Z	65	 48% 40% 9% .
51	a	223	 37% 20% . 40%
52	3	1539	 66% 31% .
53	1	2903	 67% 29% .

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Mol	Chain	Length	Quality of chain
54	2	120	66% 28% 7%
55	5	77	78% 21%
55	6	77	62% 34%
56	4	18	11% 50% 50%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 148592 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	b	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

- Molecule 2 is a protein called 50S ribosomal protein L3.

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

- Molecule 3 is a protein called 50S ribosomal protein L4.

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

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	e	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	f	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 6 is a protein called 50S ribosomal protein L9.

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

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	h	131	Total	C	N	O	S	0	0
			989	625	175	184	5		

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	i	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 9 is a protein called 50S ribosomal protein L13.

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

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	k	122	Total	C	N	O	S	0	0
			939	587	180	166	6		

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	l	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 12 is a protein called 50S ribosomal protein L16.

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

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	n	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

- Molecule 14 is a protein called 50S ribosomal protein L18.

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

- Molecule 15 is a protein called 50S ribosomal protein L19.

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

- Molecule 16 is a protein called 50S ribosomal protein L20.

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

- Molecule 17 is a protein called 50S ribosomal protein L21.

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

- Molecule 18 is a protein called 50S ribosomal protein L22.

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

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	t	93	Total	C	N	O	S	0
			739	466	139	132	2	0

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	u	102	Total	C	N	O		0
			780	492	146	142		0

- Molecule 21 is a protein called 50S ribosomal protein L25.

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

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	w	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 23 is a protein called 50S ribosomal protein L28.

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

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 26 is a protein called 50S ribosomal protein L32.

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

- Molecule 27 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	C	50	Total	C	N	O	0	0
			410	263	75	72		

- Molecule 28 is a protein called 50S ribosomal protein L34.

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

- Molecule 29 is a protein called 50S ribosomal protein L35.

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

- Molecule 30 is a protein called 50S ribosomal protein L36.

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

- Molecule 31 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	G	225	Total	C	N	O	S	0	0
			1757	1111	315	323	8		

- Molecule 32 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	H	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 33 is a protein called 30S ribosomal protein S4.

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

- Molecule 34 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	J	157	Total	C	N	O	S	0	0
			1157	719	218	214	6		

- Molecule 35 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	K	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 36 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	L	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 37 is a protein called 30S ribosomal protein S8.

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

- Molecule 38 is a protein called 30S ribosomal protein S9.

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

- Molecule 39 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	O	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 40 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	P	116	Total	C	N	O	S	0	0
			870	535	173	159	3		

- Molecule 41 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Q	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 42 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	R	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 43 is a protein called 30S ribosomal protein S14.

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

- Molecule 44 is a protein called 30S ribosomal protein S15.

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

- Molecule 45 is a protein called 30S ribosomal protein S16.

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

- Molecule 46 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	V	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 47 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	W	65	Total	C	N	O	S	0	0
			536	339	100	96	1		

- Molecule 48 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	X	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 49 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Y	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 50 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Z	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

- Molecule 51 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	a	134	Total	C	N	O	S	0	0
			1027	645	186	194	2		

- Molecule 52 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 53 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	1	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 1036415628

- Molecule 54 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	2	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	120	A	-	insertion	GB 1370526515

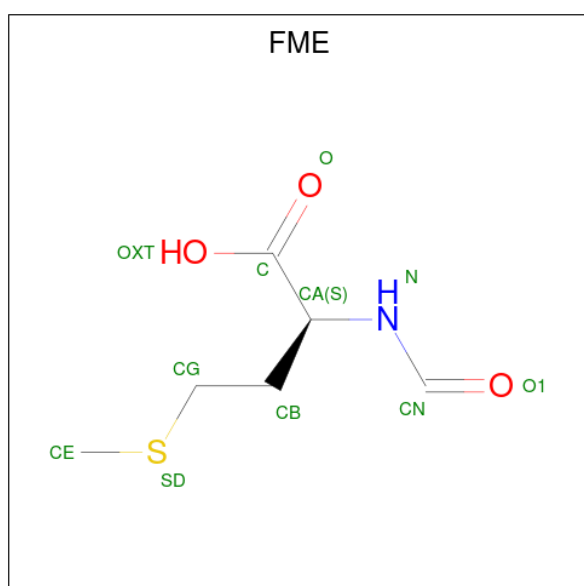
- Molecule 55 is a RNA chain called tRNAfMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	5	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		
55	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 56 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	4	18	Total	C	N	O	P	0	0
			388	175	76	120	17		

- Molecule 57 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C₆H₁₁NO₃S).

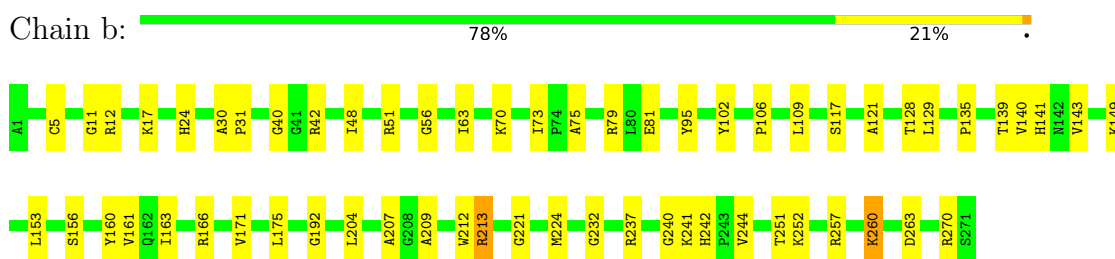


Mol	Chain	Residues	Atoms					AltConf
57	5	1	Total	C	N	O	S	0
			10	6	1	2	1	

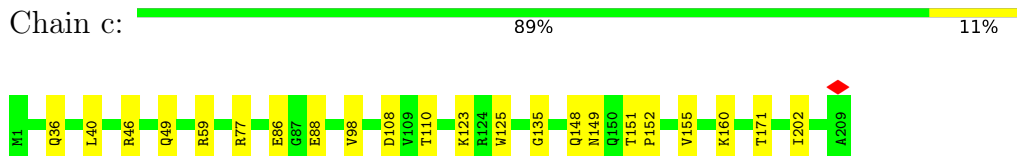
3 Residue-property plots

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.

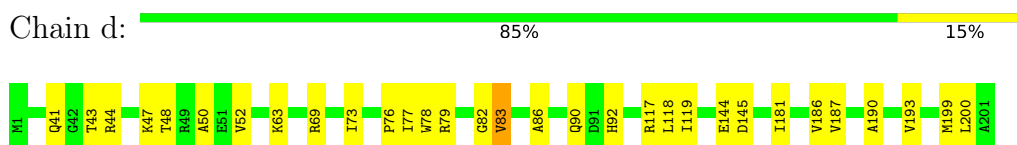
- Molecule 1: 50S ribosomal protein L2



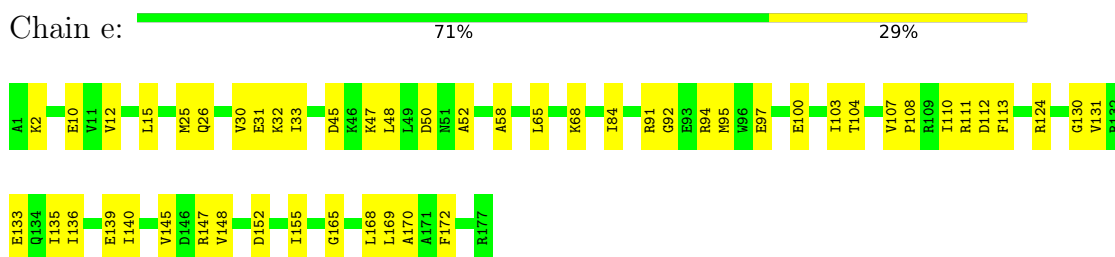
- Molecule 2: 50S ribosomal protein L3



- Molecule 3: 50S ribosomal protein L4

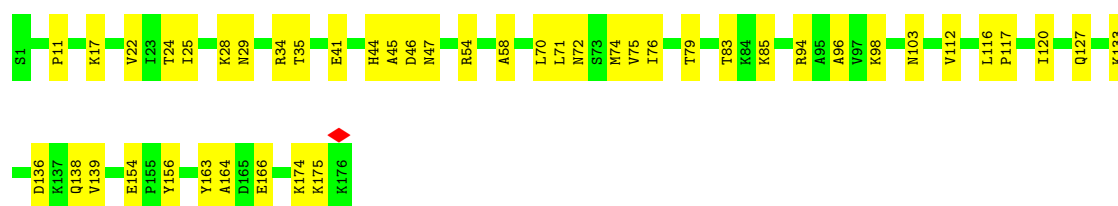


- Molecule 4: 50S ribosomal protein L5



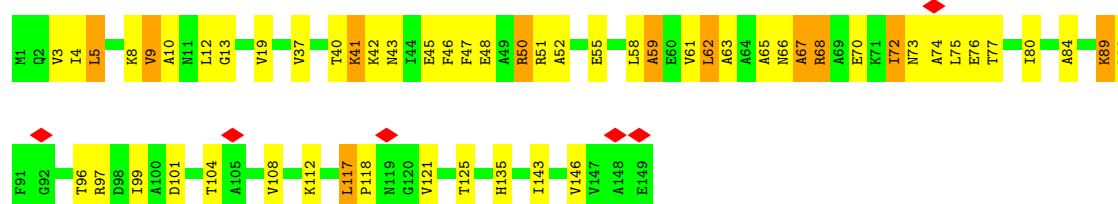
- Molecule 5: 50S ribosomal protein L6

Chain f:  74% 26%



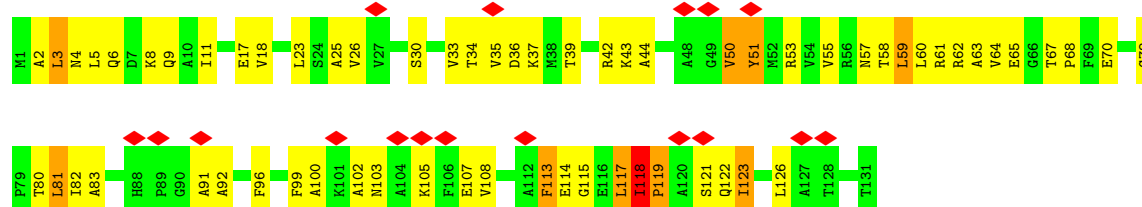
• Molecule 6: 50S ribosomal protein L9

Chain g:  62% 30% 7%



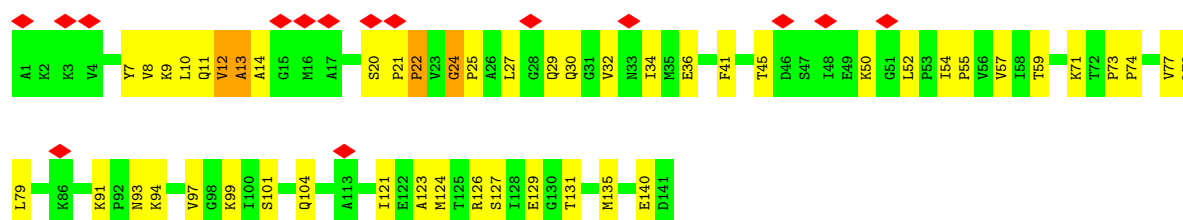
• Molecule 7: 50S ribosomal protein L10

Chain h:  13% 51% 41% 7%



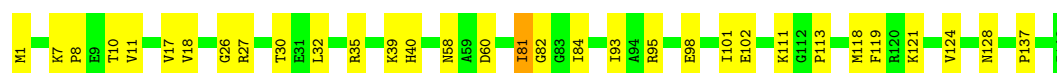
• Molecule 8: 50S ribosomal protein L11

Chain i:  11% 65% 32%



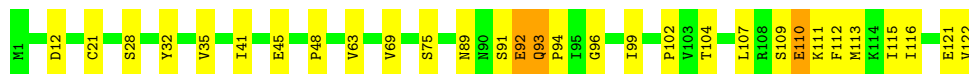
• Molecule 9: 50S ribosomal protein L13

Chain j:  77% 22%



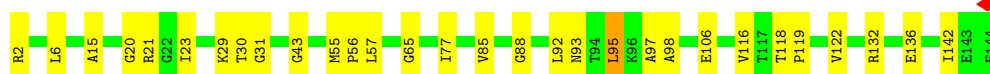
- Molecule 10: 50S ribosomal protein L14

Chain k:  75% 22%



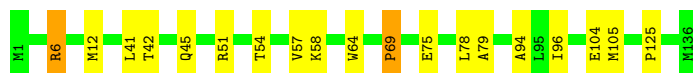
- Molecule 11: 50S ribosomal protein L15

Chain l:  79% 20%



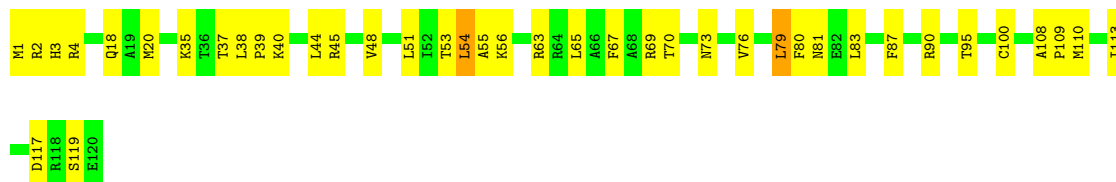
- Molecule 12: 50S ribosomal protein L16

Chain m:  86% 12%



- Molecule 13: 50S ribosomal protein L17

Chain n:  67% 32%



- Molecule 14: 50S ribosomal protein L18

Chain o:  84% 15%



- Molecule 15: 50S ribosomal protein L19

Chain p:  78% 22%



- Molecule 16: 50S ribosomal protein L20

Chain q:  83% 17%



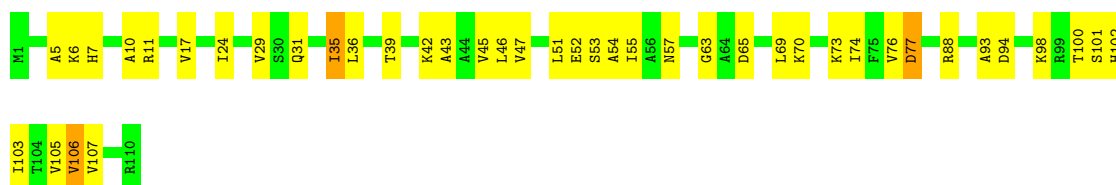
- Molecule 17: 50S ribosomal protein L21

Chain r: 68% 31%



- Molecule 18: 50S ribosomal protein L22

Chain s: 62% 35%



- Molecule 19: 50S ribosomal protein L23

Chain t: 71% 27%



- Molecule 20: 50S ribosomal protein L24

Chain u: 71% 28%



- Molecule 21: 50S ribosomal protein L25

Chain v: 80% 19%



- Molecule 22: 50S ribosomal protein L27

Chain w: 89% 11%



- Molecule 23: 50S ribosomal protein L28

Chain x:  82% 18%



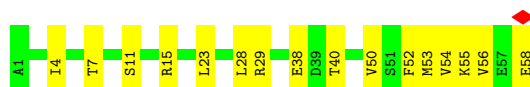
- Molecule 24: 50S ribosomal protein L29

Chain y:  60% 40%



- Molecule 25: 50S ribosomal protein L30

Chain z:  72% 28%



- Molecule 26: 50S ribosomal protein L32

Chain B:  88% 12%



- Molecule 27: 50S ribosomal protein L33

Chain C:  76% 24%



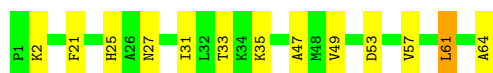
- Molecule 28: 50S ribosomal protein L34

Chain D:  72% 26%



- Molecule 29: 50S ribosomal protein L35

Chain E:  80% 19%



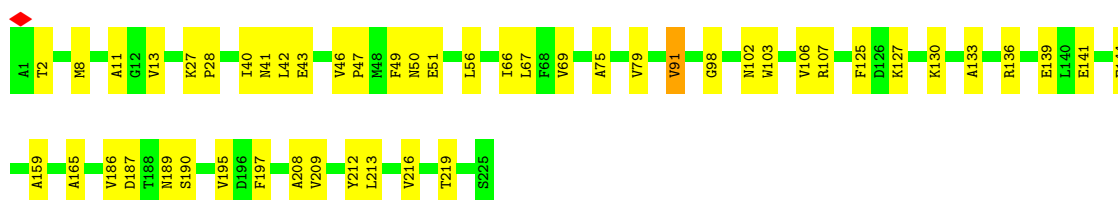
- Molecule 30: 50S ribosomal protein L36

Chain F:  74% 24% .



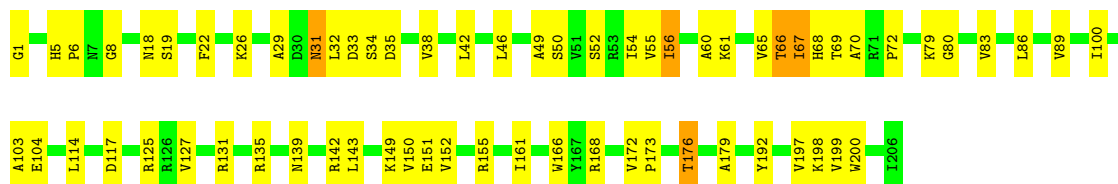
- Molecule 31: 30S ribosomal protein S2

Chain G:  78% 21%



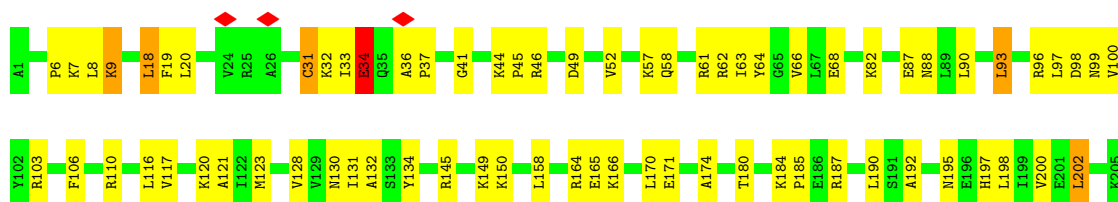
- Molecule 32: 30S ribosomal protein S3

Chain H:  68% 30% .



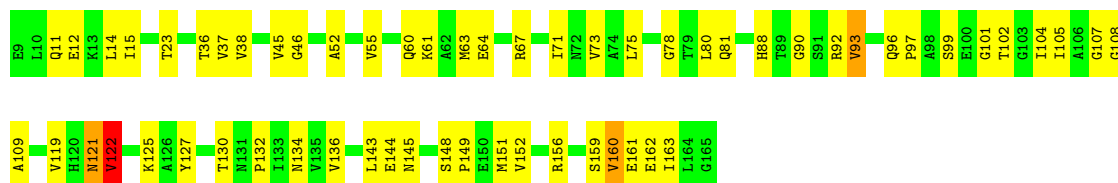
- Molecule 33: 30S ribosomal protein S4

Chain I:  65% 32% .



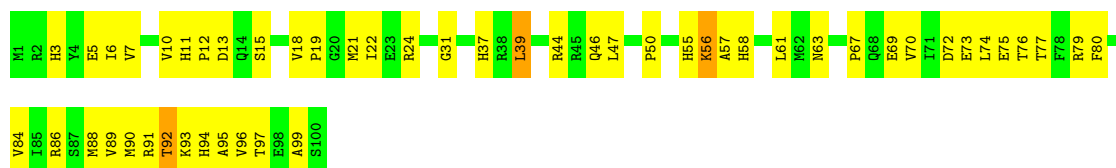
- Molecule 34: 30S ribosomal protein S5

Chain J:  62% 35% .



- Molecule 35: 30S ribosomal protein S6

Chain K:  49% 48% .



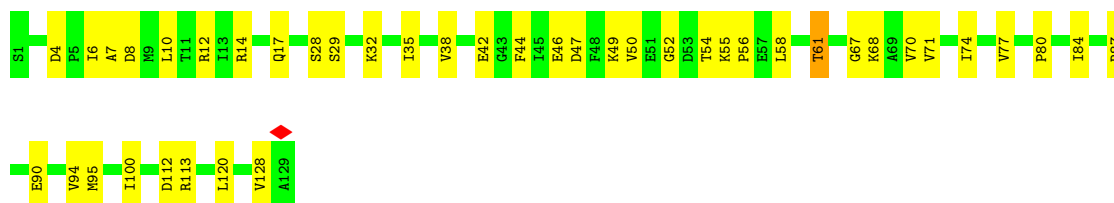
- Molecule 36: 30S ribosomal protein S7

Chain L: 77% 21% .



- Molecule 37: 30S ribosomal protein S8

Chain M: 67% 32% .



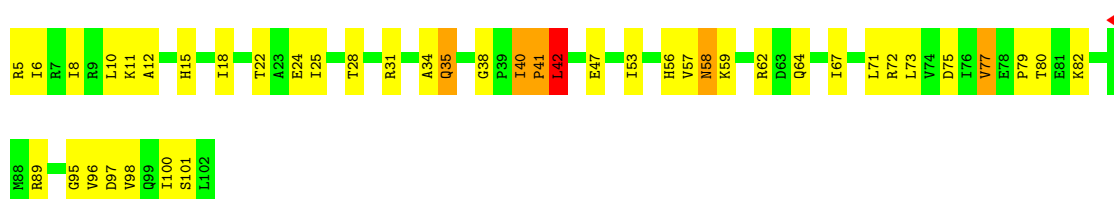
- Molecule 38: 30S ribosomal protein S9

Chain N: 59% 37% .



- Molecule 39: 30S ribosomal protein S10

Chain O: 56% 38% 5% .

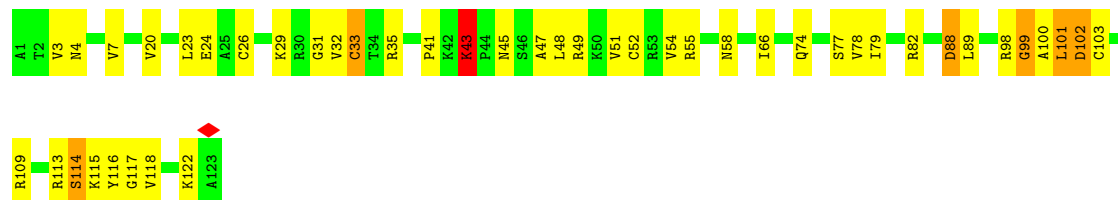


- Molecule 40: 30S ribosomal protein S11

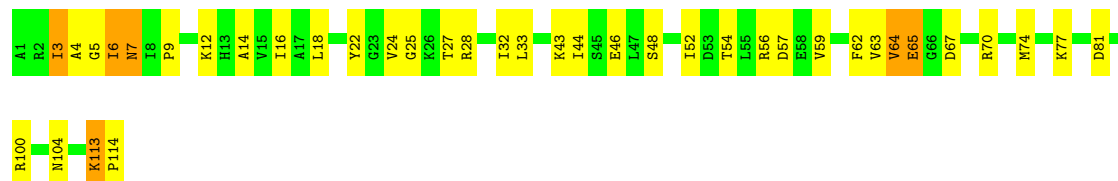
Chain P: 63% 34% .



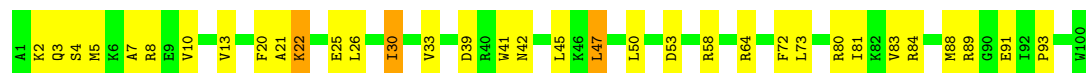
- Molecule 41: 30S ribosomal protein S12



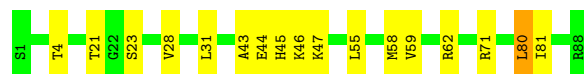
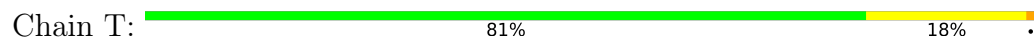
- Molecule 42: 30S ribosomal protein S13



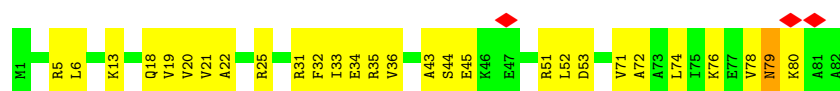
- Molecule 43: 30S ribosomal protein S14



- Molecule 44: 30S ribosomal protein S15



- Molecule 45: 30S ribosomal protein S16



- Molecule 46: 30S ribosomal protein S17

- Molecule 47: 30S ribosomal protein S18

- Molecule 48: 30S ribosomal protein S19

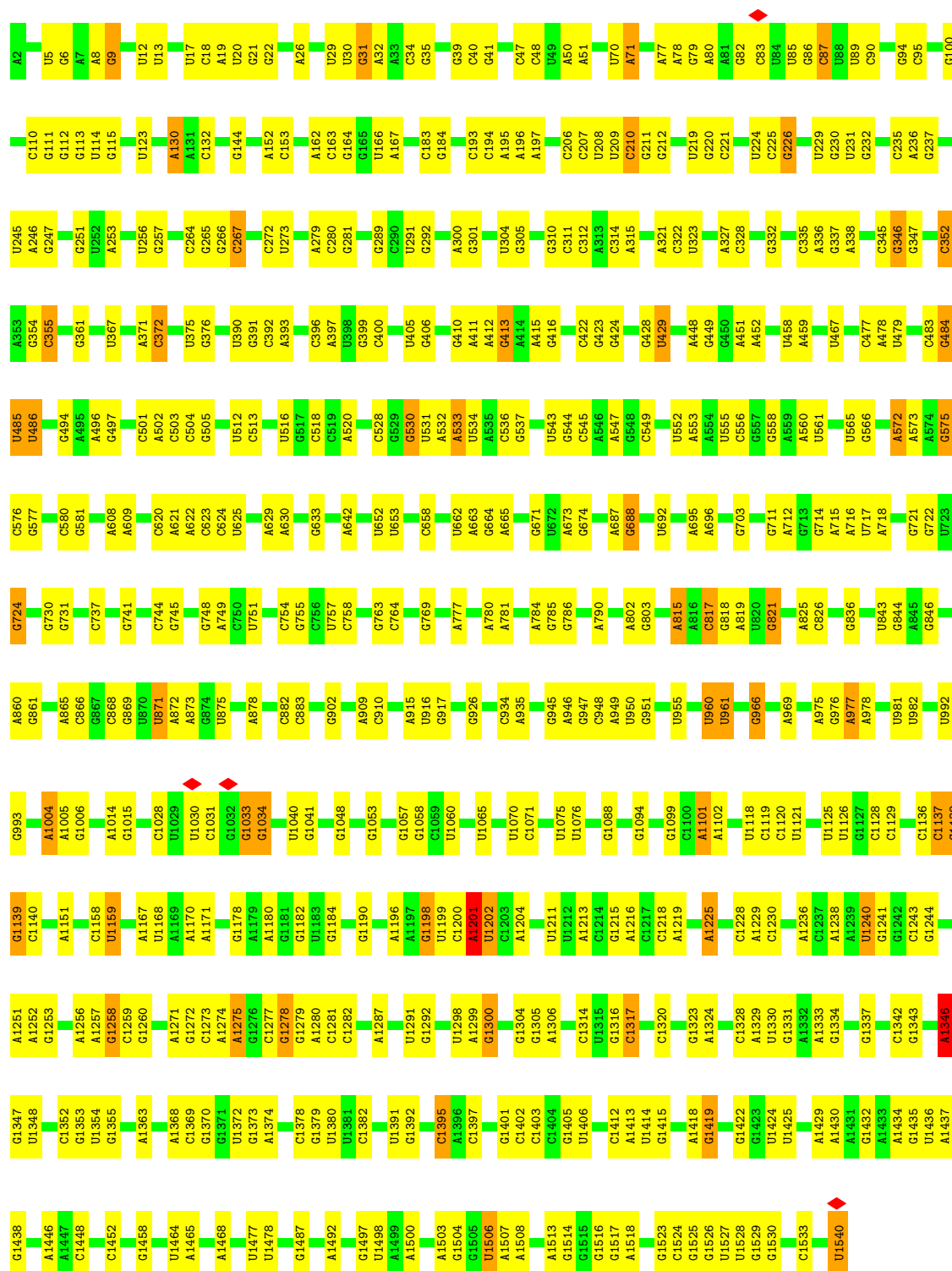
- Molecule 49: 30S ribosomal protein S20

- Molecule 50: 30S ribosomal protein S21

- Molecule 51: 50S ribosomal protein L1

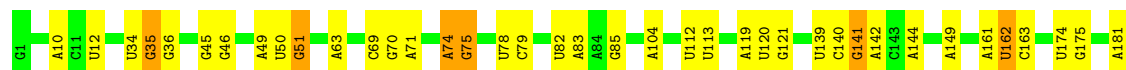
- Molecule 52: 16S ribosomal RNA



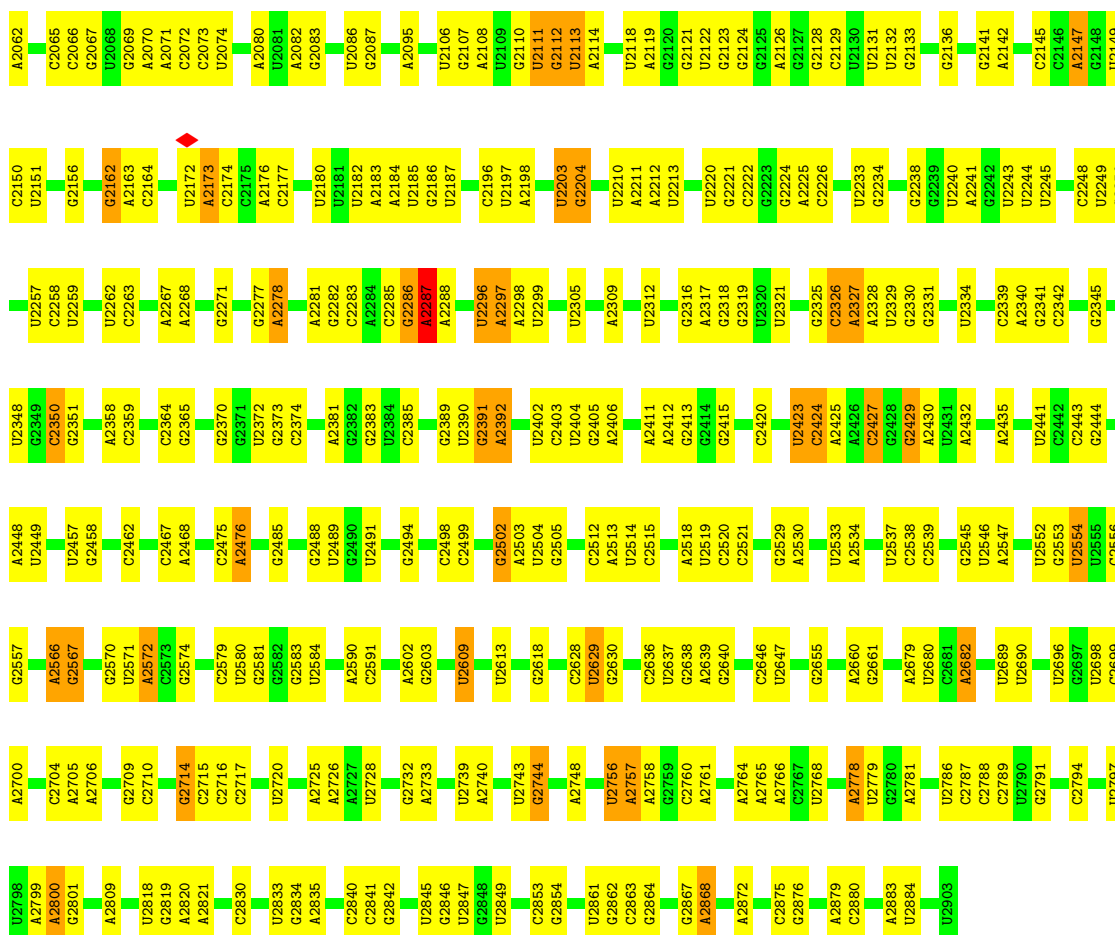


• Molecule 53: 23S ribosomal RNA

Chain 1: .

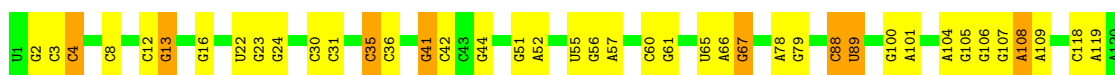


U1943	G1816	G1715	A1569	G1430	G1300	G1138	G1056	G942	U807	U688	U573	G467	A311	G189
U1944	U1818	G1720	A1570	A1431	A1301	G1139	A1057	C946	G808	C692	A574	G468	G312	A190
U1955	U1827	G1721	A1571	G1432	A1302	G1140	U1058	A947	G809	A693	U575	G469	C323	A191
U1956	G1828	U1729	G1581	A1433	C1306	U1141	G1059	C948	U810	U694	U576	G473	G329	C192
C1957	A1829	C1730	U1584	A1434	A1307	U1142	U1060	G949	C812	G695	G577	G474	A330	U193
U1963	G1830	G1731	U1584	G1435	A1308	A1143	U1061	C957	A819	A699	G579	A477	A331	A196
G1964	G1831	G1732	A1603	U1437	A1309	C1152	U1065	C961	A820	G700	U580	A478	C340	A197
C1965	C1837	A1735	A1603	U1438	C1320	G1153	U1066	G962	G822	U703	C581	G481	C341	C198
A1966	G1846	U1736	C1606	G1444	A1321	A1155	A1070	C967	U827	G704	G585	G482	A342	A199
C1967	A1847	U1739	C1607	G1445	U1326	A1156	G1071	C968	U828	G713	U588	C490	G205	G205
A1970	U1856	G1740	A1608	C1454	A1327	A1175	G1072	C969	A829	G491	U589	C491	G361	U206
U1971	G1857	A1744	A1609	U1461	U1328	U1176	A1073	G971	G830	G494	A590	G494	A362	A207
G1972	A1858	A1745	C1611	C1461	U1329	G1177	G1074	A972	G831	U499	G578	U499	G363	C208
U1979	U1859	U1468	A1614	U1468	G1331	C1178	A1077	A973	U832	G723	G579	A503	A371	G215
G1980	G1860	G1763	C1615	U1475	G1332	G1179	C1078	G974	A833	G725	C595	A504	G372	A216
U1991	A1871	A1754	A1616	U1476	U1344	U1180	C1079	A975	G834	G726	U594	A505	G386	A221
G1992	G1872	U1758	C1625	U1476	U1345	U1183	A1080	A979	A845	A727	U598	A505	U387	A222
U1993	G1873	A1759	A1626	G1482	C1345	G1186	U1081	C982	U846	G728	A599	G512	G396	U224
C1996	C1874	C1760	A1637	U1490	U1352	U1188	U1082	A983	U847	G729	A603	G512	U395	C225
C1997	G1875	G1761	G1642	A1491	A1353	U1189	A1083	C987	G858	C740	A613	A528	A404	A226
G2004	A1876	A1762	G1643	G1491	G1354	A1189	A1084	A988	G859	U741	A614	A529	U405	A227
A2005	G1877	C1764	G1644	C1498	G1355	G1190	A1085	G989	U860	U742	A616	G530	G406	C228
G2010	G1878	C1764	G1644	C1498	G1356	G1191	A1088	C995	A861	A743	G617	C531	G230	C229
U2011	A1884	A1773	G1645	C1507	C1357	G1210	G1092	A996	G864	C747	A627	A532	G411	A231
G2012	A1885	G1774	C1646	A1508	A1358	C1211	G1093	A997	C865	G628	G629	U534	C414	G242
A2019	A1889	G1776	U1647	A1509	G1360	G1212	A1095	G997	G865	A752	G629	G535	A415	G248
A2020	A1890	U1779	U1648	G1510	G1361	A1213	A1096	C1005	C873	G760	A637	A538	C420	C249
C2021	G1893	A1780	G1651	A1515	A1365	G1236	U1097	C1006	G874	U762	G638	C542	G254	G254
C2022	C1894	A1784	U1657	A1522	A1366	G1239	C1102	C1007	A878	G763	U639	G544	A256	A256
C2023	A1899	A1785	C1658	U1523	A1367	U1240	A1103	U1012	C885	A764	C640	C544	C433	A265
G2029	A1900	A1786	U1662	G1524	G1368	C1251	U1105	U1013	A886	U545	A644	U545	U434	A266
A2031	A1901	G1790	G1663	A1525	C1370	G1252	G1106	U1019	U887	G770	U646	A547	C435	G266
G2032	C1902	A1791	A1664	A1528	G1371	A1253	G1107	A1021	C888	C772	U646	G548	C436	G275
C2035	G1905	G1674	G1674	G1529	A1373	G1256	G1110	G1022	C890	U773	C650	G549	U437	C276
C2036	G1906	A1794	A1678	A1535	A1378	C1257	A1111	U1023	G891	U554	A654	U554	G438	U276
A2042	G1907	C1795	A1679	C1536	A1379	U1258	G1112	U1023	A892	G555	C440	G439	G277	U277
C2043	A1913	U1796	U1680	G1537	A1383	G1268	U1113	G1026	C893	G555	U441	A439	A278	A278
G2048	G1929	G1798	G1681	U1539	U1394	A1269	C1114	A1027	U894	U779	A668	G442	U280	U280
C2049	G1930	C1800	G1685	G1540	U1405	C1270	G1115	A1028	U895	A782	G669	A443	C281	C281
G2055	U1931	A1801	C1686	G1545	U1406	A1271	G1122	U1033	A896	A783	A670	C444	G444	G444
C2056	A1932	G1807	A1701	G1555	U1405	A1272	G1125	C1045	A910	G785	G674	U448	U448	U290
A1933	G1933	A1808	G1702	U1559	U1415	C1278	U1130	A1046	A917	G799	A677	A457	A294	A294
G1935	C1934	A1809	G1703	G1560	G1416	G1279	U1132	G1047	A917	A800	G682	C564	G458	G458
A1936	G1935	A1810	C1704	C1564	C1419	C1289	U1133	C1053	U932	G805	U686	C565	U459	U459
A1937	A1937	G1811	A1705	C1565	A1419	C1289	A1134	A1054	U932	G805	U686	C565	U459	U459
A1938	A1938			A1566	A1420	C1287	C1135	G1055	A941	C806	C687	U571	G301	G301



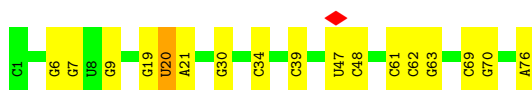
- Molecule 54: 5S ribosomal RNA

Chain 2: 66% 28% 7%



- Molecule 55: tRNAfMet

Chain 5: 78% 21%

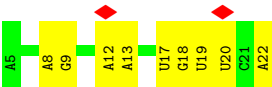


- Molecule 55: tRNAfMet

Chain 6: 62% 34%



- Molecule 56: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	115115	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	27.527	Depositor
Minimum map value	-12.932	Depositor
Average map value	0.110	Depositor
Map value standard deviation	1.011	Depositor
Recommended contour level	1	Depositor
Map size (Å)	383.904, 383.904, 383.904	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.333, 1.333, 1.333	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	b	0.30	0/2122	0.91	6/2852 (0.2%)
2	c	0.28	0/1586	0.80	0/2134
3	d	0.28	0/1571	0.81	1/2113 (0.0%)
4	e	0.29	0/1435	0.91	5/1926 (0.3%)
5	f	0.29	0/1343	0.87	2/1816 (0.1%)
6	g	0.33	0/1122	1.11	10/1515 (0.7%)
7	h	0.35	0/1002	1.15	11/1350 (0.8%)
8	i	0.37	0/1046	0.98	6/1410 (0.4%)
9	j	0.28	0/1152	0.79	0/1551
10	k	0.28	0/948	0.89	1/1268 (0.1%)
11	l	0.30	0/1054	0.95	4/1403 (0.3%)
12	m	0.29	0/1093	0.76	0/1460
13	n	0.29	0/974	0.92	4/1301 (0.3%)
14	o	0.29	0/902	0.85	3/1209 (0.2%)
15	p	0.29	0/929	0.79	1/1242 (0.1%)
16	q	0.30	0/960	0.86	2/1278 (0.2%)
17	r	0.28	0/829	0.81	0/1107
18	s	0.27	0/864	0.89	1/1156 (0.1%)
19	t	0.28	0/745	0.82	1/994 (0.1%)
20	u	0.29	0/788	0.88	1/1051 (0.1%)
21	v	0.29	0/766	0.83	1/1025 (0.1%)
22	w	0.26	0/582	0.73	0/769
23	x	0.29	0/635	0.85	0/848
24	y	0.28	0/510	0.90	1/677 (0.1%)
25	z	0.28	0/453	0.79	1/605 (0.2%)
26	B	0.27	0/450	0.80	0/599
27	C	0.33	0/417	0.81	0/554
28	D	0.32	0/380	0.93	1/498 (0.2%)
29	E	0.28	0/513	0.83	0/676
30	F	0.32	0/303	0.86	0/397
31	G	0.29	0/1788	0.93	5/2408 (0.2%)
32	H	0.31	0/1652	0.88	5/2225 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.31	0/1665	0.99	7/2227 (0.3%)
34	J	0.33	0/1170	0.96	7/1573 (0.4%)
35	K	0.31	0/836	0.85	1/1128 (0.1%)
36	L	0.29	0/1196	0.90	3/1602 (0.2%)
37	M	0.30	0/989	0.92	1/1326 (0.1%)
38	N	0.32	0/1034	0.96	4/1375 (0.3%)
39	O	0.35	0/797	0.89	5/1077 (0.5%)
40	P	0.30	0/886	0.90	2/1195 (0.2%)
41	Q	0.32	0/969	0.97	6/1300 (0.5%)
42	R	0.31	0/893	0.91	2/1193 (0.2%)
43	S	0.30	0/817	0.93	3/1088 (0.3%)
44	T	0.29	0/722	0.87	4/964 (0.4%)
45	U	0.33	0/659	1.05	4/884 (0.5%)
46	V	0.28	0/658	0.89	1/881 (0.1%)
47	W	0.31	0/545	0.83	2/731 (0.3%)
48	X	0.33	0/653	0.96	5/877 (0.6%)
49	Y	0.30	0/671	0.89	2/888 (0.2%)
50	Z	0.34	0/551	1.10	6/728 (0.8%)
51	a	0.34	0/1034	1.01	10/1387 (0.7%)
52	3	0.41	0/36963	0.51	3/57662 (0.0%)
53	1	0.39	0/69796	0.51	4/108888 (0.0%)
54	2	0.40	0/2872	0.50	0/4479
55	5	0.40	0/1832	0.47	0/2855
55	6	0.41	0/1832	0.52	0/2855
56	4	0.43	0/436	0.50	0/679
All	All	0.37	0/161390	0.64	155/241259 (0.1%)

There are no bond length outliers.

All (155) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	I	9	LYS	N-CA-C	-11.47	97.78	112.23
6	g	67	ALA	N-CA-C	-11.06	98.30	112.23
37	M	67	GLY	N-CA-C	-10.62	101.31	114.16
34	J	161	GLU	N-CA-C	8.48	120.14	111.07
51	a	178	VAL	N-CA-C	8.25	118.34	110.42
32	H	34	SER	N-CA-C	-8.23	102.69	112.89
6	g	59	ALA	N-CA-C	-8.01	102.96	112.89
1	b	213	ARG	N-CA-C	-7.78	103.77	113.18
7	h	50	VAL	N-CA-C	7.75	119.80	111.58
44	T	43	ALA	N-CA-C	-7.74	102.78	111.14
50	Z	31	VAL	N-CA-C	-7.69	105.06	112.29

Continued on next page...

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	h	42	ARG	N-CA-C	-7.69	103.70	113.23
4	e	148	VAL	N-CA-C	-7.66	105.10	111.91
36	L	116	ALA	N-CA-C	-7.59	102.94	111.14
21	v	80	HIS	N-CA-C	-7.49	100.64	109.93
33	I	7	LYS	N-CA-C	7.44	120.26	111.71
43	S	30	ILE	N-CA-C	-7.34	104.14	111.77
39	O	77	VAL	N-CA-C	7.33	117.85	110.23
45	U	36	VAL	N-CA-C	7.17	113.88	106.21
18	s	35	ILE	N-CA-C	-7.09	104.07	111.58
31	G	42	LEU	N-CA-C	7.09	119.01	111.28
34	J	160	VAL	N-CA-C	7.09	117.85	110.62
44	T	81	ILE	N-CA-C	7.08	117.84	110.62
7	h	118	ILE	CA-C-N	-7.00	111.10	119.84
7	h	118	ILE	C-N-CA	-7.00	111.10	119.84
8	i	78	LEU	N-CA-C	-6.87	103.86	111.82
4	e	170	ALA	N-CA-C	-6.86	103.59	112.23
41	Q	114	SER	N-CA-C	-6.79	103.94	111.82
47	W	69	TYR	N-CA-C	-6.67	103.82	112.23
45	U	72	ALA	N-CA-C	-6.60	104.16	111.36
31	G	91	VAL	N-CA-C	-6.58	99.67	108.35
20	u	89	GLY	N-CA-C	-6.55	104.42	115.62
51	a	55	SER	N-CA-C	6.51	119.20	111.71
6	g	10	ALA	N-CA-C	6.51	120.68	112.87
50	Z	58	LYS	N-CA-C	-6.49	104.06	112.23
6	g	117	LEU	CA-C-N	6.46	125.69	118.97
6	g	117	LEU	C-N-CA	6.46	125.69	118.97
7	h	100	ALA	N-CA-C	-6.43	104.19	111.14
43	S	50	LEU	N-CA-C	-6.43	101.96	109.93
53	1	1130	U	C2'-C3'-O3'	6.41	119.11	109.50
6	g	72	ILE	N-CA-C	-6.36	103.14	111.09
6	g	68	ARG	N-CA-C	-6.29	104.50	111.36
48	X	40	PHE	CA-C-N	6.28	127.69	119.84
48	X	40	PHE	C-N-CA	6.28	127.69	119.84
51	a	195	ALA	N-CA-C	-6.28	105.11	112.89
38	N	87	MET	N-CA-C	-6.26	104.70	112.90
7	h	43	LYS	N-CA-C	-6.24	104.58	111.82
41	Q	43	LYS	N-CA-C	6.23	123.58	109.81
41	Q	88	ASP	N-CA-C	-6.16	107.60	114.62
32	H	67	ILE	N-CA-C	6.14	117.42	108.58
6	g	5	LEU	N-CA-C	6.14	118.83	110.55
19	t	89	GLU	N-CA-C	6.10	118.43	111.11
31	G	139	GLU	N-CA-C	-6.07	105.70	113.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	i	24	GLY	CA-C-N	6.07	127.42	119.84
8	i	24	GLY	C-N-CA	6.07	127.42	119.84
7	h	65	GLU	N-CA-C	-6.06	105.85	113.18
48	X	63	ASP	N-CA-C	6.05	118.84	111.82
6	g	63	ALA	N-CA-C	-6.04	104.61	112.23
51	a	197	LYS	N-CA-C	-6.03	104.70	111.28
45	U	80	LYS	N-CA-C	-6.01	105.91	113.72
31	G	127	LYS	N-CA-C	-6.00	106.95	114.56
7	h	123	ILE	N-CA-C	5.97	117.43	109.37
40	P	69	CYS	N-CA-C	-5.97	106.16	113.50
25	z	56	VAL	N-CA-C	5.96	117.18	108.53
14	o	116	GLN	N-CA-C	5.96	117.90	108.67
16	q	49	ARG	N-CA-C	-5.95	106.02	113.28
5	f	47	ASN	N-CA-C	-5.94	105.87	113.23
52	3	1201	A	C2'-C3'-O3'	5.94	118.41	109.50
1	b	12	ARG	N-CA-C	-5.93	105.36	113.30
32	H	5	HIS	CA-C-N	5.91	126.06	119.32
32	H	5	HIS	C-N-CA	5.91	126.06	119.32
44	T	80	LEU	N-CA-C	5.87	117.35	111.07
7	h	117	LEU	N-CA-C	5.82	117.81	109.14
32	H	56	ILE	N-CA-C	5.81	116.96	108.53
11	l	95	LEU	N-CA-C	-5.79	105.05	111.36
13	n	79	LEU	N-CA-C	-5.78	102.75	110.55
14	o	62	LEU	N-CA-C	5.75	118.60	110.14
3	d	73	ILE	N-CA-C	-5.74	106.20	112.80
33	I	31	CYS	N-CA-C	-5.74	106.08	114.39
8	i	36	GLU	N-CA-C	-5.67	105.24	111.82
34	J	101	GLY	N-CA-C	-5.67	106.71	115.73
36	L	67	ASN	N-CA-C	-5.63	106.57	113.50
16	q	37	ALA	N-CA-C	-5.60	105.09	111.14
34	J	145	ASN	N-CA-C	-5.59	105.67	112.88
50	Z	8	ASN	N-CA-C	5.59	122.70	110.80
42	R	113	LYS	N-CA-C	5.55	122.08	109.81
13	n	67	PHE	N-CA-C	-5.55	107.06	113.88
33	I	166	LYS	CA-C-N	5.50	125.50	119.89
33	I	166	LYS	C-N-CA	5.50	125.50	119.89
48	X	9	PHE	N-CA-C	5.50	117.66	109.25
51	a	184	LYS	N-CA-C	5.49	117.69	111.11
40	P	70	ALA	N-CA-C	-5.48	105.39	111.36
50	Z	49	ALA	N-CA-C	-5.48	105.39	111.36
42	R	3	ILE	N-CA-C	5.43	116.73	108.80
44	T	4	THR	N-CA-C	5.43	117.90	111.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	e	10	GLU	N-CA-C	5.43	117.06	111.03
7	h	119	PRO	N-CA-C	-5.43	101.29	112.47
45	U	76	LYS	N-CA-C	-5.43	105.79	112.90
51	a	194	VAL	N-CA-C	-5.40	105.67	113.07
33	I	19	PHE	N-CA-C	5.39	119.44	112.86
14	o	20	GLU	N-CA-C	-5.37	105.46	112.23
8	i	127	SER	N-CA-C	-5.36	105.48	112.23
51	a	59	VAL	N-CA-C	5.36	116.49	109.21
48	X	35	ARG	N-CA-C	-5.32	106.29	112.89
41	Q	74	GLN	N-CA-C	5.31	116.57	107.28
7	h	44	ALA	N-CA-C	-5.31	105.67	111.82
1	b	207	ALA	N-CA-C	-5.29	105.68	111.82
24	y	17	GLU	N-CA-C	-5.29	105.60	111.36
38	N	6	TYR	N-CA-C	5.28	117.84	109.50
39	O	42	LEU	CA-C-N	5.28	126.44	119.84
39	O	42	LEU	C-N-CA	5.28	126.44	119.84
43	S	22	LYS	N-CA-C	-5.28	107.50	114.04
53	1	1020	A	C2'-C3'-O3'	5.28	117.42	109.50
36	L	140	VAL	N-CA-C	-5.27	105.39	110.72
11	l	97	ALA	N-CA-C	-5.27	106.35	112.89
34	J	122	VAL	N-CA-C	5.25	120.26	109.34
28	D	30	VAL	N-CA-C	-5.24	105.43	110.72
53	1	669	G	N9-C1'-C2'	5.23	119.85	112.00
38	N	57	VAL	N-CA-C	5.23	120.22	109.34
34	J	88	HIS	N-CA-C	5.22	116.08	107.20
49	Y	69	ASN	N-CA-C	-5.21	106.07	112.90
33	I	202	LEU	N-CA-C	5.19	117.61	111.33
34	J	55	VAL	CB-CA-C	-5.18	108.86	114.35
6	g	74	ALA	N-CA-C	-5.18	106.80	113.01
4	e	26	GLN	N-CA-C	-5.17	106.74	113.16
46	V	49	ASN	N-CA-C	5.16	121.80	110.80
47	W	66	LEU	N-CA-C	-5.15	107.00	113.28
15	p	100	ARG	N-CA-C	-5.14	106.51	112.89
50	Z	24	LYS	N-CA-C	5.11	121.69	110.80
49	Y	84	LYS	N-CA-C	-5.11	105.89	111.82
11	l	43	GLY	N-CA-C	-5.11	108.23	115.43
35	K	31	GLY	N-CA-C	-5.10	107.99	114.16
31	G	49	PHE	N-CA-C	-5.09	105.81	111.36
38	N	105	ARG	N-CA-C	-5.09	106.58	112.89
52	3	1300	G	N9-C1'-C2'	5.09	119.64	112.00
4	e	52	ALA	N-CA-C	-5.09	105.82	112.23
51	a	191	ALA	N-CA-C	5.08	116.63	111.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	Q	99	GLY	N-CA-C	-5.06	108.13	115.27
53	1	2287	A	N9-C1'-C2'	5.06	119.59	112.00
52	3	1346	A	N9-C1'-C2'	5.06	119.59	112.00
50	Z	44	ARG	N-CA-C	-5.05	105.23	111.40
1	b	11	GLY	N-CA-C	-5.04	107.89	113.79
41	Q	115	LYS	N-CA-C	-5.04	102.31	110.32
39	O	40	ILE	CA-C-N	5.04	126.13	119.84
39	O	40	ILE	C-N-CA	5.04	126.13	119.84
1	b	204	LEU	N-CA-C	5.03	116.77	111.28
51	a	200	LYS	CA-C-N	5.03	124.97	119.78
51	a	200	LYS	C-N-CA	5.03	124.97	119.78
13	n	119	SER	N-CA-C	-5.03	104.66	111.55
1	b	237	ARG	N-CA-C	5.02	117.30	111.02
10	k	32	TYR	N-CA-C	5.02	117.18	109.95
8	i	97	VAL	N-CA-C	5.02	115.63	110.36
13	n	54	LEU	N-CA-C	-5.01	106.68	112.89
11	l	98	ALA	N-CA-C	-5.01	106.76	112.92
5	f	58	ALA	N-CA-C	5.00	116.54	111.14

There are no chirality outliers.

There are no planarity outliers.

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	b	2083	0	2157	35	0
2	c	1565	0	1616	16	0
3	d	1552	0	1619	24	0
4	e	1411	0	1447	29	0
5	f	1323	0	1374	25	0
6	g	1111	0	1148	48	0
7	h	989	0	1025	47	0
8	i	1032	0	1088	42	0
9	j	1129	0	1162	29	0
10	k	939	0	1012	20	0
11	l	1045	0	1117	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	m	1074	0	1157	12	0
13	n	961	0	1000	27	0
14	o	892	0	923	11	0
15	p	917	0	965	19	0
16	q	947	0	1022	15	0
17	r	816	0	839	26	0
18	s	857	0	922	25	0
19	t	739	0	807	23	0
20	u	780	0	834	21	0
21	v	753	0	780	13	0
22	w	575	0	592	5	0
23	x	625	0	655	8	0
24	y	509	0	543	19	0
25	z	449	0	491	10	0
26	B	444	0	461	6	0
27	C	410	0	440	8	0
28	D	377	0	418	11	0
29	E	504	0	574	9	0
30	F	302	0	343	12	0
31	G	1757	0	1787	29	0
32	H	1625	0	1699	44	0
33	I	1643	0	1710	52	0
34	J	1157	0	1199	35	0
35	K	818	0	808	39	0
36	L	1182	0	1240	26	0
37	M	979	0	1034	33	0
38	N	1022	0	1070	35	0
39	O	787	0	828	31	0
40	P	870	0	878	35	0
41	Q	955	0	1019	39	0
42	R	884	0	944	30	0
43	S	805	0	847	25	0
44	T	714	0	737	9	0
45	U	649	0	666	22	0
46	V	649	0	691	16	0
47	W	536	0	552	6	0
48	X	638	0	665	17	0
49	Y	665	0	714	25	0
50	Z	545	0	579	34	0
51	a	1027	0	1092	42	0
52	3	33012	0	16618	347	0
53	1	62317	0	31346	579	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
54	2	2568	0	1303	31	0
55	5	1640	0	836	8	0
55	6	1640	0	837	17	0
56	4	388	0	196	5	0
57	5	10	0	10	0	0
All	All	148592	0	100436	1975	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 8.

All (1975) 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)
40:P:118:ASN:HD21	52:3:718:A:H5'	1.00	1.12
53:1:45:G:H5''	53:1:46:G:H5'	1.31	1.12
52:3:405:U:H3'	52:3:406:G:H5'	1.42	1.01
53:1:821:A:H5''	53:1:822:G:H5''	1.41	1.01
53:1:1906:G:H2'	53:1:1907:G:H5''	1.44	0.98
10:k:35:VAL:HG21	10:k:69:VAL:HG22	1.43	0.98
40:P:118:ASN:ND2	52:3:718:A:H5'	1.76	0.98
40:P:118:ASN:HD21	52:3:718:A:C5'	1.79	0.96
34:J:107:GLY:HA3	52:3:9:G:H5'	1.48	0.93
52:3:484:G:H4'	52:3:485:U:H5''	1.51	0.93
38:N:83:THR:HG21	38:N:102:PHE:HB3	1.54	0.89
8:i:123:ALA:HB1	53:1:1081:U:H4'	1.55	0.87
45:U:5:ARG:HB2	52:3:376:G:H5''	1.55	0.87
10:k:110:GLU:H	10:k:113:MET:HE2	1.40	0.86
12:m:12:MET:HA	53:1:910:A:H62	1.41	0.86
8:i:12:VAL:HG12	8:i:13:ALA:H	1.41	0.85
6:g:8:LYS:O	6:g:9:VAL:HG22	1.76	0.85
19:t:1:MET:HG3	19:t:2:ILE:HD12	1.58	0.85
21:v:20:LEU:HD11	21:v:41:GLU:HG3	1.56	0.85
35:K:3:HIS:H	35:K:92:THR:HG22	1.40	0.84
42:R:113:LYS:HG3	42:R:114:PRO:HD3	1.58	0.84
4:e:84:ILE:HD11	53:1:2312:U:H5'	1.59	0.84
40:P:124:LYS:HE3	52:3:780:A:H5''	1.60	0.83
1:b:106:PRO:HD2	1:b:109:LEU:HD22	1.60	0.83
53:1:2286:G:H5''	53:1:2287:A:OP1	1.80	0.82
8:i:25:PRO:HB2	53:1:1095:A:H61	1.45	0.82
36:L:115:MET:HA	36:L:118:ARG:HB2	1.62	0.81
54:2:13:G:H21	54:2:16:G:H1'	1.45	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:858:G:H5'	53:1:859:G:OP2	1.79	0.81
20:u:85:ARG:HD3	20:u:87:GLU:HG3	1.63	0.81
51:a:27:ILE:HD13	51:a:182:ALA:HA	1.64	0.80
53:1:275:C:H2'	53:1:276:U:H4'	1.64	0.79
2:c:151:THR:HB	2:c:152:PRO:HD3	1.65	0.79
9:j:81:ILE:HG23	9:j:82:GLY:H	1.47	0.79
55:6:13:C:H2'	55:6:14:A:H5''	1.62	0.79
50:Z:9:GLU:HG3	50:Z:10:PRO:HD3	1.62	0.79
16:q:108:LEU:HA	17:r:48:LYS:HE2	1.65	0.78
40:P:124:LYS:HE2	52:3:1523:G:H5''	1.65	0.78
40:P:126:ARG:HB3	50:Z:33:ARG:HH11	1.48	0.78
53:1:542:C:H2'	53:1:543:G:H5''	1.65	0.78
31:G:66:ILE:HG22	31:G:159:ALA:HB3	1.64	0.78
53:1:1053:C:H2'	53:1:1054:A:H5''	1.65	0.78
8:i:74:PRO:HB2	8:i:77:VAL:HG22	1.64	0.78
53:1:2277:G:H2'	53:1:2278:A:H5''	1.66	0.78
10:k:121:GLU:HG2	10:k:122:VAL:HG23	1.65	0.77
36:L:56:SER:HB3	36:L:59:GLU:HG2	1.66	0.77
1:b:153:LEU:HD13	1:b:175:LEU:HD21	1.65	0.77
9:j:26:GLY:HA3	53:1:1140:C:H5'	1.67	0.76
6:g:58:LEU:O	6:g:61:VAL:HG22	1.85	0.76
53:1:1906:G:C2'	53:1:1907:G:H5''	2.16	0.76
5:f:163:TYR:HB2	5:f:166:GLU:HB2	1.66	0.76
53:1:1020:A:H1'	53:1:1021:A:OP2	1.86	0.76
52:3:208:U:H2'	52:3:210:C:H1'	1.66	0.76
53:1:2267:A:H5''	53:1:2268:A:H5'	1.68	0.75
7:h:17:GLU:HG3	7:h:53:ARG:HD2	1.67	0.75
38:N:91:GLU:HA	38:N:94:ARG:HB2	1.69	0.75
36:L:78:ARG:NH1	52:3:1382:C:H4'	2.01	0.75
52:3:1201:A:H1'	52:3:1202:U:OP2	1.86	0.74
53:1:1936:A:H2	53:1:1943:U:H3	1.35	0.74
52:3:769:G:H4'	52:3:1513:A:H4'	1.70	0.74
30:F:1:MET:HE2	30:F:36:ARG:HB2	1.67	0.74
38:N:98:ARG:HD2	38:N:103:VAL:HG21	1.69	0.73
20:u:6:ARG:O	20:u:24:VAL:HG13	1.88	0.73
29:E:33:THR:HG23	53:1:2420:C:OP1	1.88	0.73
34:J:108:GLY:H	52:3:9:G:H4'	1.52	0.73
53:1:546:U:H2'	53:1:547:A:H4'	1.69	0.73
13:n:44:LEU:HD23	13:n:113:ILE:HD13	1.70	0.73
41:Q:23:LEU:HD22	41:Q:29:LYS:HZ3	1.53	0.73
33:I:195:ASN:HD21	33:I:197:HIS:HB3	1.53	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:121:G:H4'	53:1:149:A:H5'	1.71	0.72
6:g:55:GLU:HA	6:g:58:LEU:HG	1.69	0.72
44:T:71:ARG:HH22	52:3:754:C:H5'	1.52	0.72
51:a:12:ARG:HH22	53:1:2106:U:H5''	1.52	0.72
31:G:69:VAL:HG12	31:G:91:VAL:HG22	1.72	0.72
37:M:6:ILE:HD11	37:M:35:ILE:HD12	1.70	0.72
41:Q:109:ARG:HB2	41:Q:118:VAL:HG21	1.71	0.72
6:g:65:ALA:O	6:g:68:ARG:HB3	1.90	0.72
31:G:213:LEU:HA	31:G:216:VAL:HG22	1.71	0.72
36:L:78:ARG:HH11	52:3:1382:C:H4'	1.54	0.72
41:Q:23:LEU:HD22	41:Q:29:LYS:HD3	1.72	0.72
52:3:664:G:H22	52:3:741:G:H1	1.36	0.72
42:R:16:ILE:H	42:R:16:ILE:HD12	1.54	0.71
33:I:18:LEU:HD23	33:I:18:LEU:H	1.56	0.71
52:3:1306:A:N6	52:3:1331:G:H1'	2.06	0.70
53:1:1900:A:H1'	53:1:1970:A:H2'	1.73	0.70
53:1:2287:A:O2'	53:1:2288:A:H2'	1.91	0.70
45:U:78:VAL:O	45:U:79:ASN:HB2	1.90	0.70
7:h:55:VAL:HA	53:1:1084:A:H4'	1.72	0.70
6:g:73:ASN:O	6:g:76:GLU:HG3	1.92	0.69
8:i:25:PRO:HB2	53:1:1095:A:N6	2.06	0.69
51:a:54:LYS:NZ	55:6:63:G:H4'	2.07	0.69
22:w:39:THR:H	53:1:2331:G:H4'	1.56	0.69
6:g:9:VAL:CG2	6:g:13:GLY:H	2.06	0.69
26:B:54:ILE:HG23	26:B:56:LYS:H	1.56	0.69
38:N:54:VAL:HG12	38:N:55:ASP:H	1.57	0.69
52:3:352:C:H4'	52:3:354:G:OP1	1.93	0.69
40:P:23:HIS:HB3	40:P:30:ILE:HG13	1.74	0.69
32:H:1:GLY:HA3	52:3:1060:U:H5	1.57	0.69
53:1:2296:U:H5''	53:1:2297:A:OP1	1.92	0.68
37:M:10:LEU:HB3	37:M:74:ILE:HG21	1.74	0.68
6:g:96:THR:HG23	6:g:112:LYS:HE3	1.76	0.68
33:I:57:LYS:HD3	33:I:202:LEU:HD23	1.75	0.68
33:I:98:ASP:HB3	33:I:132:ALA:HB1	1.75	0.68
54:2:3:C:H3'	54:2:4:C:H5''	1.74	0.68
53:1:1133:A:H4'	53:1:1134:A:H5''	1.76	0.68
16:q:36:GLN:HA	16:q:39:ILE:HG12	1.76	0.68
18:s:42:LYS:HB2	53:1:2010:G:H5''	1.74	0.68
7:h:6:GLN:O	7:h:9:GLN:HG3	1.92	0.68
14:o:29:HIS:HB3	14:o:36:TYR:HB2	1.75	0.68
53:1:704:G:H2'	53:1:726:G:H22	1.58	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1394:U:H4'	53:1:1603:A:H4'	1.74	0.68
6:g:66:ASN:HD21	6:g:135:HIS:CD2	2.12	0.67
52:3:960:U:H4'	52:3:961:U:O5'	1.92	0.67
53:1:1077:A:H2'	53:1:1078:U:H5'	1.76	0.67
32:H:55:VAL:HG13	32:H:66:THR:HG23	1.77	0.67
45:U:33:ILE:HG22	45:U:34:GLU:HG3	1.76	0.67
53:1:1807:G:H2'	53:1:1808:A:H5'	1.76	0.67
53:1:215:G:H4'	53:1:216:A:H4'	1.76	0.67
6:g:84:ALA:HB2	6:g:90:LEU:HD23	1.77	0.66
49:Y:34:VAL:HG11	49:Y:78:LEU:HD21	1.75	0.66
10:k:63:VAL:HG12	10:k:107:LEU:HD21	1.75	0.66
33:I:195:ASN:ND2	33:I:197:HIS:HB3	2.11	0.66
53:1:2136:G:H22	53:1:2156:G:H1'	1.61	0.66
21:v:9:ARG:HG2	21:v:41:GLU:HB2	1.77	0.66
5:f:96:ALA:HB3	5:f:103:ASN:HB3	1.77	0.66
20:u:48:VAL:HG22	20:u:50:ALA:H	1.59	0.66
30:F:36:ARG:O	30:F:37:GLN:HB2	1.96	0.66
50:Z:9:GLU:CG	50:Z:10:PRO:HD3	2.25	0.66
41:Q:24:GLU:H	41:Q:24:GLU:CD	2.03	0.66
37:M:28:SER:OG	37:M:56:PRO:HB2	1.96	0.66
52:3:1418:A:H3'	52:3:1419:G:H5''	1.78	0.66
53:1:687:C:H6	53:1:687:C:H5'	1.59	0.66
16:q:5:ARG:NH1	53:1:585:G:N7	2.44	0.66
3:d:190:ALA:O	3:d:193:VAL:HG12	1.96	0.66
35:K:50:PRO:HG3	35:K:55:HIS:CE1	2.31	0.66
51:a:206:GLY:HA2	53:1:1860:G:H5''	1.78	0.66
6:g:66:ASN:HD21	6:g:135:HIS:HD2	1.41	0.65
34:J:104:ILE:H	34:J:104:ILE:HD12	1.60	0.65
7:h:81:LEU:H	7:h:81:LEU:HD12	1.61	0.65
39:O:59:LYS:HE2	39:O:62:ARG:HH22	1.61	0.65
27:C:34:GLU:HB3	27:C:47:ILE:HD11	1.77	0.65
42:R:64:VAL:HG12	42:R:65:GLU:H	1.61	0.65
49:Y:23:ARG:O	49:Y:26:MET:HG3	1.96	0.65
52:3:1137:C:H5'	52:3:1138:G:H5'	1.79	0.65
4:e:92:GLY:O	4:e:95:MET:HG3	1.96	0.65
8:i:9:LYS:NZ	53:1:1060:U:H5''	2.12	0.65
27:C:41:VAL:HG13	27:C:42:VAL:HG23	1.79	0.65
35:K:67:PRO:HG2	35:K:70:VAL:HG23	1.78	0.65
48:X:15:LEU:HA	48:X:18:VAL:HG12	1.79	0.65
33:I:97:LEU:HA	33:I:100:VAL:HG12	1.80	0.64
54:2:88:C:H4'	54:2:89:U:OP1	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:r:54:VAL:HG12	17:r:55:ASP:OD1	1.98	0.64
20:u:42:LYS:HE2	53:1:499:U:H5''	1.78	0.64
31:G:75:ALA:HB1	31:G:79:VAL:HG23	1.79	0.64
53:1:1141:U:H4'	53:1:1142:A:O4'	1.96	0.64
4:e:131:VAL:HG21	4:e:136:ILE:HD13	1.80	0.64
16:q:50:ARG:HG2	53:1:1156:A:C8	2.33	0.64
35:K:76:THR:HA	35:K:79:ARG:HD2	1.79	0.64
49:Y:26:MET:HB3	52:3:1458:G:H5'	1.78	0.64
35:K:96:VAL:HG22	35:K:97:THR:H	1.63	0.64
16:q:106:THR:O	16:q:109:VAL:HG12	1.98	0.64
13:n:45:ARG:HG2	13:n:95:THR:HG21	1.79	0.64
35:K:21:MET:HG2	35:K:24:ARG:HH22	1.62	0.64
54:2:3:C:C3'	54:2:4:C:H5''	2.28	0.64
52:3:327:A:O2'	52:3:328:C:H4'	1.98	0.63
49:Y:4:LYS:HD3	52:3:332:G:OP1	1.98	0.63
51:a:181:ASP:HB3	51:a:184:LYS:HD3	1.79	0.63
35:K:5:GLU:HA	35:K:63:ASN:HA	1.80	0.63
53:1:2277:G:C2'	53:1:2278:A:H5''	2.27	0.63
32:H:29:ALA:O	32:H:32:LEU:HD23	1.99	0.63
51:a:215:SER:HB2	51:a:221:GLY:HA2	1.81	0.63
8:i:93:ASN:OD1	53:1:1077:A:H5'	1.99	0.62
35:K:3:HIS:N	35:K:92:THR:HG22	2.13	0.62
41:Q:32:VAL:HG12	41:Q:55:ARG:HB3	1.81	0.62
53:1:783:A:H2'	53:1:784:G:H5'	1.81	0.62
53:1:1019:U:H3	53:1:1142:A:H62	1.47	0.62
53:1:2423:U:O2'	53:1:2425:A:H2'	1.99	0.62
13:n:2:ARG:HG2	13:n:2:ARG:O	1.98	0.62
19:t:8:LEU:HD13	24:y:21:LEU:HB3	1.81	0.62
52:3:1306:A:H61	52:3:1331:G:H1'	1.61	0.62
53:1:2682:A:H61	53:1:2728:U:H1'	1.63	0.62
10:k:110:GLU:HA	10:k:113:MET:HG2	1.80	0.62
31:G:46:VAL:HG23	31:G:47:PRO:HD3	1.82	0.62
51:a:3:LYS:HE3	53:1:2107:G:H3'	1.81	0.62
33:I:58:GLN:O	33:I:62:ARG:HG2	2.00	0.62
50:Z:19:LYS:HG3	50:Z:24:LYS:HD2	1.82	0.62
52:3:1158:C:H2'	52:3:1159:U:H4'	1.82	0.62
8:i:30:GLN:HB2	8:i:32:VAL:HG23	1.81	0.62
9:j:27:ARG:NH2	53:1:1142:A:H4'	2.15	0.62
48:X:38:THR:HG22	48:X:39:ILE:H	1.65	0.62
52:3:1033:G:H2'	52:3:1034:G:H5''	1.82	0.62
52:3:1271:A:H5'	52:3:1314:C:H5''	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1373:A:C5'	53:1:2212:A:H1'	2.29	0.62
1:b:81:GLU:HG3	1:b:102:TYR:HE1	1.63	0.62
7:h:58:THR:HG21	7:h:82:ILE:HB	1.82	0.62
35:K:91:ARG:HG3	35:K:92:THR:H	1.65	0.62
37:M:100:ILE:HB	37:M:128:VAL:HG13	1.82	0.62
52:3:1198:G:H5'	52:3:1198:G:H8	1.65	0.61
53:1:1300:G:H4'	53:1:1301:A:C5'	2.30	0.61
25:z:4:ILE:HG13	25:z:58:GLU:HA	1.82	0.61
52:3:744:C:H2'	52:3:745:G:H8	1.64	0.61
15:p:51:ASN:C	15:p:52:ARG:HD2	2.26	0.61
39:O:56:HIS:ND1	39:O:57:VAL:HG23	2.14	0.61
45:U:6:LEU:HG	45:U:19:VAL:HG12	1.81	0.61
53:1:1110:G:H2'	53:1:1111:A:H8	1.66	0.61
39:O:5:ARG:HG2	39:O:79:PRO:HB3	1.81	0.61
1:b:48:ILE:HG22	53:1:779:U:OP1	2.00	0.61
6:g:117:LEU:HD23	6:g:117:LEU:H	1.65	0.61
8:i:71:LYS:HE2	53:1:1059:G:O5'	2.00	0.61
53:1:2277:G:C3'	53:1:2278:A:H5''	2.30	0.61
31:G:69:VAL:HG12	31:G:91:VAL:CG2	2.30	0.61
41:Q:49:ARG:HB2	41:Q:89:LEU:HD21	1.82	0.61
52:3:950:U:H2'	52:3:951:G:H8	1.66	0.61
13:n:53:THR:HG21	53:1:2840:C:H5''	1.82	0.61
52:3:405:U:C3'	52:3:406:G:H5'	2.26	0.61
53:1:542:C:C2'	53:1:543:G:H5''	2.31	0.61
7:h:33:VAL:HG12	53:1:1055:G:H5''	1.83	0.60
29:E:2:LYS:HG3	53:1:242:G:C8	2.35	0.60
51:a:4:LEU:HD21	51:a:9:ARG:HB2	1.84	0.60
41:Q:33:CYS:H	41:Q:54:VAL:HG23	1.65	0.60
8:i:27:LEU:HD13	8:i:34:ILE:HD13	1.83	0.60
29:E:61:LEU:HD12	29:E:64:ALA:HB3	1.83	0.60
44:T:28:VAL:HG23	44:T:62:ARG:HG3	1.83	0.60
53:1:1801:A:H5''	53:1:2203:U:H2'	1.82	0.60
53:1:310:A:C2'	53:1:311:A:H5''	2.31	0.60
53:1:2141:G:H22	53:1:2151:U:H1'	1.66	0.60
28:D:10:LEU:HD23	53:1:770:G:H5''	1.83	0.60
3:d:76:PRO:HA	3:d:82:GLY:CA	2.31	0.60
25:z:23:LEU:HD11	25:z:53:MET:SD	2.41	0.60
52:3:291:U:O2'	52:3:292:G:H5'	2.01	0.60
5:f:17:LYS:HE3	5:f:24:THR:HB	1.82	0.60
33:I:63:ILE:O	33:I:110:ARG:HD2	2.01	0.60
44:T:44:GLU:O	44:T:45:HIS:HB2	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1373:A:H5'	53:1:2212:A:H1'	1.84	0.60
23:x:17:ARG:HE	23:x:23:ALA:HB2	1.67	0.60
24:y:2:LYS:HD2	53:1:78:U:OP1	2.02	0.60
18:s:93:ALA:HB2	53:1:1614:A:N1	2.17	0.59
19:t:30:ILE:HG23	19:t:85:VAL:HG13	1.83	0.59
51:a:174:THR:HB	53:1:2124:G:H4'	1.83	0.59
13:n:53:THR:HA	13:n:56:LYS:HG3	1.84	0.59
19:t:2:ILE:HG21	53:1:144:A:H4'	1.82	0.59
52:3:744:C:H2'	52:3:745:G:C8	2.38	0.59
35:K:19:PRO:O	35:K:22:ILE:HG22	2.02	0.59
9:j:95:ARG:HH22	53:1:2768:U:H4'	1.66	0.59
53:1:1300:G:H4'	53:1:1301:A:H5'	1.84	0.59
6:g:12:LEU:HD23	6:g:12:LEU:H	1.67	0.59
33:I:61:ARG:HH21	33:I:68:GLU:H	1.49	0.59
36:L:111:GLY:HA2	36:L:118:ARG:HD3	1.85	0.59
41:Q:23:LEU:HB3	41:Q:26:CYS:SG	2.43	0.59
53:1:1319:C:O2'	53:1:1320:C:H5'	2.03	0.59
55:6:13:C:C2'	55:6:14:A:H5''	2.30	0.59
28:D:12:ARG:NE	28:D:44:VAL:HG21	2.18	0.59
46:V:48:GLU:HB2	46:V:51:GLU:OE1	2.02	0.59
49:Y:32:LYS:NZ	52:3:1438:G:H5''	2.18	0.59
50:Z:66:ARG:HH21	52:3:1099:G:H4'	1.67	0.59
51:a:53:ARG:HD3	55:6:61:C:O2'	2.02	0.59
52:3:78:A:H2'	52:3:79:G:O4'	2.02	0.59
52:3:346:G:C2'	52:3:347:G:H5'	2.33	0.59
52:3:1218:C:H2'	52:3:1219:A:C8	2.38	0.59
6:g:40:THR:HB	6:g:43:ASN:HD22	1.68	0.59
6:g:59:ALA:O	6:g:62:LEU:HD23	2.01	0.59
52:3:346:G:H2'	52:3:347:G:H5'	1.84	0.59
12:m:45:GLN:NE2	53:1:2485:G:H5''	2.17	0.58
38:N:105:ARG:O	38:N:105:ARG:HD3	2.03	0.58
5:f:41:GLU:HA	5:f:54:ARG:HH21	1.68	0.58
8:i:21:PRO:HB2	8:i:22:PRO:HD3	1.86	0.58
9:j:30:THR:HG21	53:1:1005:C:O2'	2.03	0.58
13:n:20:MET:HE1	13:n:40:LYS:HD3	1.85	0.58
51:a:8:MET:HE3	53:1:2174:C:H4'	1.85	0.58
3:d:199:MET:SD	3:d:200:LEU:HD22	2.43	0.58
4:e:107:VAL:HG23	4:e:108:PRO:HD3	1.84	0.58
7:h:2:ALA:H	7:h:6:GLN:HG2	1.68	0.58
27:C:22:THR:HG22	27:C:23:THR:H	1.68	0.58
3:d:69:ARG:HD3	53:1:674:G:H1'	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:d:48:THR:HG22	3:d:86:ALA:HB3	1.85	0.58
7:h:34:THR:O	7:h:37:LYS:HB3	2.03	0.58
8:i:8:VAL:HG12	8:i:9:LYS:H	1.68	0.58
50:Z:50:SER:HA	50:Z:53:LYS:HE2	1.84	0.58
53:1:974:G:H1'	53:1:975:A:C8	2.39	0.58
41:Q:23:LEU:CD2	41:Q:29:LYS:HD3	2.33	0.58
53:1:2285:C:O2'	53:1:2287:A:H1'	2.04	0.58
12:m:42:THR:OG1	12:m:45:GLN:HG3	2.02	0.58
35:K:10:VAL:HG12	35:K:58:HIS:HB3	1.85	0.58
51:a:209:ILE:HD11	51:a:212:VAL:HG22	1.84	0.58
53:1:704:G:H2'	53:1:726:G:N2	2.18	0.58
53:1:2233:U:H2'	53:1:2234:G:C8	2.39	0.58
13:n:54:LEU:HD11	13:n:65:LEU:HD23	1.86	0.58
53:1:310:A:O2'	53:1:311:A:H5''	2.03	0.58
53:1:1367:A:H2'	53:1:1368:G:H5'	1.83	0.58
53:1:2799:A:H2'	53:1:2800:A:H5'	1.85	0.58
7:h:34:THR:HG21	53:1:1057:A:H1'	1.84	0.58
15:p:88:ARG:HH11	15:p:112:ARG:HE	1.52	0.58
16:q:89:ILE:HA	17:r:11:GLN:HE22	1.68	0.58
32:H:173:PRO:HB2	32:H:176:THR:HG22	1.86	0.58
37:M:70:VAL:HG13	37:M:71:VAL:H	1.69	0.58
17:r:49:ILE:HD12	17:r:52:PRO:HA	1.86	0.58
33:I:46:ARG:H	33:I:46:ARG:HD3	1.69	0.58
20:u:17:ASP:HB3	20:u:20:LYS:HB2	1.86	0.57
33:I:33:ILE:HG22	33:I:34:GLU:H	1.69	0.57
38:N:112:ARG:NH2	39:O:64:GLN:HE22	2.02	0.57
53:1:329:G:O4'	53:1:477:A:H1'	2.03	0.57
53:1:2286:G:H4'	53:1:2287:A:O4'	2.04	0.57
53:1:2553:G:H3'	53:1:2554:U:H5''	1.84	0.57
54:2:3:C:H2'	54:2:4:C:H5''	1.86	0.57
6:g:67:ALA:HA	6:g:70:GLU:HG3	1.84	0.57
39:O:11:LYS:HD3	39:O:71:LEU:HD12	1.85	0.57
12:m:64:TRP:HB2	12:m:104:GLU:HB2	1.85	0.57
37:M:77:VAL:HG12	37:M:84:ILE:HD12	1.85	0.57
2:c:59:ARG:HH11	53:1:2830:C:H3'	1.69	0.57
3:d:63:LYS:HD2	53:1:2444:G:OP2	2.05	0.57
5:f:85:LYS:HB3	5:f:164:ALA:HB2	1.86	0.57
35:K:7:VAL:HG22	35:K:61:LEU:HD12	1.86	0.57
35:K:10:VAL:CG1	35:K:58:HIS:HB3	2.34	0.57
50:Z:57:LYS:HE2	50:Z:57:LYS:HA	1.86	0.57
33:I:190:LEU:HD12	33:I:192:ALA:H	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:d:47:LYS:O	3:d:83:VAL:HB	2.03	0.57
28:D:14:ARG:HD2	53:1:771:G:OP1	2.05	0.57
39:O:53:ILE:HG22	43:S:84:ARG:HD2	1.87	0.57
50:Z:16:ARG:HB2	50:Z:19:LYS:HD3	1.87	0.57
52:3:555:U:H2'	52:3:556:C:C6	2.39	0.57
52:3:1414:U:H2'	52:3:1415:G:H8	1.68	0.57
53:1:704:G:H1'	53:1:727:A:N6	2.19	0.57
8:i:93:ASN:ND2	53:1:1077:A:H5'	2.20	0.57
18:s:70:LYS:O	18:s:107:VAL:HG23	2.04	0.57
44:T:28:VAL:HG11	44:T:80:LEU:HD21	1.85	0.57
55:5:6:G:O2'	55:5:7:G:H5'	2.03	0.57
36:L:78:ARG:HB3	36:L:83:THR:HG22	1.86	0.57
33:I:90:LEU:HD12	33:I:93:LEU:HD11	1.85	0.57
52:3:946:A:H2'	52:3:947:G:C8	2.39	0.57
31:G:103:TRP:HA	31:G:106:VAL:HG12	1.86	0.56
33:I:164:ARG:HG2	33:I:165:GLU:H	1.70	0.56
33:I:187:ARG:HH12	33:I:192:ALA:HA	1.70	0.56
39:O:57:VAL:O	39:O:58:ASN:HB2	2.05	0.56
51:a:185:LEU:HA	51:a:188:ASN:HD22	1.70	0.56
34:J:75:LEU:HD13	34:J:78:GLY:H	1.70	0.56
37:M:42:GLU:HG2	37:M:100:ILE:HG13	1.87	0.56
7:h:64:VAL:O	7:h:67:THR:HG22	2.03	0.56
8:i:99:LYS:HD3	8:i:140:GLU:HG2	1.87	0.56
16:q:88:GLU:OE1	17:r:52:PRO:HB3	2.04	0.56
35:K:3:HIS:H	35:K:92:THR:CG2	2.16	0.56
38:N:35:GLU:HA	38:N:39:GLY:HA3	1.87	0.56
41:Q:29:LYS:HE2	41:Q:58:ASN:HD22	1.70	0.56
41:Q:43:LYS:HE2	41:Q:43:LYS:HA	1.86	0.56
52:3:77:A:H2'	52:3:78:A:H8	1.70	0.56
52:3:1005:A:H2'	52:3:1006:G:O4'	2.05	0.56
4:e:107:VAL:CG2	4:e:108:PRO:HD3	2.35	0.56
22:w:66:GLU:OE1	22:w:68:LYS:HE2	2.05	0.56
34:J:14:LEU:HA	34:J:36:THR:HG22	1.88	0.56
39:O:10:LEU:HD23	39:O:10:LEU:H	1.71	0.56
52:3:314:C:O2'	52:3:315:A:H5'	2.05	0.56
53:1:613:A:H2'	53:1:613:A:N3	2.21	0.56
53:1:644:A:H2'	53:1:645:C:C4'	2.35	0.56
53:1:821:A:C5'	53:1:822:G:H5''	2.27	0.56
3:d:76:PRO:HA	3:d:82:GLY:HA2	1.88	0.56
9:j:17:VAL:HG23	9:j:137:PRO:HB2	1.88	0.56
25:z:50:VAL:O	25:z:54:VAL:HG22	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:6:PRO:HB2	33:I:9:LYS:HB3	1.87	0.56
41:Q:113:ARG:HB2	41:Q:118:VAL:HB	1.86	0.56
50:Z:39:LYS:HA	50:Z:39:LYS:HE2	1.87	0.56
9:j:7:LYS:HB2	9:j:10:THR:HG22	1.86	0.56
12:m:75:GLU:OE2	53:1:957:C:H5'	2.05	0.56
23:x:18:SER:OG	53:1:2080:A:H5'	2.06	0.56
21:v:51:GLN:HE22	21:v:86:LEU:HD21	1.70	0.56
52:3:29:U:O2'	52:3:30:U:H5'	2.05	0.56
52:3:70:U:H4'	52:3:71:A:H8	1.70	0.56
52:3:663:A:H5'	52:3:836:G:OP1	2.05	0.56
55:6:69:C:H2'	55:6:70:G:H5'	1.87	0.56
1:b:221:GLY:HA2	1:b:224:MET:HE3	1.87	0.56
32:H:50:SER:HB3	32:H:114:LEU:HD11	1.88	0.56
53:1:554:U:H2'	53:1:555:G:O4'	2.06	0.56
38:N:40:ARG:HH21	52:3:1292:G:H4'	1.70	0.56
38:N:64:ILE:HD12	38:N:64:ILE:N	2.21	0.56
38:N:115:VAL:HG11	39:O:62:ARG:HB2	1.87	0.56
52:3:950:U:H2'	52:3:951:G:C8	2.41	0.56
53:1:2800:A:H3'	53:1:2801:G:H5'	1.88	0.56
53:1:2834:G:H2'	53:1:2879:A:N6	2.21	0.56
51:a:3:LYS:HE2	53:1:2108:A:OP2	2.06	0.56
52:3:335:C:H2'	52:3:336:A:C8	2.41	0.56
11:l:132:ARG:O	11:l:136:GLU:HG3	2.07	0.55
53:1:45:G:H5''	53:1:46:G:C5'	2.20	0.55
53:1:1872:A:H2'	53:1:1873:G:O4'	2.05	0.55
8:i:7:TYR:HB3	8:i:59:THR:HA	1.89	0.55
46:V:18:LYS:HZ2	46:V:49:ASN:H	1.53	0.55
24:y:59:GLU:OE2	24:y:60:LYS:HG3	2.07	0.55
37:M:54:THR:C	37:M:56:PRO:HD3	2.32	0.55
38:N:57:VAL:HG23	38:N:58:GLU:H	1.70	0.55
40:P:126:ARG:HB3	50:Z:33:ARG:NH1	2.20	0.55
53:1:615:U:H5''	53:1:616:A:OP2	2.07	0.55
53:1:1779:U:H5	53:1:1784:A:N7	2.04	0.55
5:f:154:GLU:OE1	5:f:156:TYR:HB2	2.07	0.55
8:i:93:ASN:HD21	53:1:1077:A:H5'	1.71	0.55
31:G:195:VAL:HG12	31:G:197:PHE:H	1.71	0.55
35:K:18:VAL:HG12	35:K:19:PRO:HD3	1.88	0.55
37:M:8:ASP:O	37:M:12:ARG:HG3	2.07	0.55
53:1:703:U:H2'	53:1:704:G:O4'	2.06	0.55
9:j:27:ARG:HH22	53:1:1142:A:H4'	1.72	0.55
49:Y:4:LYS:HE2	49:Y:6:ALA:C	2.32	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1053:C:C2'	53:1:1054:A:H5''	2.33	0.55
53:1:2629:U:O2'	53:1:2630:G:H5''	2.06	0.55
4:e:45:ASP:HB3	4:e:48:LEU:HB2	1.89	0.55
49:Y:43:LYS:HE2	49:Y:43:LYS:HA	1.88	0.55
14:o:39:VAL:HG12	14:o:49:VAL:H	1.72	0.55
52:3:354:G:H2'	52:3:355:C:H5'	1.87	0.55
52:3:1352:C:H2'	52:3:1353:G:C8	2.42	0.55
53:1:1026:G:H2'	53:1:1027:A:H8	1.72	0.55
53:1:2646:C:H2'	53:1:2647:U:O4'	2.07	0.55
4:e:25:MET:HE2	54:2:57:A:N1	2.22	0.55
17:r:24:LYS:HA	17:r:94:THR:HG22	1.89	0.55
32:H:55:VAL:HG13	32:H:66:THR:CG2	2.36	0.55
32:H:56:ILE:HD12	32:H:65:VAL:HG12	1.87	0.55
32:H:143:LEU:O	32:H:143:LEU:HD23	2.07	0.55
37:M:52:GLY:HA3	37:M:56:PRO:HA	1.87	0.55
50:Z:6:ARG:C	50:Z:8:ASN:H	2.13	0.55
50:Z:48:LYS:NZ	52:3:724:G:OP1	2.39	0.55
52:3:77:A:H2'	52:3:78:A:C8	2.42	0.55
53:1:2345:G:N3	53:1:2381:A:H2'	2.22	0.55
20:u:73:ASN:ND2	20:u:75:ALA:HB3	2.21	0.55
53:1:1111:A:O2'	53:1:1112:G:H4'	2.07	0.55
37:M:94:VAL:HG12	37:M:95:MET:HG2	1.88	0.55
50:Z:48:LYS:HA	50:Z:51:ALA:HB3	1.89	0.55
53:1:962:G:H21	53:1:2250:G:H1	1.53	0.55
53:1:2112:G:H2'	53:1:2113:U:H5'	1.88	0.55
6:g:112:LYS:NZ	53:1:2220:U:H5''	2.22	0.54
7:h:55:VAL:HA	53:1:1084:A:C4'	2.37	0.54
18:s:88:ARG:HG3	18:s:94:ASP:OD2	2.07	0.54
36:L:37:THR:HG21	52:3:1240:U:H4'	1.88	0.54
7:h:18:VAL:HG12	7:h:70:GLU:HB3	1.88	0.54
10:k:48:PRO:HG3	52:3:1422:G:H5'	1.89	0.54
38:N:71:ILE:HG13	38:N:72:SER:H	1.72	0.54
50:Z:58:LYS:O	50:Z:61:ARG:HD2	2.07	0.54
53:1:2243:U:H2'	53:1:2244:U:C6	2.43	0.54
17:r:47:VAL:O	17:r:47:VAL:HG13	2.08	0.54
33:I:123:MET:HE2	33:I:145:ARG:HA	1.87	0.54
50:Z:64:ALA:C	50:Z:66:ARG:H	2.15	0.54
53:1:2432:A:H1'	55:6:75:C:O4'	2.07	0.54
53:1:2834:G:H2'	53:1:2879:A:H61	1.72	0.54
3:d:41:GLN:HG2	3:d:43:THR:HG23	1.88	0.54
13:n:63:ARG:HD3	53:1:1454:C:O4'	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:u:35:VAL:HG13	20:u:38:ILE:HG13	1.89	0.54
25:z:23:LEU:HD22	25:z:28:LEU:HD12	1.89	0.54
36:L:87:PRO:HG3	36:L:148:LYS:HA	1.89	0.54
40:P:87:GLY:H	40:P:113:THR:HG22	1.72	0.54
42:R:22:TYR:HD2	42:R:65:GLU:HA	1.71	0.54
49:Y:32:LYS:HZ3	52:3:1438:G:H5''	1.72	0.54
50:Z:16:ARG:HH21	50:Z:19:LYS:HE2	1.73	0.54
52:3:868:C:H2'	52:3:869:G:O4'	2.07	0.54
53:1:1326:U:H2'	53:1:1327:A:H8	1.72	0.54
53:1:2514:U:H2'	53:1:2515:C:C6	2.42	0.54
7:h:59:LEU:HD12	53:1:1107:G:OP1	2.08	0.54
35:K:96:VAL:HG22	35:K:97:THR:N	2.22	0.54
39:O:28:THR:HA	39:O:31:ARG:NH1	2.23	0.54
53:1:414:C:H2'	53:1:415:A:C8	2.43	0.54
53:1:1758:U:C5	53:1:2696:U:H5'	2.42	0.54
53:1:2875:C:H2'	53:1:2876:G:C8	2.42	0.54
26:B:54:ILE:HG23	26:B:56:LYS:N	2.23	0.54
30:F:37:GLN:HE21	53:1:1125:G:H5'	1.73	0.54
50:Z:23:GLU:O	50:Z:25:ALA:N	2.40	0.54
53:1:1810:A:H2'	53:1:1811:G:O4'	2.06	0.54
2:c:123:LYS:HE2	13:n:1:MET:HE1	1.90	0.54
7:h:23:LEU:HD13	7:h:118:ILE:HB	1.90	0.54
13:n:38:LEU:HB3	13:n:39:PRO:HD3	1.88	0.54
44:T:23:SER:HA	52:3:751:U:H4'	1.89	0.54
52:3:1088:G:H21	52:3:1167:A:H61	1.53	0.54
52:3:1429:A:H2'	52:3:1430:A:H8	1.73	0.54
53:1:2233:U:H2'	53:1:2234:G:H8	1.73	0.54
53:1:2391:G:H2'	53:1:2424:C:N4	2.23	0.54
53:1:2743:U:C3'	53:1:2744:G:H5''	2.37	0.54
8:i:121:ILE:HA	8:i:124:MET:HE3	1.89	0.54
15:p:52:ARG:HH22	53:1:2720:U:H5''	1.73	0.54
33:I:49:ASP:O	33:I:52:VAL:HG22	2.07	0.54
53:1:967:U:H2'	53:1:968:C:C6	2.43	0.54
53:1:1637:A:H5'	53:1:1760:C:O2'	2.07	0.54
53:1:1664:A:H61	53:1:1996:C:H42	1.55	0.54
53:1:2210:U:H4'	53:1:2211:A:H2	1.71	0.54
4:e:103:ILE:HG13	4:e:104:THR:HG23	1.88	0.54
7:h:25:ALA:HA	7:h:115:GLY:HA2	1.90	0.54
8:i:12:VAL:HG13	53:1:1061:U:H3	1.73	0.54
51:a:53:ARG:HB3	55:6:62:C:H4'	1.90	0.54
52:3:448:A:H3'	52:3:449:G:C8	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:248:G:O5'	53:1:249:C:H5'	2.08	0.54
53:1:639:U:H2'	53:1:640:C:C6	2.43	0.54
53:1:1611:C:H6	53:1:1611:C:H5'	1.73	0.54
53:1:2537:U:H2'	53:1:2538:C:C6	2.42	0.54
6:g:125:THR:HG23	6:g:146:VAL:HG13	1.89	0.53
32:H:151:GLU:HG2	32:H:166:TRP:HB3	1.89	0.53
34:J:159:SER:HB3	34:J:162:GLU:OE2	2.08	0.53
41:Q:88:ASP:HB3	41:Q:89:LEU:HD12	1.89	0.53
53:1:2086:U:H2'	53:1:2087:G:C8	2.42	0.53
7:h:118:ILE:O	7:h:118:ILE:HG22	2.08	0.53
17:r:49:ILE:O	17:r:49:ILE:HG13	2.08	0.53
52:3:396:C:H2'	52:3:397:A:H5''	1.90	0.53
38:N:55:ASP:HB3	38:N:59:LYS:HG3	1.89	0.53
52:3:130:A:O2'	52:3:264:C:H5'	2.08	0.53
52:3:715:A:H2'	52:3:716:A:C8	2.43	0.53
53:1:917:A:H5''	53:1:2268:A:H61	1.73	0.53
13:n:69:ARG:O	13:n:70:THR:OG1	2.19	0.53
32:H:55:VAL:CG1	32:H:66:THR:HG23	2.38	0.53
35:K:47:LEU:HD21	35:K:57:ALA:HB3	1.91	0.53
50:Z:6:ARG:HG2	50:Z:8:ASN:H	1.74	0.53
52:3:86:G:H4'	52:3:87:C:C5	2.43	0.53
52:3:231:U:H2'	52:3:232:G:H8	1.73	0.53
53:1:1045:C:OP1	53:1:1047:G:H5'	2.09	0.53
17:r:81:LYS:HE3	53:1:973:A:OP2	2.08	0.53
52:3:79:G:O2'	52:3:80:A:H5'	2.08	0.53
53:1:2679:A:O2'	53:1:2680:U:H5'	2.08	0.53
12:m:41:LEU:HG	12:m:96:ILE:HG13	1.90	0.53
31:G:216:VAL:HA	31:G:219:THR:HG22	1.90	0.53
41:Q:82:ARG:NH1	52:3:552:U:H5'	2.23	0.53
52:3:17:U:H2'	52:3:18:C:C6	2.44	0.53
7:h:61:ARG:NH2	53:1:1046:A:OP2	2.41	0.53
52:3:673:A:H2'	52:3:674:G:C8	2.44	0.53
53:1:528:A:N1	53:1:2042:A:H2'	2.24	0.53
53:1:1060:U:H4'	53:1:1061:U:H5'	1.91	0.53
53:1:2114:A:H2'	53:1:2114:A:N3	2.23	0.53
8:i:93:ASN:CG	53:1:1077:A:H5'	2.34	0.53
10:k:21:CYS:HA	10:k:41:ILE:HG22	1.90	0.53
53:1:441:U:O2'	53:1:442:G:H5'	2.08	0.53
53:1:2743:U:H2'	53:1:2744:G:H5''	1.90	0.53
54:2:88:C:C4'	54:2:89:U:OP1	2.57	0.53
20:u:27:VAL:HG22	20:u:33:VAL:HG12	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:P:19:VAL:HG12	40:P:82:GLU:HB2	1.91	0.53
51:a:10:VAL:HG12	51:a:14:LYS:NZ	2.24	0.53
31:G:47:PRO:O	31:G:51:GLU:HG3	2.09	0.53
52:3:123:U:H5''	52:3:311:C:O2'	2.08	0.53
53:1:45:G:C5'	53:1:46:G:H5'	2.22	0.53
28:D:34:ARG:NH2	28:D:39:ARG:HD2	2.24	0.52
45:U:22:ALA:HA	45:U:33:ILE:HD12	1.91	0.52
48:X:6:LYS:HE2	48:X:6:LYS:HA	1.91	0.52
51:a:54:LYS:HZ3	55:6:63:G:H4'	1.74	0.52
52:3:390:U:H2'	52:3:391:G:C8	2.44	0.52
53:1:580:U:H2'	53:1:581:C:C6	2.43	0.52
53:1:2799:A:C2'	53:1:2800:A:H5'	2.39	0.52
20:u:71:ILE:HD11	20:u:82:VAL:HB	1.90	0.52
24:y:21:LEU:HD23	24:y:25:GLN:HG2	1.90	0.52
41:Q:32:VAL:HA	41:Q:78:VAL:HG12	1.91	0.52
53:1:668:A:H2'	53:1:670:A:H62	1.75	0.52
53:1:1796:U:H2'	53:1:1797:G:H8	1.74	0.52
53:1:1857:G:N2	53:1:1884:G:H2'	2.24	0.52
53:1:2238:G:H2'	53:1:2238:G:N3	2.24	0.52
1:b:70:LYS:HE3	1:b:73:ILE:HD12	1.91	0.52
14:o:49:VAL:HG21	14:o:82:ALA:HA	1.89	0.52
18:s:53:SER:O	18:s:57:ASN:HB2	2.10	0.52
21:v:77:VAL:HG12	21:v:89:ILE:HG22	1.91	0.52
33:I:61:ARG:HH21	33:I:68:GLU:N	2.07	0.52
41:Q:82:ARG:HH11	52:3:552:U:H5'	1.75	0.52
52:3:757:U:H2'	52:3:758:C:O4'	2.09	0.52
53:1:1071:G:OP1	53:1:1071:G:H3'	2.09	0.52
53:1:1794:A:H2'	53:1:1795:C:C6	2.44	0.52
34:J:60:GLN:O	34:J:64:GLU:HG3	2.10	0.52
35:K:6:ILE:HG12	35:K:89:VAL:HG12	1.90	0.52
52:3:70:U:H4'	52:3:71:A:C8	2.45	0.52
52:3:545:C:O2'	52:3:549:C:H5''	2.09	0.52
52:3:784:A:H2'	52:3:785:G:C8	2.44	0.52
52:3:1412:C:H2'	52:3:1413:A:C8	2.44	0.52
53:1:1077:A:C2'	53:1:1078:U:H5'	2.39	0.52
53:1:1251:C:O2'	53:1:1252:G:H3'	2.09	0.52
53:1:1856:U:H2'	53:1:1857:G:O4'	2.09	0.52
4:e:133:GLU:HG3	4:e:135:ILE:HG22	1.91	0.52
7:h:103:ASN:HD22	7:h:113:PHE:HE1	1.58	0.52
40:P:17:ASP:HB3	40:P:36:ARG:HH21	1.75	0.52
52:3:70:U:H5''	52:3:71:A:OP1	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1506:U:O2'	52:3:1507:A:H5'	2.10	0.52
53:1:2111:U:H3	53:1:2147:A:H1'	1.75	0.52
33:I:131:ILE:HG12	52:3:620:C:C2	2.44	0.52
36:L:78:ARG:HD3	52:3:1382:C:H5'	1.90	0.52
39:O:57:VAL:O	39:O:58:ASN:CB	2.57	0.52
41:Q:122:LYS:HE2	41:Q:122:LYS:HA	1.91	0.52
53:1:2389:G:H5''	53:1:2390:U:O4'	2.10	0.52
11:l:23:ILE:H	11:l:23:ILE:HD12	1.75	0.52
16:q:111:LYS:HG2	17:r:48:LYS:HD2	1.91	0.52
36:L:139:ASP:HA	36:L:142:ARG:HB2	1.92	0.52
38:N:105:ARG:HH11	38:N:107:ALA:HA	1.75	0.52
52:3:410:G:H2'	52:3:429:U:C4	2.44	0.52
52:3:1211:U:H4'	52:3:1213:A:N3	2.24	0.52
53:1:581:C:H2'	53:1:582:A:C8	2.45	0.52
53:1:1434:A:H2'	53:1:1435:G:C8	2.45	0.52
53:1:2128:G:H1'	53:1:2173:A:N3	2.25	0.52
54:2:65:U:H3'	54:2:108:A:N6	2.25	0.52
56:4:19:U:H2'	56:4:20:U:C6	2.45	0.52
6:g:5:LEU:HD12	6:g:5:LEU:N	2.25	0.52
9:j:118:MET:HA	9:j:121:LYS:HE2	1.92	0.52
24:y:24:GLU:O	24:y:28:LEU:HB2	2.10	0.52
28:D:30:VAL:O	28:D:34:ARG:HG2	2.09	0.52
42:R:6:ILE:HG13	42:R:7:ASN:H	1.73	0.52
51:a:33:LEU:HB3	51:a:219:GLY:HA3	1.90	0.52
52:3:113:G:H1'	52:3:354:G:H5'	1.90	0.52
52:3:909:A:H2'	52:3:910:C:O4'	2.10	0.52
53:1:1213:A:N6	53:1:1236:G:H1'	2.24	0.52
26:B:32:THR:HG22	26:B:50:GLY:HA2	1.92	0.52
30:F:2:LYS:HB2	30:F:35:GLN:HB3	1.92	0.52
40:P:49:SER:HB3	40:P:68:ARG:HD3	1.90	0.52
44:T:31:LEU:HD22	44:T:58:MET:HB2	1.92	0.52
44:T:45:HIS:O	44:T:47:LYS:N	2.43	0.52
52:3:1418:A:H3'	52:3:1419:G:C5'	2.39	0.52
53:1:2756:U:H4'	53:1:2757:A:OP1	2.10	0.52
6:g:101:ASP:O	6:g:104:THR:HG22	2.09	0.52
9:j:81:ILE:HG23	9:j:82:GLY:N	2.21	0.52
19:t:47:VAL:HG23	19:t:51:PHE:HD2	1.74	0.52
30:F:24:ARG:NH2	30:F:36:ARG:HG3	2.25	0.52
30:F:36:ARG:O	30:F:37:GLN:CB	2.58	0.52
35:K:21:MET:HE1	35:K:84:VAL:HG13	1.92	0.52
40:P:44:ALA:HB3	40:P:69:CYS:HB2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:S:20:PHE:O	43:S:21:ALA:HB3	2.10	0.52
44:T:21:THR:HG21	52:3:658:C:H1'	1.92	0.52
53:1:1509:A:H2'	53:1:1510:G:C8	2.45	0.52
54:2:3:C:C2'	54:2:4:C:H5''	2.39	0.52
13:n:73:ASN:HA	13:n:76:VAL:HG12	1.90	0.51
18:s:47:VAL:HG12	18:s:103:ILE:HG21	1.92	0.51
18:s:100:THR:HG22	18:s:101:SER:H	1.74	0.51
34:J:71:ILE:CD1	34:J:144:GLU:HG2	2.39	0.51
35:K:69:GLU:O	35:K:72:ASP:OD1	2.28	0.51
52:3:622:A:H2'	52:3:623:C:H5'	1.91	0.51
52:3:948:C:H2'	52:3:949:A:H8	1.76	0.51
52:3:1004:A:H2'	52:3:1005:A:O4'	2.09	0.51
53:1:1130:U:O2'	53:1:1131:G:OP1	2.27	0.51
53:1:2636:C:H2'	53:1:2637:U:C6	2.45	0.51
1:b:143:VAL:HG21	1:b:161:VAL:HG21	1.92	0.51
11:l:77:ILE:HD12	11:l:77:ILE:N	2.26	0.51
50:Z:34:ARG:HB3	50:Z:36:PHE:CZ	2.45	0.51
53:1:278:A:H2'	53:1:278:A:N3	2.25	0.51
53:1:669:G:H2'	53:1:669:G:N3	2.25	0.51
53:1:1357:C:H2'	53:1:1358:G:O4'	2.11	0.51
3:d:119:ILE:HB	3:d:187:VAL:HG12	1.92	0.51
15:p:52:ARG:NH2	53:1:2720:U:H5''	2.25	0.51
34:J:148:SER:O	34:J:151:MET:HG3	2.10	0.51
37:M:55:LYS:HD3	52:3:652:U:O2'	2.09	0.51
52:3:335:C:H2'	52:3:336:A:H8	1.75	0.51
53:1:1111:A:H2'	53:1:1112:G:H4'	1.92	0.51
53:1:1186:G:H2'	53:1:1187:G:O4'	2.11	0.51
53:1:1437:C:H2'	53:1:1438:U:C6	2.46	0.51
43:S:4:SER:OG	52:3:1216:A:H5''	2.09	0.51
49:Y:49:ALA:O	49:Y:52:GLU:HG2	2.11	0.51
52:3:31:G:N2	52:3:47:C:H5''	2.25	0.51
3:d:144:GLU:HG2	3:d:145:ASP:N	2.26	0.51
10:k:102:PRO:HB3	10:k:121:GLU:HB3	1.92	0.51
32:H:80:GLY:O	32:H:83:VAL:HG12	2.11	0.51
38:N:98:ARG:NH2	52:3:1178:G:N7	2.58	0.51
53:1:528:A:C2	53:1:2042:A:H2'	2.46	0.51
53:1:2743:U:H3'	53:1:2744:G:H5''	1.92	0.51
39:O:38:GLY:O	39:O:40:ILE:HD12	2.10	0.51
40:P:34:THR:HG22	40:P:40:ALA:HA	1.93	0.51
41:Q:52:CYS:HB3	41:Q:66:ILE:HD11	1.92	0.51
45:U:31:ARG:HB2	52:3:310:G:H5''	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:225:C:C3'	52:3:226:G:H5''	2.41	0.51
31:G:186:VAL:HG23	31:G:190:SER:HB2	1.91	0.51
37:M:70:VAL:HG13	37:M:71:VAL:N	2.25	0.51
42:R:70:ARG:O	42:R:74:MET:HG2	2.11	0.51
46:V:60:ILE:HG21	46:V:72:TRP:HB3	1.92	0.51
52:3:536:C:H2'	52:3:537:G:H8	1.76	0.51
53:1:1111:A:H2'	53:1:1111:A:N3	2.25	0.51
53:1:2698:U:H2'	53:1:2699:C:C6	2.46	0.51
5:f:22:VAL:HG12	5:f:35:THR:HG22	1.91	0.51
43:S:7:ALA:O	43:S:10:VAL:HG12	2.11	0.51
51:a:7:ARG:HH21	51:a:8:MET:HE1	1.75	0.51
51:a:186:LYS:HA	51:a:186:LYS:HE2	1.93	0.51
53:1:1535:A:H3'	53:1:1536:C:H5'	1.92	0.51
53:1:2183:A:H2'	53:1:2184:A:C8	2.46	0.51
9:j:7:LYS:HG2	53:1:538:A:H4'	1.93	0.51
41:Q:51:VAL:HG22	41:Q:52:CYS:H	1.75	0.51
41:Q:98:ARG:HB2	41:Q:116:TYR:HA	1.92	0.51
45:U:21:VAL:HG12	45:U:34:GLU:O	2.10	0.51
51:a:12:ARG:NH2	53:1:2106:U:H5''	2.23	0.51
52:3:1368:A:O2'	52:3:1369:C:H5'	2.11	0.51
53:1:161:A:H3'	53:1:162:U:H5''	1.93	0.51
53:1:2048:G:H2'	53:1:2049:G:H5''	1.93	0.51
53:1:2788:C:H2'	53:1:2789:C:C6	2.45	0.51
36:L:145:GLU:O	36:L:148:LYS:HG2	2.10	0.51
46:V:19:SER:HB3	46:V:70:LYS:NZ	2.26	0.51
46:V:30:HIS:HD2	46:V:33:TYR:H	1.58	0.51
52:3:79:G:H2'	52:3:80:A:O4'	2.11	0.51
52:3:110:C:H2'	52:3:111:G:O4'	2.11	0.51
52:3:484:G:H4'	52:3:485:U:C5'	2.32	0.51
52:3:1516:G:H2'	52:3:1518:A:OP2	2.11	0.51
1:b:56:GLY:HA2	1:b:212:TRP:HA	1.92	0.50
19:t:15:HIS:H	19:t:32:LEU:HA	1.76	0.50
22:w:38:GLY:HA2	53:1:2330:G:H21	1.76	0.50
31:G:56:LEU:O	31:G:56:LEU:HD23	2.11	0.50
35:K:69:GLU:O	35:K:73:GLU:OE1	2.29	0.50
53:1:473:G:O2'	53:1:474:G:H5'	2.11	0.50
53:1:543:G:H2'	53:1:544:C:O4'	2.11	0.50
36:L:112:ASP:H	36:L:118:ARG:HD3	1.77	0.50
43:S:2:LYS:HD2	43:S:5:MET:HE3	1.92	0.50
52:3:1497:G:O2'	52:3:1498:U:H5'	2.11	0.50
53:1:226:A:H2'	53:1:227:A:O4'	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:340:A:H2'	53:1:341:C:O4'	2.12	0.50
53:1:2875:C:H2'	53:1:2876:G:H8	1.76	0.50
20:u:6:ARG:HG3	20:u:7:ASP:OD1	2.12	0.50
32:H:33:ASP:OD1	43:S:64:ARG:HB2	2.12	0.50
53:1:2467:C:H2'	53:1:2468:A:O4'	2.10	0.50
48:X:52:ASN:OD1	48:X:53:GLY:N	2.39	0.50
53:1:1045:C:P	53:1:1047:G:H5'	2.52	0.50
53:1:2432:A:H1'	55:6:75:C:C4'	2.41	0.50
17:r:28:ALA:HB3	17:r:31:GLU:OE2	2.12	0.50
31:G:40:ILE:H	31:G:40:ILE:HD12	1.76	0.50
33:I:158:LEU:HD21	33:I:174:ALA:HA	1.92	0.50
39:O:22:THR:HA	39:O:25:ILE:HG22	1.94	0.50
52:3:422:C:H5'	52:3:423:G:N3	2.26	0.50
52:3:543:U:H2'	52:3:544:G:H8	1.76	0.50
52:3:948:C:H2'	52:3:949:A:C8	2.47	0.50
52:3:1402:C:H2'	52:3:1403:C:O4'	2.11	0.50
53:1:704:G:H1'	53:1:727:A:H61	1.77	0.50
32:H:68:HIS:HA	32:H:103:ALA:O	2.11	0.50
42:R:28:ARG:NH2	42:R:62:PHE:HB2	2.27	0.50
51:a:27:ILE:HD12	51:a:185:LEU:HB3	1.94	0.50
53:1:1190:G:H2'	53:1:1191:G:H8	1.76	0.50
7:h:33:VAL:HA	53:1:1055:G:H4'	1.93	0.50
28:D:12:ARG:HE	28:D:44:VAL:HG21	1.77	0.50
52:3:946:A:H2'	52:3:947:G:H8	1.76	0.50
53:1:799:G:H5''	53:1:800:A:H2'	1.92	0.50
53:1:1360:G:H2'	53:1:1361:G:H5'	1.94	0.50
53:1:1874:C:H2'	53:1:1875:G:O4'	2.11	0.50
9:j:111:LYS:H	9:j:111:LYS:HD2	1.76	0.50
17:r:53:PHE:O	17:r:54:VAL:C	2.55	0.50
25:z:7:THR:OG1	25:z:55:LYS:HB3	2.12	0.50
33:I:123:MET:HG2	33:I:128:VAL:HG12	1.93	0.50
51:a:69:THR:HA	51:a:176:GLY:HA2	1.93	0.50
52:3:608:A:H2'	52:3:609:A:O4'	2.12	0.50
52:3:1128:C:O2'	52:3:1129:C:H5'	2.11	0.50
52:3:1200:C:H5''	52:3:1201:A:H3'	1.94	0.50
53:1:1979:U:O2'	53:1:1980:G:H5'	2.11	0.50
6:g:51:ARG:HB3	6:g:55:GLU:HB2	1.94	0.50
7:h:67:THR:N	7:h:68:PRO:CD	2.75	0.50
8:i:10:LEU:HG	53:1:1070:A:N1	2.27	0.50
37:M:28:SER:HB3	37:M:58:LEU:HB2	1.93	0.50
39:O:80:THR:HG22	39:O:82:LYS:H	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:477:C:H2'	52:3:478:A:C8	2.47	0.50
53:1:2404:U:H2'	53:1:2405:G:O4'	2.11	0.50
2:c:149:ASN:HB3	53:1:2572:A:OP2	2.11	0.49
5:f:94:ARG:HG3	5:f:127:GLN:HB3	1.94	0.49
7:h:33:VAL:HG23	7:h:35:VAL:H	1.77	0.49
9:j:58:ASN:HD21	9:j:128:ASN:HB2	1.77	0.49
17:r:74:ILE:N	17:r:74:ILE:HD12	2.26	0.49
38:N:51:LEU:HD11	38:N:62:LEU:HD11	1.94	0.49
38:N:121:ARG:HG3	52:3:1348:U:H4'	1.94	0.49
39:O:40:ILE:HB	39:O:73:LEU:HD21	1.93	0.49
52:3:981:U:H2'	52:3:982:U:C5	2.47	0.49
52:3:1316:G:H2'	52:3:1317:C:H5''	1.92	0.49
52:3:1330:U:H2'	52:3:1331:G:O4'	2.12	0.49
53:1:2163:A:H2'	53:1:2164:C:H5'	1.94	0.49
5:f:44:HIS:O	5:f:46:ASP:N	2.45	0.49
6:g:8:LYS:O	6:g:9:VAL:HG13	2.12	0.49
34:J:15:ILE:HD11	34:J:37:VAL:HG22	1.93	0.49
42:R:56:ARG:O	42:R:59:VAL:HG12	2.11	0.49
49:Y:59:ARG:NH2	52:3:194:C:H5''	2.27	0.49
52:3:265:G:H2'	52:3:267:C:H5	1.77	0.49
52:3:575:G:O2'	52:3:821:G:H5'	2.12	0.49
52:3:730:G:H2'	52:3:731:G:H5'	1.94	0.49
53:1:503:A:H4'	53:1:505:A:H5''	1.94	0.49
53:1:1213:A:H62	53:1:1236:G:H1'	1.77	0.49
53:1:2070:A:H2'	53:1:2071:A:O4'	2.12	0.49
53:1:2282:G:H4'	53:1:2389:G:O2'	2.11	0.49
55:5:20:U:H3'	55:5:21:A:H5'	1.93	0.49
52:3:245:U:O2'	52:3:246:A:H5'	2.12	0.49
52:3:664:G:N2	52:3:741:G:H1	2.08	0.49
53:1:1434:A:H2'	53:1:1435:G:H8	1.77	0.49
53:1:1932:A:H2'	53:1:1933:G:O4'	2.13	0.49
53:1:2011:U:H2'	53:1:2012:G:O4'	2.12	0.49
53:1:2029:G:O6	53:1:2032:G:H5''	2.11	0.49
5:f:34:ARG:HE	5:f:70:LEU:HD13	1.78	0.49
7:h:96:PHE:HE2	7:h:126:LEU:H	1.58	0.49
15:p:105:LYS:O	15:p:108:ARG:HG2	2.13	0.49
33:I:120:LYS:O	33:I:145:ARG:HD2	2.12	0.49
37:M:14:ARG:HD2	52:3:875:U:O2'	2.12	0.49
41:Q:100:ALA:O	41:Q:101:LEU:O	2.30	0.49
51:a:170:ILE:HG12	53:1:2177:C:O2'	2.12	0.49
53:1:310:A:H2'	53:1:311:A:H5''	1.91	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1796:U:H2'	53:1:1797:G:C8	2.48	0.49
53:1:2427:C:C5'	53:1:2429:G:H5'	2.42	0.49
4:e:111:ARG:NH2	4:e:112:ASP:OD2	2.45	0.49
6:g:8:LYS:C	6:g:9:VAL:HG13	2.37	0.49
6:g:96:THR:O	6:g:99:ILE:HG22	2.12	0.49
8:i:126:ARG:HA	8:i:129:GLU:HG3	1.94	0.49
13:n:79:LEU:O	13:n:80:PHE:HB2	2.12	0.49
14:o:108:ASP:O	14:o:112:GLU:HG2	2.12	0.49
18:s:73:LYS:HB2	18:s:106:VAL:CG1	2.42	0.49
31:G:165:ALA:HB3	31:G:190:SER:HB3	1.93	0.49
33:I:82:LYS:HD2	52:3:5:U:O4	2.13	0.49
37:M:4:ASP:HB2	37:M:80:PRO:HG3	1.94	0.49
43:S:89:ARG:HB3	43:S:91:GLU:OE1	2.13	0.49
52:3:1527:U:H2'	52:3:1528:U:C6	2.47	0.49
53:1:1444:G:H2'	53:1:1445:G:H8	1.78	0.49
1:b:242:HIS:O	1:b:244:VAL:HG13	2.13	0.49
20:u:32:LYS:HE2	20:u:65:GLN:OE1	2.13	0.49
40:P:13:LYS:HD2	40:P:13:LYS:N	2.28	0.49
53:1:74:A:H4'	53:1:75:G:O5'	2.12	0.49
53:1:1830:C:H2'	53:1:1831:G:H8	1.78	0.49
5:f:28:LYS:HD2	5:f:28:LYS:C	2.37	0.49
17:r:39:LEU:O	17:r:49:ILE:HG23	2.12	0.49
24:y:21:LEU:HA	24:y:25:GLN:HB3	1.93	0.49
39:O:24:GLU:O	39:O:28:THR:HG23	2.13	0.49
50:Z:19:LYS:HD2	50:Z:19:LYS:N	2.28	0.49
52:3:225:C:H2'	52:3:226:G:H5''	1.95	0.49
4:e:68:LYS:NZ	54:2:41:G:H1	2.11	0.49
6:g:8:LYS:O	6:g:9:VAL:CG2	2.56	0.49
17:r:59:ILE:HG23	17:r:101:ILE:HD13	1.93	0.49
27:C:20:TYR:OH	53:1:2348:U:H5'	2.13	0.49
37:M:4:ASP:OD2	37:M:7:ALA:HB2	2.13	0.49
43:S:5:MET:HA	43:S:8:ARG:HB3	1.94	0.49
43:S:5:MET:HE1	52:3:982:U:H5''	1.95	0.49
49:Y:81:GLN:O	49:Y:84:LYS:HB3	2.12	0.49
52:3:505:G:H4'	52:3:534:U:C4	2.48	0.49
52:3:695:A:H2'	52:3:696:A:C8	2.47	0.49
53:1:1539:U:H2'	53:1:1540:G:H8	1.77	0.49
53:1:2488:G:H2'	53:1:2489:U:C6	2.47	0.49
54:2:30:C:H2'	54:2:31:C:O4'	2.12	0.49
9:j:102:GLU:HG2	9:j:119:PHE:HZ	1.78	0.49
15:p:30:TRP:CE3	15:p:37:LYS:HG2	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:s:11:ARG:NH2	18:s:98:LYS:HD2	2.27	0.49
33:I:18:LEU:HB2	33:I:63:ILE:CD1	2.43	0.49
36:L:134:VAL:HG22	36:L:138:GLU:OE2	2.12	0.49
42:R:12:LYS:HE2	42:R:16:ILE:HG22	1.95	0.49
43:S:41:TRP:HZ2	48:X:10:ILE:HD11	1.78	0.49
52:3:12:U:H2'	52:3:13:U:H5''	1.94	0.49
52:3:543:U:H2'	52:3:544:G:C8	2.48	0.49
53:1:784:G:H5'	53:1:785:G:OP1	2.13	0.49
53:1:2533:U:H2'	53:1:2534:A:O4'	2.13	0.49
6:g:80:ILE:HD12	6:g:80:ILE:N	2.28	0.49
9:j:39:LYS:HD2	53:1:1007:C:OP1	2.13	0.49
50:Z:13:VAL:HG22	50:Z:14:ALA:H	1.78	0.49
53:1:1111:A:C2'	53:1:1112:G:H4'	2.42	0.49
53:1:1476:U:H3	53:1:1515:A:H62	1.61	0.49
55:5:69:C:H2'	55:5:70:G:H8	1.77	0.49
3:d:77:ILE:HG13	3:d:78:TRP:HD1	1.77	0.48
5:f:136:ASP:HB3	5:f:139:VAL:HG22	1.95	0.48
37:M:50:VAL:HG22	37:M:50:VAL:O	2.13	0.48
42:R:43:LYS:HB2	42:R:46:GLU:OE1	2.12	0.48
53:1:2297:A:N6	53:1:2319:G:H1'	2.27	0.48
53:1:2512:C:H2'	53:1:2513:A:O4'	2.13	0.48
53:1:2552:U:C6	53:1:2554:U:H5'	2.48	0.48
1:b:209:ALA:HA	1:b:212:TRP:CE2	2.48	0.48
24:y:39:GLN:HB3	24:y:41:HIS:CE1	2.49	0.48
52:3:1014:A:H2'	52:3:1015:G:O4'	2.13	0.48
53:1:112:U:H2'	53:1:113:U:H5'	1.95	0.48
53:1:891:G:H2'	53:1:892:A:H8	1.78	0.48
53:1:1930:G:O2'	53:1:1931:U:C6	2.66	0.48
53:1:2257:U:O2'	53:1:2258:C:H5'	2.14	0.48
53:1:2732:G:O2'	53:1:2733:A:H5'	2.13	0.48
2:c:135:GLY:HA2	53:1:743:A:OP1	2.12	0.48
6:g:47:PHE:O	6:g:52:ALA:N	2.45	0.48
32:H:54:ILE:HD12	32:H:54:ILE:N	2.28	0.48
33:I:96:ARG:HB2	33:I:99:ASN:HD22	1.77	0.48
42:R:59:VAL:HG22	42:R:64:VAL:HG21	1.95	0.48
48:X:30:LEU:HB2	48:X:48:ILE:HG22	1.95	0.48
52:3:219:U:H2'	52:3:220:G:H8	1.78	0.48
52:3:1277:C:H2'	52:3:1278:G:H5''	1.94	0.48
53:1:570:G:H2'	53:1:2030:A:N7	2.28	0.48
53:1:1297:C:OP1	53:1:2710:C:H4'	2.14	0.48
53:1:1565:C:O2'	53:1:1566:A:H2'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2149:U:H2'	53:1:2150:C:O4'	2.13	0.48
53:1:2329:U:H2'	53:1:2330:G:C8	2.47	0.48
53:1:2443:C:O2'	53:1:2444:G:H5'	2.13	0.48
7:h:8:LYS:O	7:h:11:ILE:HG22	2.14	0.48
10:k:12:ASP:HB2	10:k:96:GLY:HA3	1.96	0.48
15:p:92:ARG:HD3	53:1:1753:G:H5''	1.96	0.48
17:r:41:ILE:O	17:r:47:VAL:HG12	2.14	0.48
51:a:33:LEU:HD22	51:a:220:ALA:H	1.79	0.48
52:3:530:G:H3'	52:3:530:G:N3	2.28	0.48
52:3:1118:U:H2'	52:3:1119:C:C6	2.49	0.48
53:1:49:A:H5'	53:1:51:G:O4'	2.13	0.48
53:1:2846:G:H2'	53:1:2847:U:O4'	2.13	0.48
8:i:9:LYS:C	8:i:10:LEU:HD12	2.39	0.48
8:i:131:THR:O	8:i:135:MET:HG2	2.12	0.48
9:j:84:ILE:HG23	9:j:84:ILE:O	2.14	0.48
31:G:40:ILE:HD12	31:G:40:ILE:N	2.29	0.48
38:N:14:SER:HB3	38:N:69:GLY:HA3	1.94	0.48
51:a:185:LEU:HA	51:a:188:ASN:ND2	2.28	0.48
52:3:1436:U:H2'	52:3:1437:A:C8	2.48	0.48
53:1:534:U:H2'	53:1:535:G:C8	2.49	0.48
53:1:1239:G:H2'	53:1:1240:U:O4'	2.12	0.48
53:1:1268:A:H2'	53:1:1269:A:O4'	2.13	0.48
53:1:1432:G:H2'	53:1:1433:A:C8	2.48	0.48
53:1:2760:C:O2'	53:1:2761:A:H5'	2.13	0.48
4:e:110:ILE:O	4:e:113:PHE:HB2	2.13	0.48
13:n:2:ARG:O	13:n:2:ARG:CG	2.61	0.48
17:r:80:ARG:HG2	17:r:80:ARG:HH11	1.79	0.48
52:3:494:G:O2'	52:3:496:A:H1'	2.13	0.48
53:1:2405:G:H2'	53:1:2411:A:H62	1.78	0.48
31:G:11:ALA:HB1	31:G:208:ALA:HA	1.94	0.48
32:H:198:LYS:HE3	52:3:1058:G:OP1	2.14	0.48
34:J:107:GLY:CA	52:3:9:G:H5'	2.32	0.48
39:O:47:GLU:HB2	39:O:67:ILE:HB	1.95	0.48
45:U:78:VAL:O	45:U:79:ASN:CB	2.60	0.48
53:1:2590:A:O2'	53:1:2591:C:H5'	2.13	0.48
3:d:76:PRO:HA	3:d:82:GLY:HA3	1.96	0.48
7:h:55:VAL:HA	53:1:1084:A:C5'	2.44	0.48
18:s:31:GLN:O	18:s:35:ILE:HG13	2.14	0.48
34:J:71:ILE:HD11	34:J:144:GLU:HG2	1.94	0.48
45:U:5:ARG:HD2	52:3:376:G:H4'	1.96	0.48
52:3:371:A:H2'	52:3:372:C:O4'	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:721:G:H4'	52:3:722:G:O4'	2.13	0.48
52:3:1405:G:O2'	52:3:1406:U:H5'	2.13	0.48
53:1:1539:U:H2'	53:1:1540:G:C8	2.49	0.48
53:1:2141:G:H2'	53:1:2142:A:H8	1.77	0.48
1:b:166:ARG:HG3	1:b:171:VAL:HG22	1.95	0.48
32:H:52:SER:HB3	32:H:114:LEU:HD23	1.96	0.48
32:H:54:ILE:HG23	32:H:67:ILE:HD13	1.96	0.48
41:Q:79:ILE:HG22	41:Q:103:CYS:HB2	1.96	0.48
51:a:3:LYS:HG2	53:1:2107:G:H5''	1.95	0.48
52:3:1256:A:H1'	52:3:1258:G:C4	2.49	0.48
53:1:1739:A:H2'	53:1:1740:G:O4'	2.14	0.48
53:1:2457:U:O2'	53:1:2458:G:H5'	2.14	0.48
10:k:28:SER:HB2	53:1:2566:A:N1	2.29	0.48
33:I:87:GLU:HG3	33:I:187:ARG:HD3	1.95	0.48
33:I:197:HIS:O	33:I:200:VAL:HG12	2.14	0.48
38:N:86:LEU:HD22	38:N:89:TYR:HD2	1.79	0.48
45:U:21:VAL:HG13	45:U:21:VAL:O	2.14	0.48
49:Y:68:LYS:NZ	52:3:224:U:OP1	2.44	0.48
52:3:235:C:H2'	52:3:236:A:H8	1.78	0.48
52:3:687:A:N3	52:3:688:G:H1'	2.28	0.48
52:3:1252:A:H2'	52:3:1253:G:O4'	2.13	0.48
53:1:995:C:H6	53:1:995:C:H5'	1.79	0.48
53:1:2350:C:H2'	53:1:2351:G:O4'	2.14	0.48
6:g:42:LYS:O	6:g:45:GLU:HG3	2.14	0.47
7:h:8:LYS:HA	7:h:11:ILE:HG22	1.96	0.47
12:m:69:PRO:HA	12:m:94:ALA:HB2	1.95	0.47
17:r:25:LEU:H	17:r:94:THR:HG21	1.79	0.47
32:H:26:LYS:HE2	52:3:1256:A:H3'	1.96	0.47
39:O:71:LEU:HD23	39:O:72:ARG:N	2.29	0.47
51:a:6:LYS:HG3	51:a:7:ARG:H	1.79	0.47
52:3:1256:A:H4'	52:3:1258:G:O4'	2.13	0.47
53:1:1507:C:H2'	53:1:1508:A:O4'	2.14	0.47
53:1:1827:U:C2'	53:1:1828:G:H5'	2.44	0.47
5:f:25:ILE:HD11	5:f:74:MET:HB3	1.96	0.47
10:k:75:SER:HB2	15:p:72:VAL:O	2.13	0.47
20:u:6:ARG:N	53:1:85:G:OP1	2.46	0.47
24:y:9:LYS:HG3	24:y:11:VAL:HG12	1.96	0.47
29:E:25:HIS:NE2	29:E:47:ALA:HB2	2.29	0.47
45:U:20:VAL:HG12	45:U:35:ARG:HA	1.97	0.47
45:U:22:ALA:HA	45:U:33:ILE:CD1	2.44	0.47
48:X:65:MET:HE2	48:X:73:PHE:CE1	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:395:U:H2'	53:1:396:G:C8	2.49	0.47
53:1:742:A:H2'	53:1:743:A:C8	2.49	0.47
53:1:1344:U:H3'	53:1:1345:C:H5'	1.94	0.47
4:e:32:LYS:HD3	4:e:91:ARG:NH2	2.28	0.47
4:e:140:ILE:N	4:e:140:ILE:HD12	2.29	0.47
6:g:12:LEU:HD23	6:g:12:LEU:N	2.29	0.47
6:g:46:PHE:O	6:g:50:ARG:HB2	2.14	0.47
38:N:56:MET:HG3	38:N:57:VAL:N	2.29	0.47
40:P:85:VAL:HG21	40:P:92:ARG:HG3	1.97	0.47
53:1:987:C:H2'	53:1:988:A:O4'	2.14	0.47
15:p:29:VAL:HG13	15:p:79:VAL:HG22	1.96	0.47
32:H:139:ASN:HD22	32:H:142:ARG:HE	1.62	0.47
36:L:63:VAL:O	36:L:67:ASN:ND2	2.47	0.47
50:Z:35:GLU:OE1	50:Z:37:TYR:HB2	2.13	0.47
52:3:1236:A:H4'	52:3:1304:G:H4'	1.96	0.47
53:1:1028:A:N6	53:1:1125:G:H2'	2.29	0.47
53:1:2126:A:H2'	53:1:2162:G:C2	2.48	0.47
53:1:2427:C:H5''	53:1:2429:G:H5'	1.96	0.47
17:r:94:THR:O	17:r:94:THR:HG23	2.13	0.47
30:F:25:VAL:HB	30:F:35:GLN:HG3	1.96	0.47
31:G:2:THR:HB	31:G:50:ASN:HD21	1.80	0.47
45:U:25:ARG:NH1	45:U:25:ARG:HB2	2.30	0.47
45:U:44:SER:OG	45:U:45:GLU:N	2.47	0.47
52:3:235:C:H2'	52:3:236:A:C8	2.49	0.47
53:1:1138:G:H2'	53:1:1139:G:O4'	2.14	0.47
53:1:1444:G:H2'	53:1:1445:G:C8	2.49	0.47
53:1:1564:C:H2'	53:1:1565:C:O4'	2.14	0.47
53:1:1701:A:H2'	53:1:1702:G:H5'	1.95	0.47
53:1:2391:G:H4'	53:1:2392:A:OP1	2.14	0.47
54:2:118:C:H2'	54:2:119:A:C8	2.49	0.47
2:c:98:VAL:HG22	2:c:98:VAL:O	2.14	0.47
6:g:4:ILE:HG23	6:g:37:VAL:HG23	1.96	0.47
8:i:14:ALA:HB2	8:i:54:ILE:HG21	1.96	0.47
9:j:98:GLU:HB2	9:j:124:VAL:HG23	1.96	0.47
36:L:75:LYS:O	36:L:86:VAL:HG12	2.15	0.47
37:M:17:GLN:HE21	37:M:71:VAL:HG12	1.79	0.47
38:N:38:PHE:HZ	38:N:47:VAL:HG11	1.80	0.47
49:Y:2:ASN:ND2	49:Y:3:ILE:HG22	2.30	0.47
49:Y:35:TYR:HD1	49:Y:38:ILE:HD12	1.80	0.47
52:3:225:C:H3'	52:3:226:G:H5''	1.97	0.47
52:3:662:U:H2'	52:3:663:A:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:882:C:O2'	52:3:883:C:H5'	2.15	0.47
52:3:1199:U:H2'	52:3:1200:C:H5'	1.96	0.47
52:3:1260:G:H21	52:3:1275:A:H62	1.62	0.47
53:1:69:C:O2'	53:1:70:G:H5'	2.15	0.47
53:1:1078:U:H4'	53:1:1079:C:H5''	1.97	0.47
1:b:156:SER:HB2	53:1:1818:U:H5'	1.96	0.47
2:c:155:VAL:HG21	53:1:2618:G:H21	1.79	0.47
5:f:28:LYS:HD2	5:f:29:ASN:N	2.30	0.47
15:p:51:ASN:O	53:1:2845:U:H5''	2.14	0.47
25:z:7:THR:HG1	25:z:55:LYS:HB3	1.79	0.47
31:G:141:GLU:HA	31:G:144:GLU:HG3	1.97	0.47
39:O:15:HIS:O	39:O:18:ILE:HG22	2.15	0.47
43:S:39:ASP:HA	43:S:42:ASN:HD22	1.80	0.47
48:X:15:LEU:O	48:X:18:VAL:HG12	2.14	0.47
52:3:163:C:H2'	52:3:164:G:O4'	2.15	0.47
52:3:304:U:O2'	52:3:305:G:H5'	2.15	0.47
52:3:536:C:H2'	52:3:537:G:C8	2.49	0.47
52:3:915:A:H2'	52:3:916:U:H5'	1.96	0.47
53:1:598:U:H2'	53:1:599:A:C8	2.50	0.47
53:1:713:G:H21	53:1:718:A:H62	1.62	0.47
53:1:729:G:H4'	53:1:763:G:H5'	1.96	0.47
53:1:1965:C:H5''	53:1:1966:A:H2'	1.96	0.47
53:1:2475:C:C2'	53:1:2476:A:H5'	2.45	0.47
2:c:110:THR:OG1	2:c:202:ILE:HB	2.15	0.47
21:v:64:VAL:HA	21:v:69:GLU:HA	1.97	0.47
34:J:96:GLN:HG2	34:J:97:PRO:HD2	1.96	0.47
34:J:119:VAL:HG12	34:J:121:ASN:H	1.80	0.47
43:S:47:LEU:HD23	43:S:47:LEU:O	2.15	0.47
46:V:60:ILE:CG2	46:V:72:TRP:HB3	2.45	0.47
51:a:54:LYS:HZ2	55:6:63:G:H4'	1.76	0.47
52:3:485:U:H5'	52:3:486:U:OP2	2.15	0.47
52:3:860:A:H2'	52:3:861:G:O4'	2.15	0.47
52:3:1513:A:H2'	52:3:1514:G:C8	2.50	0.47
53:1:534:U:H2'	53:1:535:G:H8	1.79	0.47
53:1:1430:G:H2'	53:1:1431:A:O4'	2.15	0.47
53:1:1678:A:H2'	53:1:1679:A:O4'	2.15	0.47
53:1:2066:C:O2'	53:1:2067:G:H5'	2.15	0.47
1:b:135:PRO:HG2	35:K:80:PHE:CD1	2.49	0.47
31:G:130:LYS:HA	31:G:133:ALA:HB3	1.95	0.47
36:L:41:ILE:HG23	36:L:116:ALA:HA	1.96	0.47
50:Z:9:GLU:CD	50:Z:10:PRO:HD3	2.40	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:a:54:LYS:HG3	51:a:56:ASP:OD2	2.15	0.47
52:3:211:G:H2'	52:3:212:G:H5'	1.96	0.47
52:3:1228:C:H2'	52:3:1229:A:H8	1.79	0.47
52:3:1372:U:H2'	52:3:1373:G:O4'	2.15	0.47
53:1:82:U:H3	53:1:104:A:H61	1.63	0.47
53:1:783:A:C2'	53:1:784:G:H5'	2.45	0.47
53:1:1176:U:H2'	53:1:1177:G:C8	2.50	0.47
53:1:1790:C:H2'	53:1:1791:A:C5	2.49	0.47
53:1:2639:A:H2'	53:1:2640:G:O4'	2.15	0.47
55:6:31:G:H2'	55:6:32:C:H5'	1.95	0.47
4:e:58:ALA:O	4:e:139:GLU:HG2	2.14	0.47
38:N:33:SER:OG	38:N:36:GLN:HG2	2.15	0.47
52:3:955:U:H3	52:3:1225:A:H61	1.61	0.47
52:3:1323:G:H2'	52:3:1324:A:C8	2.50	0.47
53:1:435:C:H2'	53:1:436:C:H5'	1.97	0.47
55:6:68:C:H2'	55:6:69:C:O4'	2.14	0.47
11:l:93:ASN:C	11:l:95:LEU:H	2.23	0.46
33:I:18:LEU:H	33:I:18:LEU:CD2	2.27	0.46
40:P:124:LYS:O	40:P:125:LYS:O	2.33	0.46
52:3:300:A:H1'	52:3:565:U:O2	2.15	0.46
52:3:560:A:H5'	52:3:566:G:N2	2.31	0.46
52:3:1354:U:H2'	52:3:1355:G:C8	2.50	0.46
53:1:174:U:H2'	53:1:175:G:C8	2.50	0.46
53:1:1278:C:H2'	53:1:1279:G:H8	1.80	0.46
53:1:1786:A:H1'	53:1:1938:A:N6	2.30	0.46
53:1:2462:C:H1'	53:1:2491:U:O4	2.14	0.46
53:1:2475:C:H2'	53:1:2476:A:H5'	1.95	0.46
30:F:36:ARG:HD2	30:F:36:ARG:C	2.41	0.46
33:I:64:TYR:CE2	33:I:93:LEU:HD13	2.50	0.46
34:J:45:VAL:HG22	34:J:46:GLY:H	1.79	0.46
52:3:784:A:H2'	52:3:785:G:H8	1.80	0.46
52:3:1354:U:H2'	52:3:1355:G:H8	1.80	0.46
53:1:1858:A:H1'	53:1:1885:A:C2	2.50	0.46
53:1:2391:G:H2'	53:1:2424:C:H41	1.79	0.46
18:s:105:VAL:O	18:s:105:VAL:HG13	2.15	0.46
33:I:33:ILE:O	33:I:34:GLU:HG2	2.16	0.46
37:M:120:LEU:HD23	37:M:120:LEU:H	1.80	0.46
39:O:35:GLN:HE22	39:O:77:VAL:HG21	1.80	0.46
52:3:1391:U:H2'	52:3:1392:G:C8	2.51	0.46
53:1:740:C:O2'	53:1:741:U:H5'	2.14	0.46
8:i:20:SER:HB2	8:i:21:PRO:HD3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:p:43:GLU:OE1	15:p:43:GLU:N	2.48	0.46
15:p:90:ALA:HB2	15:p:112:ARG:HA	1.98	0.46
29:E:57:VAL:HG13	29:E:61:LEU:HD21	1.98	0.46
31:G:98:GLY:O	31:G:102:ASN:HB3	2.15	0.46
35:K:6:ILE:HD13	35:K:74:LEU:HD23	1.97	0.46
42:R:6:ILE:HG13	42:R:7:ASN:N	2.30	0.46
42:R:100:ARG:HD2	52:3:950:U:OP2	2.15	0.46
52:3:422:C:H4'	52:3:423:G:H5''	1.98	0.46
53:1:192:C:H2'	53:1:193:U:H5'	1.98	0.46
53:1:2196:C:O2'	53:1:2197:U:H5'	2.15	0.46
53:1:2327:A:H2'	53:1:2328:A:C8	2.50	0.46
7:h:99:PHE:HA	7:h:102:ALA:HB3	1.97	0.46
16:q:57:ARG:NH1	53:1:1154:G:OP2	2.49	0.46
19:t:2:ILE:HD12	19:t:2:ILE:H	1.81	0.46
32:H:172:VAL:O	32:H:172:VAL:HG13	2.15	0.46
33:I:44:LYS:HD2	33:I:45:PRO:HD2	1.96	0.46
35:K:91:ARG:HG3	35:K:92:THR:N	2.28	0.46
39:O:6:ILE:HG23	39:O:100:ILE:HD11	1.98	0.46
47:W:25:ILE:HA	47:W:28:LEU:HB2	1.97	0.46
53:1:1827:U:O2'	53:1:1828:G:H5'	2.15	0.46
53:1:1837:C:H2'	53:1:1899:A:H61	1.81	0.46
53:1:2298:A:H2'	53:1:2299:U:O4'	2.16	0.46
13:n:3:HIS:O	13:n:4:ARG:HB2	2.15	0.46
20:u:92:VAL:HG22	20:u:93:ARG:N	2.31	0.46
36:L:75:LYS:NZ	52:3:1378:C:H42	2.14	0.46
40:P:71:ASP:O	40:P:72:ALA:HB3	2.14	0.46
52:3:195:A:H2'	52:3:196:A:C8	2.50	0.46
52:3:393:A:H5'	52:3:483:C:O2'	2.16	0.46
52:3:1070:U:H2'	52:3:1071:C:C6	2.51	0.46
53:1:2475:C:H42	53:1:2529:G:H22	1.64	0.46
53:1:2637:U:H2'	53:1:2638:G:O4'	2.15	0.46
23:x:63:ILE:O	23:x:67:LEU:HD13	2.16	0.46
32:H:176:THR:HG23	32:H:179:ALA:HB2	1.97	0.46
33:I:18:LEU:HD11	33:I:62:ARG:HB2	1.97	0.46
34:J:107:GLY:HA2	52:3:8:A:H1'	1.97	0.46
35:K:50:PRO:HG3	35:K:55:HIS:HE1	1.79	0.46
42:R:3:ILE:HG22	42:R:56:ARG:CZ	2.45	0.46
46:V:39:ARG:HA	52:3:280:C:O2	2.16	0.46
53:1:548:G:H2'	53:1:549:G:O4'	2.16	0.46
53:1:589:U:H2'	53:1:590:A:C8	2.50	0.46
53:1:752:A:H62	53:1:2609:U:H3	1.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1300:G:H4'	53:1:1301:A:H5''	1.98	0.46
54:2:106:G:H2'	54:2:107:G:O4'	2.16	0.46
9:j:1:MET:HE1	17:r:13:ARG:HH21	1.80	0.46
13:n:100:CYS:HA	26:B:42:ILE:HG12	1.97	0.46
17:r:65:ALA:HB3	17:r:95:ASP:OD1	2.15	0.46
19:t:55:VAL:HG11	19:t:85:VAL:HG23	1.98	0.46
32:H:69:THR:OG1	32:H:70:ALA:N	2.49	0.46
32:H:152:VAL:HG12	32:H:197:VAL:HG22	1.98	0.46
38:N:78:ILE:HG22	38:N:82:ILE:HG13	1.97	0.46
40:P:30:ILE:HG22	40:P:45:THR:HG22	1.97	0.46
51:a:26:ALA:HA	51:a:222:VAL:HG11	1.98	0.46
52:3:516:U:H3	52:3:533:A:H62	1.62	0.46
52:3:621:A:H2'	52:3:622:A:O4'	2.16	0.46
52:3:784:A:H4'	53:1:1837:C:OP1	2.16	0.46
53:1:78:U:H2'	53:1:79:C:C6	2.51	0.46
53:1:511:U:H2'	53:1:512:G:H5'	1.97	0.46
54:2:22:U:H2'	54:2:23:G:C8	2.51	0.46
54:2:104:A:H2'	54:2:105:G:O4'	2.16	0.46
24:y:47:ARG:O	24:y:50:VAL:HG22	2.16	0.46
34:J:45:VAL:HG22	34:J:46:GLY:N	2.31	0.46
34:J:156:ARG:HD2	37:M:44:PHE:CE1	2.51	0.46
38:N:60:LEU:N	38:N:60:LEU:HD23	2.30	0.46
40:P:60:PHE:O	40:P:63:GLN:HB3	2.16	0.46
41:Q:101:LEU:HB3	41:Q:102:ASP:H	1.46	0.46
52:3:26:A:N6	52:3:558:G:H1'	2.31	0.46
52:3:34:C:H2'	52:3:35:G:C8	2.50	0.46
52:3:483:C:H2'	52:3:484:G:C8	2.51	0.46
52:3:711:G:O2'	52:3:712:A:H5'	2.15	0.46
52:3:1477:U:H2'	52:3:1478:U:C6	2.51	0.46
53:1:255:A:H2'	53:1:256:A:O4'	2.16	0.46
53:1:577:G:OP1	53:1:2502:G:H2'	2.15	0.46
53:1:832:U:H2'	53:1:833:A:C8	2.51	0.46
53:1:1956:U:H2'	53:1:1957:C:H5'	1.96	0.46
53:1:2756:U:H1'	53:1:2757:A:H5''	1.98	0.46
53:1:2834:G:O2'	53:1:2835:A:H5'	2.15	0.46
12:m:51:ARG:HA	12:m:54:THR:HG22	1.98	0.46
13:n:37:THR:HG22	13:n:110:MET:HE1	1.97	0.46
18:s:7:HIS:CD2	18:s:10:ALA:HB2	2.51	0.46
20:u:92:VAL:HG22	20:u:93:ARG:H	1.81	0.46
32:H:19:SER:O	43:S:93:PRO:HG3	2.15	0.46
32:H:38:VAL:O	32:H:42:LEU:HD13	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:18:LEU:HB2	33:I:63:ILE:HD11	1.97	0.46
34:J:12:GLU:HB3	34:J:38:VAL:HG12	1.97	0.46
34:J:73:VAL:HG21	34:J:143:LEU:HB3	1.98	0.46
42:R:14:ALA:HB1	42:R:33:LEU:HD21	1.97	0.46
42:R:25:GLY:H	52:3:1329:A:H5'	1.81	0.46
45:U:51:ARG:C	45:U:52:LEU:HD12	2.40	0.46
45:U:71:VAL:HA	45:U:74:LEU:HB2	1.98	0.46
52:3:219:U:H2'	52:3:220:G:C8	2.51	0.46
52:3:321:A:O2'	52:3:322:C:H5'	2.15	0.46
52:3:802:A:H2'	52:3:803:G:O4'	2.16	0.46
53:1:215:G:C4'	53:1:216:A:H4'	2.42	0.46
53:1:1102:C:H2'	53:1:1103:A:H8	1.81	0.46
53:1:1735:A:H2'	53:1:1736:U:O4'	2.16	0.46
53:1:1758:U:H5	53:1:2696:U:H5'	1.81	0.46
54:2:66:A:H4'	54:2:67:G:N7	2.31	0.46
3:d:48:THR:C	3:d:50:ALA:H	2.24	0.45
3:d:117:ARG:HH12	11:l:2:ARG:HG2	1.80	0.45
6:g:40:THR:HB	6:g:43:ASN:ND2	2.31	0.45
7:h:30:SER:O	53:1:1054:A:H4'	2.16	0.45
14:o:40:ILE:HD13	54:2:8:C:O2'	2.16	0.45
19:t:6:ARG:O	19:t:10:VAL:HG23	2.16	0.45
20:u:73:ASN:HD21	20:u:75:ALA:HB3	1.82	0.45
32:H:168:ARG:HD2	32:H:168:ARG:C	2.40	0.45
34:J:160:VAL:O	34:J:163:ILE:HG12	2.17	0.45
37:M:112:ASP:OD1	37:M:113:ARG:N	2.49	0.45
43:S:81:ILE:HG21	52:3:1202:U:N3	2.31	0.45
46:V:16:MET:HB3	46:V:19:SER:O	2.16	0.45
46:V:25:GLU:HG3	46:V:40:THR:HG22	1.98	0.45
47:W:61:ALA:HB3	47:W:67:LEU:HD12	1.98	0.45
52:3:785:G:O2'	52:3:786:G:H5'	2.16	0.45
7:h:25:ALA:HB3	7:h:99:PHE:CE2	2.51	0.45
18:s:5:ALA:HB3	18:s:54:ALA:HB2	1.98	0.45
31:G:41:ASN:OD1	31:G:43:GLU:HG2	2.16	0.45
35:K:18:VAL:CG1	35:K:19:PRO:HD3	2.46	0.45
35:K:73:GLU:O	35:K:77:THR:HG23	2.15	0.45
52:3:1125:U:H2'	52:3:1126:U:H2'	1.99	0.45
52:3:1201:A:C1'	52:3:1202:U:OP2	2.60	0.45
53:1:2281:A:O2'	53:1:2282:G:H5'	2.16	0.45
54:2:51:G:H2'	54:2:52:A:O4'	2.16	0.45
8:i:12:VAL:HG12	8:i:13:ALA:N	2.21	0.45
17:r:36:ALA:HA	17:r:58:VAL:HG12	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:18:LEU:HG	33:I:20:LEU:HD23	1.98	0.45
46:V:26:ARG:NH2	52:3:237:G:H5''	2.31	0.45
52:3:355:C:H5'	52:3:355:C:H6	1.81	0.45
52:3:790:A:H5'	55:5:39:C:H5'	1.97	0.45
52:3:1088:G:N2	52:3:1167:A:H61	2.14	0.45
53:1:1023:U:O2'	53:1:1122:G:H5'	2.17	0.45
53:1:1073:A:H2'	53:1:1074:G:O4'	2.16	0.45
53:1:1112:G:O2'	53:1:1113:U:H5'	2.17	0.45
53:1:2221:G:O2'	53:1:2222:C:H5'	2.16	0.45
55:6:13:C:C3'	55:6:14:A:H5''	2.46	0.45
31:G:27:LYS:N	31:G:28:PRO:CD	2.79	0.45
32:H:65:VAL:HG22	32:H:100:ILE:HG12	1.98	0.45
34:J:108:GLY:O	34:J:109:ALA:HB3	2.16	0.45
35:K:79:ARG:HH22	52:3:671:G:H4'	1.82	0.45
40:P:78:ILE:HD12	40:P:78:ILE:N	2.31	0.45
52:3:40:C:H2'	52:3:41:G:H8	1.81	0.45
53:1:948:C:H2'	53:1:949:G:C8	2.51	0.45
53:1:1930:G:O2'	53:1:1931:U:H6	2.00	0.45
53:1:2182:U:H2'	53:1:2183:A:C8	2.52	0.45
53:1:2224:G:H4'	53:1:2226:C:C2	2.50	0.45
2:c:110:THR:HG22	2:c:171:THR:HG23	1.98	0.45
28:D:18:PHE:CE1	28:D:31:LEU:HD21	2.52	0.45
40:P:111:ASP:OD2	50:Z:24:LYS:HG2	2.16	0.45
47:W:33:THR:HG22	47:W:37:LYS:O	2.16	0.45
53:1:2176:A:H2'	53:1:2177:C:C6	2.52	0.45
13:n:55:ALA:HA	13:n:80:PHE:CE1	2.51	0.45
18:s:42:LYS:O	18:s:45:VAL:HG12	2.16	0.45
18:s:77:ASP:OD1	18:s:102:HIS:HB2	2.17	0.45
32:H:86:LEU:HA	32:H:89:VAL:HG12	1.97	0.45
55:5:69:C:H2'	55:5:70:G:C8	2.51	0.45
4:e:145:VAL:HG12	4:e:147:ARG:H	1.81	0.45
6:g:89:LYS:HE2	6:g:89:LYS:HA	1.99	0.45
38:N:71:ILE:HG13	38:N:72:SER:N	2.32	0.45
40:P:46:ALA:HB1	40:P:61:ALA:HB1	1.99	0.45
51:a:40:GLU:HB3	51:a:217:THR:HG22	1.98	0.45
51:a:206:GLY:CA	53:1:1860:G:H5''	2.46	0.45
52:3:113:G:H1'	52:3:354:G:C5'	2.46	0.45
52:3:166:U:H2'	52:3:167:A:C8	2.52	0.45
52:3:1504:G:OP1	52:3:1507:A:H4'	2.16	0.45
53:1:783:A:H2'	53:1:784:G:C5'	2.46	0.45
53:1:2073:C:O2'	53:1:2074:U:H5'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2339:C:H2'	53:1:2340:A:C8	2.51	0.45
53:1:2743:U:C2'	53:1:2744:G:H5''	2.46	0.45
8:i:45:THR:HG22	8:i:50:LYS:HD3	1.98	0.45
25:z:29:ARG:NE	53:1:1183:U:H5''	2.32	0.45
35:K:88:MET:HE2	35:K:90:MET:HE2	1.99	0.45
39:O:40:ILE:HD12	39:O:40:ILE:H	1.82	0.45
43:S:25:GLU:O	43:S:30:ILE:HG12	2.17	0.45
52:3:1057:G:H2'	52:3:1058:G:O4'	2.16	0.45
53:1:861:A:H2'	53:1:862:G:O4'	2.16	0.45
53:1:2244:U:H2'	53:1:2245:U:O4'	2.17	0.45
2:c:40:LEU:HD12	2:c:46:ARG:HG3	1.98	0.45
15:p:91:VAL:HG12	15:p:92:ARG:H	1.80	0.45
16:q:23:TYR:CD1	53:1:533:G:H5'	2.52	0.45
41:Q:78:VAL:HG23	41:Q:101:LEU:HD23	1.98	0.45
44:T:55:LEU:O	44:T:59:VAL:HG23	2.16	0.45
47:W:31:TYR:HB3	47:W:54:LEU:HD21	1.99	0.45
52:3:392:C:H2'	52:3:393:A:H8	1.82	0.45
53:1:2121:G:H2'	53:1:2122:U:O4'	2.17	0.45
53:1:2358:A:H2'	53:1:2359:C:O4'	2.17	0.45
53:1:2786:U:O2'	53:1:2787:C:H5'	2.17	0.45
5:f:174:LYS:HE3	5:f:175:LYS:HG3	1.99	0.45
9:j:113:PRO:HD2	53:1:558:U:P	2.57	0.45
21:v:72:VAL:HG12	21:v:93:ARG:HA	1.99	0.45
32:H:155:ARG:NH1	32:H:192:TYR:O	2.50	0.45
42:R:54:THR:HA	42:R:57:ASP:OD2	2.16	0.45
46:V:12:VAL:HG12	46:V:21:VAL:O	2.17	0.45
52:3:748:G:H2'	52:3:749:A:C8	2.52	0.45
52:3:1243:C:H2'	52:3:1244:G:C8	2.52	0.45
52:3:1305:G:H22	52:3:1331:G:H2'	1.82	0.45
53:1:1307:A:H2'	53:1:1308:A:O4'	2.16	0.45
53:1:1889:A:H2'	53:1:1890:A:C8	2.52	0.45
54:2:3:C:H3'	54:2:4:C:C5'	2.45	0.45
7:h:3:LEU:HD23	7:h:4:ASN:H	1.82	0.44
9:j:101:ILE:N	9:j:101:ILE:HD12	2.32	0.44
17:r:14:VAL:HG21	17:r:98:ILE:HG13	1.98	0.44
21:v:5:ASN:HA	21:v:64:VAL:HG13	1.98	0.44
39:O:72:ARG:NH2	52:3:1151:A:O2'	2.51	0.44
41:Q:45:ASN:ND2	52:3:528:C:H41	2.15	0.44
49:Y:66:ILE:CG2	49:Y:70:LYS:HB3	2.47	0.44
50:Z:39:LYS:N	50:Z:40:PRO:CD	2.80	0.44
53:1:760:G:H2'	53:1:761:A:O4'	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:948:C:H2'	53:1:949:G:H8	1.81	0.44
53:1:1645:G:H5''	53:1:1646:C:H5'	1.98	0.44
53:1:2818:U:H2'	53:1:2819:G:H8	1.82	0.44
7:h:67:THR:HG22	7:h:68:PRO:HD3	1.99	0.44
8:i:79:LEU:HD13	8:i:135:MET:HG3	1.99	0.44
20:u:96:LYS:C	20:u:98:ASN:H	2.25	0.44
32:H:150:VAL:HG23	32:H:199:VAL:HG12	1.98	0.44
35:K:22:ILE:HD11	35:K:39:LEU:HG	1.99	0.44
37:M:12:ARG:CZ	52:3:826:C:H5'	2.48	0.44
41:Q:31:GLY:HA3	41:Q:54:VAL:CG2	2.48	0.44
42:R:48:SER:O	42:R:52:ILE:HG13	2.16	0.44
50:Z:13:VAL:HG22	50:Z:14:ALA:N	2.32	0.44
50:Z:38:GLU:HB2	52:3:1526:G:P	2.57	0.44
51:a:189:LEU:HD12	51:a:190:GLU:N	2.31	0.44
52:3:1342:C:H2'	52:3:1343:G:C8	2.52	0.44
53:1:191:A:H2'	53:1:192:C:C6	2.52	0.44
53:1:433:C:O2'	53:1:434:U:H5'	2.17	0.44
53:1:467:G:O2'	53:1:468:G:H5'	2.18	0.44
53:1:687:C:H2'	53:1:688:U:O4'	2.16	0.44
53:1:2248:C:C2'	53:1:2249:U:H5'	2.47	0.44
54:2:2:G:H2'	54:2:3:C:C6	2.52	0.44
5:f:83:THR:HG22	5:f:133:LYS:HG2	1.99	0.44
6:g:9:VAL:HG21	6:g:13:GLY:H	1.81	0.44
31:G:8:MET:HE2	31:G:13:VAL:HG21	2.00	0.44
32:H:6:PRO:HG2	32:H:200:TRP:HE1	1.81	0.44
41:Q:23:LEU:HD22	41:Q:29:LYS:CD	2.43	0.44
52:3:390:U:H2'	52:3:391:G:H8	1.82	0.44
52:3:714:G:H2'	52:3:715:A:C8	2.53	0.44
52:3:1040:U:H2'	52:3:1041:G:C8	2.53	0.44
52:3:1139:G:H5''	52:3:1140:C:H5	1.83	0.44
52:3:1170:A:H2'	52:3:1171:A:O4'	2.17	0.44
52:3:1352:C:H2'	52:3:1353:G:H8	1.81	0.44
53:1:207:A:H2'	53:1:208:C:O4'	2.17	0.44
53:1:594:U:H2'	53:1:595:C:C6	2.52	0.44
1:b:149:LYS:HD3	53:1:2204:G:H4'	1.99	0.44
6:g:41:LYS:HA	6:g:41:LYS:HD2	1.87	0.44
21:v:56:PHE:CE1	21:v:61:LEU:HD21	2.52	0.44
33:I:37:PRO:HD2	33:I:41:GLY:HA3	2.00	0.44
33:I:195:ASN:ND2	33:I:198:LEU:HD23	2.33	0.44
42:R:16:ILE:HD12	42:R:16:ILE:N	2.26	0.44
52:3:82:G:H2'	52:3:83:C:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:825:A:H2'	52:3:826:C:C6	2.52	0.44
52:3:1200:C:H1'	52:3:1204:A:N6	2.33	0.44
52:3:1436:U:H2'	52:3:1437:A:H8	1.83	0.44
53:1:225:C:H2'	53:1:226:A:O4'	2.17	0.44
53:1:490:C:H4'	53:1:491:G:OP2	2.18	0.44
56:4:17:U:O2'	56:4:18:G:H5'	2.18	0.44
7:h:5:LEU:O	7:h:5:LEU:HD23	2.18	0.44
19:t:55:VAL:HG13	19:t:86:THR:O	2.17	0.44
20:u:24:VAL:HA	20:u:35:VAL:HA	1.99	0.44
33:I:117:VAL:O	33:I:130:ASN:HA	2.18	0.44
42:R:77:LYS:HG2	42:R:81:ASP:OD2	2.17	0.44
52:3:423:G:H2'	52:3:424:G:H5'	1.98	0.44
52:3:1429:A:H2'	52:3:1430:A:C8	2.52	0.44
53:1:971:G:H2'	53:1:972:A:O4'	2.18	0.44
53:1:2128:G:H21	53:1:2173:A:H1'	1.82	0.44
4:e:33:ILE:HG22	4:e:155:ILE:HA	1.99	0.44
7:h:57:ASN:HB3	7:h:62:ARG:HD2	1.99	0.44
13:n:87:PHE:HD1	13:n:90:ARG:HD3	1.82	0.44
16:q:24:TYR:HE2	53:1:2020:A:H4'	1.83	0.44
18:s:17:VAL:HG12	18:s:76:VAL:HG21	1.99	0.44
25:z:38:GLU:HG3	25:z:40:THR:HG23	1.99	0.44
30:F:37:GLN:NE2	53:1:1125:G:H5'	2.32	0.44
41:Q:48:LEU:HB2	52:3:520:A:OP1	2.18	0.44
42:R:28:ARG:O	42:R:32:ILE:HG12	2.17	0.44
51:a:47:ASN:HB2	51:a:211:LYS:H	1.83	0.44
52:3:422:C:H5'	52:3:423:G:C2	2.53	0.44
53:1:1366:A:H2'	53:1:1367:A:O4'	2.18	0.44
53:1:1528:A:H2'	53:1:1529:G:O4'	2.18	0.44
53:1:1905:C:H2'	53:1:1930:G:O4'	2.17	0.44
53:1:2581:G:H2'	53:1:2581:G:N3	2.32	0.44
53:1:2628:C:H3'	53:1:2629:U:H5'	1.99	0.44
1:b:40:GLY:O	1:b:42:ARG:NH1	2.51	0.44
1:b:48:ILE:HD11	1:b:51:ARG:HA	2.00	0.44
10:k:99:ILE:HD13	10:k:115:ILE:HG23	1.99	0.44
12:m:125:PRO:HB3	53:1:2485:G:O3'	2.17	0.44
15:p:31:VAL:HG21	15:p:40:GLN:HG2	2.00	0.44
18:s:43:ALA:HA	18:s:46:LEU:HB2	2.00	0.44
32:H:46:LEU:HB3	32:H:49:ALA:HB3	1.99	0.44
33:I:184:LYS:HA	33:I:185:PRO:HD3	1.83	0.44
38:N:9:GLY:HA2	38:N:80:HIS:ND1	2.33	0.44
50:Z:34:ARG:HB3	50:Z:36:PHE:CE1	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:781:A:OP1	52:3:1523:G:H5'	2.17	0.44
52:3:1401:G:H2'	52:3:1402:C:O4'	2.17	0.44
53:1:864:G:O2'	53:1:865:C:H5'	2.17	0.44
53:1:1060:U:H4'	53:1:1061:U:C5'	2.48	0.44
53:1:1524:G:H2'	53:1:1525:A:C8	2.53	0.44
3:d:181:ILE:HD13	11:l:6:LEU:HD11	1.99	0.44
7:h:91:ALA:O	7:h:92:ALA:HB3	2.17	0.44
13:n:79:LEU:C	13:n:81:ASN:H	2.26	0.44
18:s:69:LEU:HG	18:s:107:VAL:HG22	1.98	0.44
27:C:7:LYS:HA	27:C:23:THR:HA	1.99	0.44
33:I:171:GLU:HB2	33:I:180:THR:HG23	1.99	0.44
40:P:127:ARG:HG2	40:P:127:ARG:HH11	1.83	0.44
41:Q:4:ASN:O	41:Q:7:VAL:HG22	2.17	0.44
42:R:18:LEU:HD23	42:R:18:LEU:O	2.17	0.44
50:Z:39:LYS:O	50:Z:42:THR:HG22	2.17	0.44
53:1:1642:G:O2'	53:1:1643:G:H5'	2.18	0.44
5:f:72:ASN:O	5:f:76:ILE:HG13	2.18	0.44
6:g:68:ARG:HD2	6:g:68:ARG:C	2.42	0.44
10:k:113:MET:SD	10:k:116:ILE:HD11	2.58	0.44
11:l:57:LEU:HD22	29:E:53:ASP:HB3	1.99	0.44
15:p:1:SER:O	15:p:5:LYS:HB2	2.18	0.44
18:s:24:ILE:HD13	18:s:36:LEU:HD11	1.99	0.44
23:x:18:SER:OG	23:x:19:HIS:N	2.51	0.44
33:I:36:ALA:N	33:I:37:PRO:HD3	2.33	0.44
35:K:44:ARG:HA	35:K:58:HIS:HA	2.00	0.44
40:P:30:ILE:HG22	40:P:45:THR:CG2	2.47	0.44
41:Q:47:ALA:HB1	52:3:520:A:OP2	2.17	0.44
49:Y:66:ILE:HG23	49:Y:70:LYS:HB3	2.00	0.44
52:3:413:G:N2	52:3:428:G:H1'	2.32	0.44
52:3:1273:C:H2'	52:3:1274:A:O4'	2.17	0.44
53:1:578:G:H21	53:1:1252:G:N2	2.15	0.44
53:1:1326:U:H2'	53:1:1327:A:C8	2.52	0.44
1:b:117:SER:HB2	1:b:128:THR:HB	2.00	0.43
24:y:24:GLU:HA	24:y:28:LEU:HD23	2.00	0.43
35:K:11:HIS:NE2	35:K:13:ASP:OD2	2.51	0.43
37:M:29:SER:HB3	37:M:32:LYS:HG3	2.00	0.43
37:M:46:GLU:O	37:M:61:THR:HG23	2.18	0.43
38:N:78:ILE:O	38:N:82:ILE:HG13	2.17	0.43
39:O:12:ALA:HB2	39:O:96:VAL:HA	2.00	0.43
43:S:20:PHE:C	43:S:22:LYS:H	2.25	0.43
46:V:44:HIS:O	46:V:70:LYS:HA	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:211:G:C2'	52:3:212:G:H5'	2.48	0.43
52:3:423:G:C2'	52:3:424:G:H5'	2.48	0.43
52:3:512:U:H2'	52:3:513:C:C6	2.53	0.43
53:1:833:A:H2'	53:1:834:G:C8	2.53	0.43
53:1:1078:U:H5''	53:1:1079:C:H5''	2.00	0.43
53:1:1106:G:H5'	53:1:1106:G:H8	1.82	0.43
53:1:2628:C:O2'	53:1:2781:A:H2'	2.18	0.43
53:1:2699:C:H2'	53:1:2700:A:C8	2.53	0.43
2:c:46:ARG:NH2	2:c:88:GLU:O	2.52	0.43
4:e:47:LYS:O	4:e:50:ASP:OD2	2.35	0.43
12:m:57:VAL:HG11	12:m:105:MET:SD	2.57	0.43
18:s:6:LYS:HG2	53:1:494:G:H4'	1.99	0.43
31:G:46:VAL:HG23	31:G:47:PRO:CD	2.46	0.43
43:S:10:VAL:HA	43:S:13:VAL:HG12	2.00	0.43
49:Y:25:SER:OG	52:3:1458:G:H5''	2.18	0.43
50:Z:65:ARG:NH1	52:3:1088:G:H4'	2.33	0.43
52:3:815:A:H4'	52:3:817:C:C4	2.53	0.43
53:1:242:G:N2	53:1:254:G:H2'	2.33	0.43
53:1:2391:G:O2'	53:1:2392:A:O5'	2.33	0.43
4:e:165:GLY:O	4:e:168:LEU:HB3	2.18	0.43
8:i:101:SER:HA	8:i:140:GLU:O	2.17	0.43
13:n:48:VAL:HA	13:n:51:LEU:HD12	2.00	0.43
16:q:90:ASP:OD2	53:1:996:A:H4'	2.18	0.43
40:P:88:PRO:HG3	50:Z:28:LEU:HG	2.00	0.43
40:P:126:ARG:NH2	52:3:692:U:H5''	2.33	0.43
41:Q:41:PRO:HG3	41:Q:49:ARG:HG3	1.99	0.43
41:Q:114:SER:HB3	52:3:35:G:H21	1.84	0.43
51:a:170:ILE:HD12	51:a:170:ILE:N	2.33	0.43
52:3:1137:C:H4'	52:3:1138:G:N2	2.34	0.43
52:3:1251:A:O2'	52:3:1370:G:H5'	2.18	0.43
52:3:1258:G:O2'	52:3:1259:C:H5'	2.18	0.43
52:3:1291:U:H2'	52:3:1292:G:C8	2.53	0.43
52:3:1413:A:H2	52:3:1487:G:H22	1.63	0.43
53:1:82:U:H2'	53:1:83:A:O4'	2.18	0.43
53:1:1370:C:H2'	53:1:1371:G:O4'	2.18	0.43
53:1:2277:G:H3'	53:1:2278:A:H5''	1.99	0.43
53:1:2339:C:H2'	53:1:2340:A:H8	1.83	0.43
54:2:35:C:H2'	54:2:36:C:H5'	2.00	0.43
5:f:136:ASP:OD2	5:f:138:GLN:HB3	2.19	0.43
8:i:29:GLN:HE22	53:1:1097:U:H3	1.64	0.43
8:i:41:PHE:HZ	8:i:54:ILE:HG21	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:p:7:LEU:O	15:p:7:LEU:HD23	2.18	0.43
19:t:80:TRP:HZ3	19:t:82:LYS:HB3	1.83	0.43
30:F:30:GLU:H	30:F:30:GLU:CD	2.27	0.43
42:R:63:VAL:HG23	42:R:67:ASP:HB3	1.99	0.43
45:U:22:ALA:CB	45:U:32:PHE:HA	2.49	0.43
48:X:49:ALA:HB1	48:X:56:HIS:HB3	2.00	0.43
52:3:1138:G:H3'	52:3:1138:G:N3	2.34	0.43
52:3:1333:A:H2'	52:3:1334:G:O4'	2.18	0.43
52:3:1500:A:H5''	52:3:1508:A:H5''	2.00	0.43
52:3:1540:U:O2	52:3:1540:U:H3'	2.18	0.43
53:1:873:C:H2'	53:1:874:G:C8	2.53	0.43
53:1:1685:C:H2'	53:1:1686:C:H6	1.83	0.43
53:1:2030:A:N3	53:1:2499:C:H5''	2.33	0.43
1:b:48:ILE:HG22	53:1:779:U:P	2.59	0.43
5:f:116:LEU:HD13	5:f:120:ILE:O	2.19	0.43
7:h:36:ASP:HA	7:h:39:THR:HG23	2.00	0.43
11:l:20:GLY:O	11:l:21:ARG:NH2	2.48	0.43
11:l:65:GLY:C	53:1:2415:G:H4'	2.44	0.43
18:s:36:LEU:HA	18:s:39:THR:HG22	2.01	0.43
28:D:26:ASN:CG	53:1:682:G:H5'	2.44	0.43
32:H:32:LEU:O	32:H:35:ASP:HB3	2.18	0.43
33:I:64:TYR:HB2	33:I:66:VAL:HG23	2.00	0.43
33:I:171:GLU:HB2	33:I:180:THR:CG2	2.49	0.43
40:P:79:LYS:HE2	40:P:79:LYS:HA	2.01	0.43
45:U:6:LEU:HD11	45:U:71:VAL:HG13	1.99	0.43
52:3:624:C:H2'	52:3:625:U:O4'	2.18	0.43
52:3:1298:U:H4'	52:3:1299:A:O4'	2.17	0.43
52:3:1432:G:H1'	52:3:1468:A:N6	2.33	0.43
53:1:35:G:H2'	53:1:36:G:O4'	2.18	0.43
53:1:460:A:H2'	53:1:461:C:O4'	2.19	0.43
53:1:2519:U:H5'	53:1:2567:G:H21	1.84	0.43
53:1:2529:G:H5''	53:1:2530:A:H5''	2.00	0.43
1:b:141:HIS:ND1	1:b:192:GLY:O	2.52	0.43
2:c:125:TRP:CE3	2:c:160:LYS:HD3	2.53	0.43
7:h:121:SER:OG	7:h:122:GLN:N	2.50	0.43
13:n:18:GLN:NE2	53:1:2709:G:OP1	2.51	0.43
17:r:33:VAL:HG13	17:r:61:ALA:HB3	2.01	0.43
19:t:11:LEU:HB2	24:y:26:PHE:HE1	1.83	0.43
28:D:34:ARG:CZ	28:D:39:ARG:HD2	2.48	0.43
35:K:12:PRO:O	35:K:15:SER:HB2	2.19	0.43
52:3:1101:A:H4'	52:3:1102:A:O5'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1397:C:N4	56:4:22:A:H2'	2.32	0.43
52:3:1434:A:H2'	52:3:1435:G:O4'	2.19	0.43
53:1:230:G:O2'	53:1:231:A:H5'	2.19	0.43
53:1:438:G:H2'	53:1:439:A:C8	2.53	0.43
53:1:1331:G:O2'	53:1:1332:G:H5''	2.18	0.43
54:2:78:A:H2'	54:2:79:G:O4'	2.19	0.43
54:2:100:G:H2'	54:2:101:A:O4'	2.19	0.43
2:c:46:ARG:CZ	2:c:86:GLU:HA	2.49	0.43
6:g:5:LEU:HD22	6:g:13:GLY:HA3	2.00	0.43
6:g:97:ARG:HG2	6:g:112:LYS:HD2	2.00	0.43
8:i:101:SER:HB3	8:i:104:GLN:HG3	1.99	0.43
15:p:47:ILE:HD13	15:p:61:ARG:HB2	2.01	0.43
19:t:14:PRO:HD3	24:y:30:MET:SD	2.59	0.43
19:t:32:LEU:HD12	19:t:32:LEU:O	2.19	0.43
19:t:88:LYS:O	19:t:91:GLN:HG2	2.18	0.43
27:C:21:THR:HG23	29:E:33:THR:HG22	2.00	0.43
38:N:49:GLN:O	38:N:52:GLU:HG2	2.19	0.43
46:V:18:LYS:HA	46:V:49:ASN:HA	2.00	0.43
49:Y:2:ASN:CG	49:Y:3:ILE:H	2.26	0.43
52:3:123:U:OP1	52:3:312:C:H5'	2.18	0.43
52:3:337:G:H2'	52:3:338:A:C8	2.54	0.43
52:3:399:G:H2'	52:3:400:C:C6	2.52	0.43
52:3:1498:U:C4	56:4:17:U:H5''	2.54	0.43
53:1:279:A:H2'	53:1:280:U:H5'	1.99	0.43
53:1:807:U:H2'	53:1:808:G:C8	2.54	0.43
53:1:1570:A:H2'	53:1:1571:A:C8	2.54	0.43
53:1:1662:U:O2'	53:1:1663:G:H5'	2.18	0.43
1:b:140:VAL:HG23	1:b:161:VAL:CG2	2.48	0.43
6:g:112:LYS:HZ3	53:1:2220:U:H5''	1.83	0.43
6:g:121:VAL:HG22	6:g:121:VAL:O	2.19	0.43
18:s:51:LEU:O	18:s:55:ILE:HG13	2.19	0.43
19:t:39:THR:O	19:t:43:ILE:HG13	2.18	0.43
34:J:96:GLN:O	34:J:122:VAL:HG23	2.19	0.43
35:K:92:THR:OG1	35:K:93:LYS:N	2.30	0.43
52:3:70:U:H2'	52:3:94:G:O6	2.19	0.43
52:3:415:A:H2'	52:3:416:G:O4'	2.18	0.43
52:3:501:C:H2'	52:3:502:A:C8	2.54	0.43
52:3:715:A:H2'	52:3:716:A:H8	1.84	0.43
52:3:1524:C:H2'	52:3:1525:G:C8	2.54	0.43
53:1:1092:C:H2'	53:1:1093:G:O4'	2.18	0.43
53:1:2082:A:H2'	53:1:2083:G:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2863:C:H2'	53:1:2864:G:C8	2.53	0.43
7:h:105:LYS:HE2	7:h:105:LYS:HB3	1.90	0.43
13:n:39:PRO:HG2	53:1:1651:G:H4'	2.01	0.43
14:o:3:LYS:HE3	54:2:30:C:OP1	2.19	0.43
46:V:17:GLU:C	46:V:19:SER:H	2.27	0.43
51:a:15:VAL:HG21	51:a:33:LEU:HD21	2.01	0.43
52:3:1228:C:H2'	52:3:1229:A:C8	2.54	0.43
53:1:558:U:H2'	53:1:559:G:H8	1.83	0.43
53:1:941:A:H2'	53:1:942:G:O4'	2.18	0.43
53:1:1415:U:H2'	53:1:1416:G:H4'	2.01	0.43
8:i:93:ASN:HD21	53:1:1077:A:C5'	2.30	0.43
12:m:78:LEU:O	12:m:79:ALA:HB3	2.19	0.43
21:v:92:VAL:HG13	21:v:92:VAL:O	2.19	0.43
33:I:8:LEU:HD11	33:I:31:CYS:SG	2.59	0.43
35:K:18:VAL:N	35:K:19:PRO:CD	2.82	0.43
52:3:966:G:C2	55:5:34:C:H5'	2.54	0.43
53:1:859:G:HO2'	53:1:860:U:H5	1.63	0.43
53:1:1300:G:C4'	53:1:1301:A:H5''	2.49	0.43
53:1:1657:U:H2'	53:1:1658:C:C6	2.54	0.43
53:1:1773:A:N7	53:1:1829:A:H1'	2.33	0.43
53:1:2065:C:H1'	53:1:2449:U:H3	1.83	0.43
53:1:2520:C:O2'	53:1:2521:C:H5'	2.19	0.43
5:f:11:PRO:HG2	5:f:79:THR:HG21	2.01	0.42
9:j:35:ARG:HA	9:j:40:HIS:HD2	1.84	0.42
10:k:93:GLN:HA	10:k:94:PRO:HD2	1.81	0.42
31:G:125:PHE:HE1	31:G:136:ARG:HD3	1.84	0.42
32:H:131:ARG:HE	32:H:135:ARG:HH21	1.65	0.42
33:I:103:ARG:HB3	33:I:170:LEU:HD11	2.00	0.42
37:M:49:LYS:O	37:M:58:LEU:HD12	2.19	0.42
43:S:80:ARG:O	43:S:83:VAL:HG12	2.18	0.42
46:V:12:VAL:HG13	46:V:21:VAL:HG13	2.01	0.42
49:Y:43:LYS:HD2	49:Y:85:LEU:HB3	2.00	0.42
52:3:20:U:H2'	52:3:21:G:O4'	2.19	0.42
52:3:193:C:H2'	52:3:194:C:C6	2.54	0.42
52:3:620:C:H2'	52:3:621:A:O4'	2.19	0.42
52:3:1230:C:H5'	55:5:30:G:H5''	2.00	0.42
53:1:196:A:N3	53:1:196:A:H2'	2.34	0.42
53:1:1857:G:H1'	53:1:1885:A:N6	2.34	0.42
55:6:11:A:H2'	55:6:12:G:H8	1.84	0.42
1:b:42:ARG:HH11	1:b:42:ARG:HG3	1.84	0.42
10:k:92:GLU:O	10:k:93:GLN:O	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:q:60:TRP:CZ2	16:q:92:LYS:HG3	2.54	0.42
24:y:22:LEU:HG	24:y:23:ARG:HD3	2.01	0.42
32:H:22:PHE:HB2	39:O:95:GLY:O	2.19	0.42
34:J:148:SER:O	34:J:152:VAL:HG23	2.19	0.42
38:N:28:VAL:HG13	38:N:63:TYR:HD1	1.84	0.42
38:N:60:LEU:HD23	38:N:60:LEU:H	1.84	0.42
45:U:18:GLN:O	45:U:20:VAL:HG13	2.18	0.42
49:Y:70:LYS:HG3	49:Y:73:ARG:NH2	2.34	0.42
52:3:89:U:H2'	52:3:90:C:O4'	2.19	0.42
52:3:945:G:H2'	52:3:945:G:N3	2.33	0.42
53:1:468:G:H2'	53:1:469:G:O4'	2.20	0.42
53:1:562:U:O4'	53:1:2036:C:H5'	2.19	0.42
53:1:772:C:O2'	53:1:773:U:H5'	2.19	0.42
53:1:2412:A:H2'	53:1:2413:G:O4'	2.19	0.42
1:b:129:LEU:N	1:b:129:LEU:HD23	2.34	0.42
32:H:125:ARG:HB2	32:H:127:VAL:HG23	2.01	0.42
36:L:29:LEU:HD12	36:L:104:VAL:HG13	2.01	0.42
36:L:41:ILE:HD13	36:L:115:MET:HE2	2.01	0.42
41:Q:20:VAL:HG21	52:3:553:A:H5''	2.01	0.42
42:R:3:ILE:HG22	42:R:56:ARG:NE	2.34	0.42
42:R:6:ILE:O	42:R:7:ASN:C	2.61	0.42
45:U:22:ALA:HB2	45:U:32:PHE:CB	2.49	0.42
48:X:66:VAL:HG13	48:X:67:GLY:N	2.34	0.42
52:3:977:A:H2'	52:3:978:A:H5''	2.02	0.42
52:3:1033:G:H2'	52:3:1034:G:C5'	2.49	0.42
53:1:1020:A:C1'	53:1:1021:A:OP2	2.61	0.42
53:1:1367:A:C2'	53:1:1368:G:H5'	2.49	0.42
53:1:1775:U:H2'	53:1:1776:G:H5'	2.02	0.42
53:1:2725:A:O2'	53:1:2726:A:C8	2.72	0.42
56:4:8:A:H2'	56:4:9:G:H8	1.84	0.42
4:e:169:LEU:HA	4:e:172:PHE:HD2	1.83	0.42
6:g:77:THR:HA	6:g:143:ILE:O	2.19	0.42
7:h:58:THR:HA	7:h:63:ALA:HB3	2.01	0.42
7:h:114:GLU:O	7:h:123:ILE:HB	2.19	0.42
8:i:12:VAL:HG22	53:1:1061:U:O2	2.19	0.42
11:l:55:MET:HE3	53:1:2392:A:C2	2.54	0.42
14:o:16:ARG:HE	14:o:19:GLN:HE21	1.66	0.42
21:v:26:PHE:HE1	21:v:44:HIS:HA	1.84	0.42
24:y:2:LYS:NZ	24:y:6:LEU:HD22	2.34	0.42
30:F:16:ILE:N	30:F:16:ILE:HD12	2.34	0.42
32:H:22:PHE:CD2	39:O:97:ASP:HB2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:J:80:LEU:HD13	34:J:122:VAL:HB	2.00	0.42
37:M:35:ILE:O	37:M:38:VAL:HG12	2.20	0.42
41:Q:101:LEU:C	41:Q:103:CYS:H	2.28	0.42
52:3:1346:A:H2'	52:3:1346:A:N3	2.34	0.42
53:1:807:U:H2'	53:1:808:G:H8	1.84	0.42
53:1:1609:A:H1'	53:1:1616:A:O4'	2.18	0.42
53:1:2019:A:H2	53:1:2035:G:H22	1.67	0.42
53:1:2185:U:H2'	53:1:2186:G:C8	2.55	0.42
53:1:2853:C:H2'	53:1:2854:G:C8	2.54	0.42
1:b:5:CYS:SG	1:b:17:LYS:HE2	2.59	0.42
4:e:130:GLY:HA2	4:e:152:ASP:HA	2.02	0.42
19:t:73:ARG:N	19:t:73:ARG:HD2	2.35	0.42
24:y:4:LYS:HG3	24:y:7:ARG:HH22	1.84	0.42
32:H:61:LYS:HD3	32:H:61:LYS:N	2.34	0.42
32:H:161:ILE:HD12	32:H:161:ILE:N	2.34	0.42
38:N:104:THR:HG22	52:3:1180:A:OP1	2.19	0.42
53:1:629:G:H5''	53:1:650:C:O2'	2.18	0.42
53:1:859:G:O2'	53:1:860:U:P	2.77	0.42
53:1:2849:U:H4'	53:1:2868:A:C2	2.55	0.42
1:b:241:LYS:O	53:1:1902:C:H4'	2.20	0.42
6:g:12:LEU:HD12	6:g:19:VAL:HG11	2.00	0.42
7:h:50:VAL:HG13	53:1:1083:U:OP2	2.19	0.42
7:h:80:THR:O	7:h:81:LEU:C	2.62	0.42
35:K:46:GLN:HA	35:K:56:LYS:HG2	2.02	0.42
36:L:37:THR:O	36:L:41:ILE:HG13	2.19	0.42
39:O:100:ILE:HG13	39:O:101:SER:N	2.34	0.42
51:a:3:LYS:HG3	51:a:4:LEU:N	2.35	0.42
52:3:229:U:H2'	52:3:230:G:C8	2.55	0.42
52:3:272:C:H2'	52:3:273:U:C6	2.55	0.42
52:3:458:U:H2'	52:3:459:A:C8	2.55	0.42
52:3:763:G:H2'	52:3:764:C:C6	2.54	0.42
53:1:699:A:H2'	53:1:700:G:O4'	2.19	0.42
53:1:996:A:H2'	53:1:997:G:H8	1.84	0.42
1:b:70:LYS:O	1:b:117:SER:OG	2.34	0.42
6:g:48:GLU:HA	6:g:52:ALA:HB2	2.02	0.42
8:i:57:VAL:O	8:i:57:VAL:HG13	2.20	0.42
11:l:30:THR:HG22	53:1:810:U:O4	2.19	0.42
11:l:118:THR:HA	11:l:119:PRO:HD3	1.88	0.42
20:u:31:GLY:O	20:u:66:VAL:HG13	2.20	0.42
34:J:125:LYS:HG2	34:J:127:TYR:CZ	2.54	0.42
34:J:134:ASN:ND2	52:3:19:A:OP1	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:M:71:VAL:O	37:M:71:VAL:HG13	2.20	0.42
39:O:42:LEU:HD22	39:O:73:LEU:HD22	2.02	0.42
48:X:62:THR:HG22	48:X:65:MET:SD	2.59	0.42
50:Z:38:GLU:HB2	52:3:1526:G:OP2	2.19	0.42
52:3:114:U:O2'	52:3:115:G:H5'	2.19	0.42
52:3:1379:G:O2'	52:3:1380:U:H5'	2.19	0.42
53:1:2186:G:H2'	53:1:2187:U:O4'	2.20	0.42
53:1:2704:C:H2'	53:1:2705:A:O4'	2.20	0.42
2:c:77:ARG:O	2:c:77:ARG:HG3	2.20	0.42
3:d:79:ARG:HD3	53:1:1258:U:H4'	2.01	0.42
3:d:186:VAL:O	3:d:186:VAL:HG13	2.20	0.42
4:e:2:LYS:HE3	4:e:100:GLU:HG2	2.02	0.42
9:j:11:VAL:HG13	9:j:11:VAL:O	2.19	0.42
9:j:113:PRO:HD2	53:1:558:U:OP1	2.19	0.42
36:L:27:ASN:HB3	52:3:1374:A:O2'	2.19	0.42
49:Y:54:GLN:N	49:Y:55:PRO:HD2	2.35	0.42
53:1:1524:G:H2'	53:1:1525:A:H8	1.85	0.42
53:1:2545:G:H2'	53:1:2546:U:O4'	2.20	0.42
53:1:2705:A:H2'	53:1:2706:A:O4'	2.19	0.42
53:1:2861:U:H2'	53:1:2862:G:C8	2.54	0.42
18:s:52:GLU:HA	18:s:55:ILE:HD12	2.01	0.42
27:C:34:GLU:HA	27:C:48:TYR:O	2.20	0.42
27:C:43:ARG:NH1	53:1:2370:G:H4'	2.34	0.42
31:G:187:ASP:HB3	31:G:189:ASN:OD1	2.20	0.42
33:I:116:LEU:HG	33:I:121:ALA:HB3	2.01	0.42
34:J:52:ALA:HB2	34:J:61:LYS:HE2	2.01	0.42
42:R:9:PRO:HG2	42:R:44:ILE:HG13	2.02	0.42
49:Y:17:ARG:HB3	52:3:323:U:H5'	2.01	0.42
51:a:7:ARG:HB3	53:1:2129:C:OP1	2.20	0.42
52:3:162:A:H2'	52:3:163:C:O4'	2.19	0.42
52:3:1395:C:H6	52:3:1395:C:H5'	1.85	0.42
53:1:1078:U:C5'	53:1:1079:C:H5''	2.50	0.42
53:1:1893:C:H2'	53:1:1894:C:H5'	2.01	0.42
1:b:251:THR:OG1	1:b:252:LYS:N	2.53	0.42
4:e:84:ILE:CD1	53:1:2312:U:H5'	2.41	0.42
7:h:3:LEU:O	7:h:6:GLN:HB2	2.19	0.42
14:o:33:ARG:HG2	14:o:34:HIS:CD2	2.55	0.42
35:K:89:VAL:HG23	52:3:737:C:H5'	2.01	0.42
36:L:68:VAL:HA	36:L:137:ARG:HD3	2.02	0.42
38:N:20:ILE:HD11	38:N:60:LEU:CD1	2.49	0.42
40:P:115:ILE:O	40:P:115:ILE:HG13	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:Q:99:GLY:HA3	41:Q:117:GLY:HA3	2.02	0.42
52:3:231:U:H2'	52:3:232:G:C8	2.54	0.42
52:3:572:A:H5''	52:3:917:G:H4'	2.01	0.42
52:3:580:C:H2'	52:3:581:G:O4'	2.20	0.42
53:1:692:C:O2'	53:1:693:A:H5'	2.20	0.42
53:1:1270:C:H5''	53:1:1271:G:O5'	2.20	0.42
53:1:2861:U:H2'	53:1:2862:G:H8	1.84	0.42
54:2:55:U:O2'	54:2:56:G:H5'	2.20	0.42
10:k:107:LEU:O	10:k:112:PHE:HB2	2.21	0.41
17:r:49:ILE:HG22	17:r:54:VAL:HG22	2.02	0.41
28:D:44:VAL:O	28:D:44:VAL:HG13	2.20	0.41
32:H:31:ASN:HD22	32:H:31:ASN:HA	1.63	0.41
52:3:392:C:H2'	52:3:393:A:C8	2.54	0.41
53:1:1152:C:H2'	53:1:1153:C:C6	2.55	0.41
53:1:2004:G:H2'	53:1:2005:A:O4'	2.20	0.41
53:1:2248:C:H2'	53:1:2249:U:H5'	2.02	0.41
54:2:60:C:H2'	54:2:61:G:C8	2.54	0.41
5:f:72:ASN:O	5:f:75:VAL:HG22	2.20	0.41
7:h:26:VAL:HG23	7:h:83:ALA:H	1.85	0.41
10:k:92:GLU:O	10:k:93:GLN:C	2.63	0.41
10:k:110:GLU:N	10:k:113:MET:HE2	2.21	0.41
15:p:63:ILE:HG23	15:p:63:ILE:O	2.20	0.41
15:p:102:ARG:NH2	53:1:1754:A:O3'	2.53	0.41
24:y:49:ASP:O	24:y:53:VAL:HG23	2.20	0.41
25:z:15:ARG:HE	25:z:52:PHE:HE2	1.68	0.41
38:N:21:LYS:O	38:N:61:ASP:N	2.53	0.41
40:P:80:ASN:HB3	40:P:105:ARG:HB3	2.02	0.41
41:Q:23:LEU:HD22	41:Q:29:LYS:NZ	2.29	0.41
45:U:13:LYS:HE3	52:3:392:C:H5'	2.03	0.41
52:3:1342:C:H2'	52:3:1343:G:H8	1.85	0.41
53:1:331:C:H41	53:1:1210:G:N2	2.18	0.41
53:1:565:C:H4'	53:1:1253:A:C6	2.55	0.41
53:1:979:A:H2'	53:1:982:C:H42	1.84	0.41
53:1:1079:C:H2'	53:1:1080:A:C8	2.55	0.41
53:1:1681:G:N3	53:1:1762:A:H2'	2.35	0.41
53:1:1801:A:H5''	53:1:2203:U:C2'	2.48	0.41
3:d:44:ARG:HD2	53:1:444:C:OP2	2.21	0.41
3:d:118:LEU:HD12	3:d:186:VAL:O	2.20	0.41
4:e:30:VAL:HG13	4:e:30:VAL:O	2.21	0.41
5:f:98:LYS:NZ	5:f:103:ASN:HB2	2.35	0.41
6:g:51:ARG:HG2	6:g:55:GLU:OE1	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:i:91:LYS:HB3	8:i:94:LYS:HB2	2.03	0.41
13:n:108:ALA:HA	13:n:109:PRO:HD3	1.94	0.41
25:z:11:SER:HB2	53:1:989:G:OP2	2.20	0.41
28:D:24:THR:HG22	28:D:25:LYS:N	2.35	0.41
33:I:149:LYS:HG2	33:I:150:LYS:N	2.35	0.41
34:J:132:PRO:O	34:J:136:VAL:HG23	2.19	0.41
34:J:148:SER:OG	34:J:149:PRO:HD2	2.20	0.41
35:K:37:HIS:CE1	35:K:95:ALA:HB3	2.55	0.41
39:O:40:ILE:HA	39:O:41:PRO:HD3	1.90	0.41
41:Q:77:SER:OG	41:Q:102:ASP:HB3	2.20	0.41
42:R:114:PRO:CG	52:3:1228:C:H5'	2.51	0.41
49:Y:6:ALA:C	49:Y:8:LYS:H	2.26	0.41
49:Y:67:HIS:HE1	52:3:132:C:O3'	2.03	0.41
51:a:194:VAL:O	51:a:197:LYS:HB3	2.20	0.41
51:a:209:ILE:HG23	51:a:209:ILE:O	2.20	0.41
52:3:152:A:H2'	52:3:153:C:H5'	2.02	0.41
52:3:1391:U:H2'	52:3:1392:G:H8	1.84	0.41
53:1:859:G:C2'	53:1:860:U:OP2	2.68	0.41
53:1:1475:G:C2'	53:1:1476:U:OP2	2.68	0.41
53:1:1744:A:H3'	53:1:1745:A:H8	1.85	0.41
53:1:2296:U:C5'	53:1:2297:A:OP1	2.66	0.41
53:1:2714:G:O2'	53:1:2715:C:H5'	2.20	0.41
54:2:55:U:H2'	54:2:56:G:C8	2.56	0.41
2:c:36:GLN:HB3	2:c:49:GLN:HE21	1.84	0.41
2:c:108:ASP:OD1	2:c:108:ASP:N	2.54	0.41
8:i:8:VAL:HG12	8:i:9:LYS:N	2.34	0.41
8:i:14:ALA:HB2	8:i:54:ILE:CG2	2.50	0.41
21:v:69:GLU:O	21:v:69:GLU:HG2	2.19	0.41
23:x:70:LEU:HD23	23:x:73:ARG:HH21	1.85	0.41
52:3:1120:C:H2'	52:3:1121:U:C6	2.55	0.41
53:1:677:A:O2'	53:1:2071:A:H5'	2.19	0.41
53:1:1306:C:H41	53:1:1606:C:H2'	1.85	0.41
53:1:1354:A:H2'	53:1:1355:G:O4'	2.19	0.41
53:1:1405:U:H2'	53:1:1406:U:C6	2.56	0.41
53:1:1468:U:H2'	53:1:1522:A:N6	2.34	0.41
53:1:1775:U:C2'	53:1:1776:G:H5'	2.50	0.41
53:1:2297:A:H62	53:1:2319:G:H1'	1.85	0.41
53:1:2579:C:O2'	53:1:2580:U:H5'	2.20	0.41
4:e:124:ARG:NH2	53:1:2316:G:H4'	2.35	0.41
7:h:117:LEU:C	7:h:119:PRO:HD2	2.46	0.41
13:n:35:LYS:HE2	13:n:100:CYS:SG	2.60	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:o:94:ARG:HB3	14:o:97:PHE:O	2.20	0.41
16:q:30:VAL:HG13	53:1:580:U:O3'	2.20	0.41
37:M:17:GLN:HG3	37:M:71:VAL:HG13	2.01	0.41
40:P:12:ARG:C	40:P:14:GLN:H	2.29	0.41
43:S:41:TRP:O	43:S:45:LEU:HD13	2.21	0.41
52:3:220:G:O2'	52:3:221:C:H5'	2.21	0.41
53:1:572:A:H5''	53:1:573:U:OP2	2.21	0.41
53:1:2180:U:H4'	55:6:17(A):U:H5'	2.02	0.41
53:1:2238:G:N3	53:1:2238:G:C2'	2.83	0.41
55:5:62:C:H2'	55:5:63:G:C8	2.55	0.41
3:d:90:GLN:HG3	3:d:92:HIS:CE1	2.56	0.41
4:e:12:VAL:O	4:e:15:LEU:HD23	2.21	0.41
8:i:73:PRO:HA	8:i:74:PRO:HD3	1.91	0.41
11:l:116:VAL:O	11:l:116:VAL:HG13	2.21	0.41
19:t:13:ALA:HB1	24:y:33:ALA:HB1	2.03	0.41
20:u:33:VAL:HG13	20:u:66:VAL:HG12	2.02	0.41
20:u:65:GLN:HB2	20:u:68:ASN:OD1	2.21	0.41
21:v:51:GLN:NE2	21:v:86:LEU:HD21	2.34	0.41
30:F:30:GLU:HA	30:F:31:PRO:HD3	1.80	0.41
32:H:149:LYS:HG3	32:H:168:ARG:HB3	2.01	0.41
47:W:62:ARG:HD3	47:W:69:TYR:CD1	2.56	0.41
52:3:50:A:N6	52:3:361:G:H4'	2.35	0.41
52:3:1065:U:P	52:3:1190:G:H22	2.44	0.41
52:3:1464:U:H2'	52:3:1465:A:C8	2.55	0.41
53:1:1685:C:H2'	53:1:1686:C:C6	2.55	0.41
53:1:2538:C:H2'	53:1:2539:C:C6	2.55	0.41
54:2:30:C:C2'	54:2:31:C:H5'	2.50	0.41
55:6:13:C:H2'	55:6:14:A:C5'	2.43	0.41
3:d:52:VAL:HG13	3:d:52:VAL:O	2.20	0.41
3:d:200:LEU:HD13	3:d:200:LEU:HA	1.97	0.41
9:j:7:LYS:HA	9:j:8:PRO:HD3	1.90	0.41
9:j:60:ASP:HA	9:j:93:ILE:HD11	2.03	0.41
14:o:62:LEU:H	14:o:62:LEU:HD23	1.85	0.41
14:o:105:ALA:HA	14:o:108:ASP:OD2	2.20	0.41
23:x:10:ARG:NH1	23:x:10:ARG:HB2	2.35	0.41
24:y:49:ASP:HA	24:y:52:ARG:NH2	2.36	0.41
29:E:27:ASN:O	29:E:35:LYS:HE2	2.20	0.41
42:R:27:THR:HG21	52:3:1328:C:H5''	2.02	0.41
48:X:24:SER:HB3	48:X:27:LYS:HD2	2.03	0.41
48:X:57:VAL:HA	48:X:58:PRO:HD3	1.85	0.41
52:3:865:A:O2'	52:3:866:C:H5'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1075:U:H2'	52:3:1076:U:C6	2.56	0.41
52:3:1414:U:H2'	52:3:1415:G:C8	2.53	0.41
53:1:189:G:H2'	53:1:205:G:N2	2.36	0.41
53:1:341:C:H2'	53:1:342:A:C8	2.56	0.41
53:1:827:U:H4'	53:1:828:U:C5	2.55	0.41
53:1:2297:A:N1	53:1:2321:U:H5	2.19	0.41
53:1:2364:C:H2'	53:1:2365:G:O4'	2.20	0.41
53:1:2716:C:O2'	53:1:2717:C:H5'	2.20	0.41
5:f:70:LEU:HD11	53:1:2758:A:C2	2.55	0.41
6:g:67:ALA:CA	6:g:70:GLU:HG3	2.49	0.41
13:n:79:LEU:HD23	13:n:83:LEU:HB2	2.03	0.41
19:t:56:GLU:HG3	19:t:88:LYS:HE2	2.02	0.41
29:E:21:PHE:O	29:E:49:VAL:HG23	2.21	0.41
32:H:8:GLY:HA3	43:S:88:MET:HE3	2.02	0.41
33:I:134:TYR:HD1	52:3:620:C:H4'	1.86	0.41
34:J:156:ARG:HH11	37:M:100:ILE:HD11	1.86	0.41
38:N:27:ILE:N	38:N:27:ILE:HD12	2.36	0.41
45:U:35:ARG:HG3	45:U:35:ARG:O	2.21	0.41
48:X:62:THR:CG2	48:X:65:MET:HG3	2.51	0.41
48:X:68:HIS:HB3	48:X:72:GLU:OE1	2.21	0.41
53:1:807:U:O2'	53:1:808:G:H5'	2.21	0.41
53:1:893:C:H2'	53:1:894:U:O4'	2.21	0.41
53:1:2122:U:H2'	53:1:2123:G:O4'	2.20	0.41
53:1:2372:U:H2'	53:1:2373:G:H8	1.85	0.41
53:1:2660:A:H2'	53:1:2661:G:O4'	2.21	0.41
53:1:2766:A:N3	53:1:2766:A:H2'	2.36	0.41
55:6:46:G:H3'	55:6:47:U:H5'	2.03	0.41
1:b:24:HIS:HB2	1:b:79:ARG:HD2	2.02	0.41
1:b:30:ALA:HB3	1:b:31:PRO:HD3	2.03	0.41
1:b:209:ALA:O	1:b:213:ARG:HG2	2.21	0.41
1:b:257:ARG:HD3	53:1:1799:G:OP1	2.19	0.41
1:b:260:LYS:HA	1:b:263:ASP:OD2	2.20	0.41
6:g:117:LEU:HA	6:g:118:PRO:HD3	1.87	0.41
7:h:117:LEU:O	7:h:118:ILE:HB	2.20	0.41
9:j:18:VAL:HG11	9:j:32:LEU:HD21	2.03	0.41
9:j:26:GLY:HA3	53:1:1140:C:C5'	2.44	0.41
11:l:122:VAL:HG22	11:l:142:ILE:HG12	2.03	0.41
17:r:64:VAL:HG23	17:r:65:ALA:H	1.85	0.41
18:s:74:ILE:HG23	18:s:74:ILE:O	2.21	0.41
22:w:14:ALA:HB1	53:1:2271:G:OP1	2.21	0.41
22:w:22:PHE:O	22:w:25:GLU:HG3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:B:6:LYS:O	26:B:6:LYS:HG3	2.21	0.41
31:G:103:TRP:NE1	31:G:107:ARG:HH21	2.19	0.41
33:I:101:VAL:HG13	33:I:106:PHE:HB2	2.02	0.41
34:J:73:VAL:O	34:J:73:VAL:HG13	2.21	0.41
36:L:26:VAL:HG22	36:L:42:VAL:HG21	2.01	0.41
39:O:8:ILE:HD11	39:O:98:VAL:CG1	2.51	0.41
39:O:57:VAL:HG12	39:O:58:ASN:N	2.36	0.41
40:P:127:ARG:HG2	40:P:127:ARG:NH1	2.36	0.41
41:Q:89:LEU:HD12	41:Q:89:LEU:N	2.36	0.41
46:V:18:LYS:HD3	46:V:49:ASN:N	2.36	0.41
47:W:54:LEU:O	47:W:58:ILE:HG12	2.20	0.41
49:Y:14:GLU:O	49:Y:17:ARG:HG3	2.20	0.41
50:Z:19:LYS:HA	50:Z:24:LYS:CE	2.51	0.41
52:3:451:A:H4'	52:3:452:A:O4'	2.20	0.41
52:3:1225:A:H2'	52:3:1225:A:N3	2.36	0.41
53:1:198:C:O2'	53:1:199:A:H5'	2.21	0.41
53:1:420:C:H2'	53:1:421:C:O4'	2.21	0.41
53:1:1114:C:H2'	53:1:1115:G:C8	2.56	0.41
53:1:2326:C:O2'	53:1:2327:A:OP1	2.36	0.41
53:1:2556:C:H2'	53:1:2557:G:O4'	2.19	0.41
53:1:2638:G:H1'	53:1:2778:A:H61	1.86	0.41
53:1:2739:U:O2'	53:1:2740:A:H5'	2.21	0.41
53:1:2841:C:H2'	53:1:2842:G:C8	2.56	0.41
54:2:65:U:H3'	54:2:108:A:H61	1.86	0.41
54:2:65:U:H2'	54:2:66:A:H5'	2.02	0.41
1:b:75:ALA:HB2	1:b:95:TYR:CD1	2.56	0.41
1:b:163:ILE:HG23	1:b:171:VAL:HG13	2.03	0.41
6:g:72:ILE:HB	6:g:108:VAL:HG22	2.02	0.41
7:h:37:LYS:HD3	53:1:1085:A:N6	2.35	0.41
7:h:60:LEU:O	7:h:64:VAL:HB	2.21	0.41
19:t:89:GLU:CD	19:t:89:GLU:H	2.29	0.41
23:x:6:VAL:HG23	23:x:50:VAL:HG12	2.03	0.41
23:x:9:LYS:HE3	23:x:53:LYS:HE3	2.03	0.41
26:B:9:ARG:H	26:B:9:ARG:HG3	1.65	0.41
31:G:67:LEU:HG	31:G:69:VAL:HG13	2.03	0.41
32:H:72:PRO:HB3	32:H:104:GLU:HG2	2.03	0.41
34:J:92:ARG:O	34:J:93:VAL:C	2.64	0.41
36:L:39:GLU:HA	36:L:42:VAL:HG22	2.04	0.41
37:M:68:LYS:HE3	37:M:68:LYS:HB3	1.95	0.41
51:a:200:LYS:HA	51:a:201:PRO:HD3	1.87	0.41
52:3:86:G:H4'	52:3:87:C:C4	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:112:G:H21	52:3:354:G:H5'	1.85	0.41
52:3:871:U:H5''	52:3:872:A:OP2	2.21	0.41
52:3:1279:G:H4'	52:3:1281:C:H41	1.86	0.41
52:3:1424:U:H2'	52:3:1425:U:O4'	2.20	0.41
53:1:141:G:N3	53:1:141:G:O4'	2.54	0.41
53:1:414:C:H2'	53:1:415:A:H8	1.85	0.41
53:1:616:A:H2'	53:1:617:G:O4'	2.20	0.41
53:1:873:C:H2'	53:1:874:G:H8	1.86	0.41
53:1:890:C:H2'	53:1:891:G:O4'	2.21	0.41
53:1:2262:U:O2'	53:1:2263:C:H5'	2.21	0.41
3:d:79:ARG:HH21	53:1:448:U:C4'	2.34	0.40
4:e:65:LEU:HD22	54:2:42:C:C5	2.56	0.40
8:i:24:GLY:HA3	8:i:25:PRO:HD3	1.82	0.40
19:t:80:TRP:CZ3	19:t:82:LYS:HB3	2.56	0.40
31:G:209:VAL:HA	31:G:212:TYR:HD2	1.86	0.40
34:J:63:MET:O	34:J:67:ARG:HD3	2.21	0.40
36:L:2:ARG:HA	52:3:1380:U:C5	2.56	0.40
37:M:87:ARG:H	37:M:90:GLU:HB2	1.86	0.40
38:N:128:LYS:HD2	52:3:966:G:H21	1.86	0.40
43:S:26:LEU:HD23	43:S:26:LEU:O	2.21	0.40
48:X:38:THR:HG22	48:X:39:ILE:N	2.33	0.40
52:3:503:C:H2'	52:3:504:C:C6	2.56	0.40
52:3:1412:C:H2'	52:3:1413:A:H8	1.85	0.40
53:1:277:G:H1'	53:1:361:G:O6	2.21	0.40
53:1:580:U:H2'	53:1:581:C:H6	1.87	0.40
53:1:859:G:H1'	53:1:860:U:H5	1.85	0.40
53:1:2240:U:O2'	53:1:2241:A:H5'	2.20	0.40
53:1:2267:A:H5''	53:1:2268:A:C5'	2.45	0.40
53:1:2340:A:H2'	53:1:2341:G:H8	1.86	0.40
1:b:139:THR:HG23	1:b:160:TYR:CD2	2.56	0.40
4:e:31:GLU:OE2	4:e:91:ARG:NH2	2.50	0.40
4:e:94:ARG:HA	4:e:97:GLU:OE1	2.21	0.40
5:f:112:VAL:O	5:f:112:VAL:HG13	2.21	0.40
6:g:75:LEU:O	6:g:77:THR:HG22	2.21	0.40
9:j:7:LYS:HB2	9:j:10:THR:CG2	2.51	0.40
9:j:27:ARG:NH1	53:1:1143:A:N7	2.70	0.40
13:n:113:ILE:O	13:n:113:ILE:HG23	2.22	0.40
34:J:81:GLN:NE2	34:J:149:PRO:HD2	2.35	0.40
36:L:136:LYS:O	36:L:140:VAL:HG23	2.21	0.40
37:M:80:PRO:HG2	52:3:878:A:C5'	2.51	0.40
41:Q:109:ARG:NH1	52:3:537:G:H5''	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:X:12:LEU:HA	48:X:15:LEU:CD2	2.51	0.40
52:3:206:C:H2'	52:3:207:C:O4'	2.21	0.40
52:3:375:U:H2'	52:3:376:G:C8	2.57	0.40
52:3:947:G:H2'	52:3:948:C:O4'	2.22	0.40
52:3:1033:G:C2'	52:3:1034:G:H5''	2.49	0.40
53:1:723:C:H2'	53:1:724:U:C6	2.56	0.40
53:1:1053:C:C3'	53:1:1054:A:H5''	2.52	0.40
53:1:1720:U:H2'	53:1:1721:G:O4'	2.21	0.40
53:1:2065:C:H2'	53:1:2066:C:C6	2.56	0.40
53:1:2317:A:H2'	53:1:2318:G:O4'	2.22	0.40
53:1:2457:U:H3	53:1:2494:G:H1	1.67	0.40
53:1:2572:A:OP1	53:1:2574:G:H4'	2.20	0.40
5:f:71:LEU:HA	5:f:74:MET:HB2	2.03	0.40
7:h:5:LEU:HA	7:h:8:LYS:HB2	2.02	0.40
8:i:8:VAL:HG11	53:1:1097:U:O2'	2.21	0.40
8:i:52:LEU:HD23	8:i:52:LEU:H	1.86	0.40
10:k:91:SER:O	10:k:92:GLU:C	2.64	0.40
19:t:53:VAL:HB	19:t:91:GLN:HE21	1.87	0.40
33:I:130:ASN:OD1	33:I:131:ILE:HD12	2.21	0.40
35:K:47:LEU:HD12	35:K:55:HIS:HA	2.03	0.40
40:P:118:ASN:ND2	52:3:717:U:O3'	2.55	0.40
43:S:2:LYS:HA	52:3:1048:G:OP1	2.21	0.40
52:3:629:A:H2'	52:3:630:A:O4'	2.21	0.40
52:3:1272:G:H2'	52:3:1273:C:O4'	2.21	0.40
53:1:1625:C:H2'	53:1:1626:A:O4'	2.21	0.40
53:1:1846:G:H2'	53:1:1847:A:O4'	2.21	0.40
53:1:2342:C:O2'	53:1:2374:C:H5''	2.22	0.40
6:g:66:ASN:ND2	6:g:135:HIS:HB2	2.37	0.40
11:l:55:MET:HA	11:l:56:PRO:HD3	1.93	0.40
11:l:92:LEU:HD11	11:l:106:GLU:O	2.21	0.40
12:m:6:ARG:HH11	12:m:6:ARG:HG2	1.86	0.40
18:s:29:VAL:HG21	18:s:55:ILE:HG12	2.04	0.40
20:u:73:ASN:O	20:u:74:ALA:HB3	2.21	0.40
32:H:18:ASN:ND2	43:S:89:ARG:O	2.55	0.40
40:P:123:PRO:O	50:Z:34:ARG:N	2.54	0.40
42:R:24:VAL:HG23	42:R:28:ARG:HB3	2.03	0.40
42:R:67:ASP:HA	42:R:70:ARG:HH11	1.87	0.40
43:S:53:ASP:HA	43:S:58:ARG:HD3	2.03	0.40
52:3:256:U:H2'	52:3:257:G:C8	2.57	0.40
52:3:300:A:H2'	52:3:301:G:O4'	2.22	0.40
53:1:290:U:H2'	53:1:291:G:H8	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:819:A:C4	53:1:1189:A:C2	3.09	0.40
53:1:1877:A:H2'	53:1:1878:G:O4'	2.22	0.40
53:1:1935:G:H1'	53:1:1964:G:N2	2.37	0.40
53:1:2583:G:H2'	53:1:2584:U:O4'	2.21	0.40
1:b:270:ARG:HB3	1:b:270:ARG:NH1	2.37	0.40
10:k:109:SER:O	10:k:111:LYS:N	2.51	0.40
16:q:23:TYR:CE1	53:1:533:G:H5'	2.56	0.40
19:t:56:GLU:CD	19:t:88:LYS:HG2	2.47	0.40
21:v:72:VAL:HA	21:v:94:ALA:H	1.87	0.40
24:y:2:LYS:HE2	24:y:6:LEU:HD13	2.04	0.40
33:I:88:ASN:HD22	33:I:88:ASN:HA	1.76	0.40
33:I:190:LEU:HD12	33:I:192:ALA:N	2.36	0.40
40:P:27:ASN:HA	40:P:57:SER:OG	2.20	0.40
43:S:72:PHE:C	43:S:73:LEU:HD12	2.47	0.40
52:3:1353:G:O2'	52:3:1354:U:H5'	2.21	0.40
53:1:644:A:H2'	53:1:645:C:H4'	2.02	0.40
53:1:1077:A:C3'	53:1:1078:U:H5'	2.52	0.40
53:1:1704:C:H2'	53:1:1705:A:C8	2.56	0.40
53:1:2538:C:H2'	53:1:2539:C:H6	1.87	0.40
53:1:2570:G:H2'	53:1:2571:U:O4'	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b	269/271 (99%)	239 (89%)	25 (9%)	5 (2%)	6	30
2	c	207/209 (99%)	194 (94%)	12 (6%)	1 (0%)	24	60
3	d	199/201 (99%)	184 (92%)	14 (7%)	1 (0%)	24	60
4	e	175/177 (99%)	151 (86%)	24 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	f	174/176 (99%)	159 (91%)	13 (8%)	2 (1%)	11	43
6	g	147/149 (99%)	121 (82%)	21 (14%)	5 (3%)	3	17
7	h	129/131 (98%)	92 (71%)	30 (23%)	7 (5%)	1	9
8	i	139/141 (99%)	118 (85%)	16 (12%)	5 (4%)	2	16
9	j	140/142 (99%)	134 (96%)	5 (4%)	1 (1%)	18	53
10	k	120/122 (98%)	99 (82%)	17 (14%)	4 (3%)	3	17
11	l	141/143 (99%)	118 (84%)	18 (13%)	5 (4%)	3	16
12	m	134/136 (98%)	125 (93%)	6 (4%)	3 (2%)	5	26
13	n	118/120 (98%)	103 (87%)	14 (12%)	1 (1%)	16	50
14	o	114/116 (98%)	105 (92%)	8 (7%)	1 (1%)	14	48
15	p	112/114 (98%)	99 (88%)	13 (12%)	0	100	100
16	q	115/117 (98%)	111 (96%)	4 (4%)	0	100	100
17	r	101/103 (98%)	89 (88%)	9 (9%)	3 (3%)	3	19
18	s	108/110 (98%)	97 (90%)	9 (8%)	2 (2%)	6	30
19	t	91/93 (98%)	83 (91%)	7 (8%)	1 (1%)	11	43
20	u	100/102 (98%)	86 (86%)	12 (12%)	2 (2%)	6	28
21	v	92/94 (98%)	85 (92%)	6 (6%)	1 (1%)	11	43
22	w	73/75 (97%)	67 (92%)	6 (8%)	0	100	100
23	x	75/77 (97%)	68 (91%)	7 (9%)	0	100	100
24	y	61/63 (97%)	60 (98%)	1 (2%)	0	100	100
25	z	56/58 (97%)	50 (89%)	6 (11%)	0	100	100
26	B	54/56 (96%)	50 (93%)	4 (7%)	0	100	100
27	C	48/50 (96%)	43 (90%)	4 (8%)	1 (2%)	5	27
28	D	44/46 (96%)	39 (89%)	5 (11%)	0	100	100
29	E	62/64 (97%)	55 (89%)	6 (10%)	1 (2%)	7	34
30	F	36/38 (95%)	30 (83%)	5 (14%)	1 (3%)	4	21
31	G	223/225 (99%)	208 (93%)	15 (7%)	0	100	100
32	H	204/206 (99%)	189 (93%)	13 (6%)	2 (1%)	12	45
33	I	203/205 (99%)	178 (88%)	23 (11%)	2 (1%)	12	45
34	J	155/157 (99%)	127 (82%)	20 (13%)	8 (5%)	1	9
35	K	98/100 (98%)	79 (81%)	13 (13%)	6 (6%)	1	7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	L	149/151 (99%)	133 (89%)	16 (11%)	0	100	100
37	M	127/129 (98%)	116 (91%)	10 (8%)	1 (1%)	16	50
38	N	125/127 (98%)	101 (81%)	20 (16%)	4 (3%)	3	18
39	O	96/98 (98%)	75 (78%)	14 (15%)	7 (7%)	1	4
40	P	114/116 (98%)	96 (84%)	14 (12%)	4 (4%)	3	16
41	Q	121/123 (98%)	93 (77%)	22 (18%)	6 (5%)	1	10
42	R	112/114 (98%)	94 (84%)	12 (11%)	6 (5%)	1	9
43	S	98/100 (98%)	84 (86%)	12 (12%)	2 (2%)	6	28
44	T	86/88 (98%)	79 (92%)	6 (7%)	1 (1%)	10	40
45	U	80/82 (98%)	69 (86%)	9 (11%)	2 (2%)	4	23
46	V	78/80 (98%)	66 (85%)	10 (13%)	2 (3%)	4	23
47	W	63/65 (97%)	57 (90%)	5 (8%)	1 (2%)	7	34
48	X	77/79 (98%)	64 (83%)	9 (12%)	4 (5%)	1	9
49	Y	83/85 (98%)	78 (94%)	3 (4%)	2 (2%)	4	24
50	Z	63/65 (97%)	42 (67%)	15 (24%)	6 (10%)	0	2
51	a	130/223 (58%)	120 (92%)	7 (5%)	3 (2%)	5	25
All	All	5919/6112 (97%)	5202 (88%)	595 (10%)	122 (2%)	8	27

All (122) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	232	GLY
5	f	45	ALA
7	h	81	LEU
7	h	108	VAL
7	h	118	ILE
10	k	89	ASN
10	k	110	GLU
17	r	54	VAL
20	u	99	SER
30	F	37	GLN
34	J	93	VAL
34	J	122	VAL
38	N	57	VAL
38	N	90	ASP
39	O	58	ASN

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Mol	Chain	Res	Type
40	P	125	LYS
41	Q	43	LYS
41	Q	101	LEU
42	R	7	ASN
42	R	65	GLU
44	T	46	LYS
45	U	43	ALA
46	V	49	ASN
50	Z	24	LYS
50	Z	34	ARG
1	b	240	GLY
5	f	117	PRO
6	g	9	VAL
9	j	81	ILE
10	k	92	GLU
11	l	15	ALA
11	l	85	VAL
12	m	58	LYS
12	m	69	PRO
18	s	63	GLY
18	s	65	ASP
20	u	6	ARG
35	K	92	THR
39	O	34	ALA
40	P	89	GLY
42	R	5	GLY
42	R	6	ILE
45	U	79	ASN
48	X	4	LEU
49	Y	67	HIS
50	Z	64	ALA
1	b	121	ALA
6	g	41	LYS
6	g	89	LYS
7	h	51	TYR
8	i	11	GLN
11	l	29	LYS
11	l	31	GLY
19	t	52	GLU
33	I	34	GLU
35	K	39	LEU
35	K	99	ALA

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Mol	Chain	Res	Type
37	M	47	ASP
39	O	89	ARG
40	P	14	GLN
40	P	88	PRO
41	Q	102	ASP
43	S	3	GLN
48	X	34	SER
50	Z	9	GLU
50	Z	25	ALA
2	c	148	GLN
6	g	3	VAL
7	h	107	GLU
8	i	13	ALA
12	m	6	ARG
13	n	117	ASP
33	I	32	LYS
34	J	23	THR
34	J	90	GLY
34	J	99	SER
35	K	56	LYS
35	K	86	ARG
39	O	35	GLN
39	O	41	PRO
39	O	75	ASP
41	Q	33	CYS
41	Q	35	ARG
42	R	4	ALA
42	R	104	ASN
46	V	17	GLU
49	Y	68	LYS
51	a	26	ALA
1	b	260	LYS
6	g	50	ARG
7	h	78	GLY
7	h	113	PHE
10	k	93	GLN
14	o	34	HIS
21	v	93	ARG
32	H	79	LYS
34	J	102	THR
38	N	107	ALA
39	O	42	LEU

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Mol	Chain	Res	Type
41	Q	3	VAL
50	Z	10	PRO
17	r	44	GLY
29	E	31	ILE
32	H	60	ALA
34	J	11	GLN
34	J	121	ASN
35	K	94	HIS
38	N	30	ASN
47	W	13	THR
51	a	208	TYR
8	i	12	VAL
8	i	22	PRO
8	i	55	PRO
17	r	56	GLY
51	a	23	ILE
3	d	83	VAL
48	X	41	PRO
48	X	53	GLY
1	b	63	ILE
11	l	88	GLY
27	C	40	PRO
43	S	33	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	
1	b	216/216 (100%)	216 (100%)	0	100	100
2	c	164/164 (100%)	164 (100%)	0	100	100
3	d	165/165 (100%)	165 (100%)	0	100	100
4	e	148/148 (100%)	148 (100%)	0	100	100
5	f	137/137 (100%)	137 (100%)	0	100	100
6	g	114/114 (100%)	113 (99%)	1 (1%)	70	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	h	100/100 (100%)	97 (97%)	3 (3%)	36	69
8	i	109/109 (100%)	109 (100%)	0	100	100
9	j	116/116 (100%)	116 (100%)	0	100	100
10	k	103/103 (100%)	101 (98%)	2 (2%)	50	76
11	l	102/102 (100%)	102 (100%)	0	100	100
12	m	109/109 (100%)	109 (100%)	0	100	100
13	n	100/100 (100%)	100 (100%)	0	100	100
14	o	86/86 (100%)	86 (100%)	0	100	100
15	p	99/99 (100%)	99 (100%)	0	100	100
16	q	89/89 (100%)	88 (99%)	1 (1%)	65	83
17	r	84/84 (100%)	83 (99%)	1 (1%)	63	82
18	s	93/93 (100%)	91 (98%)	2 (2%)	45	74
19	t	80/80 (100%)	79 (99%)	1 (1%)	61	81
20	u	83/83 (100%)	83 (100%)	0	100	100
21	v	78/78 (100%)	78 (100%)	0	100	100
22	w	57/57 (100%)	56 (98%)	1 (2%)	51	77
23	x	67/67 (100%)	66 (98%)	1 (2%)	57	80
24	y	55/55 (100%)	55 (100%)	0	100	100
25	z	48/48 (100%)	48 (100%)	0	100	100
26	B	47/47 (100%)	47 (100%)	0	100	100
27	C	45/45 (100%)	45 (100%)	0	100	100
28	D	38/38 (100%)	37 (97%)	1 (3%)	40	72
29	E	51/51 (100%)	50 (98%)	1 (2%)	48	76
30	F	34/34 (100%)	34 (100%)	0	100	100
31	G	186/186 (100%)	186 (100%)	0	100	100
32	H	170/170 (100%)	166 (98%)	4 (2%)	43	73
33	I	172/172 (100%)	169 (98%)	3 (2%)	53	78
34	J	119/119 (100%)	117 (98%)	2 (2%)	53	78
35	K	87/87 (100%)	86 (99%)	1 (1%)	65	83
36	L	124/124 (100%)	123 (99%)	1 (1%)	73	86
37	M	104/104 (100%)	103 (99%)	1 (1%)	68	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	N	105/105 (100%)	103 (98%)	2 (2%)	50	76
39	O	86/86 (100%)	86 (100%)	0	100	100
40	P	89/89 (100%)	89 (100%)	0	100	100
41	Q	103/103 (100%)	103 (100%)	0	100	100
42	R	92/92 (100%)	91 (99%)	1 (1%)	65	83
43	S	83/83 (100%)	82 (99%)	1 (1%)	63	82
44	T	76/76 (100%)	76 (100%)	0	100	100
45	U	65/65 (100%)	64 (98%)	1 (2%)	57	80
46	V	74/74 (100%)	73 (99%)	1 (1%)	59	80
47	W	56/56 (100%)	56 (100%)	0	100	100
48	X	70/70 (100%)	69 (99%)	1 (1%)	59	80
49	Y	65/65 (100%)	65 (100%)	0	100	100
50	Z	55/55 (100%)	54 (98%)	1 (2%)	51	77
51	a	110/174 (63%)	108 (98%)	2 (2%)	51	77
All	All	4908/4972 (99%)	4871 (99%)	37 (1%)	70	86

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	g	62	LEU
7	h	3	LEU
7	h	51	TYR
7	h	59	LEU
10	k	45	GLU
10	k	104	THR
16	q	110	GLU
17	r	22	LEU
18	s	77	ASP
18	s	106	VAL
19	t	85	VAL
22	w	67	VAL
23	x	33	HIS
28	D	1	MET
29	E	61	LEU
32	H	31	ASN
32	H	66	THR
32	H	117	ASP

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Mol	Chain	Res	Type
32	H	176	THR
33	I	18	LEU
33	I	34	GLU
33	I	93	LEU
34	J	105	ILE
34	J	130	THR
35	K	75	GLU
36	L	66	GLU
37	M	61	THR
38	N	52	GLU
38	N	60	LEU
42	R	64	VAL
43	S	47	LEU
45	U	53	ASP
46	V	59	GLU
48	X	11	ASP
50	Z	10	PRO
51	a	53	ARG
51	a	185	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (104) such sidechains are listed below:

Mol	Chain	Res	Type
1	b	36	ASN
1	b	127	ASN
1	b	199	HIS
1	b	238	ASN
2	c	32	ASN
2	c	36	GLN
2	c	49	GLN
2	c	67	HIS
2	c	94	GLN
2	c	173	GLN
3	d	41	GLN
3	d	92	HIS
3	d	97	ASN
3	d	195	GLN
4	e	51	ASN
5	f	19	ASN
5	f	72	ASN
6	g	2	GLN
6	g	28	ASN

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Mol	Chain	Res	Type
6	g	33	GLN
6	g	43	ASN
6	g	66	ASN
7	h	4	ASN
7	h	103	ASN
8	i	5	GLN
8	i	29	GLN
8	i	104	GLN
9	j	58	ASN
9	j	135	GLN
11	l	35	HIS
12	m	22	GLN
13	n	18	GLN
14	o	19	GLN
14	o	98	GLN
14	o	100	HIS
14	o	104	GLN
15	p	40	GLN
16	q	19	GLN
16	q	71	ASN
17	r	6	GLN
17	r	11	GLN
17	r	86	GLN
19	t	59	ASN
20	u	73	ASN
22	w	8	ASN
22	w	72	ASN
23	x	15	ASN
23	x	19	HIS
23	x	35	HIS
24	y	15	ASN
24	y	36	GLN
26	B	3	GLN
27	C	44	GLN
28	D	29	GLN
31	G	18	GLN
31	G	50	ASN
31	G	119	GLN
31	G	167	HIS
31	G	176	ASN
31	G	177	ASN
31	G	202	ASN

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Mol	Chain	Res	Type
32	H	2	GLN
32	H	7	ASN
32	H	18	ASN
32	H	24	ASN
32	H	31	ASN
32	H	122	GLN
32	H	139	ASN
33	I	35	GLN
33	I	73	ASN
33	I	88	ASN
33	I	99	ASN
33	I	195	ASN
33	I	197	HIS
34	J	81	GLN
34	J	121	ASN
35	K	52	ASN
36	L	85	GLN
36	L	121	ASN
36	L	147	ASN
39	O	35	GLN
39	O	58	ASN
39	O	64	GLN
40	P	14	GLN
40	P	117	HIS
40	P	118	ASN
41	Q	45	ASN
41	Q	95	HIS
42	R	99	GLN
43	S	42	ASN
43	S	65	GLN
44	T	36	ASN
44	T	49	HIS
44	T	61	GLN
45	U	26	ASN
45	U	63	GLN
46	V	30	HIS
47	W	18	GLN
47	W	53	GLN
49	Y	2	ASN
49	Y	12	GLN
49	Y	67	HIS
49	Y	69	ASN

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Mol	Chain	Res	Type
50	Z	8	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	142 (9%)	2 (0%)
53	1	2902/2903 (99%)	322 (11%)	11 (0%)
54	2	119/120 (99%)	11 (9%)	1 (0%)
55	5	76/77 (98%)	7 (9%)	0
55	6	76/77 (98%)	16 (21%)	0
56	4	17/18 (94%)	2 (11%)	0
All	All	4728/4734 (99%)	500 (10%)	14 (0%)

All (500) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	6	G
52	3	9	G
52	3	22	G
52	3	31	G
52	3	32	A
52	3	39	G
52	3	48	C
52	3	51	A
52	3	71	A
52	3	85	U
52	3	87	C
52	3	95	C
52	3	100	G
52	3	130	A
52	3	144	G
52	3	183	C
52	3	184	G
52	3	197	A
52	3	209	U
52	3	210	C
52	3	226	G
52	3	247	G
52	3	251	G
52	3	253	A
52	3	266	G

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Mol	Chain	Res	Type
52	3	267	C
52	3	279	A
52	3	281	G
52	3	289	G
52	3	345	C
52	3	346	G
52	3	352	C
52	3	355	C
52	3	367	U
52	3	372	C
52	3	411	A
52	3	412	A
52	3	413	G
52	3	429	U
52	3	467	U
52	3	479	U
52	3	484	G
52	3	485	U
52	3	486	U
52	3	497	G
52	3	518	C
52	3	530	G
52	3	531	U
52	3	532	A
52	3	533	A
52	3	547	A
52	3	561	U
52	3	572	A
52	3	573	A
52	3	575	G
52	3	576	C
52	3	577	G
52	3	633	G
52	3	642	A
52	3	653	U
52	3	665	A
52	3	688	G
52	3	703	G
52	3	724	G
52	3	755	G
52	3	777	A
52	3	815	A

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Mol	Chain	Res	Type
52	3	817	C
52	3	818	G
52	3	819	A
52	3	821	G
52	3	843	U
52	3	844	G
52	3	846	G
52	3	871	U
52	3	873	A
52	3	902	G
52	3	926	G
52	3	934	C
52	3	935	A
52	3	960	U
52	3	961	U
52	3	966	G
52	3	969	A
52	3	975	A
52	3	976	G
52	3	977	A
52	3	992	U
52	3	993	G
52	3	1004	A
52	3	1028	C
52	3	1030	U
52	3	1031	C
52	3	1033	G
52	3	1034	G
52	3	1053	G
52	3	1094	G
52	3	1101	A
52	3	1136	C
52	3	1137	C
52	3	1138	G
52	3	1139	G
52	3	1159	U
52	3	1168	U
52	3	1182	G
52	3	1184	G
52	3	1196	A
52	3	1198	G
52	3	1201	A

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Mol	Chain	Res	Type
52	3	1202	U
52	3	1215	G
52	3	1225	A
52	3	1238	A
52	3	1240	U
52	3	1241	G
52	3	1257	A
52	3	1258	G
52	3	1275	A
52	3	1278	G
52	3	1280	A
52	3	1282	C
52	3	1287	A
52	3	1300	G
52	3	1317	C
52	3	1320	C
52	3	1337	G
52	3	1346	A
52	3	1347	G
52	3	1363	A
52	3	1395	C
52	3	1419	G
52	3	1446	A
52	3	1448	C
52	3	1452	C
52	3	1492	A
52	3	1503	A
52	3	1506	U
52	3	1517	G
52	3	1529	G
52	3	1530	G
52	3	1533	C
52	3	1540	U
53	1	10	A
53	1	12	U
53	1	34	U
53	1	35	G
53	1	50	U
53	1	51	G
53	1	63	A
53	1	71	A
53	1	74	A

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Mol	Chain	Res	Type
53	1	75	G
53	1	119	A
53	1	120	U
53	1	139	U
53	1	140	C
53	1	141	G
53	1	142	A
53	1	162	U
53	1	163	C
53	1	181	A
53	1	196	A
53	1	199	A
53	1	216	A
53	1	221	A
53	1	222	A
53	1	224	U
53	1	228	C
53	1	229	C
53	1	248	G
53	1	249	C
53	1	255	A
53	1	265	A
53	1	266	G
53	1	276	U
53	1	278	A
53	1	281	C
53	1	294	A
53	1	301	G
53	1	311	A
53	1	312	G
53	1	323	C
53	1	329	G
53	1	330	A
53	1	361	G
53	1	363	G
53	1	371	A
53	1	372	G
53	1	386	G
53	1	387	U
53	1	404	A
53	1	406	G
53	1	411	G

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Mol	Chain	Res	Type
53	1	424	G
53	1	457	A
53	1	458	G
53	1	481	G
53	1	491	G
53	1	504	A
53	1	505	A
53	1	529	A
53	1	531	C
53	1	532	A
53	1	543	G
53	1	545	U
53	1	563	A
53	1	573	U
53	1	575	A
53	1	588	U
53	1	603	A
53	1	616	A
53	1	627	A
53	1	637	A
53	1	646	U
53	1	654	A
53	1	669	G
53	1	686	U
53	1	687	C
53	1	695	G
53	1	730	A
53	1	747	C
53	1	752	A
53	1	764	A
53	1	776	G
53	1	782	A
53	1	784	G
53	1	785	G
53	1	805	G
53	1	812	C
53	1	819	A
53	1	822	G
53	1	827	U
53	1	828	U
53	1	830	G
53	1	845	A

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Mol	Chain	Res	Type
53	1	846	U
53	1	847	U
53	1	858	G
53	1	860	U
53	1	878	A
53	1	885	C
53	1	886	A
53	1	887	U
53	1	888	C
53	1	896	A
53	1	897	C
53	1	910	A
53	1	932	U
53	1	941	A
53	1	946	C
53	1	961	C
53	1	974	G
53	1	983	A
53	1	995	C
53	1	996	A
53	1	1012	U
53	1	1013	C
53	1	1021	A
53	1	1022	G
53	1	1026	G
53	1	1033	U
53	1	1045	C
53	1	1046	A
53	1	1047	G
53	1	1054	A
53	1	1060	U
53	1	1062	G
53	1	1065	U
53	1	1066	U
53	1	1070	A
53	1	1071	G
53	1	1079	C
53	1	1084	A
53	1	1088	A
53	1	1104	C
53	1	1106	G
53	1	1111	A

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Mol	Chain	Res	Type
53	1	1131	G
53	1	1132	U
53	1	1133	A
53	1	1135	C
53	1	1143	A
53	1	1175	A
53	1	1177	G
53	1	1180	U
53	1	1212	G
53	1	1251	C
53	1	1253	A
53	1	1256	G
53	1	1271	G
53	1	1272	A
53	1	1289	C
53	1	1301	A
53	1	1302	A
53	1	1321	A
53	1	1329	U
53	1	1330	C
53	1	1332	G
53	1	1345	C
53	1	1352	U
53	1	1365	A
53	1	1378	A
53	1	1379	U
53	1	1383	A
53	1	1416	G
53	1	1419	A
53	1	1420	A
53	1	1454	C
53	1	1461	C
53	1	1476	U
53	1	1482	G
53	1	1490	A
53	1	1491	G
53	1	1498	C
53	1	1515	A
53	1	1524	G
53	1	1535	A
53	1	1536	C
53	1	1537	G

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Mol	Chain	Res	Type
53	1	1555	G
53	1	1559	U
53	1	1560	G
53	1	1569	A
53	1	1581	G
53	1	1584	U
53	1	1608	A
53	1	1611	C
53	1	1616	A
53	1	1647	U
53	1	1648	U
53	1	1674	G
53	1	1715	G
53	1	1729	U
53	1	1730	C
53	1	1732	C
53	1	1758	U
53	1	1764	C
53	1	1773	A
53	1	1780	A
53	1	1791	A
53	1	1800	C
53	1	1801	A
53	1	1808	A
53	1	1816	C
53	1	1829	A
53	1	1871	A
53	1	1901	A
53	1	1906	G
53	1	1907	G
53	1	1913	A
53	1	1929	G
53	1	1930	G
53	1	1937	A
53	1	1938	A
53	1	1944	U
53	1	1955	U
53	1	1963	U
53	1	1967	C
53	1	1970	A
53	1	1971	U
53	1	1972	G

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Mol	Chain	Res	Type
53	1	1991	U
53	1	1993	U
53	1	1997	C
53	1	2022	U
53	1	2023	C
53	1	2031	A
53	1	2043	C
53	1	2049	G
53	1	2055	C
53	1	2056	G
53	1	2060	A
53	1	2061	G
53	1	2062	A
53	1	2069	G
53	1	2072	C
53	1	2095	A
53	1	2110	G
53	1	2111	U
53	1	2112	G
53	1	2113	U
53	1	2118	U
53	1	2119	A
53	1	2131	U
53	1	2132	U
53	1	2133	G
53	1	2145	C
53	1	2147	A
53	1	2162	G
53	1	2172	U
53	1	2173	A
53	1	2198	A
53	1	2203	U
53	1	2204	G
53	1	2213	U
53	1	2225	A
53	1	2259	U
53	1	2278	A
53	1	2283	C
53	1	2287	A
53	1	2297	A
53	1	2305	U
53	1	2309	A

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Mol	Chain	Res	Type
53	1	2325	G
53	1	2327	A
53	1	2334	U
53	1	2350	C
53	1	2383	G
53	1	2385	C
53	1	2392	A
53	1	2402	U
53	1	2403	C
53	1	2406	A
53	1	2423	U
53	1	2424	C
53	1	2427	C
53	1	2429	G
53	1	2430	A
53	1	2435	A
53	1	2441	U
53	1	2448	A
53	1	2476	A
53	1	2498	C
53	1	2502	G
53	1	2503	A
53	1	2504	U
53	1	2505	G
53	1	2518	A
53	1	2547	A
53	1	2554	U
53	1	2566	A
53	1	2567	G
53	1	2572	A
53	1	2602	A
53	1	2603	G
53	1	2609	U
53	1	2613	U
53	1	2629	U
53	1	2655	G
53	1	2682	A
53	1	2689	U
53	1	2690	U
53	1	2714	G
53	1	2744	G
53	1	2748	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	1	2757	A
53	1	2764	A
53	1	2765	A
53	1	2778	A
53	1	2779	U
53	1	2791	G
53	1	2794	C
53	1	2797	U
53	1	2800	A
53	1	2809	A
53	1	2820	A
53	1	2821	A
53	1	2833	U
53	1	2867	G
53	1	2868	A
53	1	2872	A
53	1	2880	C
53	1	2883	A
53	1	2884	U
54	2	4	C
54	2	12	C
54	2	13	G
54	2	24	G
54	2	35	C
54	2	41	G
54	2	44	G
54	2	67	G
54	2	89	U
54	2	108	A
54	2	109	A
55	5	9	G
55	5	19	G
55	5	20	U
55	5	47	U
55	5	48	C
55	5	61	C
55	5	76	A
55	6	3	C
55	6	8	U
55	6	9	G
55	6	10	G
55	6	14	A

Continued on next page...

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Mol	Chain	Res	Type
55	6	18	G
55	6	19	G
55	6	20	U
55	6	21	A
55	6	22	G
55	6	34	C
55	6	61	C
55	6	64	G
55	6	70	G
55	6	71	C
55	6	74	C
56	4	12	A
56	4	13	A

All (14) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
52	3	960	U
52	3	1201	A
53	1	227	A
53	1	490	C
53	1	859	G
53	1	1020	A
53	1	1130	U
53	1	1475	G
53	1	2286	G
53	1	2296	U
53	1	2326	C
53	1	2391	G
53	1	2756	U
54	2	88	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand 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	$\# Z > 2$
57	FME	5	101	55	8,9,10	0.51	0	8,9,11	0.92	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
57	FME	5	101	55	-	1/7/9/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
57	5	101	FME	CB-CA-N-CN

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

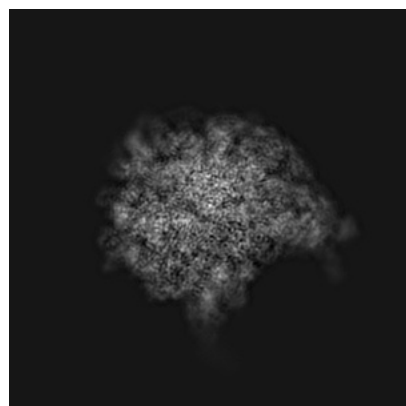
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21619. These allow visual inspection of the internal detail of the map and identification of artifacts.

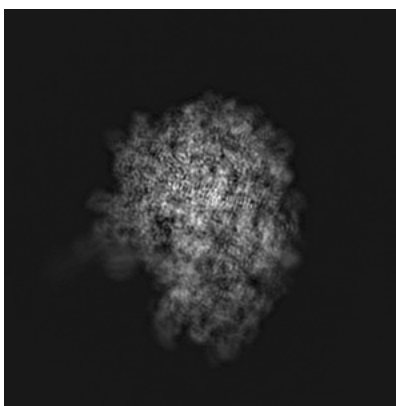
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

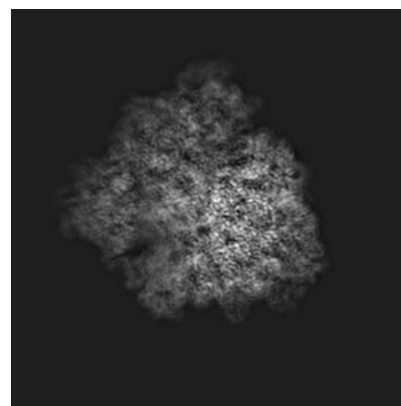
6.1.1 Primary map



X

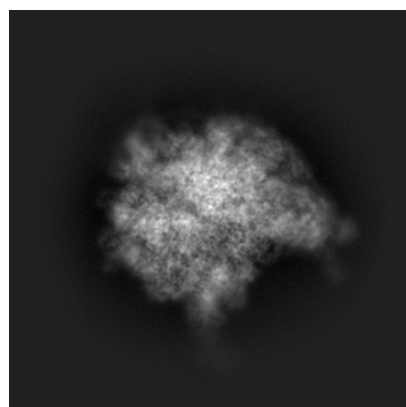


Y

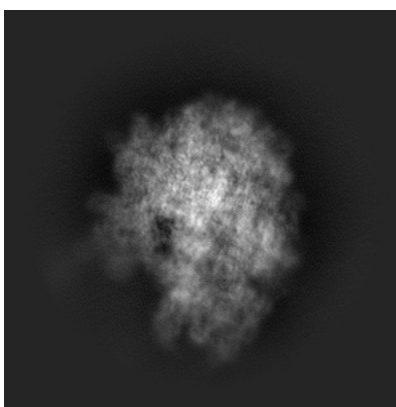


Z

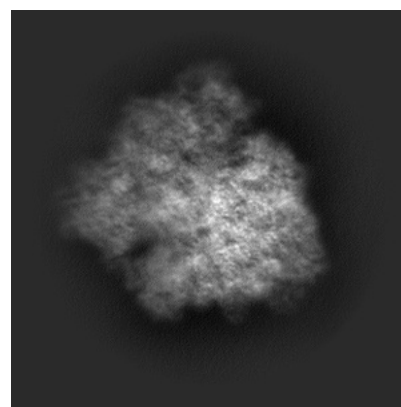
6.1.2 Raw map



X



Y

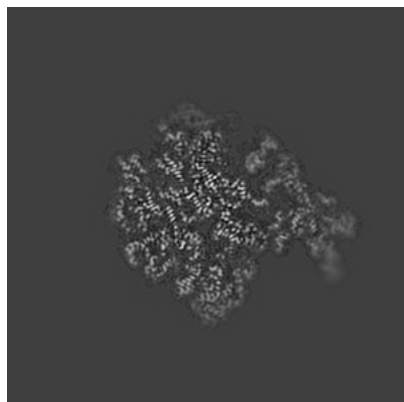


Z

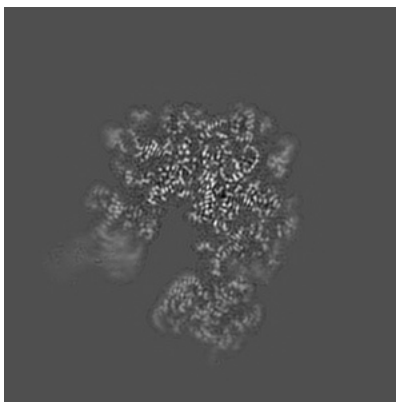
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

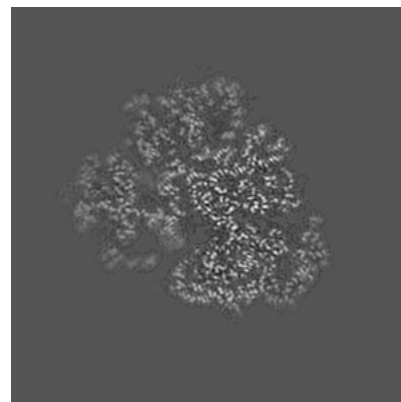
6.2.1 Primary map



X Index: 144

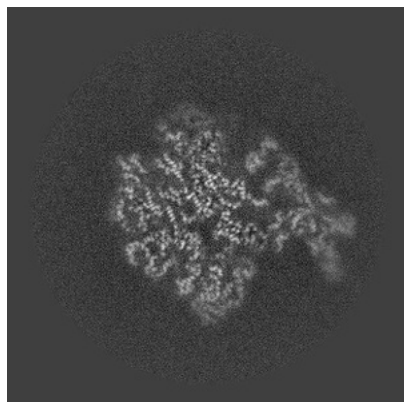


Y Index: 144

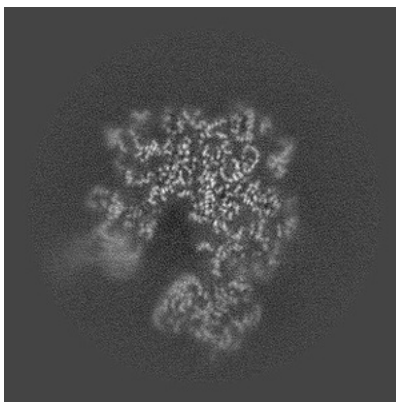


Z Index: 144

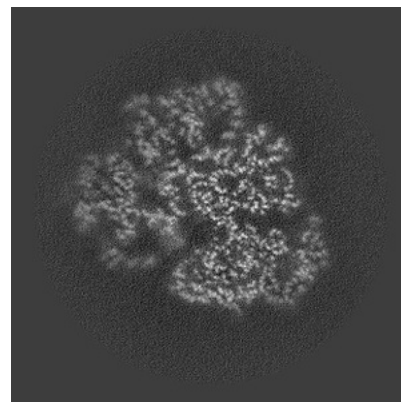
6.2.2 Raw map



X Index: 144



Y Index: 144

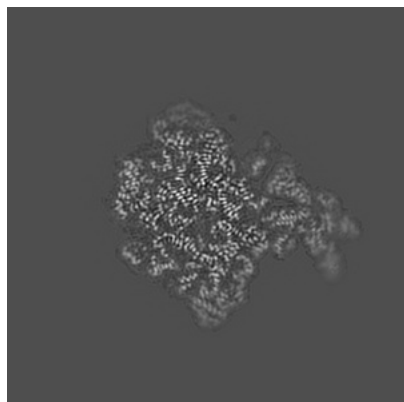


Z Index: 144

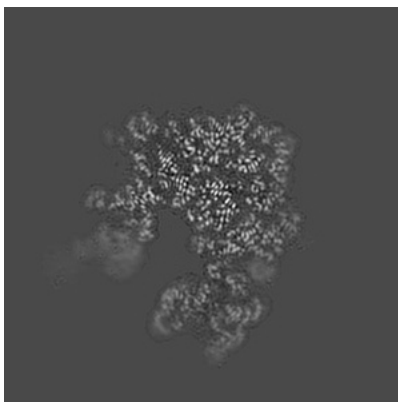
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

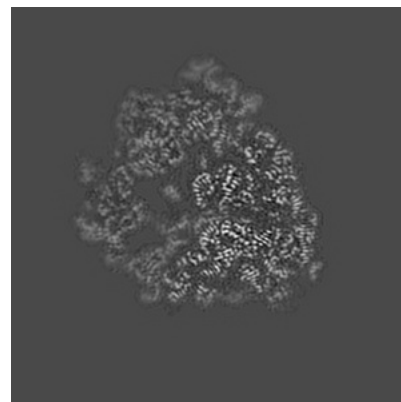
6.3.1 Primary map



X Index: 147

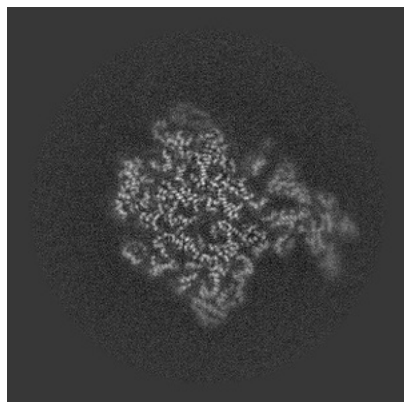


Y Index: 149

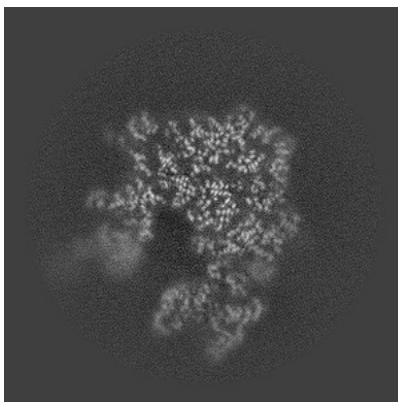


Z Index: 135

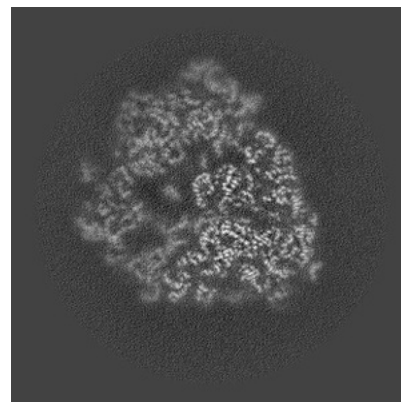
6.3.2 Raw map



X Index: 147



Y Index: 149

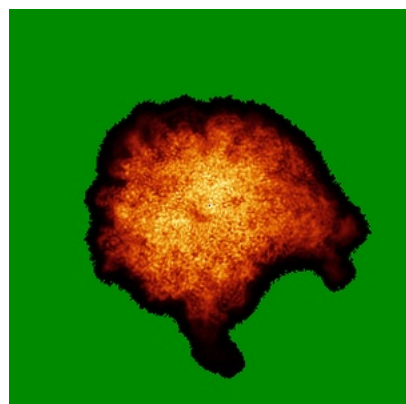


Z Index: 135

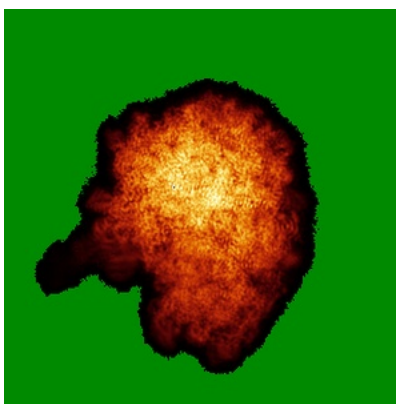
The images above show the largest variance slices of the map in three orthogonal directions.

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

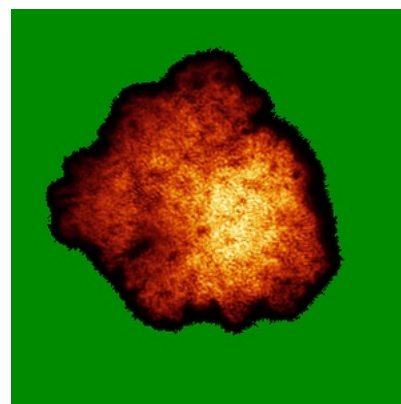
6.4.1 Primary map



X

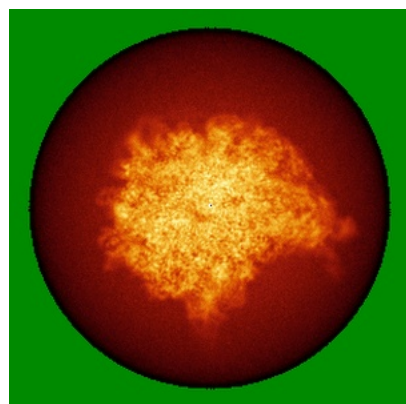


Y

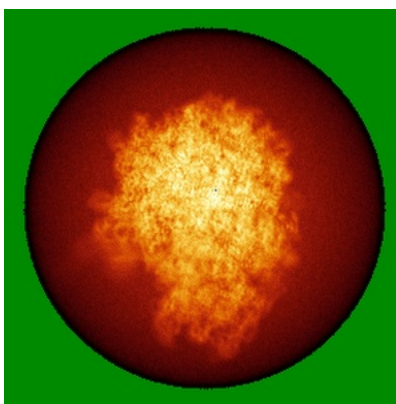


Z

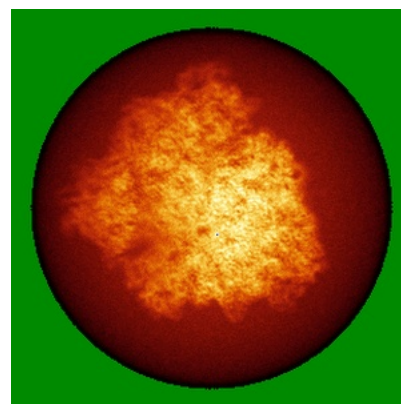
6.4.2 Raw map



X



Y

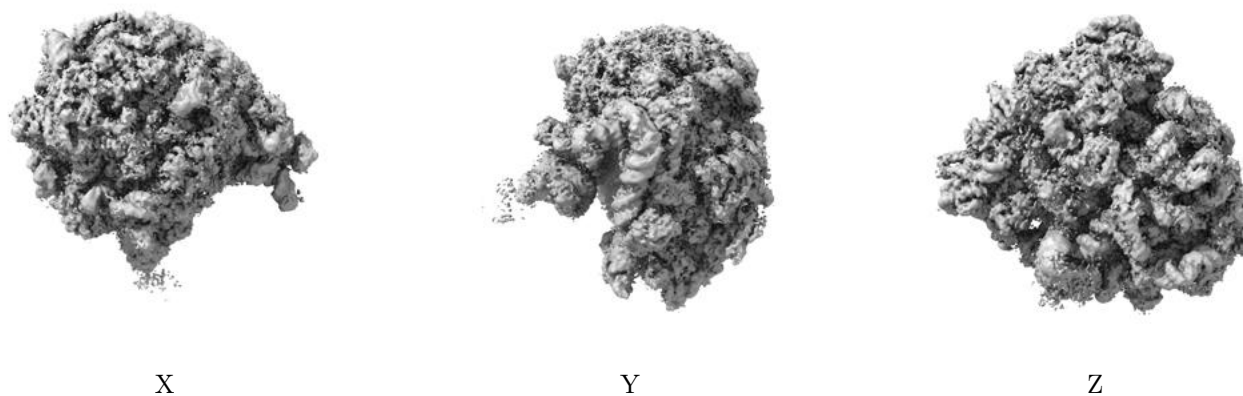


Z

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

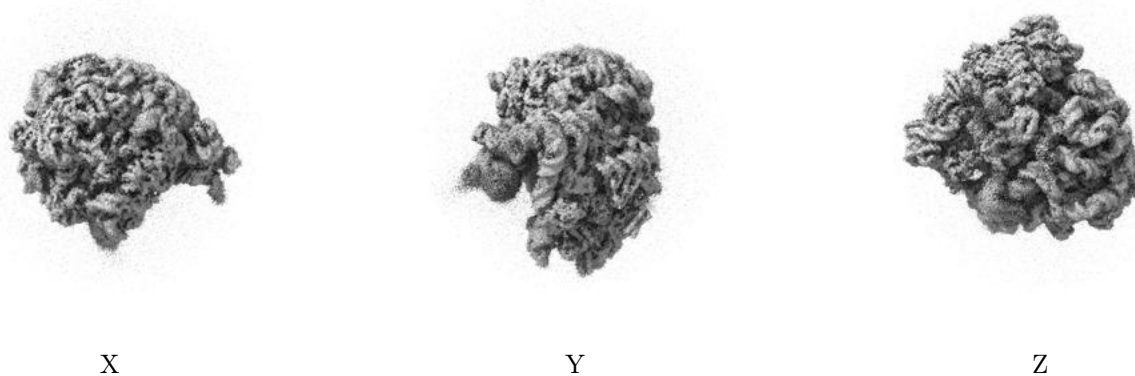
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

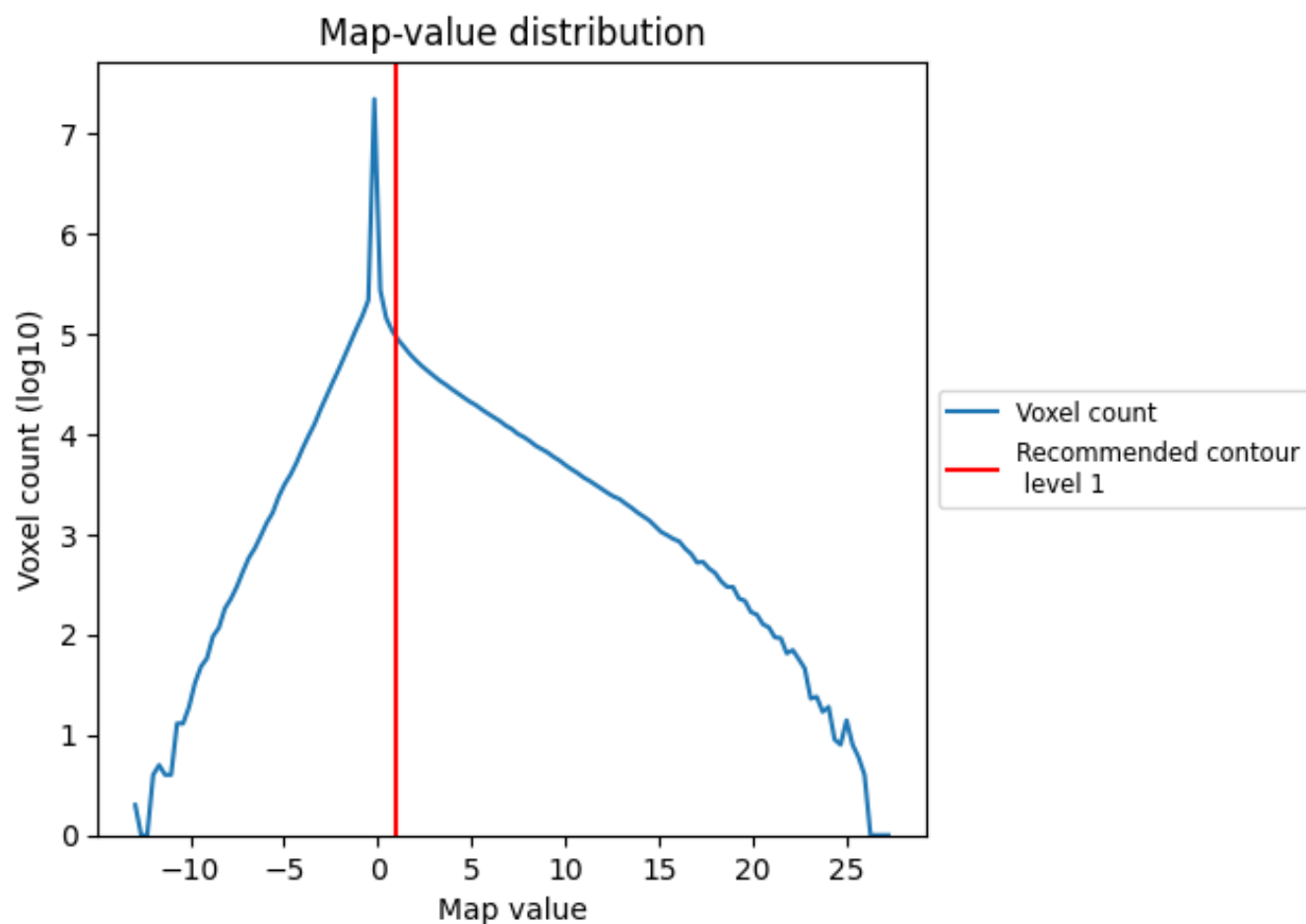
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

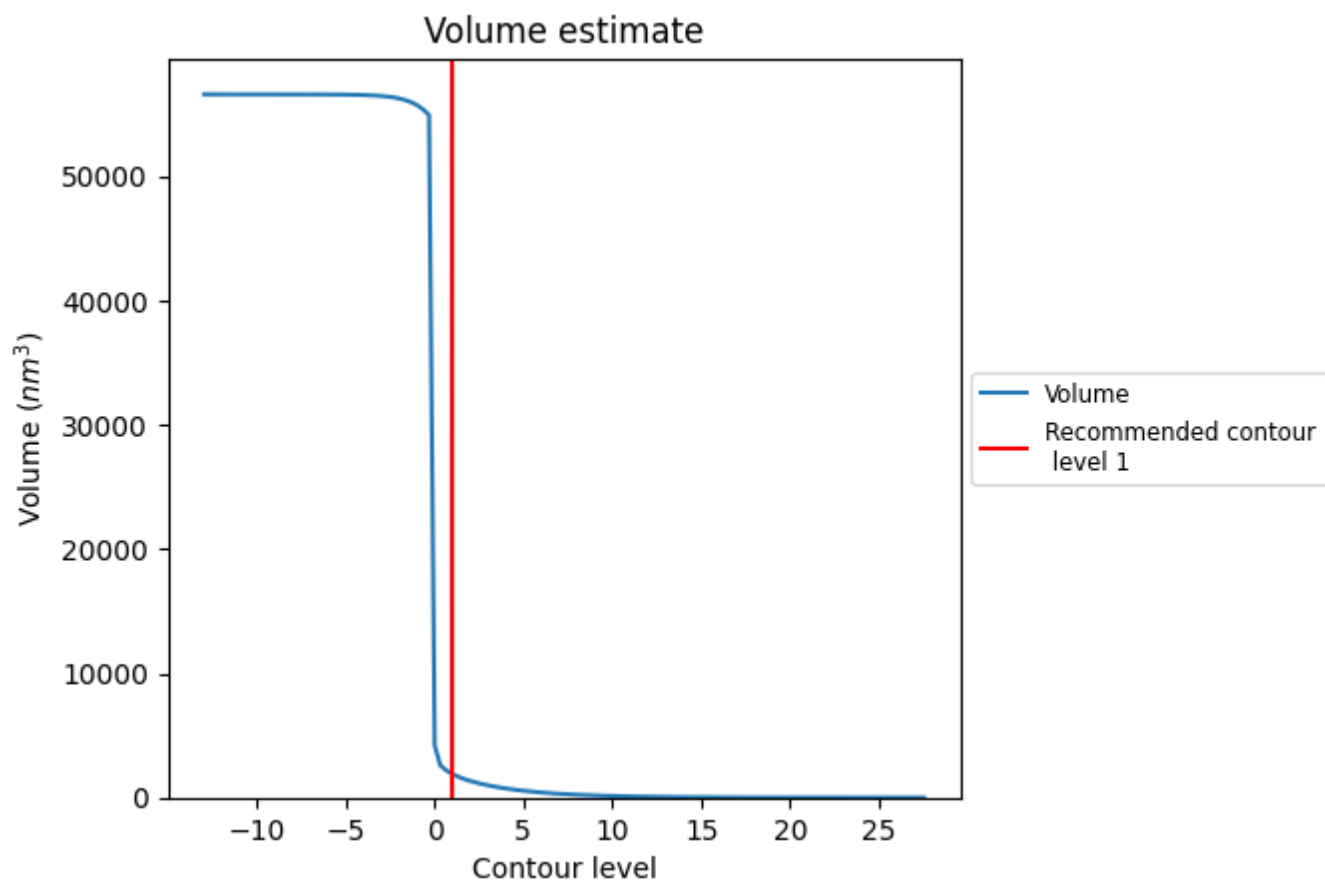
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

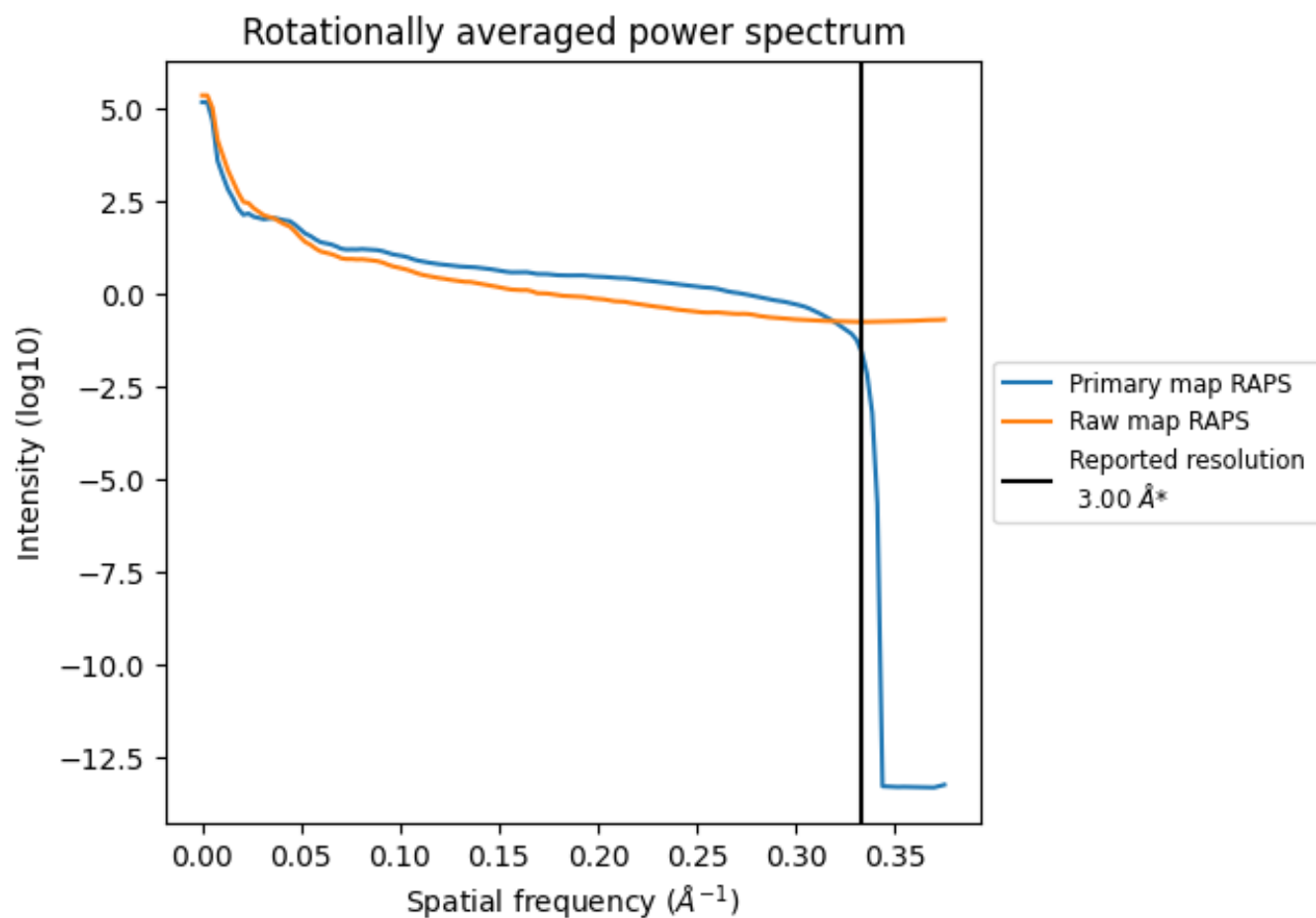
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1918 nm³; this corresponds to an approximate mass of 1732 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 ⓘ

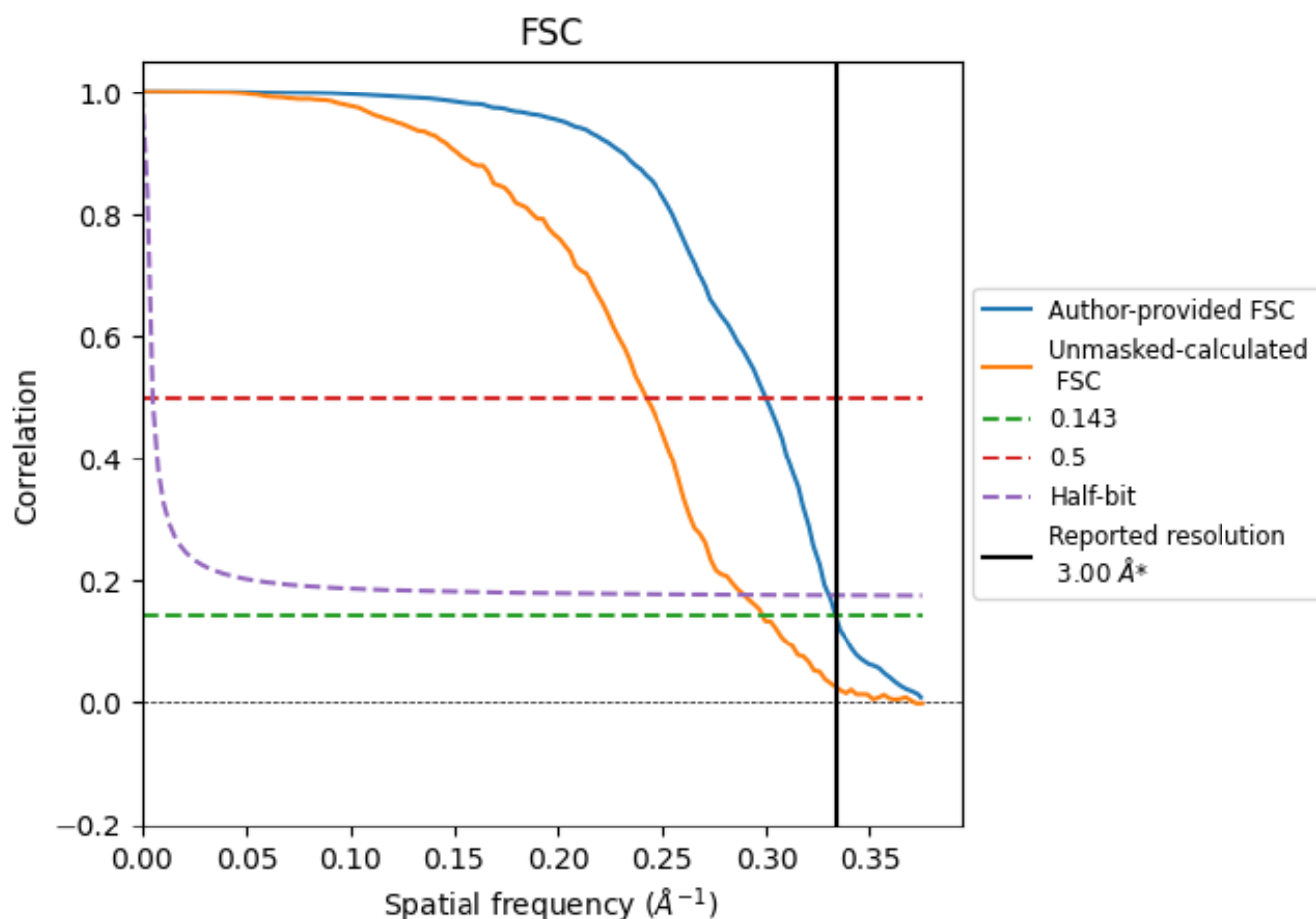


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.333 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

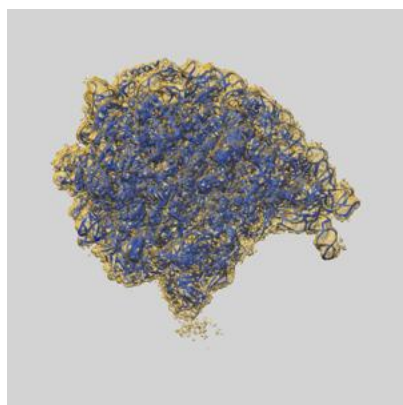
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.00	3.34	3.03
Unmasked-calculated*	3.35	4.13	3.46

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.35 differs from the reported value 3.0 by more than 10 %

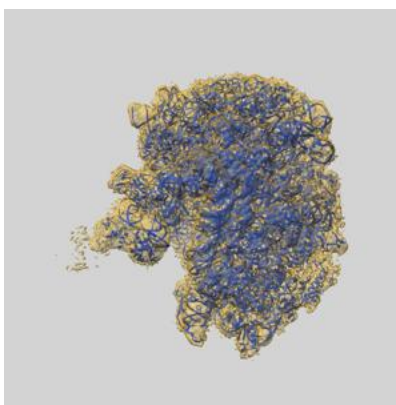
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21619 and PDB model 6WD0. Per-residue inclusion information can be found in section [3](#) on page [15](#).

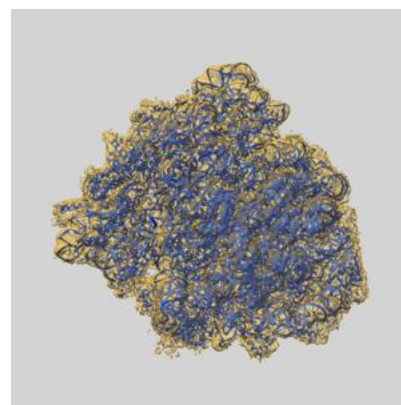
9.1 Map-model overlay [i](#)



X



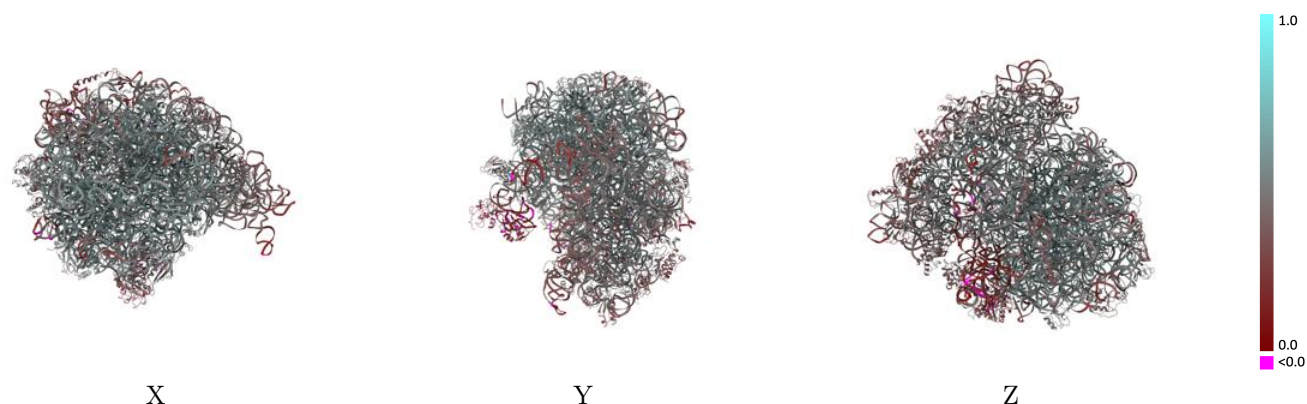
Y



Z

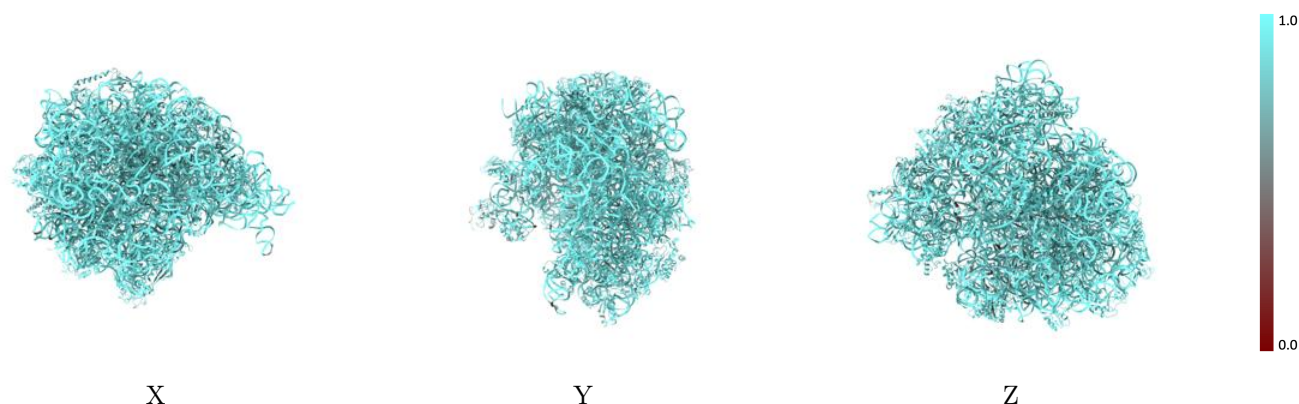
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



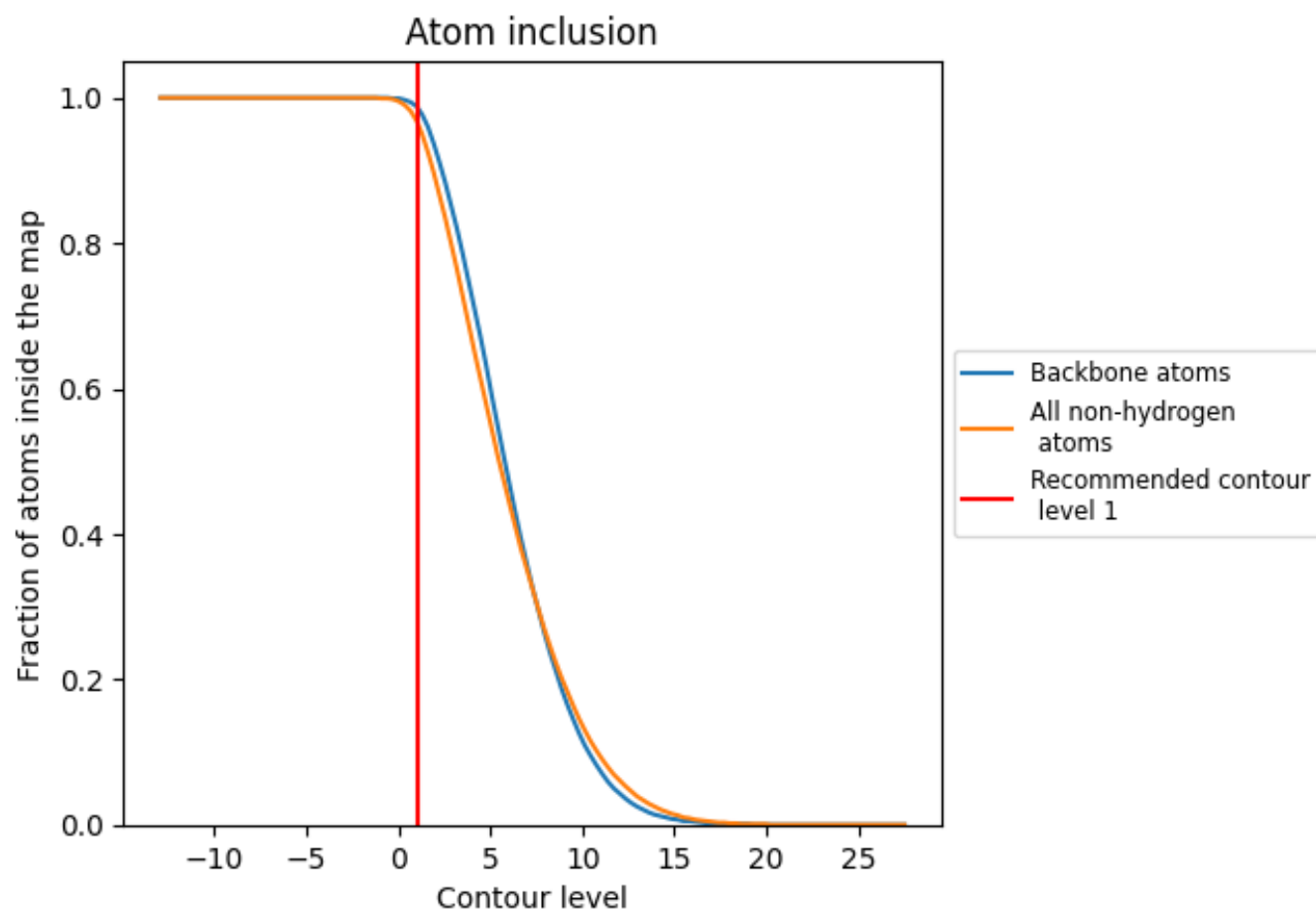
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1).

9.4 Atom inclusion ⓘ



At the recommended contour level, 99% of all backbone atoms, 97% 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 (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9680	 0.4600
1	 0.9890	 0.4910
2	 0.9900	 0.4520
3	 0.9850	 0.4450
4	 0.7760	 0.2400
5	 0.9810	 0.4280
6	 0.8370	 0.1630
B	 0.9560	 0.5200
C	 0.8860	 0.4770
D	 0.9610	 0.5500
E	 0.9840	 0.5510
F	 0.9140	 0.4900
G	 0.8900	 0.3890
H	 0.9130	 0.4320
I	 0.8730	 0.3930
J	 0.9330	 0.4700
K	 0.9520	 0.4190
L	 0.9400	 0.3980
M	 0.9170	 0.4680
N	 0.9330	 0.4050
O	 0.8390	 0.3810
P	 0.9630	 0.4570
Q	 0.9520	 0.4780
R	 0.9430	 0.3910
S	 0.9000	 0.4150
T	 0.9670	 0.4560
U	 0.9110	 0.4450
V	 0.9510	 0.4450
W	 0.9550	 0.4320
X	 0.9600	 0.4010
Y	 0.9120	 0.4150
Z	 0.8490	 0.3370
a	 0.8410	 0.2150
b	 0.9720	 0.5390
c	 0.9680	 0.5290



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Chain	Atom inclusion	Q-score
d	 0.9590	 0.4910
e	 0.9350	 0.3920
f	 0.9610	 0.4330
g	 0.8600	 0.3450
h	 0.7890	 0.1690
i	 0.8560	 0.1240
j	 0.9640	 0.5230
k	 0.9580	 0.5220
l	 0.9560	 0.5060
m	 0.9570	 0.5210
n	 0.9720	 0.5300
o	 0.9500	 0.4540
p	 0.9640	 0.5190
q	 0.9800	 0.5350
r	 0.9650	 0.4940
s	 0.9460	 0.5100
t	 0.9530	 0.4930
u	 0.9440	 0.4600
v	 0.9540	 0.4790
w	 0.9620	 0.5400
x	 0.9770	 0.5190
y	 0.9280	 0.4200
z	 0.9630	 0.5000