



Full wwPDB EM Validation Report ⓘ

Mar 29, 2026 – 06:24 AM UTC

PDB ID : 8VWQ / pdb_00008vwq
EMDB ID : EMD-43594
Title : E. coli 70S ribosome with unmodified Lys-tRNA^{Pro}(GGG) in the P/P conformation on a slippery CCC-C codon and Elongation Factor P bound (uL1 in the closed conformation)
Authors : Kimbrough, E.M.; Dunham, C.M.; Nguyen, H.A.
Deposited on : 2024-02-02
Resolution : 3.10 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

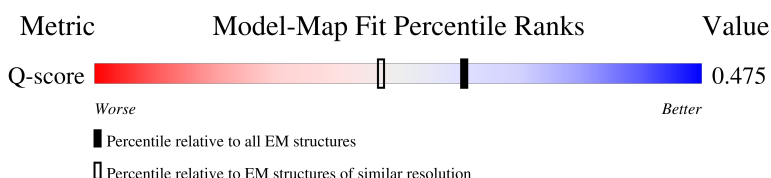
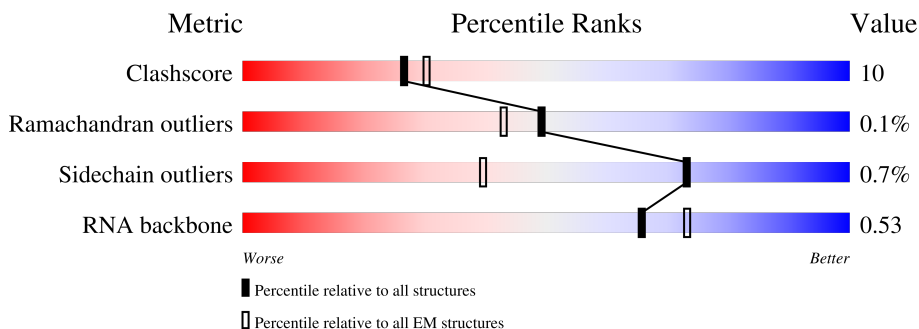
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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.



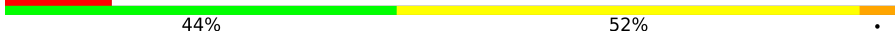
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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.

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1	1	2903	
2	2	1540	
3	3	120	

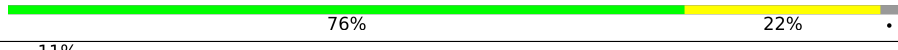
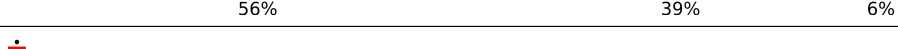
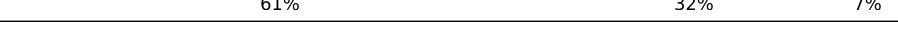
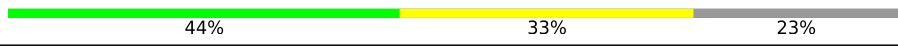
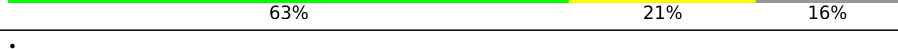
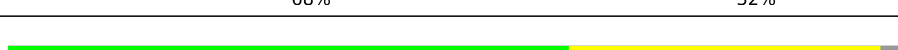
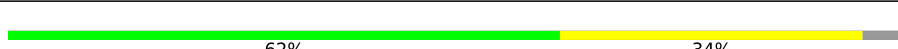
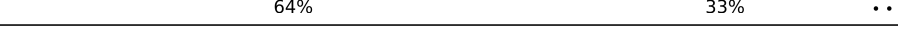
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Mol	Chain	Length	Quality of chain
4	4	18	
5	5	77	
6	6	188	
7	A	224	
8	B	273	
9	C	209	
10	D	201	
11	E	179	
12	F	177	
13	G	149	
14	J	142	
15	K	123	
16	L	144	
17	M	136	
18	N	127	
19	O	117	
20	P	115	
21	Q	118	
22	R	103	
23	S	110	
24	T	100	
25	U	104	
26	V	94	
27	W	84	
28	X	78	

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Mol	Chain	Length	Quality of chain
29	Y	63	
30	Z	59	
31	a	70	
32	b	57	
33	c	55	
34	d	46	
35	e	65	
36	f	38	
37	g	241	
38	h	233	
39	i	206	
40	j	167	
41	k	135	
42	l	179	
43	m	130	
44	n	130	
45	o	103	
46	p	129	
47	q	124	
48	r	118	
49	s	101	
50	t	89	
51	u	82	
52	v	84	
53	w	75	

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Mol	Chain	Length	Quality of chain
54	x	92	64% 26% 10%
55	y	87	79% 20%
56	z	71	20% 70% 28%

2 Entry composition [i](#)

There are 59 unique types of molecules in this entry. The entry contains 147683 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2869	Total	C	N	O	P	0	0
			61599	27479	11343	19908	2869		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 1914786293
1	1847	G	A	conflict	GB 1914786293
1	2069	A	G	conflict	GB 1914786293
1	2104	U	C	conflict	GB 1914786293

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1533	Total	C	N	O	P	0	0
			32907	14683	6036	10655	1533		

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

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

- Molecule 4 is a RNA chain called messenger RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	8	Total	C	N	O	P	0	0
			167	75	29	55	8		

- Molecule 5 is a RNA chain called tRNA^{Pro}L (GGG).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	77	Total	C	N	O	P	0	0
			1648	733	297	541	77		

- Molecule 6 is a protein called Elongation factor P.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	188	Total	C	N	O	S	0	0
			1461	928	242	286	5		

- Molecule 7 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	224	Total	C	N	O	S	0	0
			1663	1039	303	315	6		

- Molecule 8 is a protein called 50S ribosomal protein L2.

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

- Molecule 9 is a protein called 50S ribosomal protein L3.

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

- Molecule 10 is a protein called 50S ribosomal protein L4.

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

- Molecule 11 is a protein called 50S ribosomal protein L5.

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

- Molecule 12 is a protein called 50S ribosomal protein L6.

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

- Molecule 13 is a protein called Large ribosomal subunit protein bL9.

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

- Molecule 14 is a protein called 50S ribosomal protein L13.

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

- Molecule 15 is a protein called 50S ribosomal protein L14.

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

- Molecule 16 is a protein called 50S ribosomal protein L15.

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

- Molecule 17 is a protein called 50S ribosomal protein L16.

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

- Molecule 18 is a protein called Large ribosomal subunit protein bL17.

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

- Molecule 19 is a protein called 50S ribosomal protein L18.

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

- Molecule 20 is a protein called 50S ribosomal protein L19.

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

- Molecule 21 is a protein called 50S ribosomal protein L20.

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

- Molecule 22 is a protein called Ribosomal protein L21.

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

- Molecule 23 is a protein called 50S ribosomal protein L22.

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

- Molecule 24 is a protein called 50S ribosomal protein L23.

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

- Molecule 25 is a protein called 50S ribosomal protein L24.

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

- Molecule 26 is a protein called 50S ribosomal protein L25.

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

- Molecule 27 is a protein called Large ribosomal subunit protein bL27.

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

- Molecule 28 is a protein called 50S ribosomal protein L28.

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

- Molecule 29 is a protein called 50S ribosomal protein L29.

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

- Molecule 30 is a protein called Large ribosomal subunit protein uL30.

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

- Molecule 31 is a protein called 50S ribosomal protein L31.

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

- Molecule 32 is a protein called 50S ribosomal protein L32.

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

- Molecule 33 is a protein called Large ribosomal subunit protein bL33.

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

- Molecule 34 is a protein called 50S ribosomal protein L34.

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

- Molecule 35 is a protein called 50S ribosomal protein L35.

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

- Molecule 36 is a protein called 50S ribosomal protein L36.

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

- Molecule 37 is a protein called 30S ribosomal protein S2.

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

- Molecule 38 is a protein called 30S ribosomal protein S3.

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

- Molecule 39 is a protein called 30S ribosomal protein S4.

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

- Molecule 40 is a protein called 30S ribosomal protein S5.

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

- Molecule 41 is a protein called 30S ribosomal protein S6.

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

- Molecule 42 is a protein called 30S ribosomal protein S7.

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

- Molecule 43 is a protein called 30S ribosomal protein S8.

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

- Molecule 44 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 45 is a protein called 30S ribosomal protein S10.

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

- Molecule 46 is a protein called 30S ribosomal protein S11.

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

- Molecule 47 is a protein called Small ribosomal subunit protein uS12.

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

- Molecule 48 is a protein called 30S ribosomal protein S13.

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

- Molecule 49 is a protein called Small ribosomal subunit protein uS14.

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

- Molecule 50 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 51 is a protein called 30S ribosomal protein S16.

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

- Molecule 52 is a protein called Small ribosomal subunit protein uS17.

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

- Molecule 53 is a protein called 30S ribosomal protein S18.

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

- Molecule 54 is a protein called 30S ribosomal protein S19.

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

- Molecule 55 is a protein called 30S ribosomal protein S20.

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

- Molecule 56 is a protein called 30S ribosomal protein S21.

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

- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
57	1	339	Total	Mg	0
			339	339	
57	2	183	Total	Mg	0
			183	183	
57	3	12	Total	Mg	0
			12	12	
57	B	4	Total	Mg	0
			4	4	
57	C	1	Total	Mg	0
			1	1	
57	D	4	Total	Mg	0
			4	4	
57	E	1	Total	Mg	0
			1	1	
57	J	1	Total	Mg	0
			1	1	
57	K	1	Total	Mg	0
			1	1	
57	L	2	Total	Mg	0
			2	2	
57	M	1	Total	Mg	0
			1	1	
57	P	2	Total	Mg	0
			2	2	

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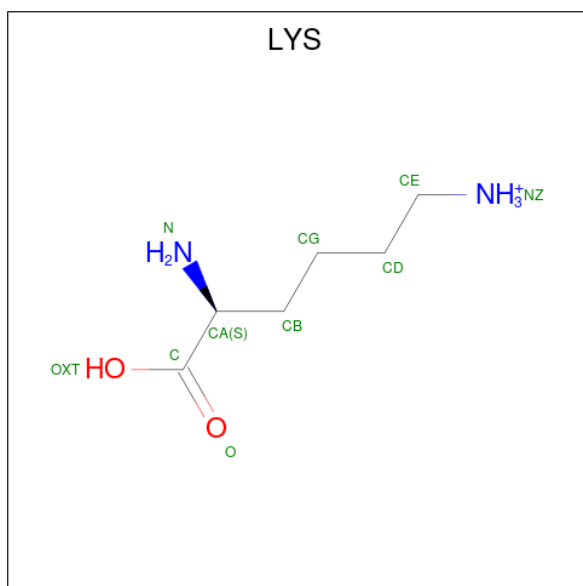
Mol	Chain	Residues	Atoms		AltConf
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57	R	3	Total 3	Mg 3	0
57	S	1	Total 1	Mg 1	0
57	T	2	Total 2	Mg 2	0
57	V	1	Total 1	Mg 1	0
57	Z	2	Total 2	Mg 2	0
57	b	2	Total 2	Mg 2	0
57	d	1	Total 1	Mg 1	0
57	e	3	Total 3	Mg 3	0
57	f	1	Total 1	Mg 1	0
57	i	3	Total 3	Mg 3	0
57	j	2	Total 2	Mg 2	0
57	k	1	Total 1	Mg 1	0
57	l	2	Total 2	Mg 2	0
57	m	1	Total 1	Mg 1	0
57	o	1	Total 1	Mg 1	0
57	q	1	Total 1	Mg 1	0
57	t	1	Total 1	Mg 1	0
57	u	1	Total 1	Mg 1	0
57	w	1	Total 1	Mg 1	0
57	y	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
57	z	2	Total	Mg	0
			2	2	

- Molecule 58 is LYSINE (CCD ID: LYS) (formula: $C_6H_{15}N_2O_2$).



Mol	Chain	Residues	Atoms				AltConf
58	5	1	Total	C	N	O	0
			9	6	2	1	

- Molecule 59 is water.

Mol	Chain	Residues	Atoms		AltConf
59	1	153	Total	O	0
			153	153	
59	2	78	Total	O	0
			78	78	
59	3	7	Total	O	0
			7	7	
59	4	1	Total	O	0
			1	1	
59	5	5	Total	O	0
			5	5	
59	6	5	Total	O	0
			5	5	
59	B	1	Total	O	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
59	C	2	Total 2	O 2	0
59	D	2	Total 2	O 2	0
59	E	9	Total 9	O 9	0
59	F	6	Total 6	O 6	0
59	G	6	Total 6	O 6	0
59	L	2	Total 2	O 2	0
59	M	2	Total 2	O 2	0
59	N	1	Total 1	O 1	0
59	O	3	Total 3	O 3	0
59	P	5	Total 5	O 5	0
59	S	3	Total 3	O 3	0
59	U	3	Total 3	O 3	0
59	V	5	Total 5	O 5	0
59	W	2	Total 2	O 2	0
59	Y	1	Total 1	O 1	0
59	a	15	Total 15	O 15	0
59	c	1	Total 1	O 1	0
59	f	1	Total 1	O 1	0
59	g	24	Total 24	O 24	0
59	h	5	Total 5	O 5	0
59	i	3	Total 3	O 3	0

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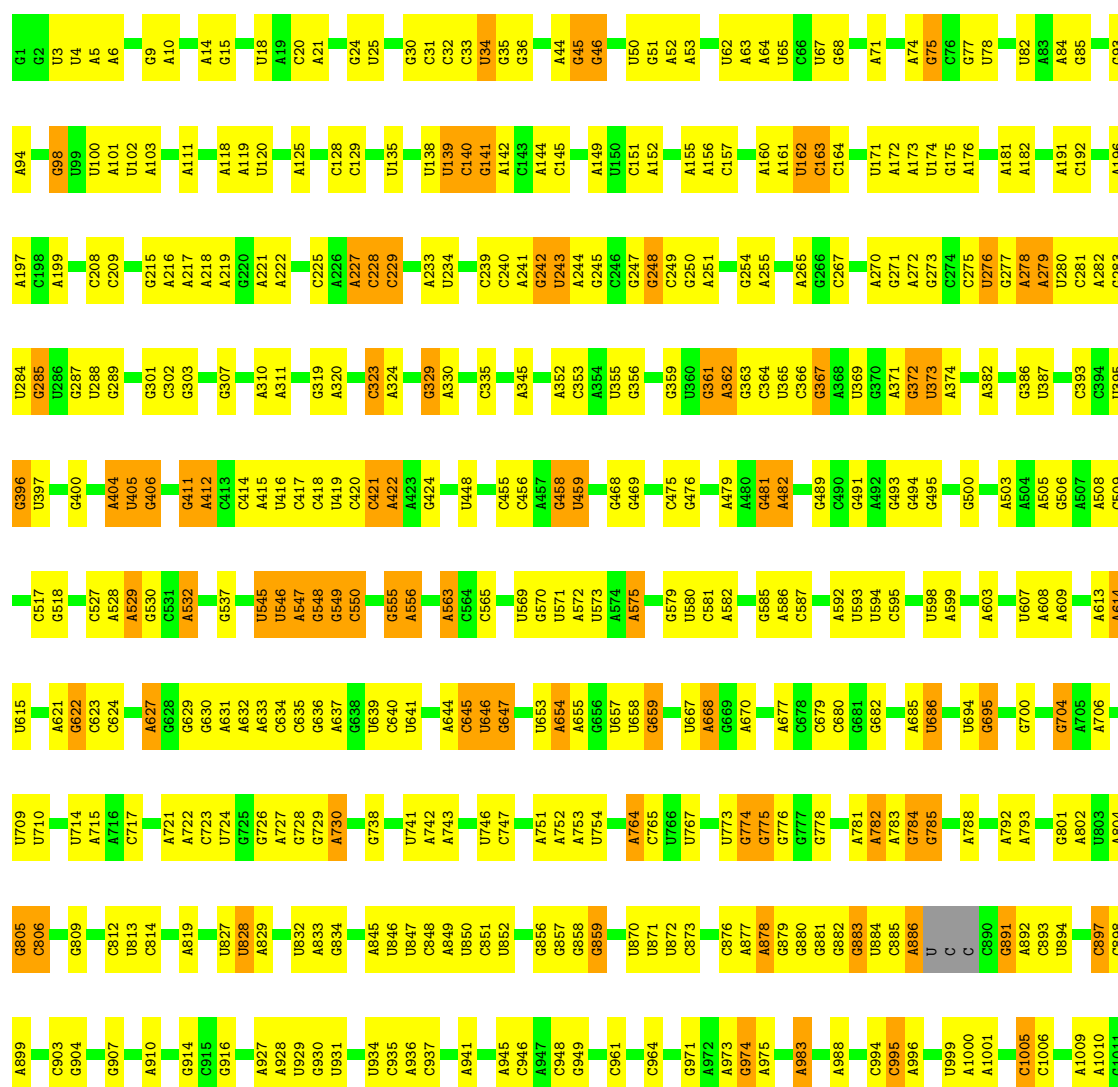
Mol	Chain	Residues	Atoms		AltConf
59	j	3	Total 3	O 3	0
59	k	4	Total 4	O 4	0
59	l	9	Total 9	O 9	0
59	m	3	Total 3	O 3	0
59	n	6	Total 6	O 6	0
59	o	4	Total 4	O 4	0
59	p	2	Total 2	O 2	0
59	q	6	Total 6	O 6	0
59	r	4	Total 4	O 4	0
59	t	1	Total 1	O 1	0
59	u	2	Total 2	O 2	0
59	v	5	Total 5	O 5	0
59	w	11	Total 11	O 11	0
59	x	1	Total 1	O 1	0
59	z	10	Total 10	O 10	0

3 Residue-property plots

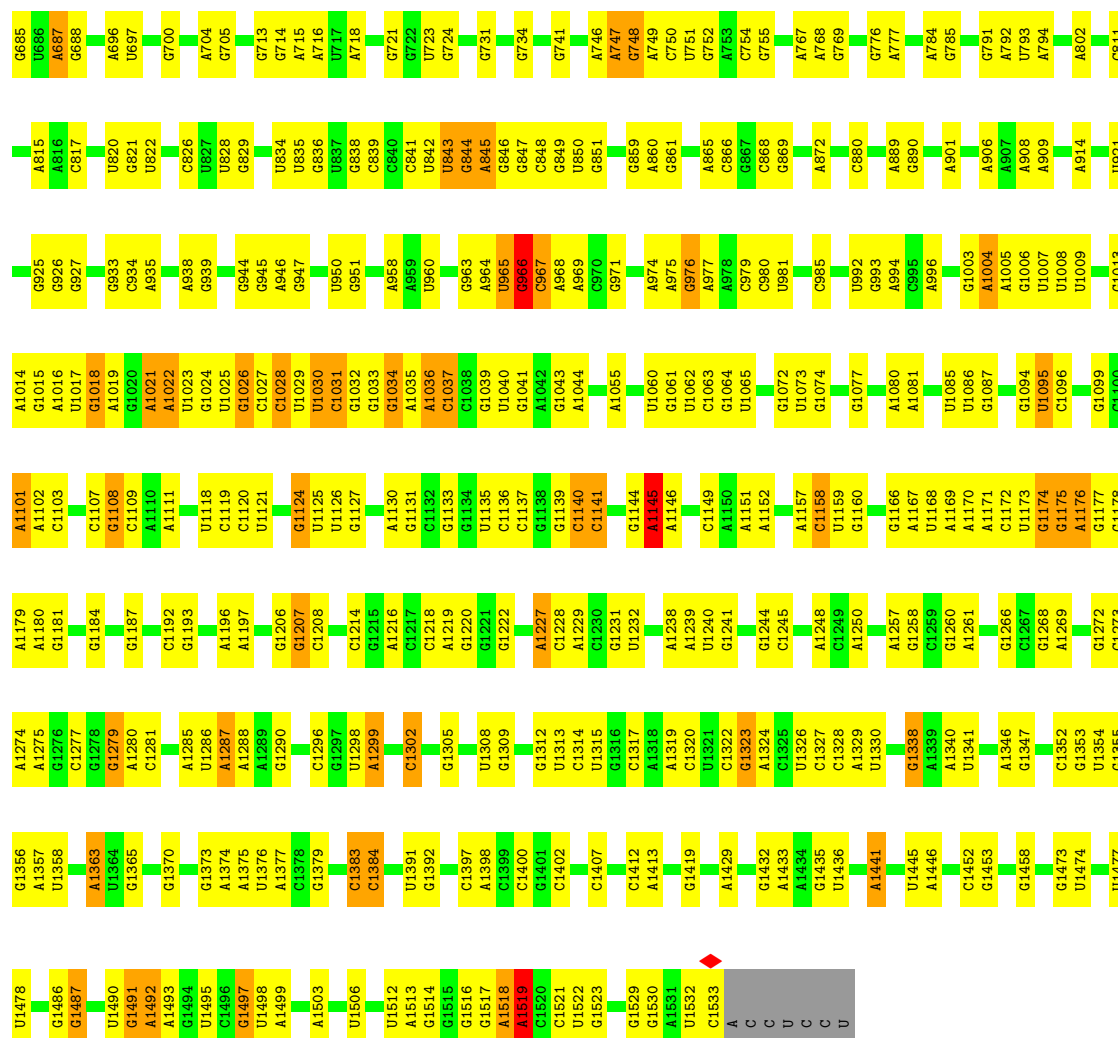
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 23S ribosomal RNA

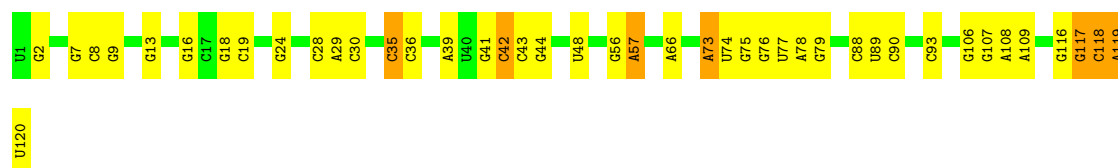
Chain 1: 



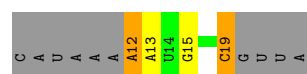
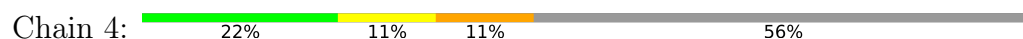
A2212	U2079	G1763	C1565	U1474	G1368	U1273	U181	G1093	U1012
U2213	A2080	C1764	A1566	G1475	G1368	A1274	G182	U1094	C1013
C2214	U2086	A1665	G1567	G1475	U1379	A1275	U183	A1095	A1014
C2215	G2087	C1771	G1568	G1478	U1379	G1278	U184	A1096	U1019
G2216	A2088	U1772	A1569	G1478	A1383	G1279	G185	U1097	U1019
U2220	U2092	A1672	A1570	G1482	A1383	G1280	G186	A1098	A1020
G2221	G2093	G1673	A1571	G1483	C1386	G1281	G190	A1099	A1021
C2222	A2094	G1674	A1572	G1484	C1387	G1282	C196	U1100	G1022
A2225	C2095	U1773	G1573	U1485	G1388	G1283	C197	U1101	U1023
C2226	C2096	U1675	C1577	U1486	G1388	A1284	C198	C1102	G1026
U2229	A2097	A1676	U1578	U1486	A1392	G1285	U198	C1104	A1027
G2230	U2098	G1681	A1579	U1486	A1393	A1286	U199	U1105	A1028
U2231	U2099	G1682	C1582	G1491	U1394	G1292	A1204	G1106	U1033
C2232	G2100	U1683	A1583	G1492	A1395	G1292	A1205	G1110	G1034
U2233	A2101	G1684	C1493	C1493	C1396	G1293	G1206	A1111	U1035
G2234	G2102	C1685	U1584	U1494	U1397	G1295	C1211	G1112	A1039
U2238	G2103	A1789	C1585	A1495	G1401	G1296	G1212	C1114	A1040
G2239	U2104	C1790	A1586	A1496	G1401	G1296	A1214	G1115	C1045
U2243	U2105	A1791	G1587	U1497	U1405	G1300	G1220	G1116	A1046
C2244	G2107	U1794	G1588	U1497	U1405	A1301	G1220	G1120	G1047
U2245	A2108	U1796	U1589	C1499	U1406	G1306	G1223	G1125	A1054
G2246	G2110	G1797	A1590	G1500	U1406	C1306	U1223	A1126	G1055
A2247	U2111	U1798	C1592	G1504	U1415	G1309	U1224	G1130	G1056
U2250	G2112	A1801	A1593	A1504	G1416	G1310	U1225	G1131	U1057
C2251	U2113	C1800	U1594	A1505	G1417	G1311	G1226	U1132	U1058
U2258	G2115	U1716	C1595	A1508	G1418	C1315	A1236	A1133	G1059
G2259	U2116	G1721	U1596	A1509	A1419	G1316	G1237	U1134	U1060
U2262	A2117	A1722	A1597	G1510	G1421	G1317	U1237	A1135	U1061
C2263	G2118	G1723	C1600	U1513	G1422	G1318	G1238	G1139	G1062
U2264	U2119	U1724	C1607	G1514	C1428	C1319	G1239	G1140	U1063
G2265	G2120	G1725	A1608	A1515	G1430	A1321	U1240	U1141	C1064
U2267	G2121	C1726	C1614	G1524	G1431	G1326	U1241	A1142	U1065
A2267	U2122	U1729	A1615	G1527	G1432	U1327	U1242	A1143	U1066
C2268	G2123	C1730	A1616	A1528	A1433	A1328	C1243	G1153	G1068
U2271	U2124	A1819	C1617	G1529	A1434	U1329	A1246	G1154	A1069
G2272	G2125	G1735	A1618	G1530	U1442	C1330	A1247	U1155	A1070
U2273	A2051	U1736	G1619	U1534	U1443	G1333	G1248	U1159	G1071
C2273	A2052	G1737	G1620	A1535	G1444	G1334	U1249	G1160	C1072
U2279	C2055	U1738	A1632	C1536	C1447	G1338	G1250	U1169	A1073
G2282	G2056	A1739	U1636	G1537	G1448	G1338	G1251	G1170	G1074
C2283	A2060	U1744	A1637	U1538	G1449	G1341	A1253	G1171	C1075
U2286	G2061	C1843	U1637	A1544	G1451	C1345	U1255	A1175	C1076
A2287	C2062	G1847	U1645	A1548	G1452	C1352	U1262	U1174	A1077
C2288	G2063	A1848	C1646	A1549	A1453	C1357	A1268	A1176	U1078
U2289	C2065	C1965	U1647	C1550	C1454	U1352	A1269	G1177	A1088
G2290	U2069	A1853	U1648	A1551	U1458	G1358	C1270	C1178	A1089
U2291	A2070	G1756	A1650	C1551	C1461	C1363	G1271	G1179	A1090
C2292	G2071	U1758	G1651	C1559	C1469	A1365	A1272	U1180	G1091
G2293	A2072	U1759	A1652	G1560	A1470				C1092
U2294	C2073	G1857	A1653						
C2295	G2074	A1858	A1654						



- Molecule 3: 5S ribosomal RNA



- Molecule 4: messenger RNA



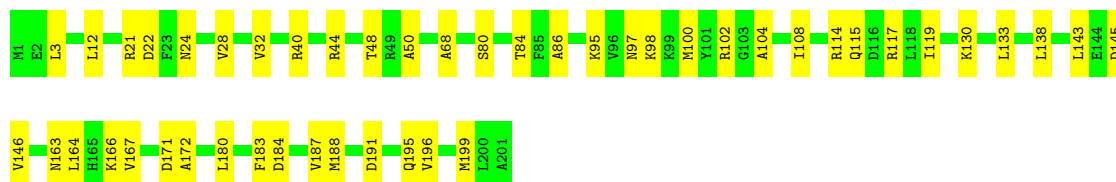
- Molecule 5: tRNA^{ProL} (GGG)





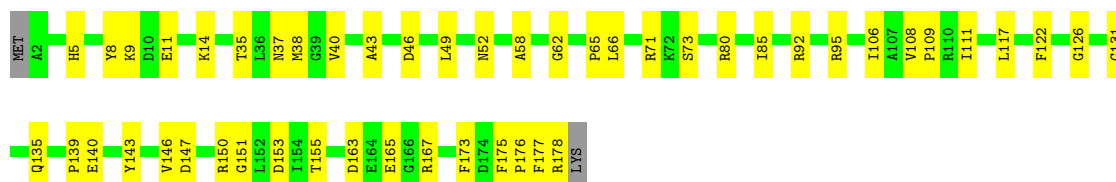
- Molecule 10: 50S ribosomal protein L4

Chain D: 77% 23%



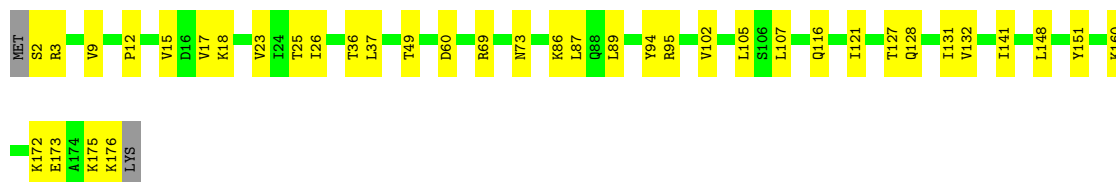
- Molecule 11: 50S ribosomal protein L5

Chain E: 72% 27%



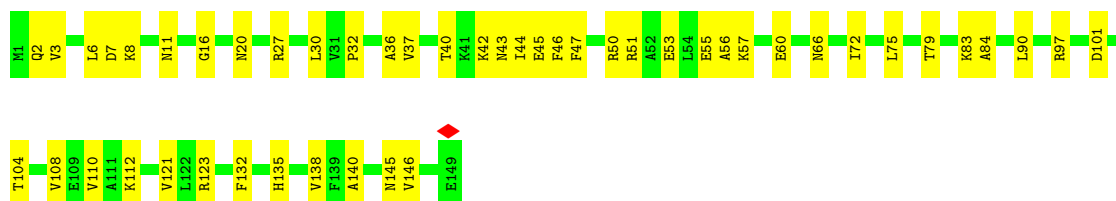
- Molecule 12: 50S ribosomal protein L6

Chain F: 77% 21%



- Molecule 13: Large ribosomal subunit protein bL9

Chain G: 68% 32%



- Molecule 14: 50S ribosomal protein L13

Chain J: 80% 20%



- Molecule 15: 50S ribosomal protein L14

Chain K: 82% 17%



- Molecule 16: 50S ribosomal protein L15

Chain L: 74% 26%



- Molecule 17: 50S ribosomal protein L16

Chain M: 79% 21%



- Molecule 18: Large ribosomal subunit protein bL17

Chain N: 69% 24% 6%



LYS
ALA
GLU
ALA
ALA
ALA
GLU

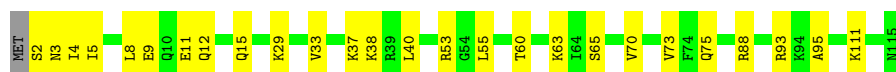
- Molecule 19: 50S ribosomal protein L18

Chain O: 77% 22%



- Molecule 20: 50S ribosomal protein L19

Chain P: 77% 23%



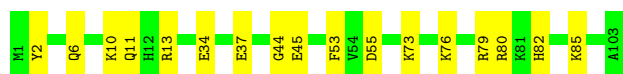
- Molecule 21: 50S ribosomal protein L20

Chain Q:  84% 15%



- Molecule 22: Ribosomal protein L21

Chain R:  83% 17%



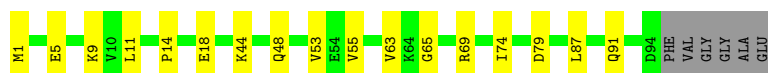
- Molecule 23: 50S ribosomal protein L22

Chain S:  77% 23%



- Molecule 24: 50S ribosomal protein L23

Chain T:  77% 17% 6%



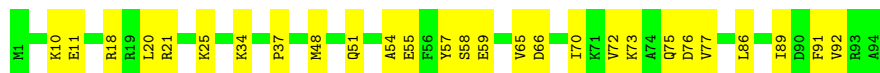
- Molecule 25: 50S ribosomal protein L24

Chain U:  77% 22%



- Molecule 26: 50S ribosomal protein L25

Chain V:  71% 29%



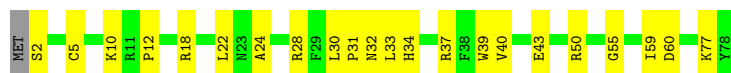
- Molecule 27: Large ribosomal subunit protein bL27

Chain W:  74% 14% 11%



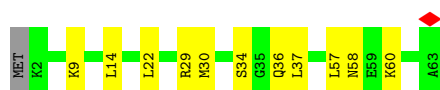
- Molecule 28: 50S ribosomal protein L28

Chain X:  71% 28%



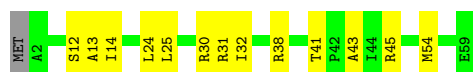
- Molecule 29: 50S ribosomal protein L29

Chain Y:  81% 17%



- Molecule 30: Large ribosomal subunit protein uL30

Chain Z:  76% 22%



- Molecule 31: 50S ribosomal protein L31

Chain a:  11% 56% 39% 6%



- Molecule 32: 50S ribosomal protein L32

Chain b:  72% 26%



- Molecule 33: Large ribosomal subunit protein bL33

Chain c:  65% 29% 5%



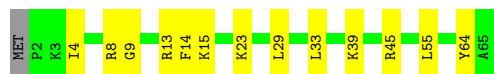
- Molecule 34: 50S ribosomal protein L34

Chain d:  78% 22%



- Molecule 35: 50S ribosomal protein L35

Chain e:  78% 20%



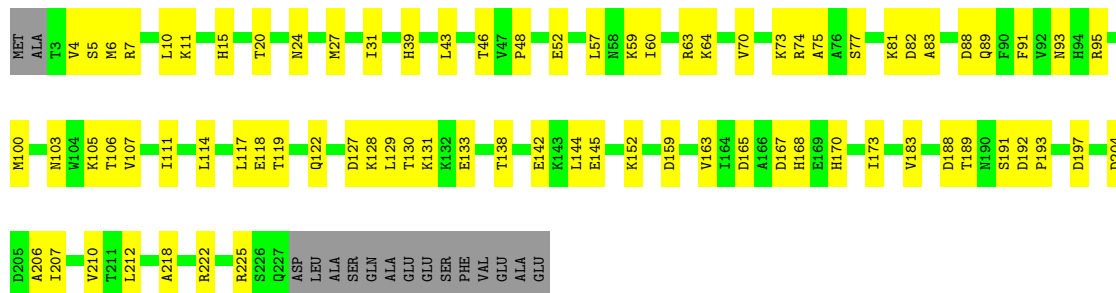
- Molecule 36: 50S ribosomal protein L36

Chain f:  76% 24%



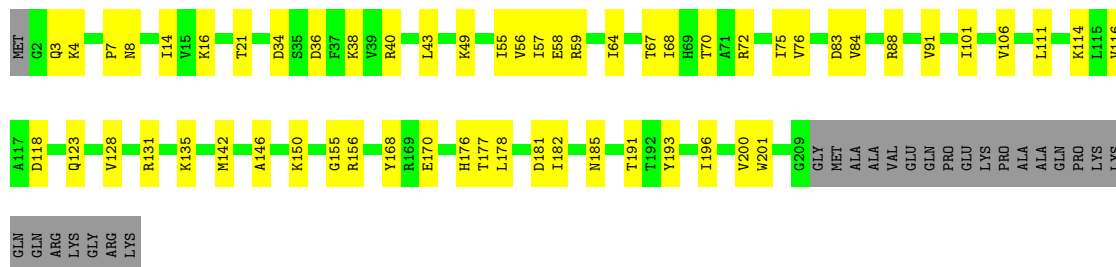
- Molecule 37: 30S ribosomal protein S2

Chain g:  61% 32% 7%



- Molecule 38: 30S ribosomal protein S3

Chain h:  65% 24% 11%



- Molecule 39: 30S ribosomal protein S4

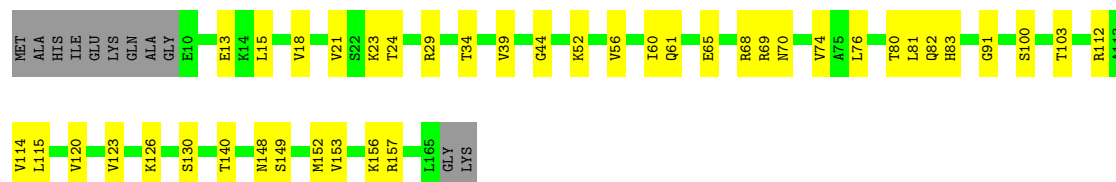
Chain i:  68% 31%





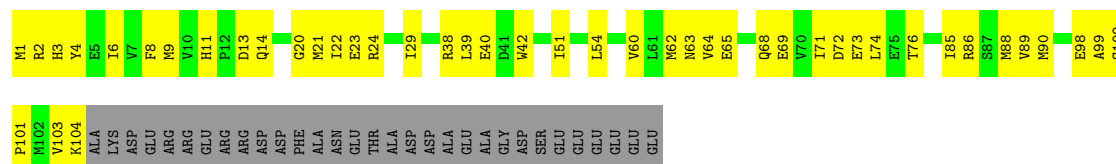
- Molecule 40: 30S ribosomal protein S5

Chain j: 69% 25% 7%



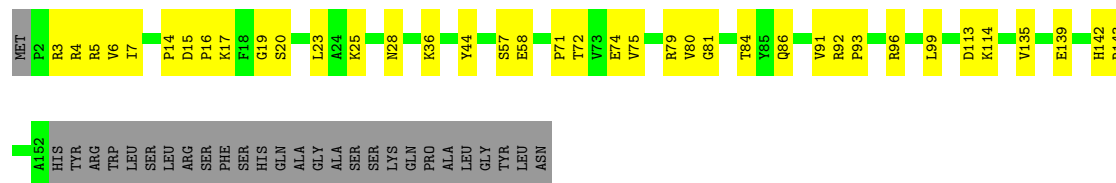
- Molecule 41: 30S ribosomal protein S6

Chain k: 44% 33% 23%



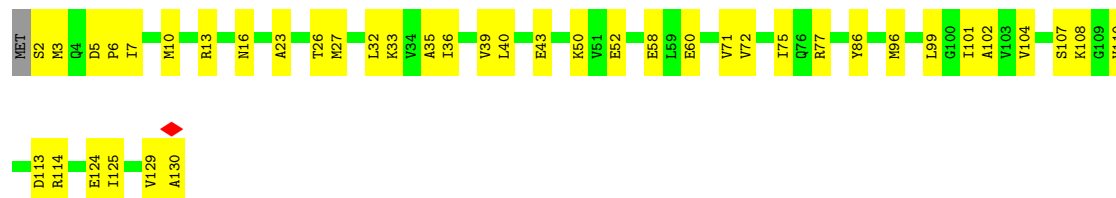
- Molecule 42: 30S ribosomal protein S7

Chain l: 63% 21% 16%



- Molecule 43: 30S ribosomal protein S8

Chain m: 68% 32% 0%

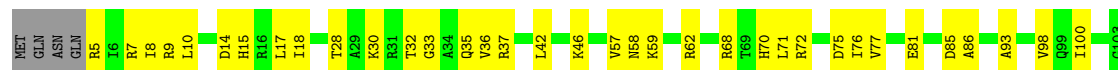


- Molecule 44: Small ribosomal subunit protein uS9

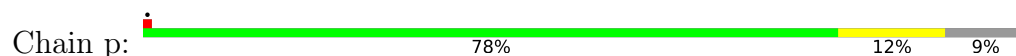
Chain n: 63% 35% 0%



- Molecule 45: 30S ribosomal protein S10



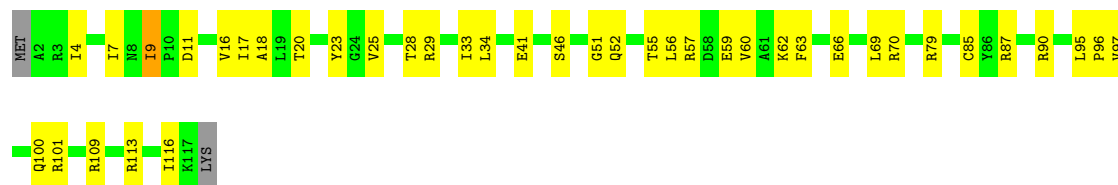
- Molecule 46: 30S ribosomal protein S11



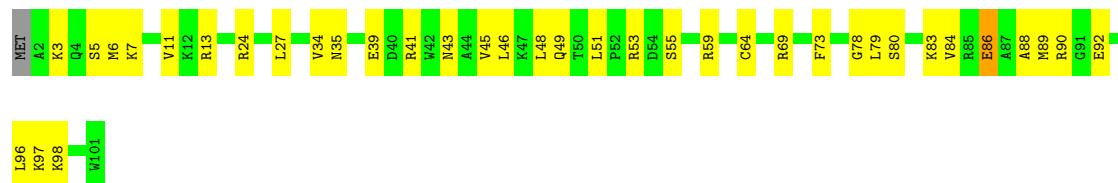
- Molecule 47: Small ribosomal subunit protein uS12



- Molecule 48: 30S ribosomal protein S13



- Molecule 49: Small ribosomal subunit protein uS14



- Molecule 50: Small ribosomal subunit protein uS15

Chain t:  71% 28% .



- Molecule 51: 30S ribosomal protein S16

Chain u:  65% 35%



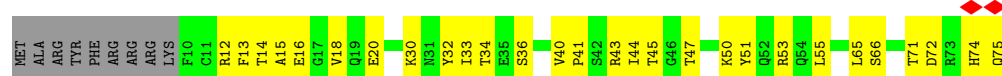
- Molecule 52: Small ribosomal subunit protein uS17

Chain v:  68% 27% 5%



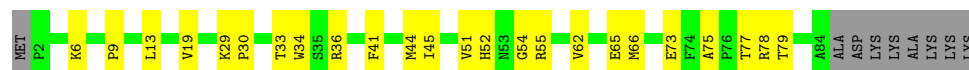
- Molecule 53: 30S ribosomal protein S18

Chain w:  51% 37% 12%



- Molecule 54: 30S ribosomal protein S19

Chain x:  64% 26% 10%



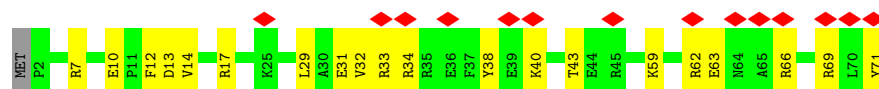
- Molecule 55: 30S ribosomal protein S20

Chain y:  79% 20%



- Molecule 56: 30S ribosomal protein S21

Chain z:  20% 70% 28%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	133607	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	56.07	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.033	Depositor
Minimum map value	-0.019	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0023	Depositor
Map size ($\text{\AA}$)	547.3792, 547.3792, 547.3792	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.0691, 1.0691, 1.0691	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: UR3, MG, MA6, 2MG, G7M, 0TD, KEO, 4OC, 5MC, PSU

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.46	0/68991	0.37	0/107624
2	2	0.39	0/36565	0.32	1/57035 (0.0%)
3	3	0.36	0/2872	0.34	0/4478
4	4	0.42	0/185	0.40	0/285
5	5	0.37	0/1841	0.56	3/2870 (0.1%)
6	6	0.85	0/1470	1.00	9/1992 (0.5%)
7	A	0.37	0/1678	0.77	9/2262 (0.4%)
8	B	0.52	1/2121 (0.0%)	0.55	0/2852
9	C	0.45	0/1586	0.52	0/2134
10	D	0.42	0/1571	0.48	0/2113
11	E	0.32	0/1434	0.48	0/1926
12	F	0.30	0/1333	0.48	0/1805
13	G	0.29	0/1122	0.52	0/1515
14	J	0.44	0/1152	0.52	0/1551
15	K	0.51	0/955	0.58	0/1279
16	L	0.57	0/1062	0.74	3/1413 (0.2%)
17	M	0.43	0/1093	0.48	0/1460
18	N	0.64	0/964	0.67	1/1289 (0.1%)
19	O	0.33	0/902	0.51	0/1209
20	P	0.44	0/929	0.48	0/1242
21	Q	0.67	2/960 (0.2%)	0.52	0/1278
22	R	0.43	0/829	0.49	0/1107
23	S	0.52	0/864	0.53	0/1156
24	T	0.38	0/752	0.45	0/1005
25	U	0.36	0/796	0.47	0/1062
26	V	0.35	0/766	0.41	0/1025
27	W	0.44	0/582	0.53	0/769
28	X	0.57	0/635	0.49	0/848
29	Y	0.33	0/502	0.44	0/667
30	Z	0.42	0/452	0.50	0/605
31	a	0.19	0/531	0.44	0/709
32	b	0.46	0/450	0.62	0/599

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	c	0.55	0/433	0.50	0/576
34	d	0.48	0/380	0.52	0/498
35	e	0.72	0/513	0.73	1/676 (0.1%)
36	f	0.42	0/303	0.58	0/397
37	g	0.24	0/1791	0.47	0/2413
38	h	0.45	0/1663	0.55	0/2241
39	i	0.36	0/1665	0.52	1/2227 (0.0%)
40	j	0.41	0/1165	0.47	0/1568
41	k	0.31	0/867	0.47	0/1171
42	l	0.55	0/1195	0.58	0/1602
43	m	0.49	0/989	0.53	1/1326 (0.1%)
44	n	0.44	0/1034	0.54	0/1375
45	o	0.31	0/800	0.49	0/1082
46	p	0.37	0/893	0.50	0/1205
47	q	0.39	0/960	0.52	0/1286
48	r	0.31	0/909	0.47	0/1215
49	s	0.45	0/817	0.49	0/1088
50	t	0.34	0/722	0.45	0/964
51	u	0.34	0/659	0.48	0/884
52	v	0.45	0/657	0.52	0/881
53	w	0.32	0/553	0.48	0/743
54	x	0.40	0/680	0.55	0/915
55	y	0.32	0/675	0.40	0/895
56	z	0.20	0/597	0.45	0/792
All	All	0.44	3/158865 (0.0%)	0.42	29/237184 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	Q	26	GLY	CA-C	-9.15	1.42	1.52
8	B	143	ASN	CA-C	-6.61	1.45	1.53
21	Q	25	TYR	CA-C	-6.23	1.44	1.52

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	L	36	LYS	N-CA-C	14.80	131.72	111.74
7	A	131	LEU	N-CA-C	9.73	121.48	111.07
39	i	23	SER	N-CA-C	9.06	120.76	111.07
5	5	2	G	C4'-C3'-O3'	8.93	122.79	109.40
35	e	33	LEU	N-CA-C	8.88	121.03	111.36
7	A	52	ALA	N-CA-C	-8.47	102.05	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	124	VAL	N-CA-C	8.25	119.05	110.72
18	N	105	GLY	N-CA-C	7.81	122.10	112.73
7	A	134	ARG	N-CA-C	-7.79	102.79	111.28
16	L	35	HIS	N-CA-C	7.10	120.09	108.52
6	6	62	ALA	N-CA-C	7.05	120.17	109.23
43	m	23	ALA	N-CA-C	6.87	118.77	111.28
7	A	128	GLY	N-CA-C	-6.70	103.98	114.10
6	6	61	SER	N-CA-C	6.61	118.91	108.79
6	6	103	ASN	N-CA-C	-6.57	103.76	113.61
5	5	74	C	C2'-C3'-O3'	-6.29	104.27	113.70
6	6	135	ILE	N-CA-C	6.19	117.39	107.73
5	5	3	G	C4'-C3'-O3'	6.16	118.64	109.40
7	A	122	ARG	N-CA-C	-6.00	104.74	111.28
6	6	71	ASN	N-CA-C	5.89	119.05	107.98
7	A	130	VAL	N-CA-C	-5.88	104.78	110.72
6	6	85	MET	N-CA-C	5.76	118.03	108.99
2	2	1145	A	C4'-C3'-O3'	-5.52	104.72	113.00
16	L	36	LYS	CB-CA-C	-5.43	104.02	111.73
6	6	59	THR	N-CA-C	5.34	117.19	111.36
7	A	125	GLY	N-CA-C	5.34	119.14	112.73
7	A	51	ASP	N-CA-C	-5.16	102.27	109.96
6	6	81	PHE	N-CA-C	5.05	117.47	109.50
6	6	136	VAL	N-CA-C	5.01	115.78	110.72

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	1	61599	0	30981	884	0
2	2	32907	0	16572	443	0
3	3	2569	0	1300	29	0
4	4	167	0	88	4	0
5	5	1648	0	833	23	0
6	6	1461	0	1421	56	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	1663	0	1746	121	0
8	B	2082	0	2154	49	0
9	C	1565	0	1615	40	0
10	D	1552	0	1619	33	0
11	E	1410	0	1444	42	0
12	F	1313	0	1358	23	0
13	G	1111	0	1148	34	0
14	J	1129	0	1162	20	0
15	K	946	0	1023	19	0
16	L	1053	0	1129	35	0
17	M	1074	0	1157	22	0
18	N	951	0	994	20	0
19	O	892	0	923	18	0
20	P	917	0	962	24	0
21	Q	947	0	1019	11	0
22	R	816	0	839	14	0
23	S	857	0	922	19	0
24	T	746	0	811	13	0
25	U	788	0	844	17	0
26	V	753	0	780	22	0
27	W	575	0	592	10	0
28	X	625	0	652	17	0
29	Y	501	0	531	9	0
30	Z	448	0	488	10	0
31	a	522	0	524	21	0
32	b	444	0	458	15	0
33	c	426	0	464	16	0
34	d	377	0	418	8	0
35	e	504	0	572	14	0
36	f	302	0	343	6	0
37	g	1760	0	1787	60	0
38	h	1636	0	1710	39	0
39	i	1643	0	1706	48	0
40	j	1152	0	1196	27	0
41	k	848	0	846	31	0
42	l	1181	0	1238	30	0
43	m	979	0	1031	27	0
44	n	1022	0	1070	41	0
45	o	790	0	831	32	0
46	p	877	0	887	16	0
47	q	957	0	1017	28	0
48	r	900	0	965	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	s	805	0	844	27	0
50	t	714	0	734	19	0
51	u	649	0	666	20	0
52	v	648	0	691	17	0
53	w	544	0	560	25	0
54	x	663	0	688	20	0
55	y	669	0	719	13	0
56	z	589	0	629	19	0
57	1	339	0	0	0	0
57	2	183	0	0	0	0
57	3	12	0	0	0	0
57	B	4	0	0	0	0
57	C	1	0	0	0	0
57	D	4	0	0	0	0
57	E	1	0	0	0	0
57	J	1	0	0	0	0
57	K	1	0	0	0	0
57	L	2	0	0	0	0
57	M	1	0	0	0	0
57	P	2	0	0	0	0
57	Q	2	0	0	0	0
57	R	3	0	0	0	0
57	S	1	0	0	0	0
57	T	2	0	0	0	0
57	V	1	0	0	0	0
57	Z	2	0	0	0	0
57	b	2	0	0	0	0
57	d	1	0	0	0	0
57	e	3	0	0	0	0
57	f	1	0	0	0	0
57	i	3	0	0	0	0
57	j	2	0	0	0	0
57	k	1	0	0	0	0
57	l	2	0	0	0	0
57	m	1	0	0	0	0
57	o	1	0	0	0	0
57	q	1	0	0	0	0
57	t	1	0	0	0	0
57	u	1	0	0	0	0
57	w	1	0	0	0	0
57	y	1	0	0	0	0
57	z	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	5	9	0	12	0	0
59	1	153	0	0	36	0
59	2	78	0	0	17	0
59	3	7	0	0	1	0
59	4	1	0	0	0	0
59	5	5	0	0	0	0
59	6	5	0	0	1	0
59	B	1	0	0	0	0
59	C	2	0	0	0	0
59	D	2	0	0	0	0
59	E	9	0	0	1	0
59	F	6	0	0	0	0
59	G	6	0	0	1	0
59	L	2	0	0	0	0
59	M	2	0	0	0	0
59	N	1	0	0	0	0
59	O	3	0	0	0	0
59	P	5	0	0	2	0
59	S	3	0	0	0	0
59	U	3	0	0	0	0
59	V	5	0	0	4	0
59	W	2	0	0	1	0
59	Y	1	0	0	0	0
59	a	15	0	0	4	0
59	c	1	0	0	2	0
59	f	1	0	0	0	0
59	g	24	0	0	4	0
59	h	5	0	0	0	0
59	i	3	0	0	1	0
59	j	3	0	0	1	0
59	k	4	0	0	0	0
59	l	9	0	0	2	0
59	m	3	0	0	1	0
59	n	6	0	0	1	0
59	o	4	0	0	0	0
59	p	2	0	0	1	0
59	q	6	0	0	0	0
59	r	4	0	0	0	0
59	t	1	0	0	0	0
59	u	2	0	0	0	0
59	v	5	0	0	0	0
59	w	11	0	0	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	x	1	0	0	0	0
59	z	10	0	0	1	0
All	All	147683	0	99713	2424	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 10.

All (2424) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2190:G:H5''	59:1:3455:HOH:O	1.28	1.27
2:2:89:U:H3'	59:2:1801:HOH:O	1.40	1.22
1:1:1071:G:H5'	59:1:3494:HOH:O	1.34	1.22
1:1:894:U:H5''	59:1:3485:HOH:O	1.45	1.14
5:5:39:G:O2'	6:6:149:THR:HG22	1.50	1.11
2:2:85:U:H2'	59:2:1822:HOH:O	1.52	1.07
42:l:143:ARG:HD3	59:l:301:HOH:O	1.51	1.07
7:A:52:ALA:HB3	7:A:53:ARG:NH2	1.72	1.04
1:1:1096:A:H1'	59:1:3496:HOH:O	1.55	1.03
7:A:52:ALA:HB3	7:A:53:ARG:HH21	1.19	1.00
59:1:3430:HOH:O	17:M:18:ARG:HD3	1.60	1.00
1:1:284:U:H3	1:1:356:G:H1	0.99	0.97
4:4:12:A:C2	4:4:12:A:OP1	2.19	0.95
1:1:2109:U:H5''	59:1:3449:HOH:O	1.67	0.94
2:2:429:U:H5'	39:i:9:LEU:HD11	1.53	0.91
1:1:1478:G:H1	1:1:1513:U:H3	1.18	0.91
26:V:72:VAL:HG11	26:V:91:PHE:HB3	1.54	0.89
1:1:586:A:H5'	10:D:84:THR:HG21	1.56	0.88
7:A:202:THR:HG22	7:A:205:LYS:HE2	1.56	0.86
7:A:154:LYS:HA	7:A:157:LYS:HG2	1.57	0.86
20:P:60:THR:HG22	20:P:73:VAL:HG12	1.57	0.86
28:X:33:LEU:HD12	28:X:50:ARG:HG2	1.58	0.85
1:1:2160:C:H1'	59:1:3407:HOH:O	1.77	0.85
59:1:3430:HOH:O	17:M:18:ARG:CD	2.22	0.84
1:1:2840:C:H5''	18:N:53:THR:HG21	1.58	0.84
5:5:39:G:H4'	6:6:149:THR:HG21	1.58	0.83
1:1:1936:A:H2	1:1:1943:U:H3	1.24	0.83
5:5:39:G:O2'	6:6:149:THR:CG2	2.26	0.83
1:1:880:G:H1	1:1:897:C:H42	1.23	0.82
44:n:91:ASP:HB3	44:n:94:LEU:HD22	1.58	0.82
33:c:17:THR:HG21	33:c:42:VAL:HG11	1.62	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1270:C:H5''	1:1:1271:G:H5'	1.61	0.81
53:w:18:VAL:HA	59:w:207:HOH:O	1.81	0.80
1:1:2119:A:H5'	59:1:3519:HOH:O	1.82	0.80
2:2:85:U:H5'	59:2:1810:HOH:O	1.82	0.79
2:2:81:A:H5'	59:2:1829:HOH:O	1.81	0.78
6:6:34:KEO:O02	6:6:34:KEO:N02	2.14	0.78
1:1:1174:U:C6	59:1:3513:HOH:O	2.37	0.77
13:G:84:ALA:HB2	13:G:90:LEU:HD23	1.64	0.77
45:o:10:LEU:HB3	45:o:18:ILE:HD11	1.66	0.77
31:a:3:LYS:HA	59:a:103:HOH:O	1.85	0.77
40:j:114:VAL:HG11	40:j:140:THR:HG21	1.67	0.77
41:k:88:MET:HE3	41:k:90:MET:HE3	1.67	0.76
52:v:17:MET:SD	52:v:20:SER:OG	2.43	0.76
6:6:16:MET:HB2	6:6:65:ALA:HB2	1.68	0.76
1:1:495:G:H21	23:S:61:ASN:HD21	1.33	0.76
7:A:64:VAL:HG12	7:A:161:VAL:HG22	1.66	0.75
1:1:1597:A:H5''	1:1:1598:A:H5'	1.66	0.75
2:2:87:C:C4	59:2:1833:HOH:O	2.39	0.75
5:5:39:G:HO2'	6:6:149:THR:HG22	1.51	0.75
1:1:1105:U:H2'	1:1:1106:G:H8	1.49	0.75
1:1:517:C:OP2	32:b:10:ARG:NH2	2.20	0.74
1:1:2286:G:OP2	33:c:6:ARG:NH2	2.20	0.74
7:A:122:ARG:HD2	7:A:126:GLN:HE22	1.50	0.74
1:1:1093:G:O2'	1:1:1098:A:N6	2.20	0.74
1:1:704:G:H2'	1:1:726:G:H22	1.52	0.74
9:C:133:THR:HG22	9:C:134:HIS:H	1.52	0.74
7:A:114:VAL:HG13	7:A:139:ASN:HD21	1.53	0.74
26:V:54:ALA:HB3	59:V:202:HOH:O	1.87	0.73
1:1:1090:A:H2'	1:1:1091:G:C8	2.23	0.73
42:l:71:PRO:HG3	42:l:99:LEU:HD11	1.70	0.73
46:p:64:GLN:HB2	46:p:99:ALA:HB2	1.68	0.73
20:P:29:LYS:HB3	20:P:40:LEU:HD12	1.68	0.73
1:1:2114:A:H2'	1:1:2115:G:C8	2.23	0.73
1:1:2115:G:H2'	1:1:2117:A:H62	1.53	0.73
33:c:53:LYS:NZ	59:c:101:HOH:O	2.21	0.73
38:h:111:LEU:HD11	38:h:146:ALA:HB2	1.70	0.73
16:L:78:ARG:HG2	16:L:113:ALA:HB3	1.71	0.73
1:1:729:G:H5''	1:1:730:A:H5''	1.70	0.73
2:2:81:A:N6	2:2:88:U:O4	2.22	0.73
42:l:28:ASN:OD1	42:l:36:LYS:NZ	2.22	0.73
23:S:22:ASP:OD2	23:S:25:ARG:NH2	2.22	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2304:G:H22	1:1:2312:U:H3	1.35	0.72
20:P:33:VAL:HG22	20:P:38:LYS:HG2	1.70	0.72
1:1:706:A:OP1	8:B:7:LYS:NZ	2.22	0.72
7:A:167:LYS:HE3	7:A:172:HIS:HA	1.70	0.72
37:g:43:LEU:HA	37:g:46:THR:HG22	1.70	0.72
39:i:60:LYS:NZ	39:i:194:ASP:O	2.22	0.72
1:1:1172:C:H3'	59:1:3424:HOH:O	1.90	0.72
16:L:123:ARG:NH2	16:L:143:GLU:OE2	2.22	0.72
53:w:12:ARG:CD	59:w:209:HOH:O	2.37	0.72
1:1:1143:A:N7	14:J:27:ARG:NH1	2.37	0.72
31:a:56:ARG:HH11	48:r:79:ARG:HD2	1.54	0.72
1:1:897:C:H5	59:1:3470:HOH:O	1.70	0.72
50:t:17:ARG:HE	50:t:18:ASP:HB2	1.54	0.72
1:1:1153:C:OP1	21:Q:92:ARG:NH2	2.21	0.71
39:i:116:GLN:OE1	39:i:154:ARG:NH2	2.21	0.71
2:2:673:A:H2'	2:2:674:G:C8	2.26	0.71
56:z:69:ARG:NH2	56:z:71:TYR:O	2.23	0.71
1:1:500:G:N1	1:1:503:A:OP2	2.23	0.71
2:2:664:G:H22	2:2:741:G:H1	1.37	0.71
41:k:9:MET:HE3	41:k:86:ARG:HB3	1.73	0.71
3:3:43:C:O2	11:E:92:ARG:NH2	2.21	0.71
1:1:355:U:H2'	1:1:356:G:H8	1.55	0.71
2:2:517:G:N2	2:2:530:G:OP1	2.22	0.71
7:A:116:ALA:HB2	7:A:124:VAL:HG21	1.72	0.71
1:1:1190:G:N7	59:1:3401:HOH:O	2.22	0.71
1:1:2006:C:O2'	1:1:2823:A:N3	2.23	0.70
9:C:5:VAL:H	9:C:32:ASN:HD21	1.39	0.70
37:g:100:MET:HA	37:g:107:VAL:HG21	1.74	0.70
2:2:841:C:H2'	2:2:843:U:H5'	1.74	0.70
31:a:16:CYS:SG	31:a:17:SER:N	2.64	0.70
2:2:634:C:H2'	2:2:635:A:H8	1.56	0.70
23:S:4:ILE:HG12	23:S:106:VAL:HG22	1.73	0.70
45:o:14:ASP:HB3	45:o:17:LEU:HB3	1.72	0.70
1:1:870:U:OP1	17:M:6:ARG:NH1	2.25	0.70
1:1:1753:G:N2	1:1:1756:G:OP2	2.25	0.70
52:v:7:THR:HG22	52:v:60:GLU:HB2	1.73	0.70
1:1:529:A:OP2	14:J:116:ARG:NH2	2.24	0.70
1:1:1827:U:H5'	1:1:1971:U:H4'	1.74	0.70
2:2:1356:G:H2'	2:2:1357:A:C8	2.27	0.70
1:1:805:G:N2	1:1:829:A:OP1	2.25	0.70
1:1:270:A:N1	1:1:369:U:O2'	2.24	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1534:U:H2'	1:1:1536:C:H5'	1.74	0.69
53:w:34:THR:HG23	53:w:36:SER:H	1.57	0.69
1:1:2189:U:H5''	59:1:3428:HOH:O	1.92	0.69
1:1:2530:A:N7	12:F:172:LYS:NZ	2.38	0.69
1:1:1858:A:N6	1:1:1884:G:O2'	2.24	0.69
1:1:281:C:H42	1:1:359:G:H1	1.38	0.69
1:1:572:A:OP2	22:R:80:ARG:NH2	2.24	0.69
1:1:2243:U:H2'	1:1:2244:U:C6	2.28	0.69
45:o:59:LYS:HE2	45:o:62:ARG:HH22	1.56	0.69
14:J:31:GLU:OE1	14:J:34:ARG:NH2	2.26	0.69
8:B:180:GLU:OE2	8:B:270:ARG:NH1	2.25	0.69
1:1:140:C:OP2	1:1:141:G:N2	2.26	0.68
2:2:206:C:N4	59:2:1804:HOH:O	2.25	0.68
4:4:12:A:OP1	4:4:12:A:N3	2.25	0.68
12:F:89:LEU:HD13	12:F:94:TYR:HB3	1.74	0.68
44:n:106:ARG:NH1	44:n:107:ASP:O	2.25	0.68
2:2:1028:C:H1'	2:2:1034:G:H22	1.58	0.68
1:1:2128:G:N7	7:A:37:LYS:NZ	2.37	0.68
2:2:1229:A:OP2	48:r:113:ARG:NH1	2.26	0.68
41:k:38:ARG:HH21	41:k:63:ASN:HD21	1.40	0.68
2:2:1126:U:OP1	45:o:7:ARG:NH2	2.26	0.68
12:F:2:SER:OG	12:F:3:ARG:N	2.26	0.68
17:M:14:LYS:O	17:M:71:LYS:NZ	2.24	0.68
47:q:100:GLY:N	47:q:104:CYS:O	2.25	0.68
44:n:12:ARG:HH22	44:n:109:ARG:HH21	1.41	0.68
2:2:337:G:H2'	2:2:338:A:C8	2.29	0.67
51:u:48:GLU:OE2	51:u:51:ARG:NH1	2.24	0.67
1:1:636:G:N7	16:L:109:LYS:NZ	2.38	0.67
38:h:49:LYS:O	38:h:72:ARG:NH1	2.26	0.67
2:2:81:A:N7	2:2:83:C:N4	2.41	0.67
2:2:130:A:H5'	52:v:65:ARG:HD3	1.75	0.67
2:2:521:G:N7	47:q:50:ARG:NH2	2.43	0.67
2:2:1013:G:N2	2:2:1016:A:OP2	2.27	0.67
7:A:55:SER:C	7:A:57:GLN:H	2.03	0.67
14:J:17:VAL:HG12	14:J:55:ILE:HB	1.77	0.67
54:x:55:ARG:HH22	54:x:79:THR:HG21	1.58	0.67
1:1:320:A:N3	10:D:163:ASN:ND2	2.43	0.67
1:1:2182:U:H2'	1:1:2183:A:C8	2.30	0.67
23:S:19:LEU:HB3	32:b:22:LEU:HD13	1.76	0.67
1:1:569:U:O2'	1:1:983:A:N1	2.26	0.67
10:D:119:ILE:HB	10:D:187:VAL:HG12	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:M:66:ARG:NH1	17:M:104:GLU:OE2	2.27	0.67
1:1:2467:C:OP1	36:f:8:LYS:NZ	2.27	0.66
7:A:69:THR:H	7:A:177:LYS:HD3	1.60	0.66
7:A:134:ARG:C	7:A:136:LEU:H	2.03	0.66
2:2:405:U:O4	39:i:2:ALA:N	2.28	0.66
2:2:1152:A:OP1	45:o:70:HIS:ND1	2.28	0.66
7:A:52:ALA:CB	7:A:53:ARG:HH21	2.01	0.66
36:f:2:LYS:NZ	36:f:32:LYS:O	2.28	0.66
50:t:2:SER:OG	50:t:3:LEU:N	2.28	0.66
1:1:1392:A:N6	24:T:18:GLU:OE2	2.27	0.66
56:z:62:ARG:HB2	59:z:202:HOH:O	1.94	0.66
37:g:31:ILE:HG21	37:g:39:HIS:HD2	1.61	0.66
42:l:15:ASP:OD1	42:l:20:SER:N	2.25	0.66
1:1:994:C:O2	22:R:10:LYS:NZ	2.28	0.66
1:1:2376:A:N3	19:O:111:ARG:NH1	2.43	0.66
29:Y:9:LYS:O	29:Y:60:LYS:NZ	2.26	0.66
33:c:27:LYS:NZ	59:c:101:HOH:O	2.28	0.66
38:h:191:THR:HG23	38:h:193:TYR:H	1.58	0.66
1:1:2191:A:H2'	1:1:2192:U:C6	2.30	0.66
1:1:1056:G:O2'	1:1:1103:A:N6	2.29	0.66
1:1:2113:U:N1	59:1:3410:HOH:O	2.28	0.66
2:2:618:C:O2'	51:u:14:ARG:NH2	2.28	0.66
2:2:1023:U:H5''	59:2:1843:HOH:O	1.95	0.66
2:2:1176:A:H2'	2:2:1177:G:C8	2.30	0.66
1:1:1779:U:OP2	1:1:1784:A:N6	2.28	0.66
1:1:2867:G:O2'	1:1:2868:A:O5'	2.13	0.66
5:5:5:A:O2'	5:5:6:C:O5'	2.13	0.66
1:1:245:G:O6	35:e:8:ARG:NH1	2.29	0.66
1:1:781:A:OP1	8:B:217:ARG:NH2	2.24	0.66
20:P:15:GLN:OE1	20:P:15:GLN:N	2.29	0.66
1:1:893:C:H2'	1:1:894:U:C6	2.31	0.65
2:2:87:C:C5	59:2:1833:HOH:O	2.49	0.65
7:A:52:ALA:CB	7:A:53:ARG:NH2	2.54	0.65
1:1:335:C:H5''	25:U:82:ARG:HD3	1.78	0.65
1:1:627:A:OP1	16:L:78:ARG:NH1	2.21	0.65
3:3:48:U:OP1	19:O:30:ARG:NH2	2.30	0.65
46:p:98:ARG:HD2	59:p:201:HOH:O	1.96	0.65
2:2:980:C:O2'	49:s:13:ARG:NH1	2.30	0.65
44:n:112:GLU:OE2	44:n:115:LYS:NZ	2.27	0.65
1:1:2822:G:OP1	9:C:164:GLN:NE2	2.30	0.65
2:2:1298:U:H5	42:l:114:LYS:HD2	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:75:G:H2'	3:3:76:G:H8	1.62	0.65
1:1:1715:G:HO2'	1:1:1716:U:H6	1.44	0.65
2:2:150:U:H2'	2:2:151:A:H8	1.62	0.65
52:v:25:ILE:HD11	52:v:61:ILE:HD11	1.78	0.65
1:1:219:A:N3	1:1:234:U:O2'	2.28	0.65
1:1:2328:A:H2'	1:1:2329:U:C6	2.33	0.64
1:1:2683:C:O2	15:K:70:ARG:NH2	2.27	0.64
2:2:501:C:OP1	47:q:114:ARG:NH2	2.29	0.64
32:b:54:VAL:HG23	32:b:55:ILE:HG23	1.79	0.64
2:2:337:G:H2'	2:2:338:A:H8	1.61	0.64
7:A:62:ALA:HB1	7:A:161:VAL:HG11	1.79	0.64
31:a:25:ARG:NH2	59:a:102:HOH:O	2.26	0.64
11:E:140:GLU:HA	31:a:28:VAL:HG12	1.79	0.64
38:h:36:ASP:OD1	38:h:59:ARG:NH2	2.30	0.64
1:1:1801:A:OP2	8:B:150:LYS:NZ	2.25	0.64
41:k:99:ALA:HB1	41:k:103:VAL:HG11	1.78	0.64
3:3:75:G:H2'	3:3:76:G:C8	2.32	0.64
5:5:26:A:H61	5:5:44:G:H1	1.45	0.64
6:6:110:GLN:HE22	7:A:126:GLN:HG2	1.63	0.64
7:A:88:LYS:HZ1	7:A:95:VAL:H	1.45	0.64
1:1:191:A:H2'	1:1:192:C:H6	1.63	0.64
1:1:1847:G:O2'	1:1:1848:A:H8	1.80	0.64
11:E:62:GLY:O	11:E:95:ARG:NH2	2.31	0.64
1:1:1570:A:H2'	1:1:1571:A:C8	2.32	0.63
6:6:93:LEU:HD21	6:6:122:PRO:HD3	1.80	0.63
13:G:72:ILE:HG22	13:G:108:VAL:HG12	1.79	0.63
1:1:2508:G:H1	1:1:2580:U:H5	1.46	0.63
2:2:946:A:H2'	2:2:947:G:C8	2.32	0.63
2:2:1040:U:H2'	2:2:1041:G:H8	1.62	0.63
50:t:12:VAL:HG21	50:t:22:THR:HG22	1.80	0.63
1:1:2175:C:H2'	1:1:2176:A:H8	1.64	0.63
1:1:2467:C:O2	17:M:123:LYS:NZ	2.32	0.63
2:2:202:G:H21	2:2:466:A:H61	1.45	0.63
6:6:72:LEU:HD21	6:6:93:LEU:HD13	1.80	0.63
27:W:37:ILE:HG22	27:W:38:VAL:HG13	1.79	0.63
44:n:87:LEU:HG	44:n:94:LEU:HD11	1.81	0.63
11:E:167:ARG:NE	59:E:302:HOH:O	2.32	0.63
48:r:7:ILE:HD11	48:r:66:GLU:HG2	1.80	0.63
1:1:2867:G:O2'	1:1:2868:A:H8	1.82	0.63
2:2:202:G:O2'	2:2:468:A:H8	1.81	0.63
8:B:129:THR:HB	8:B:191:THR:HG22	1.78	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:C:1:MET:HG2	9:C:2:ILE:H	1.64	0.63
21:Q:50:ARG:O	21:Q:54:LYS:NZ	2.31	0.63
22:R:44:GLY:O	22:R:45:GLU:HG3	1.98	0.63
1:1:2818:U:OP2	18:N:42:LYS:NZ	2.31	0.63
2:2:438:U:H3	2:2:496:A:H62	1.47	0.63
51:u:12:LYS:HG2	51:u:13:LYS:HG2	1.81	0.63
1:1:1171:G:N2	1:1:1178:C:N3	2.47	0.63
2:2:34:C:H2'	2:2:35:G:H8	1.63	0.63
2:2:1279:G:N2	59:2:1805:HOH:O	2.32	0.63
1:1:2848:G:O2'	1:1:2868:A:N6	2.31	0.62
2:2:1028:C:H2'	2:2:1029:U:C6	2.34	0.62
4:4:12:A:OP1	4:4:12:A:H2	1.76	0.62
24:T:69:ARG:HG2	24:T:74:ILE:HG12	1.80	0.62
37:g:73:LYS:NZ	37:g:204:ASP:OD1	2.32	0.62
2:2:1176:A:H2'	2:2:1177:G:H8	1.64	0.62
40:j:157:ARG:NH1	43:m:99:LEU:O	2.32	0.62
51:u:4:ILE:HG12	51:u:21:VAL:HG22	1.81	0.62
1:1:243:U:OP2	1:1:254:G:N1	2.29	0.62
1:1:1111:A:O2'	1:1:1112:G:OP1	2.16	0.62
30:Z:41:THR:HG22	30:Z:43:ALA:H	1.64	0.62
1:1:1565:C:O2'	1:1:1566:A:H2'	1.99	0.62
1:1:1667:G:H5''	15:K:5:GLN:O	2.00	0.62
1:1:1105:U:H2'	1:1:1106:G:C8	2.32	0.62
2:2:1081:A:H5'	40:j:23:LYS:HD3	1.79	0.62
49:s:46:LEU:HB3	54:x:13:LEU:HD12	1.82	0.62
1:1:319:G:H1	1:1:323:C:H5	1.47	0.62
1:1:813:U:H2'	1:1:814:C:H6	1.65	0.62
1:1:2638:G:HO2'	1:1:2639:A:H8	1.47	0.62
2:2:1218:C:H2'	2:2:1219:A:H8	1.64	0.62
45:o:37:ARG:N	45:o:75:ASP:O	2.22	0.62
51:u:44:SER:N	51:u:47:GLU:OE2	2.33	0.62
54:x:36:ARG:HH12	54:x:77:THR:HB	1.65	0.62
2:2:216:U:H2'	2:2:217:C:C6	2.34	0.62
16:L:73:ILE:HD12	16:L:106:GLU:HG3	1.81	0.62
48:r:85:CYS:HB2	54:x:73:GLU:HB3	1.82	0.62
1:1:2514:U:H2'	1:1:2515:C:H6	1.64	0.62
2:2:56:U:H2'	2:2:57:G:H8	1.65	0.62
10:D:184:ASP:OD1	16:L:2:ARG:NH2	2.33	0.62
17:M:74:THR:HG21	17:M:86:LYS:HE3	1.82	0.62
37:g:15:HIS:HB3	37:g:43:LEU:HD21	1.81	0.62
9:C:14:ILE:HD13	20:P:12:GLN:HE22	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:L:85:VAL:HG11	16:L:90:VAL:HG12	1.80	0.62
1:1:172:A:H2'	1:1:173:A:H8	1.65	0.61
1:1:2861:U:H2'	1:1:2862:G:H8	1.64	0.61
8:B:17:VAL:HG22	8:B:204:VAL:HG22	1.82	0.61
26:V:20:LEU:HD22	26:V:25:LYS:HB2	1.81	0.61
41:k:1:MET:HG2	41:k:2:ARG:H	1.64	0.61
45:o:10:LEU:HG	45:o:98:VAL:HG12	1.82	0.61
1:1:244:A:OP2	35:e:8:ARG:NH2	2.33	0.61
1:1:1064:C:N4	1:1:1069:A:OP2	2.33	0.61
1:1:746:U:O2'	23:S:90:LYS:NZ	2.32	0.61
1:1:1125:G:OP2	1:1:1126:A:O2'	2.14	0.61
1:1:1796:U:H2'	1:1:1797:G:H8	1.65	0.61
7:A:194:VAL:HA	7:A:197:LYS:HE3	1.81	0.61
1:1:2329:U:H2'	1:1:2330:G:C8	2.35	0.61
9:C:14:ILE:HD13	20:P:12:GLN:NE2	2.16	0.61
1:1:475:C:O2	1:1:479:A:N6	2.29	0.61
7:A:66:PRO:HB2	7:A:67:HIS:HD2	1.65	0.61
12:F:173:GLU:N	12:F:173:GLU:OE2	2.33	0.61
48:r:90:ARG:HG2	48:r:97:VAL:HA	1.81	0.61
1:1:1056:G:N1	1:1:1102:C:OP2	2.34	0.61
1:1:1091:G:N2	1:1:1101:U:O2	2.32	0.61
2:2:481:G:O2'	2:2:483:C:N4	2.34	0.61
2:2:1314:C:H2'	2:2:1315:U:H6	1.65	0.61
38:h:8:ASN:ND2	49:s:90:ARG:O	2.33	0.61
42:l:93:PRO:O	42:l:96:ARG:HG2	2.01	0.61
6:6:14:LYS:HG2	6:6:67:VAL:HB	1.83	0.61
6:6:72:LEU:HD23	6:6:84:PHE:HB2	1.81	0.61
7:A:22:ASP:H	7:A:25:GLU:CD	2.08	0.61
13:G:135:HIS:HB3	13:G:138:VAL:HG12	1.83	0.61
16:L:56:PRO:HG2	16:L:59:ARG:HG3	1.82	0.61
39:i:7:PRO:HB2	39:i:10:LYS:HB3	1.83	0.61
1:1:2291:U:H2'	1:1:2292:U:C6	2.35	0.61
7:A:42:VAL:HA	7:A:217:THR:HA	1.81	0.61
15:K:76:VAL:HG22	20:P:73:VAL:HG22	1.83	0.61
39:i:172:GLU:OE1	39:i:183:LYS:NZ	2.26	0.61
39:i:198:HIS:O	39:i:202:GLU:HG3	2.01	0.61
46:p:123:PRO:HD2	56:z:38:TYR:HD1	1.65	0.61
1:1:2113:U:C6	59:1:3410:HOH:O	2.53	0.60
2:2:496:A:H2'	2:2:496:A:N3	2.16	0.60
31:a:23:LYS:HE2	59:a:108:HOH:O	2.01	0.60
39:i:100:ASN:OD1	39:i:111:ARG:NH1	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:307:G:N1	1:1:310:A:OP2	2.30	0.60
1:1:372:G:O2'	1:1:373:U:OP2	2.14	0.60
1:1:2121:G:H2'	1:1:2122:U:C6	2.36	0.60
1:1:2128:G:C5	59:1:3442:HOH:O	2.53	0.60
8:B:196:GLY:O	8:B:198:ALA:N	2.34	0.60
33:c:17:THR:HG22	33:c:18:GLY:H	1.66	0.60
1:1:1012:U:O4	14:J:30:THR:HG21	2.01	0.60
35:e:9:GLY:O	35:e:13:ARG:HD2	2.01	0.60
1:1:2246:G:H2'	1:1:2247:A:C8	2.36	0.60
2:2:1003:G:N2	2:2:1005:A:O5'	2.32	0.60
47:q:66:TYR:O	47:q:97:THR:HG22	2.01	0.60
1:1:2720:U:OP1	20:P:53:ARG:NH2	2.34	0.60
1:1:2903:U:H5''	59:1:3447:HOH:O	2.00	0.60
7:A:15:VAL:HG12	7:A:222:VAL:HG21	1.83	0.60
9:C:36:GLN:HB3	9:C:49:GLN:HG2	1.84	0.60
47:q:83:ARG:HD3	47:q:98:VAL:HG12	1.83	0.60
2:2:634:C:H2'	2:2:635:A:C8	2.36	0.60
2:2:674:G:H2'	2:2:675:A:H8	1.66	0.60
2:2:933:G:O6	42:l:3:ARG:NH2	2.34	0.60
47:q:79:VAL:N	47:q:103:ASP:OD1	2.34	0.60
1:1:227:A:O2'	1:1:228:C:O5'	2.19	0.60
1:1:476:G:N1	1:1:479:A:OP2	2.33	0.60
13:G:132:PHE:HB2	13:G:140:ALA:HB3	1.84	0.60
2:2:384:G:H2'	2:2:385:C:C6	2.37	0.60
38:h:131:ARG:NE	38:h:168:TYR:OH	2.35	0.60
1:1:1724:G:O6	1:1:1737:G:N2	2.34	0.60
1:1:2246:G:H2'	1:1:2247:A:H8	1.65	0.60
2:2:1314:C:H2'	2:2:1315:U:C6	2.36	0.60
3:3:93:C:OP2	26:V:18:ARG:NH1	2.35	0.60
23:S:29:VAL:HB	23:S:55:ILE:HD11	1.82	0.60
51:u:40:ASN:ND2	51:u:42:ILE:O	2.34	0.60
1:1:2127:G:N7	7:A:37:LYS:NZ	2.48	0.59
1:1:2514:U:H2'	1:1:2515:C:C6	2.37	0.59
1:1:964:C:O2'	1:1:2273:A:N3	2.32	0.59
1:1:1469:A:H2'	1:1:1470:A:C8	2.38	0.59
6:6:5:TYR:HA	6:6:61:SER:OG	2.01	0.59
6:6:5:TYR:HD2	6:6:61:SER:HG	1.49	0.59
1:1:2822:G:H2'	1:1:2823:A:H5''	1.85	0.59
7:A:61:GLY:HA2	7:A:143:GLY:HA3	1.84	0.59
2:2:662:U:O2'	2:2:836:G:OP1	2.20	0.59
26:V:54:ALA:CB	59:V:202:HOH:O	2.47	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:x:29:LYS:HE2	54:x:30:PRO:HD2	1.85	0.59
1:1:1590:A:H2'	1:1:1591:A:H8	1.68	0.59
14:J:114:LEU:HG	14:J:118:MET:HE3	1.85	0.59
25:U:35:ILE:HD11	25:U:62:GLU:HB3	1.83	0.59
37:g:24:ASN:ND2	37:g:191:SER:O	2.35	0.59
1:1:878:A:H5'	59:1:3448:HOH:O	2.02	0.59
1:1:774:G:O2'	1:1:775:G:O5'	2.19	0.59
1:1:886:A:N3	1:1:891:G:N2	2.46	0.59
1:1:1045:C:O4'	1:1:1111:A:N6	2.36	0.59
7:A:166:ASP:HA	7:A:172:HIS:HE1	1.66	0.59
15:K:69:VAL:HG11	15:K:104:THR:HG21	1.85	0.59
20:P:37:LYS:NZ	59:P:302:HOH:O	2.36	0.59
37:g:138:THR:O	37:g:142:GLU:HG2	2.02	0.59
44:n:55:VAL:HG11	44:n:94:LEU:HD12	1.85	0.59
1:1:2638:G:H1'	1:1:2778:A:N6	2.18	0.59
42:l:5:ARG:NE	42:l:6:VAL:O	2.32	0.59
1:1:2326:C:O2'	1:1:2327:A:OP1	2.19	0.59
2:2:76:G:H2'	2:2:77:A:C8	2.37	0.59
1:1:1178:C:HO2'	1:1:1179:G:H8	1.50	0.59
1:1:2179:C:N4	59:1:3417:HOH:O	2.35	0.59
2:2:1040:U:H2'	2:2:1041:G:C8	2.37	0.59
21:Q:100:VAL:O	21:Q:103:LYS:NZ	2.36	0.59
1:1:1996:C:OP1	15:K:31:ARG:NE	2.35	0.58
1:1:2313:C:O4'	11:E:37:ASN:ND2	2.35	0.58
2:2:1218:C:H2'	2:2:1219:A:C8	2.38	0.58
17:M:64:TRP:HB2	17:M:104:GLU:HB2	1.83	0.58
37:g:111:ILE:HD12	37:g:152:LYS:HA	1.85	0.58
40:j:15:LEU:HD21	40:j:18:VAL:HG13	1.84	0.58
17:M:110:GLU:OE2	17:M:114:ARG:NE	2.30	0.58
41:k:9:MET:O	41:k:85:ILE:N	2.35	0.58
42:l:79:ARG:HA	42:l:84:THR:HA	1.84	0.58
1:1:411:G:OP2	1:1:2406:A:O2'	2.21	0.58
1:1:414:C:H2'	1:1:415:A:H8	1.68	0.58
1:1:2120:G:H2'	1:1:2121:G:H8	1.69	0.58
1:1:2839:G:N2	18:N:91:ALA:O	2.31	0.58
1:1:481:G:H1'	1:1:506:G:N2	2.19	0.58
37:g:207:ILE:HD12	37:g:207:ILE:H	1.68	0.58
49:s:79:LEU:HB2	49:s:84:VAL:HG23	1.86	0.58
1:1:111:A:O2'	29:Y:58:ASN:ND2	2.37	0.58
1:1:593:U:H2'	1:1:594:U:C6	2.39	0.58
1:1:639:U:H2'	1:1:640:C:C6	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1263:U:OP1	32:b:13:ARG:NH1	2.37	0.58
7:A:147:PRO:HG3	7:A:153:VAL:HG11	1.85	0.58
42:l:72:THR:H	42:l:142:HIS:CE1	2.21	0.58
13:G:121:VAL:HG21	13:G:123:ARG:CZ	2.34	0.58
37:g:59:LYS:HE3	37:g:63:ARG:HH12	1.69	0.58
43:m:114:ARG:NH1	59:m:301:HOH:O	2.35	0.58
19:O:76:LYS:HD2	19:O:113:ALA:HB2	1.85	0.58
24:T:5:GLU:OE1	24:T:5:GLU:N	2.36	0.58
47:q:7:LEU:HD21	47:q:12:ARG:HH11	1.68	0.58
1:1:355:U:H2'	1:1:356:G:C8	2.38	0.58
1:1:481:G:H1'	1:1:506:G:H21	1.68	0.58
1:1:828:U:H2'	1:1:829:A:C8	2.39	0.58
5:5:72:G:H1'	5:5:73:A:H5'	1.86	0.58
6:6:4:TYR:O	6:6:61:SER:HB3	2.03	0.58
10:D:3:LEU:N	10:D:12:LEU:O	2.36	0.58
1:1:935:C:H2'	1:1:936:A:H8	1.69	0.58
1:1:1060:U:C2	1:1:1088:A:H8	2.22	0.58
7:A:45:ALA:HB3	7:A:214:ILE:H	1.69	0.58
44:n:55:VAL:O	44:n:57:MET:N	2.36	0.58
1:1:458:G:O2'	1:1:459:U:OP2	2.21	0.57
1:1:1734:G:H2'	1:1:1735:A:H8	1.69	0.57
2:2:546:A:HO2'	2:2:548:G:HO2'	1.45	0.57
7:A:87:ALA:HB3	7:A:95:VAL:HG11	1.86	0.57
42:l:5:ARG:NH2	42:l:7:ILE:HA	2.19	0.57
1:1:414:C:H2'	1:1:415:A:C8	2.39	0.57
1:1:1093:G:O4'	1:1:1099:G:N2	2.37	0.57
1:1:1779:U:H5	1:1:1784:A:N7	2.02	0.57
1:1:2016:U:H1'	32:b:3:VAL:HG11	1.87	0.57
1:1:2114:A:C2	59:1:3422:HOH:O	2.57	0.57
2:2:60:A:N7	2:2:108:G:O2'	2.37	0.57
2:2:110:C:O2'	51:u:25:ARG:O	2.20	0.57
11:E:126:GLY:HA2	11:E:163:ASP:HA	1.87	0.57
14:J:17:VAL:HG13	14:J:137:PRO:HB2	1.86	0.57
37:g:114:LEU:HD12	37:g:144:LEU:HG	1.85	0.57
53:w:12:ARG:HD3	59:w:209:HOH:O	2.03	0.57
1:1:624:C:O2'	1:1:657:U:OP1	2.21	0.57
1:1:1056:G:N2	1:1:1102:C:O5'	2.36	0.57
1:1:1386:C:H2'	1:1:1387:A:C8	2.39	0.57
1:1:1582:C:O2'	1:1:1585:C:N3	2.36	0.57
1:1:2188:U:H2'	1:1:2189:U:O4'	2.05	0.57
1:1:2192:U:O2'	1:1:2193:G:H8	1.88	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:107:G:N1	55:y:6:SER:OG	2.33	0.57
2:2:1014:A:C2	2:2:1219:A:H1'	2.40	0.57
23:S:82:MET:HG3	23:S:98:LYS:HB2	1.86	0.57
53:w:45:THR:OG1	53:w:47:THR:HG22	2.05	0.57
1:1:1469:A:H2'	1:1:1470:A:H8	1.70	0.57
1:1:1568:G:H4'	8:B:59:LYS:HG2	1.86	0.57
1:1:2128:G:N2	1:1:2160:C:O2	2.37	0.57
1:1:2365:G:N7	35:e:39:LYS:NZ	2.45	0.57
2:2:460:A:H2'	2:2:461:A:H8	1.69	0.57
7:A:154:LYS:HG2	7:A:157:LYS:HE3	1.85	0.57
8:B:110:LEU:HD11	8:B:116:ILE:HD11	1.86	0.57
2:2:21:G:H2'	2:2:22:G:C8	2.40	0.57
55:y:55:GLN:HG3	55:y:76:LYS:HE2	1.85	0.57
7:A:116:ALA:CB	7:A:124:VAL:HG21	2.34	0.57
17:M:40:ARG:HB2	17:M:93:VAL:CG1	2.35	0.57
1:1:1964:G:O2'	1:1:1967:C:OP2	2.20	0.57
1:1:2128:G:C6	59:1:3442:HOH:O	2.51	0.57
8:B:78:VAL:HG13	8:B:113:GLY:H	1.69	0.57
11:E:108:VAL:O	11:E:111:ILE:HG22	2.04	0.57
37:g:27:MET:HG2	37:g:193:PRO:HD3	1.86	0.57
54:x:52:HIS:NE2	54:x:54:GLY:O	2.38	0.57
1:1:773:U:O2	1:1:778:G:O2'	2.23	0.57
1:1:813:U:H2'	1:1:814:C:C6	2.39	0.57
25:U:43:LYS:NZ	25:U:60:GLU:OE1	2.37	0.57
40:j:13:GLU:HB3	40:j:39:VAL:HG12	1.85	0.57
49:s:88:ALA:HB1	49:s:96:LEU:HD22	1.87	0.57
56:z:14:VAL:HA	56:z:17:ARG:HD3	1.87	0.57
1:1:1734:G:H2'	1:1:1735:A:C8	2.40	0.57
2:2:460:A:H2'	2:2:461:A:C8	2.40	0.57
2:2:131:A:H2'	2:2:132:C:C6	2.40	0.56
2:2:147:G:H2'	2:2:148:G:C8	2.40	0.56
2:2:1356:G:H2'	2:2:1357:A:H8	1.70	0.56
53:w:18:VAL:CA	59:w:207:HOH:O	2.45	0.56
1:1:880:G:N2	1:1:897:C:N3	2.42	0.56
1:1:1536:C:H1'	59:1:3540:HOH:O	2.05	0.56
2:2:1103:C:OP1	37:g:95:ARG:NH2	2.38	0.56
7:A:198:LYS:HZ1	7:A:201:PRO:HB3	1.69	0.56
9:C:25:THR:HG21	9:C:193:VAL:HG22	1.86	0.56
20:P:63:LYS:HE2	20:P:65:SER:HB2	1.87	0.56
38:h:43:LEU:HD13	38:h:68:ILE:HD11	1.87	0.56
1:1:644:A:H2'	1:1:645:C:O4'	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1571:A:H2'	1:1:1572:A:H8	1.70	0.56
1:1:2102:G:N2	1:1:2187:U:O2'	2.29	0.56
1:1:2243:U:H2'	1:1:2244:U:H6	1.69	0.56
2:2:376:G:H5''	51:u:5:ARG:HB2	1.86	0.56
2:2:642:A:H2'	2:2:643:C:H6	1.70	0.56
2:2:1072:G:H21	37:g:106:THR:HG21	1.69	0.56
2:2:1152:A:O3'	45:o:15:HIS:NE2	2.23	0.56
2:2:1302:C:C4	48:r:17:ILE:HD11	2.41	0.56
40:j:115:LEU:HD13	40:j:123:VAL:HG11	1.86	0.56
49:s:41:ARG:O	49:s:45:VAL:HG23	2.06	0.56
49:s:89:MET:HE1	49:s:98:LYS:HD2	1.87	0.56
50:t:29:VAL:HG21	50:t:81:LEU:HD21	1.87	0.56
52:v:44:LEU:HD21	52:v:73:TRP:CG	2.40	0.56
1:1:1450:G:O2'	1:1:1452:G:N2	2.39	0.56
2:2:206:C:C4	59:2:1804:HOH:O	2.53	0.56
2:2:324:G:N1	2:2:327:A:OP2	2.38	0.56
2:2:363:A:N6	47:q:27:CYS:SG	2.77	0.56
1:1:1170:C:H2'	1:1:1171:G:C8	2.41	0.56
1:1:2286:G:H4'	1:1:2287:A:O5'	2.05	0.56
1:1:613:A:H5''	1:1:614:A:C8	2.41	0.56
2:2:843:U:H3'	2:2:844:G:H5''	1.87	0.56
2:2:944:G:N1	2:2:1338:G:OP2	2.38	0.56
40:j:44:GLY:O	40:j:74:VAL:N	2.38	0.56
43:m:2:SER:OG	43:m:3:MET:N	2.22	0.56
48:r:59:GLU:HA	48:r:62:LYS:HD3	1.87	0.56
53:w:12:ARG:HD2	59:w:209:HOH:O	2.03	0.56
1:1:1746:A:H2'	1:1:1747:U:C6	2.40	0.56
2:2:939:G:H21	2:2:1375:A:H2	1.53	0.56
7:A:65:LEU:HD12	7:A:66:PRO:HD2	1.86	0.56
41:k:6:ILE:HG23	41:k:89:VAL:HG22	1.88	0.56
1:1:639:U:H2'	1:1:640:C:H6	1.71	0.56
1:1:1068:G:N2	1:1:1095:A:O2'	2.38	0.56
1:1:2291:U:H2'	1:1:2292:U:H6	1.71	0.56
2:2:1167:A:O2'	2:2:1169:A:N7	2.35	0.56
7:A:101:ALA:O	7:A:105:LYS:HG2	2.06	0.56
1:1:171:U:H2'	1:1:172:A:H8	1.70	0.56
1:1:548:G:H2'	1:1:549:G:O4'	2.05	0.56
1:1:1056:G:H2'	1:1:1102:C:H41	1.71	0.56
1:1:1939:U:OP1	1:1:2604:U:O2'	2.22	0.56
2:2:945:G:C2	2:2:946:A:C8	2.93	0.56
2:2:958:A:N3	2:2:985:C:O2'	2.33	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:V:55:GLU:HG3	59:V:203:HOH:O	2.06	0.56
1:1:621:A:OP2	16:L:99:ASN:ND2	2.39	0.56
1:1:2112:G:OP1	1:1:2117:A:O2'	2.20	0.56
1:1:2831:G:N2	1:1:2884:U:OP2	2.39	0.56
6:6:5:TYR:HD2	6:6:61:SER:OG	1.88	0.56
8:B:107:PRO:HD2	8:B:110:LEU:HD22	1.87	0.56
43:m:13:ARG:HD3	43:m:27:MET:HG2	1.87	0.56
53:w:41:PRO:HD2	53:w:44:ILE:HD13	1.88	0.56
1:1:1589:U:H2'	1:1:1590:A:H8	1.71	0.55
2:2:1130:A:H2'	2:2:1131:G:H8	1.71	0.55
2:2:1232:U:H5''	44:n:126:GLN:HB2	1.88	0.55
7:A:194:VAL:HA	7:A:197:LYS:HG2	1.88	0.55
37:g:81:LYS:HD2	37:g:91:PHE:CZ	2.41	0.55
37:g:131:LYS:NZ	59:g:301:HOH:O	2.25	0.55
54:x:52:HIS:CD2	54:x:54:GLY:H	2.23	0.55
1:1:587:C:OP2	16:L:21:ARG:NH2	2.32	0.55
1:1:2121:G:O2'	7:A:168:ASN:OD1	2.23	0.55
1:1:2898:U:H2'	1:1:2899:A:H8	1.71	0.55
7:A:162:ARG:HH21	7:A:177:LYS:HE3	1.70	0.55
8:B:205:LEU:HB3	8:B:210:ALA:HB3	1.88	0.55
25:U:26:LYS:HB2	25:U:35:ILE:HG23	1.88	0.55
45:o:35:GLN:HB3	45:o:77:VAL:HB	1.89	0.55
1:1:1506:U:H2'	1:1:1507:C:H6	1.71	0.55
1:1:2547:A:H2'	1:1:2548:U:C6	2.42	0.55
2:2:1029:U:O2'	2:2:1031:C:OP1	2.25	0.55
2:2:1151:A:O2'	2:2:1152:A:H5''	2.07	0.55
11:E:135:GLN:HE21	11:E:146:VAL:HG21	1.71	0.55
48:r:90:ARG:HD3	48:r:95:LEU:HB2	1.88	0.55
1:1:155:A:H2'	1:1:156:A:C8	2.40	0.55
1:1:1779:U:O2	1:1:1783:A:N6	2.39	0.55
1:1:2312:U:H5'	11:E:85:ILE:HD11	1.89	0.55
2:2:41:G:H2'	2:2:42:G:H8	1.72	0.55
2:2:459:A:H2'	2:2:460:A:C8	2.41	0.55
24:T:53:VAL:HG11	24:T:87:LEU:HD13	1.87	0.55
37:g:183:VAL:HG13	37:g:197:ASP:H	1.72	0.55
1:1:2685:G:OP1	15:K:78:ARG:NH2	2.39	0.55
38:h:40:ARG:HH21	38:h:57:ILE:HG22	1.70	0.55
44:n:57:MET:HE2	44:n:61:LEU:HD11	1.88	0.55
44:n:81:HIS:CE1	44:n:85:ARG:HH21	2.24	0.55
48:r:100:GLN:OE1	48:r:100:GLN:N	2.37	0.55
53:w:30:LYS:HA	53:w:33:ILE:HG12	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:76:G:H2'	2:2:77:A:H8	1.69	0.55
5:5:63:U:H2'	5:5:64:C:C6	2.41	0.55
27:W:85:GLU:HB2	59:W:101:HOH:O	2.06	0.55
45:o:57:VAL:O	45:o:58:ASN:ND2	2.40	0.55
1:1:404:A:H1'	1:1:406:G:C4	2.40	0.55
1:1:1326:U:HO2'	1:1:2010:G:HO2'	1.53	0.55
1:1:1329:U:O2'	1:1:1330:C:OP1	2.20	0.55
2:2:34:C:H2'	2:2:35:G:C8	2.41	0.55
2:2:1287:A:H2'	2:2:1288:A:C8	2.42	0.55
6:6:67:VAL:HG13	6:6:118:TRP:HB2	1.89	0.55
8:B:141:VAL:HG12	8:B:192:LEU:HD13	1.88	0.55
30:Z:24:LEU:HD11	30:Z:54:MET:SD	2.46	0.55
41:k:8:PHE:HE2	41:k:62:MET:HE3	1.70	0.55
1:1:155:A:H2'	1:1:156:A:H8	1.70	0.55
2:2:1326:U:H2'	2:2:1327:C:H6	1.72	0.55
49:s:24:ARG:NH1	49:s:55:SER:OG	2.40	0.55
1:1:1509:A:H2'	1:1:1510:G:H8	1.71	0.55
1:1:2812:G:H2'	1:1:2813:A:C8	2.42	0.55
2:2:81:A:OP2	2:2:83:C:N4	2.40	0.55
2:2:323:U:H2'	2:2:324:G:O4'	2.07	0.55
2:2:1031:C:O3'	2:2:1032:G:N2	2.40	0.55
6:6:117:LEU:HA	6:6:122:PRO:HA	1.89	0.55
7:A:94:LEU:HD22	7:A:100:LEU:HD22	1.88	0.55
11:E:140:GLU:OE1	11:E:140:GLU:N	2.37	0.55
12:F:95:ARG:HG3	12:F:128:GLN:HB2	1.89	0.55
20:P:88:ARG:NH1	59:P:301:HOH:O	2.40	0.55
41:k:22:ILE:HD11	41:k:60:VAL:HG11	1.89	0.55
1:1:586:A:N1	1:1:809:G:O2'	2.39	0.55
2:2:206:C:C5	59:2:1804:HOH:O	2.60	0.55
2:2:413:G:H5''	59:2:1819:HOH:O	2.07	0.55
48:r:52:GLN:O	48:r:55:THR:OG1	2.23	0.55
49:s:39:GLU:O	49:s:43:ASN:ND2	2.40	0.55
1:1:1571:A:H2'	1:1:1572:A:C8	2.42	0.54
1:1:2638:G:H1'	1:1:2778:A:H61	1.72	0.54
2:2:714:G:H2'	2:2:715:A:C8	2.43	0.54
19:O:39:VAL:HG23	19:O:48:LEU:HB2	1.90	0.54
23:S:25:ARG:NH1	23:S:74:ILE:O	2.39	0.54
38:h:83:ASP:OD1	38:h:84:VAL:N	2.41	0.54
46:p:97:ILE:HG22	56:z:12:PHE:CZ	2.42	0.54
1:1:2187:U:H2'	1:1:2188:U:C5	2.42	0.54
2:2:834:U:H2'	2:2:835:U:C6	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:974:A:OP1	49:s:69:ARG:NH1	2.41	0.54
2:2:1130:A:OP1	44:n:18:ARG:NH2	2.41	0.54
6:6:46:LEU:HD23	6:6:67:VAL:HG11	1.90	0.54
7:A:76:ALA:HB1	7:A:100:LEU:HD21	1.89	0.54
23:S:1:MET:N	23:S:1:MET:SD	2.78	0.54
52:v:55:ILE:H	52:v:55:ILE:HD12	1.72	0.54
1:1:1484:U:H2'	1:1:1485:U:C6	2.43	0.54
2:2:56:U:H2'	2:2:57:G:C8	2.42	0.54
6:6:72:LEU:HD22	6:6:115:VAL:HG11	1.89	0.54
33:c:25:LYS:NZ	33:c:30:LYS:O	2.32	0.54
1:1:151:C:H2'	1:1:152:A:H8	1.73	0.54
1:1:372:G:H1'	1:1:373:U:H5	1.73	0.54
1:1:2557:G:H2'	1:1:2558:C:C6	2.42	0.54
5:5:23:C:H5''	6:6:130:PHE:HE2	1.72	0.54
7:A:100:LEU:O	7:A:104:ILE:HG12	2.07	0.54
36:f:5:ALA:O	36:f:37:GLN:NE2	2.40	0.54
38:h:123:GLN:HB3	38:h:128:VAL:HG21	1.90	0.54
41:k:38:ARG:NH1	41:k:98:GLU:O	2.41	0.54
50:t:4:SER:OG	50:t:6:GLU:OE1	2.26	0.54
1:1:30:G:O2'	1:1:1214:A:N3	2.38	0.54
1:1:160:A:N3	1:1:2208:C:O2'	2.38	0.54
1:1:2064:C:H2'	1:1:2065:C:C6	2.43	0.54
2:2:82:G:H22	2:2:84:U:H5	1.55	0.54
2:2:335:C:O2'	2:2:1433:A:N3	2.35	0.54
2:2:451:A:OP2	51:u:70:ARG:NH2	2.31	0.54
2:2:826:C:O2	43:m:16:ASN:ND2	2.41	0.54
1:1:161:A:H3'	1:1:162:U:H5''	1.89	0.54
1:1:191:A:H2'	1:1:192:C:C6	2.42	0.54
1:1:2052:A:H4'	9:C:148:GLN:O	2.07	0.54
1:1:645:C:H2'	1:1:647:G:C8	2.43	0.54
2:2:1412:C:H2'	2:2:1413:A:C8	2.42	0.54
1:1:1590:A:H2'	1:1:1591:A:C8	2.43	0.54
2:2:269:C:H2'	2:2:270:A:C8	2.42	0.54
2:2:1023:U:H3'	2:2:1024:G:H8	1.73	0.54
2:2:1166:G:N1	2:2:1169:A:OP2	2.40	0.54
9:C:130:GLN:OE1	9:C:139:SER:OG	2.25	0.54
2:2:500:G:H2'	2:2:501:C:C6	2.43	0.54
2:2:522:C:H41	47:q:50:ARG:NH1	2.06	0.54
2:2:946:A:H2'	2:2:947:G:H8	1.72	0.54
2:2:1298:U:C5	42:l:114:LYS:HD2	2.43	0.54
7:A:6:LYS:HE2	7:A:9:ARG:HB3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:O:63:LYS:HG3	19:O:64:TYR:H	1.71	0.54
27:W:15:ASP:OD1	27:W:16:SER:N	2.39	0.54
51:u:21:VAL:HG21	51:u:60:TRP:CD1	2.42	0.54
1:1:630:G:N2	1:1:633:A:OP2	2.31	0.54
1:1:793:A:OP2	1:1:2071:A:O2'	2.26	0.54
1:1:1010:A:OP1	21:Q:66:ASN:ND2	2.26	0.54
1:1:2297:A:N1	1:1:2321:U:H5	2.06	0.54
1:1:2751:G:OP1	1:1:2751:G:N2	2.40	0.54
24:T:63:VAL:O	24:T:79:ASP:HB2	2.08	0.54
42:l:71:PRO:HA	42:l:142:HIS:HE1	1.73	0.54
1:1:1071:G:H1	1:1:1092:C:N4	2.06	0.53
1:1:1103:A:H5''	1:1:1104:C:C5	2.43	0.53
1:1:1710:G:H2'	1:1:1711:A:C8	2.44	0.53
2:2:662:U:H2'	2:2:663:A:C8	2.43	0.53
18:N:87:PHE:HD1	18:N:90:ARG:HG3	1.73	0.53
22:R:76:LYS:HD2	22:R:85:LYS:HE3	1.91	0.53
31:a:56:ARG:NE	54:x:65:GLU:OE2	2.34	0.53
33:c:40:ASP:OD1	33:c:42:VAL:HG12	2.08	0.53
1:1:1009:A:N3	1:1:1153:C:O2'	2.41	0.53
1:1:1054:A:N6	1:1:1106:G:O6	2.41	0.53
1:1:1196:C:H2'	1:1:1197:G:C8	2.44	0.53
1:1:1509:A:H2'	1:1:1510:G:C8	2.44	0.53
2:2:222:C:H2'	2:2:223:A:H8	1.73	0.53
7:A:150:ALA:HA	7:A:153:VAL:HG12	1.90	0.53
8:B:108:LYS:HA	8:B:196:GLY:HA2	1.90	0.53
46:p:18:ASP:N	46:p:18:ASP:OD1	2.41	0.53
1:1:1069:A:H3'	1:1:1073:A:H62	1.73	0.53
1:1:2655:G:H1'	1:1:2656:U:H5	1.73	0.53
34:d:3:ARG:O	34:d:6:GLN:NE2	2.40	0.53
41:k:29:ILE:HD13	41:k:64:VAL:HG21	1.91	0.53
1:1:1062:G:O6	1:1:1088:A:H2'	2.08	0.53
1:1:1141:U:H4'	1:1:1142:A:O4'	2.08	0.53
1:1:1592:C:H2'	1:1:1593:A:C8	2.43	0.53
6:6:156:LEU:HD21	6:6:174:ILE:HD11	1.90	0.53
16:L:2:ARG:H	16:L:5:THR:CG2	2.22	0.53
49:s:49:GLN:NE2	54:x:13:LEU:H	2.06	0.53
54:x:77:THR:HG23	54:x:78:ARG:HD3	1.90	0.53
1:1:1296:G:OP1	1:1:2709:G:O2'	2.22	0.53
1:1:1429:G:H2'	1:1:1430:G:H8	1.73	0.53
1:1:1506:U:H2'	1:1:1507:C:C6	2.43	0.53
2:2:451:A:H61	2:2:481:G:H5'	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1140:C:O2'	2:2:1141:C:H6	1.92	0.53
13:G:90:LEU:HD11	13:G:146:VAL:HG11	1.90	0.53
16:L:82:LEU:HD22	16:L:90:VAL:HG11	1.90	0.53
3:3:8:C:O3'	19:O:25:ARG:NH1	2.42	0.53
26:V:70:ILE:O	26:V:72:VAL:HG23	2.09	0.53
37:g:188:ASP:OD1	37:g:189:THR:N	2.39	0.53
50:t:2:SER:HG	50:t:3:LEU:H	1.50	0.53
1:1:545:U:O2	1:1:548:G:O6	2.25	0.53
1:1:636:G:N2	16:L:76:GLU:OE2	2.35	0.53
1:1:2655:G:HO2'	1:1:2656:U:P	2.31	0.53
39:i:28:ILE:HD11	39:i:34:ILE:HD13	1.90	0.53
1:1:784:G:C6	8:B:228:VAL:HG21	2.44	0.53
1:1:1196:C:H2'	1:1:1197:G:H8	1.73	0.53
2:2:501:C:H2'	2:2:502:A:C8	2.44	0.53
2:2:1120:C:H2'	2:2:1121:U:C6	2.44	0.53
3:3:118:C:N4	3:3:120:U:O4	2.42	0.53
13:G:51:ARG:O	13:G:55:GLU:HG3	2.09	0.53
38:h:182:ILE:O	38:h:182:ILE:HG13	2.09	0.53
43:m:35:ALA:HB1	43:m:110:VAL:HG11	1.90	0.53
44:n:12:ARG:NH1	44:n:107:ASP:OD1	2.42	0.53
45:o:7:ARG:NH1	45:o:75:ASP:OD2	2.42	0.53
50:t:47:LYS:O	50:t:53:ARG:NH2	2.41	0.53
1:1:848:C:H2'	1:1:849:A:H8	1.74	0.53
1:1:1069:A:H4'	1:1:1070:A:C8	2.44	0.53
1:1:1565:C:HO2'	1:1:1566:A:H2'	1.73	0.53
1:1:1913:A:N1	2:2:1492:A:H2'	2.24	0.53
1:1:2512:C:H2'	1:1:2513:A:O4'	2.09	0.53
1:1:2595:G:N2	1:1:2598:A:OP2	2.33	0.53
1:1:2698:U:H2'	1:1:2699:C:C6	2.44	0.53
2:2:17:U:H2'	2:2:18:C:C6	2.44	0.53
2:2:216:U:H4'	2:2:464:U:H4'	1.91	0.53
40:j:69:ARG:HD3	59:j:301:HOH:O	2.09	0.53
41:k:72:ASP:O	41:k:76:THR:HG23	2.07	0.53
1:1:1363:C:O2'	1:1:1809:A:N3	2.36	0.53
1:1:1900:A:H1'	1:1:1970:A:H2'	1.91	0.53
1:1:2119:A:N6	59:1:3422:HOH:O	2.41	0.53
2:2:31:G:O2'	2:2:48:C:N4	2.42	0.53
2:2:776:G:N2	2:2:802:A:OP2	2.36	0.53
2:2:880:C:OP1	47:q:5:ASN:ND2	2.42	0.53
12:F:121:ILE:HD12	12:F:141:ILE:HG22	1.91	0.53
47:q:79:VAL:O	47:q:103:ASP:HB2	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:52:A:H2'	1:1:53:A:H8	1.74	0.52
1:1:1013:C:H2'	1:1:1014:A:H8	1.72	0.52
2:2:1229:A:O2'	5:5:30:U:OP1	2.24	0.52
13:G:6:LEU:HD11	13:G:37:VAL:HG23	1.91	0.52
33:c:9:ILE:HD13	33:c:25:LYS:HD2	1.90	0.52
45:o:36:VAL:HA	45:o:76:ILE:HA	1.90	0.52
46:p:97:ILE:HG22	56:z:12:PHE:HZ	1.74	0.52
1:1:144:A:H2'	1:1:145:C:C6	2.44	0.52
1:1:1796:U:H2'	1:1:1797:G:C8	2.43	0.52
1:1:2064:C:H2'	1:1:2065:C:H6	1.74	0.52
1:1:2189:U:H2'	1:1:2190:G:C8	2.44	0.52
6:6:84:PHE:HZ	6:6:100:ILE:HD11	1.75	0.52
9:C:142:VAL:HG12	9:C:144:GLY:H	1.75	0.52
42:l:80:VAL:HG23	42:l:81:GLY:H	1.74	0.52
1:1:2116:G:H2'	59:1:3466:HOH:O	2.08	0.52
2:2:1126:U:O4	45:o:9:ARG:NH1	2.42	0.52
2:2:1277:C:HO2'	2:2:1279:G:H8	1.57	0.52
3:3:74:U:O4	26:V:37:PRO:HG2	2.09	0.52
16:L:58:TYR:O	35:e:13:ARG:NH2	2.42	0.52
28:X:32:ASN:OD1	28:X:34:HIS:NE2	2.42	0.52
31:a:48:GLN:OE1	31:a:48:GLN:N	2.43	0.52
37:g:48:PRO:O	37:g:52:GLU:HG3	2.10	0.52
47:q:81:LEU:HB3	47:q:98:VAL:HG22	1.92	0.52
48:r:16:VAL:O	48:r:20:THR:HG23	2.09	0.52
2:2:75:G:H2'	2:2:76:G:H8	1.74	0.52
2:2:1005:A:H3'	2:2:1006:G:H8	1.74	0.52
2:2:1323:G:H2'	2:2:1324:A:C8	2.45	0.52
2:2:1347:G:O6	44:n:12:ARG:NH2	2.43	0.52
11:E:117:LEU:HB2	11:E:177:PHE:HA	1.91	0.52
26:V:75:GLN:HB2	26:V:92:VAL:HG12	1.92	0.52
38:h:72:ARG:HB3	38:h:75:ILE:HG22	1.91	0.52
2:2:374:A:H5''	2:2:452:A:C2	2.44	0.52
8:B:117:GLN:N	8:B:128:ASN:OD1	2.40	0.52
39:i:121:LYS:HG2	39:i:129:VAL:HG21	1.92	0.52
49:s:41:ARG:NH2	54:x:6:LYS:O	2.42	0.52
1:1:927:A:H2'	1:1:928:A:C8	2.44	0.52
1:1:1114:C:H2'	1:1:1115:G:C8	2.45	0.52
1:1:1653:G:OP1	1:1:2822:G:N1	2.30	0.52
1:1:2177:C:H5'	7:A:214:ILE:HD12	1.91	0.52
2:2:1004:A:H62	2:2:1024:G:HO2'	1.57	0.52
10:D:138:LEU:HD11	10:D:146:VAL:HG11	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:o:42:LEU:HB2	45:o:71:LEU:HB3	1.92	0.52
1:1:856:G:H2'	1:1:857:G:C8	2.45	0.52
1:1:1099:G:O2'	1:1:1100:C:O4'	2.23	0.52
1:1:1789:A:OP2	8:B:221:ARG:NH1	2.42	0.52
1:1:2661:G:H2'	1:1:2662:A:C8	2.44	0.52
2:2:769:G:H4'	2:2:1513:A:H4'	1.92	0.52
38:h:142:MET:HE3	38:h:170:GLU:HB3	1.92	0.52
1:1:571:U:H3'	22:R:80:ARG:NH2	2.25	0.52
1:1:1684:G:H2'	1:1:1685:C:C6	2.44	0.52
2:2:1120:C:H2'	2:2:1121:U:H6	1.75	0.52
2:2:1174:G:H2'	2:2:1175:G:H5'	1.90	0.52
7:A:71:ARG:HH22	7:A:93:GLU:HG3	1.75	0.52
38:h:40:ARG:NH1	49:s:92:GLU:HG2	2.24	0.52
55:y:60:ARG:O	55:y:64:LYS:HG2	2.09	0.52
1:1:172:A:H2'	1:1:173:A:C8	2.44	0.52
1:1:1432:G:H2'	1:1:1433:A:C8	2.45	0.52
1:1:2591:C:H2'	1:1:2592:G:C8	2.45	0.52
1:1:2657:A:O3'	12:F:160:LYS:NZ	2.42	0.52
2:2:1273:C:H2'	2:2:1274:A:O4'	2.09	0.52
2:2:1391:U:H2'	2:2:1392:G:C8	2.45	0.52
2:2:821:G:H2'	2:2:822:U:C6	2.45	0.52
2:2:908:A:H2'	2:2:909:A:H8	1.75	0.52
2:2:950:U:H2'	2:2:951:G:C8	2.45	0.52
7:A:59:VAL:O	7:A:164:ARG:NH1	2.42	0.52
28:X:40:VAL:HG12	28:X:43:GLU:H	1.75	0.52
44:n:42:GLU:HA	44:n:45:ARG:HD2	1.92	0.52
1:1:581:C:H2'	1:1:582:A:H8	1.75	0.51
1:1:632:A:H2'	1:1:633:A:C8	2.45	0.51
1:1:1315:C:O2'	1:1:1392:A:N3	2.37	0.51
1:1:1918:A:O2'	1:1:1920:C:N4	2.43	0.51
1:1:2127:G:OP1	7:A:38:PHE:N	2.41	0.51
1:1:2169:A:O2'	7:A:134:ARG:HG2	2.09	0.51
2:2:176:C:H2'	2:2:177:G:N3	2.25	0.51
11:E:143:TYR:HA	11:E:146:VAL:HG12	1.92	0.51
14:J:18:VAL:HG11	14:J:142:ILE:HD12	1.92	0.51
23:S:36:LEU:HB3	23:S:48:LYS:HB2	1.92	0.51
33:c:8:LYS:HA	33:c:24:THR:HA	1.92	0.51
39:i:192:SER:OG	39:i:194:ASP:OD1	2.28	0.51
40:j:24:THR:HG22	40:j:29:ARG:HG3	1.92	0.51
1:1:9:G:O2'	1:1:2800:A:N6	2.44	0.51
1:1:1842:G:H2'	1:1:1843:C:H6	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2122:U:H1'	7:A:167:LYS:HD3	1.92	0.51
1:1:2233:U:H2'	1:1:2234:G:C8	2.44	0.51
1:1:2298:A:OP1	11:E:71:ARG:NH2	2.43	0.51
2:2:1171:A:H2'	2:2:1172:C:H6	1.75	0.51
7:A:20:GLN:HG2	7:A:226:GLN:NE2	2.26	0.51
42:l:135:VAL:O	42:l:139:GLU:HG2	2.09	0.51
1:1:1856:U:H2'	1:1:1857:G:O4'	2.10	0.51
1:1:2071:A:H2'	1:1:2072:C:C6	2.46	0.51
7:A:171:ILE:HD12	7:A:171:ILE:H	1.75	0.51
10:D:3:LEU:O	10:D:12:LEU:N	2.44	0.51
13:G:66:ASN:HD22	13:G:135:HIS:CG	2.28	0.51
31:a:30:HIS:ND1	31:a:31:ASP:O	2.43	0.51
40:j:56:VAL:O	40:j:60:ILE:HG12	2.10	0.51
41:k:1:MET:SD	41:k:1:MET:N	2.72	0.51
1:1:52:A:H2'	1:1:53:A:C8	2.45	0.51
1:1:1309:G:H5''	34:d:8:SER:HA	1.93	0.51
1:1:2014:A:H2'	1:1:2015:A:C8	2.46	0.51
1:1:2104:U:H5''	1:1:2105:U:H5	1.74	0.51
1:1:2451:A:H1'	5:5:76:A:H2'	1.91	0.51
2:2:1025:U:H4'	2:2:1026:G:C8	2.46	0.51
34:d:18:PHE:HB2	34:d:43:THR:HG21	1.92	0.51
1:1:139:U:H2'	1:1:140:C:H5	1.74	0.51
1:1:2329:U:H2'	1:1:2330:G:H8	1.75	0.51
2:2:1017:U:O2'	2:2:1018:G:H8	1.93	0.51
14:J:102:GLU:HG3	14:J:124:VAL:HG11	1.93	0.51
17:M:50:ARG:O	17:M:54:THR:HG23	2.11	0.51
37:g:64:LYS:HA	37:g:225:ARG:NH1	2.26	0.51
37:g:88:ASP:OD1	37:g:89:GLN:NE2	2.44	0.51
1:1:1396:U:H5''	1:1:1397:U:OP2	2.10	0.51
1:1:1735:A:C6	1:1:1736:U:C4	2.99	0.51
2:2:380:G:N2	2:2:383:A:OP2	2.40	0.51
2:2:1497:G:H1'	2:2:1518:MA6:H2	1.93	0.51
3:3:74:U:C4	26:V:37:PRO:HG2	2.46	0.51
7:A:9:ARG:HB2	7:A:12:ARG:NE	2.25	0.51
7:A:22:ASP:N	7:A:25:GLU:OE2	2.42	0.51
17:M:34:LYS:HA	17:M:101:VAL:HA	1.93	0.51
37:g:127:ASP:O	37:g:129:LEU:N	2.43	0.51
1:1:363:G:H2'	1:1:364:C:C6	2.45	0.51
1:1:645:C:H2'	1:1:647:G:N7	2.26	0.51
1:1:1039:A:H2'	1:1:1040:A:O4'	2.11	0.51
1:1:1857:G:HO2'	1:1:1858:A:H8	1.59	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1004:A:H2'	2:2:1005:A:O4'	2.10	0.51
18:N:83:LEU:HD11	18:N:115:LEU:HD13	1.93	0.51
42:l:16:PRO:HG3	44:n:43:THR:HG22	1.92	0.51
50:t:42:HIS:CE1	50:t:46:HIS:HD2	2.29	0.51
1:1:528:A:C2	1:1:2043:C:H4'	2.45	0.51
1:1:2590:A:N1	1:1:2604:U:H5	2.08	0.51
2:2:1174:G:C2'	2:2:1175:G:H5'	2.41	0.51
2:2:1521:C:H2'	2:2:1522:U:C6	2.45	0.51
3:3:28:C:H2'	3:3:29:A:C8	2.46	0.51
37:g:218:ALA:O	37:g:222:ARG:HG3	2.10	0.51
52:v:72:SER:O	52:v:72:SER:OG	2.28	0.51
1:1:287:G:H2'	1:1:288:U:C6	2.46	0.51
1:1:565:C:P	22:R:80:ARG:H	2.34	0.51
1:1:871:U:H2'	1:1:872:U:H6	1.76	0.51
1:1:2095:A:H5'	13:G:11:ASN:HD22	1.76	0.51
2:2:1308:U:OP1	48:r:97:VAL:N	2.30	0.51
6:6:146:THR:HG22	6:6:148:GLY:O	2.11	0.51
17:M:50:ARG:HD3	17:M:65:ILE:HD11	1.92	0.51
45:o:36:VAL:HG23	45:o:76:ILE:HG12	1.93	0.51
46:p:63:ALA:HB1	46:p:96:THR:HG23	1.93	0.51
1:1:645:C:O2'	1:1:646:U:H5'	2.11	0.51
1:1:721:A:H2'	1:1:722:A:C8	2.45	0.51
1:1:1172:C:N4	59:1:3431:HOH:O	2.44	0.51
1:1:1386:C:H2'	1:1:1387:A:H8	1.76	0.51
1:1:1931:U:OP2	1:1:1968:G:N1	2.38	0.51
1:1:2017:U:H4'	32:b:5:GLN:O	2.11	0.51
1:1:2305:U:H2'	1:1:2306:C:C6	2.45	0.51
1:1:2327:A:H2'	1:1:2328:A:C8	2.45	0.51
2:2:859:G:H2'	2:2:860:A:C8	2.46	0.51
2:2:1157:A:C2	2:2:1181:G:C4	2.99	0.51
6:6:93:LEU:HD23	6:6:94:SER:N	2.26	0.51
7:A:68:GLY:HA3	7:A:177:LYS:CD	2.41	0.51
8:B:232:HIS:CG	8:B:240:PHE:HE1	2.29	0.51
42:l:17:LYS:HB2	42:l:44:TYR:CZ	2.46	0.51
52:v:49:GLU:C	52:v:51:ASN:H	2.17	0.51
1:1:197:A:H62	1:1:2430:A:H2'	1.75	0.50
1:1:709:U:H2'	1:1:710:U:C6	2.46	0.50
1:1:782:A:N7	8:B:220:VAL:HG21	2.27	0.50
1:1:2025:C:H2'	1:1:2026:U:C6	2.45	0.50
12:F:105:LEU:HD12	12:F:107:LEU:HD21	1.92	0.50
38:h:34:ASP:O	38:h:38:LYS:HG3	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:j:80:THR:OG1	40:j:81:LEU:N	2.44	0.50
1:1:631:A:N3	1:1:2415:G:O2'	2.44	0.50
1:1:1484:U:H2'	1:1:1485:U:H6	1.76	0.50
1:1:2543:G:H2'	1:1:2544:G:C8	2.46	0.50
1:1:2812:G:H2'	1:1:2813:A:H8	1.76	0.50
2:2:390:U:H2'	2:2:391:G:H8	1.76	0.50
9:C:136:ASN:ND2	9:C:139:SER:O	2.40	0.50
18:N:57:THR:HG23	18:N:62:ASN:ND2	2.26	0.50
44:n:94:LEU:HG	44:n:98:LEU:HD13	1.93	0.50
1:1:372:G:HO2'	1:1:373:U:P	2.33	0.50
1:1:581:C:H2'	1:1:582:A:C8	2.47	0.50
1:1:1874:C:H2'	1:1:1875:G:O4'	2.12	0.50
1:1:2439:A:OP1	6:6:34:KEO:N02	2.45	0.50
2:2:46:G:O2'	2:2:365:U:O2	2.28	0.50
2:2:1014:A:H2	2:2:1219:A:H1'	1.74	0.50
6:6:76:TYR:CE2	7:A:133:PRO:HB2	2.46	0.50
7:A:14:LYS:HB2	7:A:33:LEU:HD11	1.92	0.50
10:D:104:ALA:O	10:D:108:ILE:HG23	2.12	0.50
39:i:125:VAL:HG12	39:i:126:ASN:OD1	2.11	0.50
55:y:48:GLN:OE1	55:y:52:ASN:ND2	2.45	0.50
1:1:607:U:N3	1:1:608:A:N7	2.60	0.50
1:1:1063:G:H1	1:1:1076:C:H42	1.58	0.50
1:1:1071:G:O2'	1:1:1089:A:H5''	2.11	0.50
1:1:2801:G:H2'	1:1:2802:G:H8	1.76	0.50
2:2:270:A:H2'	2:2:271:C:C6	2.46	0.50
7:A:50:ILE:HD12	7:A:57:GLN:HB3	1.92	0.50
1:1:280:U:O4	1:1:361:G:N2	2.45	0.50
1:1:364:C:H2'	1:1:365:U:C6	2.46	0.50
1:1:2125:G:H21	1:1:2174:C:H41	1.59	0.50
1:1:2682:A:H61	1:1:2728:U:H1'	1.76	0.50
2:2:231:U:H2'	2:2:232:G:H8	1.76	0.50
2:2:1073:U:O2	37:g:103:ASN:ND2	2.44	0.50
37:g:114:LEU:HD11	37:g:145:GLU:HA	1.93	0.50
39:i:50:ASP:O	39:i:54:GLN:HG3	2.10	0.50
39:i:58:LYS:HD3	39:i:203:LEU:HD22	1.94	0.50
43:m:113:ASP:OD1	43:m:114:ARG:N	2.43	0.50
48:r:66:GLU:CD	48:r:66:GLU:H	2.19	0.50
1:1:936:A:H2'	1:1:937:C:C6	2.46	0.50
1:1:1447:C:O2'	1:1:1544:A:N3	2.38	0.50
2:2:501:C:H2'	2:2:502:A:H8	1.77	0.50
2:2:933:G:OP1	42:l:4:ARG:NH1	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1086:U:H3	2:2:1099:G:H22	1.59	0.50
7:A:106:LYS:HZ3	7:A:108:GLU:HG2	1.77	0.50
11:E:135:GLN:OE1	11:E:150:ARG:N	2.45	0.50
13:G:16:GLY:HA2	13:G:47:PHE:CE2	2.46	0.50
31:a:26:SER:OG	31:a:27:THR:N	2.45	0.50
39:i:78:GLU:OE2	39:i:81:ARG:NH1	2.39	0.50
2:2:811:C:O2'	2:2:901:A:N1	2.44	0.50
8:B:144:VAL:HB	8:B:154:LEU:HB2	1.92	0.50
10:D:130:LYS:HB2	10:D:133:LEU:HG	1.93	0.50
10:D:164:LEU:HB2	10:D:167:VAL:HG22	1.94	0.50
26:V:77:VAL:HG12	26:V:89:ILE:HG23	1.94	0.50
39:i:98:LEU:O	39:i:101:VAL:N	2.45	0.50
44:n:12:ARG:HD3	44:n:13:LYS:HG3	1.92	0.50
1:1:549:G:HO2'	1:1:550:C:P	2.34	0.50
1:1:646:U:H4'	59:1:3413:HOH:O	2.12	0.50
1:1:927:A:H2'	1:1:928:A:H8	1.77	0.50
1:1:1885:A:H4'	7:A:207:VAL:HG12	1.93	0.50
1:1:2333:A:H5'	1:1:2335:A:H1'	1.93	0.50
2:2:1028:C:H2'	2:2:1029:U:H6	1.75	0.50
6:6:146:THR:OG1	42:l:79:ARG:NH2	2.44	0.50
7:A:188:ASN:O	7:A:192:LEU:HG	2.12	0.50
13:G:7:ASP:OD2	13:G:8:LYS:N	2.45	0.50
14:J:45:THR:HB	14:J:48:VAL:HG22	1.94	0.50
16:L:20:GLY:O	16:L:21:ARG:HD2	2.12	0.50
39:i:116:GLN:HE21	39:i:120:HIS:CE1	2.30	0.50
1:1:173:A:H2'	1:1:174:U:C6	2.47	0.50
1:1:1494:A:H2'	1:1:1495:A:C8	2.46	0.50
1:1:1799:G:N2	1:1:1818:U:O2'	2.45	0.50
1:1:2847:U:H2'	1:1:2848:G:O4'	2.12	0.50
1:1:2898:U:H2'	1:1:2899:A:C8	2.47	0.50
47:q:21:VAL:HG13	47:q:95:TYR:CE1	2.47	0.50
1:1:363:G:H2'	1:1:364:C:H6	1.76	0.49
1:1:372:G:O2'	1:1:373:U:P	2.70	0.49
1:1:876:C:H2'	1:1:877:A:O4'	2.12	0.49
1:1:1493:C:H5''	1:1:1494:A:OP2	2.11	0.49
1:1:2113:U:C2	59:1:3410:HOH:O	2.61	0.49
1:1:2128:G:H5''	7:A:7:ARG:NH1	2.26	0.49
1:1:2185:U:H2'	1:1:2186:G:H8	1.77	0.49
1:1:2521:C:C2	1:1:2545:G:N2	2.80	0.49
1:1:2756:U:OP2	36:f:19:ARG:NE	2.34	0.49
2:2:950:U:H2'	2:2:951:G:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:C:152:PRO:HB2	9:C:154:LYS:HG2	1.94	0.49
36:f:25:VAL:HB	36:f:35:GLN:HG2	1.94	0.49
55:y:80:THR:O	55:y:84:ASN:ND2	2.44	0.49
1:1:1615:C:OP2	1:1:1617:C:N4	2.37	0.49
1:1:2202:U:O2'	1:1:2204:G:OP1	2.26	0.49
2:2:674:G:H2'	2:2:675:A:C8	2.47	0.49
2:2:976:G:OP2	2:2:1358:U:O2'	2.30	0.49
2:2:1023:U:H3'	2:2:1024:G:C8	2.48	0.49
7:A:11:ILE:O	7:A:15:VAL:HG13	2.11	0.49
7:A:166:ASP:HA	7:A:172:HIS:CE1	2.45	0.49
26:V:51:GLN:OE1	26:V:57:TYR:OH	2.27	0.49
38:h:131:ARG:HE	38:h:135:LYS:HZ1	1.59	0.49
44:n:19:VAL:HG12	44:n:65:ILE:HG23	1.93	0.49
1:1:2230:G:H2'	1:1:2231:U:C6	2.48	0.49
1:1:2328:A:H2'	1:1:2329:U:H6	1.77	0.49
1:1:2455:G:H2'	1:1:2456:C:H6	1.78	0.49
1:1:2840:C:H5''	18:N:53:THR:CG2	2.37	0.49
2:2:636:U:H2'	2:2:637:C:C6	2.47	0.49
13:G:8:LYS:HE3	59:G:206:HOH:O	2.13	0.49
38:h:16:LYS:NZ	38:h:181:ASP:OD1	2.45	0.49
47:q:53:CYS:HB2	47:q:67:ILE:HD11	1.94	0.49
54:x:51:VAL:HG13	54:x:75:ALA:HB2	1.93	0.49
1:1:848:C:H2'	1:1:849:A:C8	2.48	0.49
1:1:1073:A:H2'	1:1:1074:G:C8	2.47	0.49
2:2:1355:G:H2'	2:2:1356:G:H8	1.77	0.49
18:N:55:ALA:HA	18:N:80:PHE:CE1	2.47	0.49
44:n:21:ILE:HD11	44:n:61:LEU:HD13	1.94	0.49
1:1:284:U:O2	1:1:356:G:N2	2.36	0.49
1:1:1664:A:H2	15:K:1:MET:HE1	1.75	0.49
1:1:2182:U:H2'	1:1:2183:A:H8	1.75	0.49
2:2:320:A:H2'	2:2:321:A:C8	2.47	0.49
2:2:516:PSU:H4'	2:2:517:G:OP1	2.12	0.49
2:2:713:G:H2'	2:2:714:G:C8	2.48	0.49
9:C:152:PRO:HG3	9:C:156:PHE:CZ	2.47	0.49
1:1:659:G:H4'	10:D:95:LYS:HD3	1.93	0.49
1:1:851:C:H2'	1:1:852:U:C6	2.48	0.49
1:1:871:U:H2'	1:1:872:U:C6	2.46	0.49
1:1:2233:U:H2'	1:1:2234:G:H8	1.76	0.49
1:1:2292:U:H2'	1:1:2293:G:H8	1.78	0.49
1:1:2899:A:H2'	1:1:2900:A:C8	2.47	0.49
2:2:269:C:H2'	2:2:270:A:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:313:A:H2'	2:2:314:C:C6	2.48	0.49
2:2:921:U:O2	40:j:24:THR:OG1	2.30	0.49
6:6:5:TYR:HD2	6:6:61:SER:CB	2.25	0.49
1:1:594:U:H2'	1:1:595:C:C6	2.47	0.49
1:1:627:A:H5''	16:L:78:ARG:NH1	2.27	0.49
1:1:1592:C:H2'	1:1:1593:A:H8	1.77	0.49
9:C:8:LYS:HB2	9:C:201:LEU:HD11	1.93	0.49
11:E:122:PHE:HB3	11:E:163:ASP:HB2	1.93	0.49
13:G:66:ASN:HD22	13:G:135:HIS:HB2	1.78	0.49
25:U:36:VAL:HG23	25:U:39:ILE:HB	1.94	0.49
25:U:48:PRO:HB3	25:U:55:PRO:O	2.13	0.49
39:i:8:LYS:HB3	39:i:21:LEU:HG	1.95	0.49
56:z:40:LYS:O	56:z:43:THR:OG1	2.28	0.49
1:1:695:G:O6	1:1:767:U:O2	2.31	0.49
1:1:1357:C:H2'	1:1:1358:G:O4'	2.12	0.49
2:2:505:G:H2'	2:2:506:G:H8	1.78	0.49
2:2:979:C:O2	49:s:59:ARG:NE	2.45	0.49
10:D:191:ASP:O	10:D:195:GLN:HG2	2.13	0.49
26:V:10:LYS:HB2	26:V:11:GLU:OE1	2.13	0.49
34:d:34:ARG:NE	34:d:42:LEU:O	2.40	0.49
1:1:1930:G:H1'	1:1:1931:U:OP2	2.13	0.49
1:1:2073:C:H5''	8:B:228:VAL:HG22	1.94	0.49
1:1:2655:G:O2'	1:1:2656:U:P	2.70	0.49
1:1:2728:U:H2'	1:1:2729:G:H8	1.78	0.49
2:2:642:A:H2'	2:2:643:C:C6	2.48	0.49
2:2:1111:A:N6	38:h:176:HIS:O	2.46	0.49
2:2:1522:U:H2'	2:2:1523:G:H8	1.78	0.49
3:3:117:G:H2'	59:3:306:HOH:O	2.12	0.49
13:G:27:ARG:NH1	28:X:60:ASP:OD2	2.46	0.49
13:G:104:THR:HA	13:G:108:VAL:O	2.13	0.49
25:U:4:LYS:O	25:U:94:ARG:NH2	2.45	0.49
37:g:206:ALA:O	37:g:210:VAL:HG23	2.12	0.49
43:m:43:GLU:HG2	43:m:101:ILE:HG21	1.95	0.49
1:1:352:A:H2'	1:1:353:C:C6	2.47	0.49
1:1:1177:G:H2'	1:1:1178:C:H5'	1.95	0.49
1:1:1262:A:N3	32:b:7:LYS:NZ	2.60	0.49
1:1:2286:G:O6	33:c:23:THR:OG1	2.20	0.49
15:K:59:LYS:NZ	15:K:89:ASN:O	2.45	0.49
16:L:40:SER:O	16:L:40:SER:OG	2.30	0.49
37:g:167:ASP:OD1	37:g:191:SER:HB2	2.13	0.49
38:h:57:ILE:CG1	38:h:64:ILE:HD11	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:q:54:ARG:HH11	47:q:62:GLU:HG3	1.78	0.49
1:1:84:A:N1	1:1:98:G:O2'	2.45	0.48
1:1:1062:G:N2	1:1:1088:A:N7	2.59	0.48
1:1:1196:C:C2	1:1:1197:G:C8	3.01	0.48
1:1:1243:C:H1'	16:L:4:ASN:O	2.13	0.48
1:1:1802:A:H2'	1:1:1803:A:C8	2.48	0.48
1:1:2126:A:N1	1:1:2163:A:O2'	2.38	0.48
1:1:2575:C:H5'	9:C:149:ASN:HB2	1.94	0.48
2:2:1036:A:H2'	2:2:1037:C:C6	2.48	0.48
3:3:39:A:C2	3:3:44:G:C2	3.01	0.48
5:5:71:C:N4	5:5:72:G:O6	2.45	0.48
9:C:13:ARG:NH1	20:P:75:GLN:OE1	2.30	0.48
9:C:51:THR:OG1	9:C:76:GLY:HA3	2.12	0.48
12:F:12:PRO:HD2	12:F:15:VAL:HG21	1.94	0.48
33:c:6:ARG:HG2	33:c:24:THR:HB	1.95	0.48
40:j:61:GLN:O	40:j:65:GLU:HG2	2.13	0.48
46:p:98:ARG:HH12	56:z:13:ASP:HA	1.77	0.48
48:r:34:LEU:HD12	48:r:41:GLU:HG3	1.94	0.48
53:w:75:GLN:NE2	59:w:203:HOH:O	2.46	0.48
1:1:45:G:H5'	1:1:46:G:H5'	1.93	0.48
1:1:251:A:OP1	16:L:58:TYR:OH	2.23	0.48
1:1:742:A:H2'	1:1:743:A:C8	2.49	0.48
1:1:1060:U:N3	1:1:1088:A:H8	2.10	0.48
1:1:1068:G:N2	1:1:1096:A:O5'	2.46	0.48
1:1:2117:A:O2'	1:1:2119:A:OP1	2.31	0.48
1:1:2169:A:H2'	1:1:2170:A:C8	2.49	0.48
2:2:933:G:N7	42:l:3:ARG:NE	2.58	0.48
2:2:1118:U:H1'	2:2:1179:A:C4	2.48	0.48
6:6:27:SER:HB2	6:6:41:VAL:HG12	1.94	0.48
37:g:167:ASP:HB3	37:g:191:SER:HA	1.94	0.48
39:i:85:ASN:OD1	39:i:88:GLU:N	2.32	0.48
52:v:76:VAL:HG23	52:v:77:ARG:HG2	1.94	0.48
1:1:585:G:N7	21:Q:6:ARG:NH1	2.60	0.48
1:1:859:G:O2'	1:1:916:G:O6	2.24	0.48
1:1:1103:A:H2'	1:1:1103:A:N3	2.28	0.48
1:1:2808:G:O2'	1:1:2809:A:H8	1.96	0.48
1:1:2808:G:HO2'	1:1:2809:A:H8	1.59	0.48
2:2:754:C:O5'	50:t:72:ARG:NH1	2.46	0.48
2:2:1023:U:H2'	2:2:1024:G:O4'	2.13	0.48
10:D:138:LEU:HD12	10:D:143:LEU:HB2	1.95	0.48
24:T:65:GLY:H	24:T:79:ASP:HB3	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:i:95:GLU:O	39:i:100:ASN:ND2	2.36	0.48
41:k:68:GLN:OE1	41:k:68:GLN:N	2.40	0.48
1:1:1248:G:P	10:D:44:ARG:HH12	2.36	0.48
1:1:1496:A:H2'	1:1:1498:C:C5	2.48	0.48
1:1:2455:G:H2'	1:1:2456:C:C6	2.48	0.48
6:6:57:LYS:O	6:6:58:SER:C	2.56	0.48
8:B:165:VAL:HG21	8:B:181:MET:HE1	1.95	0.48
12:F:175:LYS:HD3	12:F:176:LYS:N	2.29	0.48
16:L:141:LYS:HE2	16:L:143:GLU:HB3	1.96	0.48
24:T:44:LYS:HG3	24:T:55:VAL:HG11	1.95	0.48
38:h:3:GLN:HB2	38:h:4:LYS:HD2	1.95	0.48
39:i:170:TRP:CD2	39:i:186:PRO:HB3	2.48	0.48
51:u:9:HIS:O	51:u:16:PHE:N	2.46	0.48
1:1:24:G:H2'	1:1:25:U:C6	2.48	0.48
1:1:240:C:OP2	1:1:241:A:O2'	2.26	0.48
1:1:931:U:OP1	30:Z:30:ARG:NH1	2.40	0.48
1:1:1056:G:H4'	1:1:1086:A:H8	1.79	0.48
1:1:2086:U:H2'	1:1:2087:G:C8	2.49	0.48
2:2:16:A:O2'	40:j:21:VAL:HG23	2.13	0.48
7:A:48:LEU:HD11	7:A:205:LYS:HD2	1.94	0.48
8:B:3:VAL:HG12	8:B:19:VAL:HG22	1.96	0.48
9:C:156:PHE:CE1	14:J:81:ILE:HD13	2.48	0.48
39:i:147:GLU:HA	39:i:150:LYS:HD3	1.95	0.48
48:r:97:VAL:HG23	48:r:109:ARG:HH22	1.79	0.48
1:1:2087:G:H2'	1:1:2088:A:H8	1.78	0.48
1:1:2801:G:H2'	1:1:2802:G:C8	2.49	0.48
2:2:382:A:H2'	2:2:383:A:C8	2.49	0.48
11:E:135:GLN:NE2	11:E:146:VAL:HG21	2.28	0.48
25:U:100:SER:O	25:U:100:SER:OG	2.28	0.48
31:a:20:ASN:ND2	31:a:39:LYS:HD3	2.28	0.48
1:1:282:A:H2'	1:1:283:G:C8	2.49	0.48
1:1:608:A:H2'	1:1:609:A:C8	2.49	0.48
1:1:704:G:H2'	1:1:726:G:N2	2.26	0.48
1:1:714:U:OP2	50:t:88:ARG:NH2	2.21	0.48
1:1:881:G:H2'	1:1:882:G:C8	2.49	0.48
1:1:1734:G:C2	1:1:1735:A:C5	3.02	0.48
1:1:1928:A:H2'	1:1:1929:G:O4'	2.13	0.48
1:1:2115:G:H3'	1:1:2116:G:C5'	2.43	0.48
1:1:2461:A:H2'	1:1:2462:C:C6	2.49	0.48
1:1:2880:C:H1'	18:N:92:GLY:O	2.13	0.48
2:2:620:C:N1	39:i:132:ILE:HG13	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:842:U:H2'	2:2:844:G:H5'	1.95	0.48
7:A:161:VAL:O	7:A:162:ARG:HD3	2.14	0.48
13:G:2:GLN:HE22	13:G:20:ASN:HB2	1.78	0.48
1:1:2680:U:O2'	1:1:2681:C:H5'	2.14	0.48
1:1:2696:U:H2'	1:1:2697:G:H8	1.78	0.48
1:1:2848:G:C8	20:P:95:ALA:HB2	2.48	0.48
2:2:4:U:H2'	2:2:5:U:H2'	1.96	0.48
2:2:142:G:H3'	2:2:143:A:H8	1.78	0.48
2:2:845:A:H1'	59:2:1851:HOH:O	2.14	0.48
2:2:1222:G:H5''	54:x:78:ARG:HD2	1.95	0.48
7:A:9:ARG:HB2	7:A:12:ARG:HE	1.78	0.48
25:U:25:VAL:HA	25:U:36:VAL:HG12	1.94	0.48
31:a:63:ARG:HH12	54:x:9:PRO:HD3	1.78	0.48
39:i:97:ARG:HG2	39:i:99:ASP:OD1	2.13	0.48
48:r:4:ILE:HG23	48:r:57:ARG:HG2	1.95	0.48
1:1:100:U:H4'	1:1:101:A:O4'	2.14	0.48
1:1:171:U:H2'	1:1:172:A:C8	2.48	0.48
1:1:239:C:HO2'	1:1:622:G:HO2'	1.62	0.48
1:1:284:U:O4	1:1:356:G:O6	2.31	0.48
1:1:419:U:H2'	1:1:420:C:C6	2.48	0.48
1:1:1550:C:H2'	1:1:1551:A:C8	2.49	0.48
1:1:2039:U:H2'	1:1:2040:G:C8	2.48	0.48
2:2:222:C:H2'	2:2:223:A:C8	2.49	0.48
2:2:488:C:H2'	2:2:489:C:H6	1.79	0.48
16:L:95:LEU:HD23	16:L:100:ILE:HD12	1.96	0.48
25:U:28:VAL:HG23	25:U:34:VAL:HG12	1.95	0.48
37:g:64:LYS:HA	37:g:225:ARG:HH12	1.76	0.48
40:j:13:GLU:OE1	40:j:68:ARG:NH1	2.47	0.48
41:k:14:GLN:OE1	41:k:14:GLN:N	2.46	0.48
42:l:57:SER:OG	42:l:58:GLU:N	2.47	0.48
1:1:278:A:C6	1:1:362:A:C8	3.01	0.48
1:1:995:C:N4	14:J:2:LYS:HG3	2.28	0.48
1:1:1723:G:O6	1:1:1737:G:H1'	2.14	0.48
1:1:2720:U:H5''	20:P:53:ARG:NH2	2.29	0.48
2:2:412:A:H62	2:2:431:A:H61	1.60	0.48
2:2:938:A:N6	2:2:939:G:C6	2.82	0.48
6:6:162:VAL:HG21	6:6:176:VAL:HG11	1.96	0.48
7:A:134:ARG:C	7:A:136:LEU:N	2.67	0.48
11:E:131:GLY:HA2	11:E:153:ASP:HA	1.96	0.48
16:L:20:GLY:HA2	16:L:28:GLY:O	2.14	0.48
38:h:70:THR:HG21	38:h:76:VAL:HG21	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:z:63:GLU:HA	56:z:66:ARG:HG2	1.95	0.48
1:1:64:A:H2'	1:1:65:U:C6	2.48	0.47
1:1:1383:A:H1'	1:1:1405:U:O2'	2.14	0.47
2:2:22:G:H2'	2:2:23:C:H6	1.79	0.47
2:2:328:C:H4'	2:2:329:A:H5'	1.96	0.47
2:2:1338:G:N3	5:5:41:C:O2'	2.47	0.47
7:A:20:GLN:HG2	7:A:226:GLN:HE21	1.79	0.47
7:A:66:PRO:HA	7:A:160:GLN:OE1	2.13	0.47
39:i:95:GLU:HA	39:i:100:ASN:ND2	2.29	0.47
42:l:72:THR:OG1	42:l:142:HIS:NE2	2.46	0.47
47:q:87:VAL:HG11	47:q:90:LEU:HD12	1.96	0.47
49:s:3:LYS:HB2	49:s:6:MET:HG2	1.95	0.47
1:1:20:C:H2'	1:1:21:A:H8	1.79	0.47
1:1:1326:U:O2'	1:1:2010:G:O2'	2.26	0.47
1:1:1676:A:H1'	9:C:133:THR:HG21	1.96	0.47
1:1:1819:A:H5''	8:B:160:THR:HG21	1.96	0.47
1:1:2113:U:H3'	1:1:2114:A:C8	2.49	0.47
2:2:189:A:H8	2:2:189:A:OP2	1.98	0.47
2:2:718:A:H5'	46:p:119:ASN:ND2	2.28	0.47
9:C:27:ILE:HG12	9:C:201:LEU:HD12	1.95	0.47
31:a:57:VAL:O	31:a:61:ASN:ND2	2.47	0.47
1:1:418:C:H2'	1:1:419:U:C6	2.49	0.47
1:1:1857:G:H1'	1:1:1885:A:N6	2.29	0.47
2:2:458:U:H2'	2:2:459:A:C8	2.50	0.47
2:2:524:G:H2'	2:2:525:C:C6	2.49	0.47
7:A:157:LYS:HG3	7:A:158:ALA:N	2.28	0.47
22:R:73:LYS:HB2	22:R:73:LYS:HE2	1.56	0.47
39:i:202:GLU:OE1	40:j:112:ARG:NH1	2.42	0.47
44:n:58:VAL:HG13	44:n:59:GLU:HG3	1.96	0.47
46:p:89:PRO:HG3	56:z:32:VAL:HG11	1.96	0.47
54:x:33:THR:OG1	54:x:34:TRP:N	2.47	0.47
1:1:1365:A:O5'	28:X:28:ARG:NH2	2.44	0.47
1:1:1565:C:O2'	1:1:1566:A:H8	1.97	0.47
2:2:390:U:H2'	2:2:391:G:C8	2.48	0.47
2:2:963:G:N2	45:o:57:VAL:HG11	2.29	0.47
2:2:1033:G:H2'	2:2:1034:G:O4'	2.15	0.47
2:2:1309:G:OP1	48:r:87:ARG:NH2	2.47	0.47
7:A:157:LYS:HA	7:A:161:VAL:HG21	1.95	0.47
25:U:35:ILE:HD11	25:U:62:GLU:CB	2.45	0.47
1:1:1320:C:H4'	1:1:1321:A:O5'	2.14	0.47
1:1:2032:G:N2	1:1:2572:A:OP2	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2171:A:H1'	1:1:2172:U:C5	2.49	0.47
2:2:130:A:O2'	2:2:131:A:O5'	2.28	0.47
2:2:908:A:H2'	2:2:909:A:C8	2.49	0.47
2:2:1062:U:H2'	2:2:1063:C:C6	2.49	0.47
7:A:56:ASP:O	7:A:202:THR:OG1	2.28	0.47
7:A:117:SER:O	7:A:121:MET:N	2.48	0.47
9:C:46:ARG:NH2	9:C:85:ALA:O	2.48	0.47
43:m:10:MET:HE1	43:m:36:ILE:HB	1.94	0.47
48:r:33:ILE:HD11	48:r:63:PHE:CD2	2.49	0.47
1:1:715:A:H8	1:1:715:A:OP1	1.98	0.47
1:1:1155:A:H5''	21:Q:55:ARG:HD3	1.97	0.47
1:1:1333:G:C2	1:1:1334:G:C8	3.02	0.47
1:1:1508:A:O2'	1:1:1509:A:O4'	2.19	0.47
2:2:41:G:H2'	2:2:42:G:C8	2.50	0.47
2:2:339:C:H2'	2:2:340:U:C6	2.50	0.47
2:2:1244:G:H2'	2:2:1245:C:C6	2.50	0.47
7:A:118:PRO:HG2	7:A:148:ASN:HD21	1.79	0.47
10:D:115:GLN:HE22	16:L:1:MET:N	2.12	0.47
11:E:46:ASP:HB3	11:E:49:LEU:HG	1.96	0.47
17:M:70:ASP:OD1	17:M:70:ASP:N	2.34	0.47
35:e:14:PHE:O	35:e:15:LYS:HD3	2.15	0.47
42:l:74:GLU:HG2	42:l:91:VAL:HG22	1.96	0.47
43:m:72:VAL:HG23	43:m:72:VAL:O	2.15	0.47
48:r:29:ARG:HD2	48:r:63:PHE:CE2	2.49	0.47
1:1:277:G:H2'	1:1:361:G:O6	2.14	0.47
1:1:580:U:H2'	1:1:581:C:H6	1.79	0.47
1:1:704:G:H1'	1:1:727:A:N6	2.30	0.47
1:1:2169:A:H2'	1:1:2170:A:H8	1.79	0.47
1:1:2290:G:H2'	1:1:2291:U:C6	2.50	0.47
1:1:2373:G:H2'	1:1:2374:C:C6	2.50	0.47
1:1:2532:G:N2	1:1:2663:G:O2'	2.48	0.47
1:1:2861:U:H2'	1:1:2862:G:C8	2.49	0.47
2:2:131:A:H2'	2:2:132:C:H6	1.79	0.47
2:2:410:G:OP1	39:i:26:ARG:HD2	2.15	0.47
2:2:452:A:H62	2:2:480:U:H3	1.62	0.47
2:2:1266:G:N2	2:2:1269:A:OP2	2.44	0.47
2:2:1328:C:H5''	48:r:28:THR:HG21	1.95	0.47
3:3:119:A:H2'	3:3:120:U:O4'	2.14	0.47
7:A:22:ASP:HA	7:A:226:GLN:OE1	2.14	0.47
7:A:68:GLY:HA3	7:A:177:LYS:HD3	1.97	0.47
13:G:40:THR:OG1	13:G:43:ASN:OD1	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:S:40:ASN:O	23:S:41:LYS:HG2	2.14	0.47
27:W:23:VAL:HG13	27:W:38:VAL:HG12	1.96	0.47
31:a:19:GLY:HA3	59:a:109:HOH:O	2.14	0.47
37:g:82:ASP:OD1	37:g:83:ALA:N	2.47	0.47
37:g:130:THR:O	37:g:133:GLU:HG3	2.15	0.47
37:g:159:ASP:OD1	37:g:159:ASP:N	2.38	0.47
45:o:5:ARG:HH22	45:o:7:ARG:CZ	2.28	0.47
1:1:93:G:H2'	1:1:94:A:C8	2.50	0.47
1:1:151:C:H2'	1:1:152:A:C8	2.49	0.47
1:1:1666:G:C2'	1:1:1667:G:H5'	2.45	0.47
1:1:2180:U:H2'	1:1:2181:U:C6	2.49	0.47
2:2:73:C:H2'	2:2:74:A:H5'	1.95	0.47
2:2:468:A:H3'	2:2:469:C:H6	1.79	0.47
2:2:478:A:H5'	59:2:1857:HOH:O	2.14	0.47
2:2:1244:G:H2'	2:2:1245:C:H6	1.79	0.47
3:3:106:G:H2'	3:3:107:G:O4'	2.14	0.47
16:L:121:THR:HG22	16:L:141:LYS:HB3	1.96	0.47
18:N:18:GLN:HE21	18:N:22:ARG:NH1	2.12	0.47
24:T:53:VAL:HG13	24:T:91:GLN:HB3	1.97	0.47
29:Y:34:SER:OG	29:Y:36:GLN:HG2	2.15	0.47
50:t:29:VAL:CG2	50:t:81:LEU:HD21	2.45	0.47
1:1:547:A:H3'	1:1:547:A:N3	2.29	0.47
1:1:1068:G:H5'	1:1:1069:A:OP2	2.14	0.47
1:1:1198:U:H2'	1:1:1199:U:C6	2.50	0.47
1:1:1548:A:H2'	1:1:1549:A:C8	2.50	0.47
2:2:161:A:H2'	2:2:162:A:C8	2.49	0.47
2:2:746:A:H2'	2:2:747:A:C8	2.50	0.47
2:2:1173:U:C2	2:2:1174:G:C8	3.03	0.47
2:2:1227:A:N7	48:r:116:ILE:HD12	2.30	0.47
7:A:67:HIS:HB3	7:A:185:LEU:HD21	1.97	0.47
9:C:5:VAL:H	9:C:32:ASN:ND2	2.07	0.47
28:X:55:GLY:O	28:X:59:ILE:HG13	2.14	0.47
32:b:13:ARG:O	32:b:17:ARG:HG2	2.15	0.47
48:r:56:LEU:O	48:r:60:VAL:HG23	2.15	0.47
1:1:686:U:H2'	1:1:788:A:N1	2.29	0.47
1:1:729:G:C5	8:B:207:LYS:HB2	2.50	0.47
1:1:930:G:H1'	30:Z:25:LEU:HD21	1.97	0.47
1:1:1645:G:H5''	1:1:1646:C:H5'	1.95	0.47
1:1:2589:A:N1	1:1:2605:U:H5	2.13	0.47
1:1:2618:G:H21	9:C:155:VAL:HG21	1.80	0.47
2:2:203:G:O2'	2:2:465:A:N1	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1346:A:OP1	44:n:122:ARG:NH1	2.36	0.47
2:2:1375:A:H2'	2:2:1376:U:O4'	2.15	0.47
7:A:96:GLY:O	7:A:97:MET:HE2	2.15	0.47
7:A:123:VAL:O	7:A:127:LEU:HB2	2.15	0.47
10:D:145:ASP:HB3	10:D:166:LYS:HD2	1.96	0.47
16:L:2:ARG:H	16:L:5:THR:HG22	1.80	0.47
23:S:73:LYS:HB2	23:S:106:VAL:HB	1.96	0.47
39:i:101:VAL:O	39:i:105:MET:HG2	2.14	0.47
50:t:4:SER:O	50:t:8:THR:HG23	2.14	0.47
1:1:30:G:H2'	1:1:31:C:C6	2.50	0.46
1:1:93:G:H2'	1:1:94:A:H8	1.80	0.46
1:1:138:U:H5''	24:T:1:MET:SD	2.55	0.46
1:1:1180:U:H5'	1:1:1181:U:OP2	2.14	0.46
1:1:1715:G:O2'	1:1:1716:U:H6	1.97	0.46
1:1:2295:C:OP2	19:O:9:ARG:NH2	2.48	0.46
9:C:176:ASP:OD1	9:C:176:ASP:N	2.37	0.46
11:E:177:PHE:O	11:E:178:ARG:HG3	2.15	0.46
28:X:18:ARG:CZ	28:X:24:ALA:HB2	2.45	0.46
37:g:7:ARG:NH1	59:g:302:HOH:O	2.47	0.46
42:l:143:ARG:CD	59:l:301:HOH:O	2.29	0.46
55:y:80:THR:HG22	55:y:84:ASN:ND2	2.29	0.46
1:1:75:G:H22	1:1:111:A:H2	1.64	0.46
1:1:1197:G:H2'	1:1:1198:U:H6	1.79	0.46
1:1:1572:A:H2'	1:1:1573:G:H8	1.80	0.46
1:1:2015:A:C2	32:b:3:VAL:HG22	2.51	0.46
1:1:2340:A:H5'	3:3:41:G:H21	1.81	0.46
1:1:2788:C:H2'	1:1:2789:C:C6	2.49	0.46
2:2:539:A:H2'	2:2:540:G:C8	2.51	0.46
2:2:620:C:C2	39:i:132:ILE:HG13	2.50	0.46
2:2:1118:U:H1'	2:2:1179:A:C5	2.51	0.46
2:2:1145:A:O2'	2:2:1146:A:H8	1.97	0.46
2:2:1152:A:P	45:o:72:ARG:HH22	2.38	0.46
6:6:140:PRO:HA	6:6:169:GLN:HE22	1.81	0.46
17:M:38:ARG:HB2	17:M:98:PRO:HD3	1.97	0.46
20:P:2:SER:OG	20:P:3:ASN:N	2.48	0.46
22:R:55:ASP:OD1	22:R:55:ASP:N	2.47	0.46
25:U:96:PHE:CE1	25:U:103:ILE:HG12	2.50	0.46
31:a:44:PHE:CD1	31:a:45:THR:HG23	2.50	0.46
44:n:57:MET:HE1	44:n:90:TYR:CE2	2.51	0.46
49:s:53:ARG:HB3	49:s:59:ARG:NH1	2.30	0.46
53:w:65:LEU:O	53:w:66:SER:OG	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1292:G:H2'	1:1:1293:C:C6	2.50	0.46
2:2:951:G:C6	2:2:1231:G:C6	3.03	0.46
3:3:66:A:H61	3:3:107:G:H2'	1.81	0.46
6:6:8:ASP:O	6:6:10:ARG:NH1	2.48	0.46
7:A:102:ASP:HA	7:A:105:LYS:HG2	1.97	0.46
41:k:4:TYR:CD1	41:k:71:ILE:HG13	2.50	0.46
48:r:11:ASP:OD1	48:r:46:SER:N	2.48	0.46
51:u:57:ILE:HD13	51:u:75:ILE:HD11	1.98	0.46
51:u:69:ASP:OD2	51:u:69:ASP:N	2.48	0.46
1:1:2258:C:O2'	1:1:2427:C:OP2	2.29	0.46
1:1:2637:U:H2'	1:1:2638:G:O4'	2.16	0.46
12:F:9:VAL:O	12:F:49:THR:OG1	2.20	0.46
37:g:20:THR:HG23	37:g:39:HIS:HE1	1.80	0.46
46:p:94:GLU:OE1	46:p:94:GLU:N	2.48	0.46
54:x:19:VAL:HG11	54:x:44:MET:SD	2.55	0.46
1:1:2388:A:H5'	1:1:2389:G:OP2	2.15	0.46
1:1:2629:U:O2'	1:1:2630:G:H5''	2.15	0.46
2:2:1172:C:C2	2:2:1173:U:C5	3.04	0.46
11:E:8:TYR:HB2	11:E:173:PHE:CZ	2.51	0.46
12:F:87:LEU:HB2	12:F:131:ILE:HB	1.98	0.46
13:G:104:THR:HG22	13:G:110:VAL:H	1.80	0.46
32:b:31:ASP:OD2	32:b:32:LYS:N	2.49	0.46
37:g:59:LYS:HB3	37:g:63:ARG:HH12	1.80	0.46
37:g:127:ASP:OD1	37:g:127:ASP:N	2.46	0.46
45:o:28:THR:O	45:o:32:THR:HG22	2.15	0.46
1:1:242:G:H1'	1:1:243:U:OP2	2.16	0.46
1:1:1020:A:H4'	1:1:1021:A:O5'	2.16	0.46
1:1:2097:A:H2'	1:1:2098:U:C6	2.50	0.46
1:1:2723:C:H2'	1:1:2724:U:O4'	2.15	0.46
2:2:468:A:H3'	2:2:469:C:C6	2.50	0.46
2:2:529:G:O6	47:q:46:ASN:ND2	2.48	0.46
3:3:35:C:H2'	3:3:36:C:H5'	1.98	0.46
14:J:125:TYR:OH	14:J:132:HIS:NE2	2.47	0.46
18:N:35:LYS:HE3	18:N:100:CYS:SG	2.55	0.46
20:P:5:ILE:O	20:P:9:GLU:HG3	2.16	0.46
1:1:139:U:H2'	1:1:140:C:C5	2.50	0.46
1:1:208:C:H2'	1:1:209:C:H6	1.80	0.46
1:1:579:G:H2'	1:1:580:U:C6	2.50	0.46
1:1:1684:G:H2'	1:1:1685:C:H6	1.81	0.46
1:1:1799:G:N7	8:B:178:SER:OG	2.44	0.46
1:1:2859:G:H2'	1:1:2860:A:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:362:G:N2	2:2:365:U:OP2	2.49	0.46
2:2:642:A:N7	43:m:107:SER:HA	2.31	0.46
7:A:23:ILE:HG23	7:A:229:LEU:HD23	1.97	0.46
7:A:217:THR:OG1	7:A:218:MET:N	2.49	0.46
8:B:155:ALA:HB2	8:B:162:VAL:HG13	1.97	0.46
10:D:21:ARG:O	10:D:114:ARG:NH2	2.48	0.46
13:G:79:THR:HA	13:G:145:ASN:OD1	2.15	0.46
32:b:38:HIS:ND1	32:b:39:LEU:O	2.45	0.46
38:h:88:ARG:HG3	38:h:101:ILE:HG12	1.97	0.46
40:j:18:VAL:HA	40:j:34:THR:O	2.16	0.46
56:z:10:GLU:OE1	56:z:14:VAL:HG13	2.15	0.46
1:1:784:G:N1	8:B:228:VAL:HG21	2.31	0.46
1:1:1636:U:H2'	1:1:1637:A:C8	2.51	0.46
1:1:2424:C:O2	1:1:2429:G:O2'	2.33	0.46
1:1:2457:U:H5	1:1:2494:G:H1	1.63	0.46
1:1:2688:G:N1	1:1:2720:U:OP2	2.35	0.46
2:2:6:G:H4'	2:2:298:A:H4'	1.96	0.46
2:2:181:A:C6	2:2:195:A:C5	3.04	0.46
2:2:784:A:H2'	2:2:785:G:C8	2.50	0.46
2:2:820:U:H4'	2:2:821:G:OP2	2.16	0.46
2:2:965:U:H5''	2:2:966:2MG:OP1	2.15	0.46
2:2:1272:G:H2'	2:2:1273:C:C6	2.51	0.46
7:A:94:LEU:HD13	7:A:100:LEU:HD13	1.96	0.46
8:B:145:GLU:HG2	8:B:151:GLY:C	2.40	0.46
10:D:22:ASP:N	10:D:22:ASP:OD1	2.47	0.46
11:E:37:ASN:OD1	11:E:38:MET:N	2.48	0.46
1:1:751:A:H5'	23:S:90:LYS:HA	1.98	0.46
1:1:1180:U:H3'	1:1:1181:U:C6	2.50	0.46
1:1:2200:C:OP2	28:X:37:ARG:NH2	2.49	0.46
1:1:2703:C:H2'	1:1:2704:C:H6	1.80	0.46
2:2:635:A:H2'	2:2:636:U:C6	2.51	0.46
7:A:51:ASP:N	7:A:57:GLN:OE1	2.49	0.46
7:A:94:LEU:HD22	7:A:100:LEU:HB2	1.97	0.46
8:B:197:ASN:OD1	8:B:200:HIS:HB2	2.16	0.46
11:E:108:VAL:HG11	11:E:176:PRO:HG2	1.96	0.46
13:G:132:PHE:N	13:G:140:ALA:O	2.49	0.46
23:S:2:GLU:HA	23:S:108:SER:HB3	1.98	0.46
37:g:59:LYS:HE3	37:g:59:LYS:HB3	1.70	0.46
43:m:104:VAL:HG12	43:m:125:ILE:HG12	1.97	0.46
44:n:44:ALA:O	44:n:48:VAL:HG23	2.16	0.46
55:y:80:THR:HG22	55:y:84:ASN:HD21	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2282:G:H4'	1:1:2389:G:O2'	2.16	0.46
2:2:299:G:H2'	2:2:300:A:C8	2.51	0.46
2:2:513:C:H2'	2:2:514:C:C6	2.51	0.46
2:2:963:G:C2	2:2:964:A:C8	3.05	0.46
10:D:108:ILE:HD11	10:D:180:LEU:HD12	1.98	0.46
12:F:23:VAL:HA	12:F:36:THR:HA	1.98	0.46
16:L:82:LEU:O	16:L:85:VAL:HG12	2.16	0.46
16:L:109:LYS:HE2	16:L:128:THR:HG22	1.98	0.46
19:O:69:ASP:OD1	19:O:70:ALA:N	2.49	0.46
24:T:5:GLU:O	24:T:9:LYS:HG2	2.16	0.46
27:W:19:LYS:HA	27:W:19:LYS:HD3	1.81	0.46
40:j:52:LYS:HB3	40:j:52:LYS:HE2	1.63	0.46
49:s:27:LEU:HD23	49:s:48:LEU:HB2	1.98	0.46
1:1:181:A:H2'	1:1:182:A:C8	2.51	0.45
1:1:495:G:N2	23:S:61:ASN:HD21	2.07	0.45
1:1:594:U:H2'	1:1:595:C:H6	1.81	0.45
1:1:1059:G:H1'	59:1:3535:HOH:O	2.17	0.45
1:1:1482:G:C2	1:1:1483:G:C8	3.04	0.45
1:1:1652:A:OP1	18:N:8:ARG:NH2	2.46	0.45
1:1:2809:A:H2'	1:1:2810:A:C8	2.51	0.45
2:2:215:C:H2'	2:2:216:U:C6	2.51	0.45
2:2:1022:A:N7	59:2:1812:HOH:O	2.48	0.45
2:2:1319:A:C8	2:2:1323:G:C6	3.04	0.45
5:5:23:C:H5''	6:6:130:PHE:CE2	2.49	0.45
7:A:134:ARG:O	7:A:136:LEU:N	2.50	0.45
7:A:161:VAL:C	7:A:162:ARG:HD3	2.40	0.45
7:A:167:LYS:HE3	7:A:173:THR:H	1.81	0.45
28:X:31:PRO:HG2	28:X:33:LEU:HD23	1.97	0.45
1:1:641:U:O2'	1:1:2350:C:OP1	2.34	0.45
1:1:936:A:H2'	1:1:937:C:H6	1.80	0.45
1:1:1000:A:H2'	1:1:1001:A:C8	2.50	0.45
1:1:1019:U:OP1	1:1:1035:U:O2'	2.20	0.45
1:1:1405:U:H2'	1:1:1406:U:C6	2.50	0.45
1:1:2298:A:H2'	1:1:2299:U:O4'	2.15	0.45
3:3:30:C:H1'	3:3:57:A:H61	1.80	0.45
7:A:83:ASN:HA	7:A:86:ALA:HB3	1.98	0.45
15:K:108:ARG:HG3	15:K:113:MET:HE1	1.98	0.45
24:T:11:LEU:O	29:Y:29:ARG:NH1	2.47	0.45
37:g:118:GLU:O	37:g:122:GLN:HB3	2.17	0.45
51:u:6:LEU:HG	51:u:19:VAL:HG12	1.98	0.45
1:1:1224:U:H2'	1:1:1225:G:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2615:U:C2	32:b:4:GLN:HA	2.51	0.45
2:2:1175:G:N3	2:2:1176:A:C8	2.85	0.45
7:A:144:THR:O	7:A:144:THR:HG22	2.16	0.45
11:E:73:SER:OG	11:E:80:ARG:HA	2.16	0.45
38:h:70:THR:O	38:h:106:VAL:HG12	2.15	0.45
39:i:17:THR:OG1	39:i:18:ASP:N	2.49	0.45
43:m:5:ASP:OD1	43:m:77:ARG:NH1	2.49	0.45
49:s:43:ASN:HA	49:s:46:LEU:HD12	1.98	0.45
1:1:549:G:O2'	1:1:550:C:OP1	2.28	0.45
1:1:563:A:OP2	22:R:79:ARG:NH2	2.44	0.45
1:1:728:G:H4'	8:B:13:ARG:HD3	1.99	0.45
1:1:1091:G:H2'	1:1:1092:C:C6	2.52	0.45
1:1:1588:G:H2'	1:1:1589:U:C6	2.51	0.45
1:1:2799:A:C6	1:1:2801:G:C5	3.04	0.45
2:2:429:U:H3'	39:i:9:LEU:HD21	1.99	0.45
2:2:687:A:C2	2:2:704:A:C5	3.04	0.45
2:2:1130:A:C8	2:2:1146:A:N1	2.84	0.45
7:A:48:LEU:HD13	7:A:209:ILE:HA	1.98	0.45
43:m:102:ALA:HB3	43:m:113:ASP:HB3	1.97	0.45
56:z:31:GLU:OE2	56:z:34:ARG:NH2	2.41	0.45
1:1:404:A:O2'	1:1:405:U:O5'	2.35	0.45
1:1:2327:A:N7	1:1:2388:A:N6	2.65	0.45
2:2:1157:A:H4'	2:2:1158:C:O5'	2.16	0.45
2:2:1376:U:H2'	2:2:1377:A:C8	2.51	0.45
3:3:7:G:H5'	19:O:29:HIS:CE1	2.51	0.45
8:B:13:ARG:HH21	8:B:18:LYS:HE3	1.81	0.45
38:h:56:VAL:HG22	38:h:67:THR:HB	1.98	0.45
45:o:46:LYS:HG2	45:o:68:ARG:HG2	1.98	0.45
53:w:14:THR:HG22	53:w:51:TYR:CE2	2.52	0.45
1:1:629:G:N3	1:1:639:U:O2'	2.49	0.45
1:1:647:G:N2	1:1:2350:C:O2'	2.50	0.45
1:1:657:U:H2'	1:1:658:U:C6	2.51	0.45
1:1:1073:A:H2'	1:1:1074:G:H8	1.81	0.45
1:1:2545:G:H2'	1:1:2546:U:O4'	2.16	0.45
1:1:2804:U:H2'	1:1:2805:C:H6	1.81	0.45
2:2:35:G:H2'	2:2:36:C:C6	2.52	0.45
2:2:193:C:H2'	2:2:194:C:C6	2.52	0.45
2:2:407:U:H2'	2:2:408:A:H8	1.82	0.45
2:2:925:G:C2	2:2:927:G:C8	3.05	0.45
2:2:1077:G:N2	2:2:1080:A:OP2	2.49	0.45
5:5:39:G:H4'	6:6:149:THR:CG2	2.40	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:O:51:ALA:HB3	19:O:78:VAL:HB	1.98	0.45
1:1:415:A:H2'	1:1:416:U:C6	2.52	0.45
1:1:1056:G:H4'	1:1:1086:A:C8	2.52	0.45
1:1:1940:U:H4'	1:1:1941:C:O5'	2.16	0.45
1:1:2887:A:N3	32:b:27:SER:OG	2.44	0.45
2:2:261:U:OP2	55:y:71:LYS:NZ	2.46	0.45
2:2:696:A:H2'	2:2:697:U:H6	1.80	0.45
2:2:1347:G:O2'	2:2:1373:G:O6	2.29	0.45
7:A:45:ALA:HA	7:A:173:THR:HG22	1.98	0.45
9:C:53:GLY:O	9:C:76:GLY:HA2	2.16	0.45
10:D:191:ASP:OD1	10:D:191:ASP:N	2.47	0.45
15:K:64:ARG:O	15:K:82:ASN:HA	2.16	0.45
38:h:91:VAL:HG21	38:h:101:ILE:HD11	1.97	0.45
50:t:10:LYS:O	50:t:14:GLU:HG2	2.17	0.45
1:1:1094:U:N3	1:1:1097:U:OP2	2.30	0.45
1:1:1474:U:O4	1:1:1475:G:N2	2.49	0.45
2:2:373:A:C2	2:2:374:A:C8	3.05	0.45
2:2:515:G:H2'	2:2:516:PSU:O4	2.17	0.45
2:2:649:A:H2'	2:2:650:G:O4'	2.16	0.45
2:2:715:A:H2'	2:2:716:A:C8	2.52	0.45
2:2:784:A:H2'	2:2:785:G:H8	1.81	0.45
8:B:88:SER:HB3	8:B:158:ALA:HB2	1.98	0.45
17:M:40:ARG:HB2	17:M:93:VAL:HG11	1.99	0.45
17:M:110:GLU:O	17:M:114:ARG:HG2	2.16	0.45
26:V:58:SER:O	26:V:73:LYS:NZ	2.47	0.45
37:g:77:SER:OG	37:g:93:ASN:ND2	2.49	0.45
39:i:48:LEU:HD21	39:i:56:ARG:HG3	1.99	0.45
41:k:40:GLU:HG2	41:k:42:TRP:CD1	2.51	0.45
1:1:421:C:O2'	1:1:422:A:P	2.75	0.45
1:1:634:C:H2'	1:1:635:C:C6	2.52	0.45
1:1:832:U:H2'	1:1:833:A:H8	1.82	0.45
1:1:1682:G:H2'	1:1:1683:U:C6	2.52	0.45
1:1:2896:C:H2'	1:1:2897:U:C6	2.52	0.45
2:2:505:G:H2'	2:2:506:G:C8	2.52	0.45
3:3:74:U:C4	3:3:75:G:C4	3.05	0.45
9:C:148:GLN:N	9:C:148:GLN:OE1	2.50	0.45
11:E:11:GLU:O	11:E:14:LYS:HG3	2.17	0.45
13:G:46:PHE:O	13:G:50:ARG:HB3	2.17	0.45
38:h:114:LYS:NZ	38:h:118:ASP:OD2	2.49	0.45
55:y:6:SER:O	55:y:10:ARG:HG2	2.17	0.45
55:y:43:ASP:OD1	55:y:43:ASP:N	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:32:C:H2'	1:1:33:C:C6	2.52	0.45
1:1:173:A:H2'	1:1:174:U:H6	1.82	0.45
1:1:197:A:N6	1:1:2430:A:H2'	2.32	0.45
1:1:279:A:N6	1:1:361:G:O2'	2.50	0.45
1:1:898:C:H2'	1:1:899:A:O4'	2.17	0.45
1:1:1316:U:H2'	1:1:1317:G:H8	1.82	0.45
1:1:1857:G:O2'	1:1:1858:A:H8	1.99	0.45
1:1:1912:A:N7	1:1:1917:U:H5	2.15	0.45
1:1:2271:G:OP1	27:W:18:ALA:HB1	2.17	0.45
2:2:368:U:H2'	2:2:368:U:O2	2.17	0.45
2:2:1352:C:H2'	2:2:1353:G:C8	2.52	0.45
2:2:1363:A:C5	2:2:1365:G:C6	3.05	0.45
24:T:14:PRO:HD3	29:Y:30:MET:SD	2.57	0.45
1:1:382:A:C2	1:1:393:C:C2	3.05	0.44
1:1:571:U:C4	1:1:575:A:C5	3.05	0.44
1:1:883:G:N2	1:1:894:U:O4	2.51	0.44
1:1:1095:A:H2'	1:1:1096:A:C8	2.52	0.44
1:1:1417:C:HO2'	1:1:1587:G:HO2'	1.64	0.44
1:1:1527:G:N1	1:1:1544:A:OP2	2.44	0.44
1:1:2264:C:N4	27:W:15:ASP:OD2	2.43	0.44
2:2:50:A:O2'	2:2:360:G:N2	2.50	0.44
2:2:254:G:P	52:v:68:SER:HG	2.40	0.44
2:2:868:C:H2'	2:2:869:G:O4'	2.17	0.44
2:2:1169:A:H2'	2:2:1170:A:C8	2.51	0.44
2:2:1178:G:N7	44:n:99:ARG:NH1	2.64	0.44
2:2:1309:G:C6	2:2:1329:A:N1	2.85	0.44
25:U:7:ARG:O	25:U:25:VAL:HG13	2.16	0.44
37:g:6:MET:O	37:g:10:LEU:HD23	2.18	0.44
38:h:123:GLN:HB3	38:h:128:VAL:CG2	2.47	0.44
39:i:21:LEU:HD12	39:i:21:LEU:HA	1.81	0.44
47:q:81:LEU:HB3	47:q:98:VAL:CG2	2.46	0.44
1:1:1172:C:H1'	59:1:3493:HOH:O	2.15	0.44
1:1:2098:U:H2'	1:1:2099:U:O4'	2.17	0.44
1:1:2480:C:H2'	1:1:2481:G:O4'	2.18	0.44
1:1:2888:C:H2'	1:1:2889:C:H6	1.82	0.44
2:2:339:C:H2'	2:2:340:U:H6	1.83	0.44
2:2:1130:A:H2'	2:2:1131:G:C8	2.51	0.44
6:6:68:VAL:O	6:6:117:LEU:HD23	2.16	0.44
7:A:55:SER:C	7:A:57:GLN:N	2.69	0.44
12:F:37:LEU:HD23	12:F:37:LEU:HA	1.74	0.44
14:J:12:LYS:O	14:J:41:LYS:NZ	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:O:34:HIS:CD2	19:O:65:THR:HG21	2.52	0.44
28:X:18:ARG:NH2	28:X:22:LEU:O	2.50	0.44
48:r:16:VAL:HG23	48:r:17:ILE:HG13	1.99	0.44
1:1:468:G:N7	34:d:39:ARG:NH2	2.52	0.44
1:1:1681:G:O2'	1:1:1762:A:N3	2.46	0.44
1:1:1738:G:O2'	1:1:1739:A:H8	2.00	0.44
1:1:2016:U:H1'	32:b:3:VAL:CG1	2.47	0.44
1:1:2038:G:H2'	1:1:2039:U:O4'	2.16	0.44
1:1:2070:A:H2'	1:1:2071:A:C8	2.52	0.44
1:1:2127:G:H8	1:1:2127:G:OP2	2.00	0.44
2:2:371:A:H2'	2:2:372:C:O4'	2.17	0.44
2:2:750:C:H2'	2:2:751:U:H6	1.82	0.44
2:2:751:U:H2'	2:2:752:G:O4'	2.17	0.44
2:2:1158:C:C4	2:2:1160:G:C8	3.05	0.44
6:6:27:SER:HA	6:6:41:VAL:HA	2.00	0.44
6:6:42:LYS:HG2	6:6:53:GLU:OE2	2.17	0.44
7:A:150:ALA:O	7:A:154:LYS:HG3	2.16	0.44
12:F:127:THR:HG22	12:F:128:GLN:H	1.81	0.44
16:L:28:GLY:HA3	22:R:82:HIS:NE2	2.32	0.44
17:M:23:GLY:O	17:M:101:VAL:HG12	2.17	0.44
30:Z:12:SER:OG	30:Z:14:ILE:HG13	2.18	0.44
44:n:95:ARG:NH2	59:n:201:HOH:O	2.20	0.44
44:n:99:ARG:HE	44:n:104:VAL:HG11	1.82	0.44
46:p:114:THR:HG21	56:z:32:VAL:HG21	1.99	0.44
48:r:20:THR:HA	48:r:25:VAL:O	2.18	0.44
53:w:36:SER:HA	53:w:72:ASP:HB3	1.99	0.44
1:1:67:U:C2	1:1:68:G:C8	3.05	0.44
1:1:373:U:H2'	1:1:374:A:H8	1.82	0.44
1:1:753:A:H2'	1:1:754:U:H6	1.82	0.44
1:1:1070:A:O2'	1:1:1071:G:OP1	2.36	0.44
1:1:1980:G:O2'	1:1:1982:U:OP2	2.33	0.44
1:1:2455:G:C4	1:1:2456:C:C5	3.05	0.44
2:2:75:G:H2'	2:2:76:G:C8	2.52	0.44
2:2:154:U:H2'	2:2:155:A:C8	2.51	0.44
2:2:472:U:H2'	2:2:473:U:C6	2.53	0.44
2:2:1477:U:H2'	2:2:1478:U:C6	2.52	0.44
6:6:6:SER:HA	6:6:9:PHE:CE2	2.53	0.44
7:A:183:ASP:O	7:A:187:GLU:HG3	2.18	0.44
10:D:171:ASP:OD1	10:D:172:ALA:N	2.51	0.44
37:g:105:LYS:HB3	59:g:311:HOH:O	2.17	0.44
42:l:16:PRO:HB2	44:n:42:GLU:OE1	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:v:4:LYS:HE2	52:v:4:LYS:HB2	1.83	0.44
1:1:1112:G:H2'	1:1:1113:U:H6	1.82	0.44
1:1:1178:C:O2'	1:1:1179:G:H8	2.00	0.44
1:1:1599:U:H2'	1:1:1600:C:H6	1.83	0.44
1:1:1901:A:OP2	8:B:253:LYS:NZ	2.46	0.44
1:1:2100:G:H2'	1:1:2101:A:C8	2.52	0.44
1:1:2109:U:H2'	1:1:2110:G:C8	2.52	0.44
1:1:2286:G:H5''	1:1:2287:A:OP1	2.18	0.44
2:2:160:A:H2'	2:2:161:A:O4'	2.17	0.44
3:3:28:C:H2'	3:3:29:A:H8	1.82	0.44
11:E:8:TYR:HB2	11:E:173:PHE:HZ	1.83	0.44
11:E:135:GLN:CD	11:E:150:ARG:H	2.24	0.44
38:h:116:VAL:HG21	38:h:200:VAL:HG11	1.98	0.44
40:j:76:LEU:HD11	40:j:120:VAL:HG12	1.99	0.44
43:m:26:THR:HG22	43:m:60:GLU:HB2	1.99	0.44
47:q:80:ILE:HA	47:q:80:ILE:HD13	1.82	0.44
1:1:396:G:OP2	28:X:10:LYS:NZ	2.50	0.44
1:1:546:U:H2'	1:1:547:A:H4'	2.00	0.44
1:1:884:U:H1'	1:1:894:U:O2	2.17	0.44
1:1:1693:U:O2'	8:B:14:ARG:NH2	2.51	0.44
2:2:455:G:C2	2:2:456:A:C4	3.05	0.44
2:2:1458:G:OP1	55:y:30:THR:OG1	2.30	0.44
7:A:106:LYS:HE3	7:A:106:LYS:HB3	1.80	0.44
7:A:198:LYS:NZ	7:A:201:PRO:HB3	2.33	0.44
7:A:214:ILE:HG12	7:A:224:VAL:HG12	1.98	0.44
8:B:53:HIS:CE1	8:B:219:THR:HA	2.53	0.44
10:D:117:ARG:NH2	10:D:183:PHE:O	2.51	0.44
11:E:106:ILE:C	11:E:109:PRO:HD2	2.43	0.44
15:K:15:GLY:O	15:K:47:ILE:HG12	2.17	0.44
26:V:21:ARG:HA	26:V:25:LYS:O	2.17	0.44
40:j:156:LYS:HD2	43:m:71:VAL:HA	2.00	0.44
48:r:23:TYR:HB3	48:r:66:GLU:HG3	1.99	0.44
1:1:608:A:H2'	1:1:609:A:H8	1.83	0.44
1:1:653:U:N3	1:1:654:A:N1	2.66	0.44
1:1:988:A:P	30:Z:12:SER:HB3	2.57	0.44
1:1:1176:U:H2'	1:1:1177:G:C8	2.52	0.44
1:1:1387:A:C6	1:1:1401:G:N1	2.85	0.44
2:2:620:C:H2'	2:2:621:A:C8	2.53	0.44
2:2:791:G:C6	2:2:792:A:N7	2.86	0.44
2:2:1355:G:H2'	2:2:1356:G:C8	2.52	0.44
3:3:74:U:H3'	3:3:75:G:H8	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:E:5:HIS:O	11:E:9:LYS:HG3	2.18	0.44
11:E:52:ASN:HB2	11:E:150:ARG:NH2	2.32	0.44
13:G:53:GLU:O	13:G:57:LYS:HG2	2.17	0.44
13:G:97:ARG:HA	13:G:112:LYS:HE2	1.99	0.44
26:V:76:ASP:OD2	26:V:77:VAL:N	2.51	0.44
29:Y:57:LEU:HA	29:Y:57:LEU:HD23	1.75	0.44
33:c:17:THR:HG22	33:c:18:GLY:N	2.32	0.44
41:k:40:GLU:OE2	41:k:103:VAL:HB	2.18	0.44
47:q:83:ARG:HB3	47:q:98:VAL:HG13	1.99	0.44
53:w:18:VAL:HG22	53:w:20:GLU:H	1.83	0.44
1:1:30:G:H2'	1:1:31:C:H6	1.83	0.44
1:1:275:C:H2'	1:1:276:U:H4'	1.99	0.44
1:1:288:U:H2'	1:1:289:G:C8	2.53	0.44
2:2:62:U:OP1	2:2:385:C:O2'	2.35	0.44
2:2:321:A:H2'	2:2:322:C:C6	2.51	0.44
2:2:1030:U:O2'	2:2:1031:C:H5''	2.18	0.44
2:2:1124:G:N2	2:2:1125:U:O4	2.40	0.44
59:2:1851:HOH:O	53:w:15:ALA:CB	2.65	0.44
18:N:57:THR:HG23	18:N:62:ASN:HD22	1.83	0.44
26:V:86:LEU:HD13	26:V:89:ILE:HD11	2.00	0.44
38:h:155:GLY:O	38:h:196:ILE:HG13	2.17	0.44
41:k:11:HIS:HE1	41:k:13:ASP:OD1	2.01	0.44
44:n:12:ARG:HH22	44:n:109:ARG:NH2	2.10	0.44
47:q:57:LEU:HD23	47:q:57:LEU:HA	1.81	0.44
1:1:288:U:H2'	1:1:289:G:H8	1.82	0.44
1:1:1636:U:H2'	1:1:1637:A:H8	1.82	0.44
1:1:2529:G:H5''	1:1:2530:A:H5''	2.00	0.44
1:1:2696:U:H2'	1:1:2697:G:C8	2.53	0.44
2:2:500:G:H2'	2:2:501:C:H6	1.82	0.44
2:2:1326:U:H2'	2:2:1327:C:C6	2.51	0.44
7:A:202:THR:H	7:A:205:LYS:HE2	1.82	0.44
12:F:18:LYS:HB3	12:F:25:THR:HB	1.99	0.44
12:F:60:ASP:OD1	12:F:60:ASP:N	2.45	0.44
43:m:96:MET:SD	43:m:130:ALA:HB1	2.58	0.44
46:p:123:PRO:HD2	56:z:38:TYR:CD1	2.50	0.44
1:1:580:U:H2'	1:1:581:C:C6	2.53	0.43
1:1:1019:U:H3	1:1:1142:A:H62	1.66	0.43
1:1:2031:A:N3	1:1:2455:G:O2'	2.43	0.43
1:1:2350:C:OP2	35:e:45:ARG:NH1	2.50	0.43
2:2:12:U:H4'	2:2:526:C:H4'	1.99	0.43
2:2:87:C:H2'	2:2:88:U:C5	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:5:39:G:C4'	6:6:149:THR:HG21	2.40	0.43
6:6:67:VAL:HG22	6:6:118:TRP:CD1	2.53	0.43
6:6:110:GLN:HG3	6:6:110:GLN:O	2.18	0.43
13:G:83:LYS:HA	13:G:83:LYS:HD3	1.83	0.43
16:L:59:ARG:HA	35:e:13:ARG:HH22	1.82	0.43
30:Z:45:ARG:HD3	30:Z:45:ARG:HA	1.79	0.43
39:i:57:GLU:OE2	39:i:196:ASN:N	2.51	0.43
42:l:75:VAL:HG21	42:l:86:GLN:HB3	2.00	0.43
48:r:66:GLU:N	48:r:66:GLU:OE1	2.51	0.43
53:w:32:TYR:O	53:w:40:VAL:HG22	2.18	0.43
55:y:22:ALA:O	55:y:26:SER:OG	2.31	0.43
1:1:493:G:H2'	1:1:494:G:O4'	2.17	0.43
1:1:527:C:C2	1:1:2779:U:H2'	2.53	0.43
1:1:774:G:HO2'	1:1:775:G:P	2.40	0.43
1:1:784:G:H5'	1:1:785:G:OP1	2.17	0.43
1:1:1318:U:H2'	1:1:1319:C:C6	2.54	0.43
1:1:1746:A:H2'	1:1:1747:U:H6	1.83	0.43
1:1:1842:G:H2'	1:1:1843:C:C6	2.52	0.43
1:1:1853:A:H2'	1:1:1854:A:C8	2.53	0.43
1:1:2331:G:N2	1:1:2385:C:C2	2.87	0.43
2:2:418:C:H2'	2:2:419:C:C6	2.52	0.43
2:2:458:U:H2'	2:2:459:A:H8	1.83	0.43
2:2:1107:C:C4	2:2:1108:G:C8	3.06	0.43
2:2:1179:A:H2'	2:2:1180:A:O4'	2.18	0.43
2:2:1219:A:H2'	2:2:1220:G:C8	2.53	0.43
5:5:3:G:H1'	5:5:4:C:O5'	2.19	0.43
5:5:5:A:OP1	6:6:10:ARG:HG2	2.18	0.43
8:B:154:LEU:HD22	8:B:176:LEU:HD22	1.99	0.43
9:C:187:LEU:O	9:C:188:LEU:HD23	2.18	0.43
11:E:40:VAL:HG23	11:E:40:VAL:O	2.17	0.43
15:K:70:ARG:HD2	15:K:76:VAL:HG12	2.00	0.43
16:L:79:LEU:HD12	16:L:112:LEU:HD12	2.01	0.43
38:h:14:ILE:HD12	38:h:178:LEU:HB3	2.00	0.43
48:r:51:GLY:O	48:r:55:THR:HG23	2.18	0.43
1:1:44:A:H2'	1:1:45:G:O4'	2.18	0.43
1:1:764:A:H5''	8:B:209:GLY:CA	2.49	0.43
1:1:1794:A:H2'	1:1:1795:C:C6	2.53	0.43
1:1:2293:G:OP1	19:O:94:ARG:NH1	2.34	0.43
1:1:2888:C:H2'	1:1:2889:C:C6	2.53	0.43
2:2:87:C:H2'	2:2:88:U:C6	2.53	0.43
2:2:299:G:N2	2:2:565:U:O2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:628:G:H2'	2:2:629:A:C8	2.53	0.43
2:2:838:G:C6	2:2:849:G:C6	3.06	0.43
27:W:31:VAL:HG13	27:W:35:SER:OG	2.18	0.43
37:g:11:LYS:HB2	37:g:11:LYS:HE2	1.79	0.43
43:m:108:LYS:HD3	43:m:108:LYS:HA	1.64	0.43
45:o:57:VAL:O	45:o:57:VAL:HG23	2.19	0.43
49:s:83:LYS:O	49:s:86:GLU:HG3	2.18	0.43
55:y:9:LYS:HE2	55:y:13:GLN:NE2	2.33	0.43
1:1:1060:U:O2'	1:1:1062:G:OP2	2.33	0.43
1:1:1485:U:H2'	1:1:1486:U:C6	2.53	0.43
1:1:1707:G:C8	1:1:1756:G:C5	3.06	0.43
1:1:2176:A:N3	1:1:2176:A:H2'	2.34	0.43
1:1:2834:G:H2'	1:1:2879:A:H61	1.83	0.43
2:2:513:C:H2'	2:2:514:C:H6	1.83	0.43
12:F:17:VAL:HG22	12:F:26:ILE:HD12	2.00	0.43
24:T:48:GLN:HG3	24:T:55:VAL:HG12	2.00	0.43
26:V:72:VAL:HG12	26:V:73:LYS:N	2.33	0.43
36:f:6:SER:O	36:f:6:SER:OG	2.35	0.43
41:k:74:LEU:HA	41:k:74:LEU:HD23	1.80	0.43
44:n:24:GLY:H	44:n:61:LEU:HA	1.83	0.43
1:1:285:G:C6	1:1:356:G:C6	3.06	0.43
1:1:372:G:O2'	1:1:400:G:N1	2.51	0.43
1:1:764:A:H5''	8:B:209:GLY:HA2	1.99	0.43
1:1:833:A:H2'	1:1:834:G:C8	2.52	0.43
1:1:1071:G:H1'	1:1:1089:A:C8	2.54	0.43
1:1:1159:U:C2	1:1:1160:G:C8	3.07	0.43
1:1:1183:U:H2'	1:1:1184:U:C6	2.54	0.43
1:1:1443:U:H2'	1:1:1444:G:H8	1.84	0.43
1:1:1902:C:H4'	8:B:242:LYS:O	2.18	0.43
1:1:2262:U:H2'	1:1:2263:C:H6	1.82	0.43
2:2:604:G:H2'	2:2:605:U:O4'	2.18	0.43
2:2:1073:U:C2	2:2:1074:G:C8	3.07	0.43
2:2:1193:G:O6	38:h:3:GLN:NE2	2.43	0.43
2:2:1513:A:H2'	2:2:1514:G:C8	2.52	0.43
7:A:54:LYS:HB3	7:A:57:GLN:CD	2.43	0.43
17:M:40:ARG:HB2	17:M:93:VAL:HG13	2.01	0.43
33:c:8:LYS:HB3	33:c:24:THR:HG22	1.99	0.43
44:n:84:THR:HG21	44:n:103:PHE:HB3	2.00	0.43
1:1:156:A:H2'	1:1:157:C:C6	2.52	0.43
1:1:329:G:OP2	25:U:69:ASN:ND2	2.44	0.43
1:1:1093:G:H2'	1:1:1094:U:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1220:G:C2	1:1:1230:A:C2	3.06	0.43
1:1:1328:A:H2'	1:1:1330:C:C4	2.54	0.43
1:1:1567:G:OP2	8:B:83:TYR:OH	2.25	0.43
1:1:2092:U:OP1	1:1:2199:A:O2'	2.33	0.43
1:1:2259:U:C6	1:1:2427:C:C4	3.07	0.43
1:1:2267:A:H5''	1:1:2268:A:H5'	2.01	0.43
2:2:407:U:H2'	2:2:408:A:C8	2.53	0.43
2:2:528:C:H41	47:q:46:ASN:ND2	2.17	0.43
6:6:163:LYS:HB3	6:6:163:LYS:HE2	1.80	0.43
7:A:27:ILE:O	7:A:30:LEU:HG	2.18	0.43
13:G:3:VAL:CG2	13:G:36:ALA:HB1	2.49	0.43
15:K:76:VAL:H	20:P:73:VAL:HG22	1.83	0.43
15:K:79:PHE:CD1	20:P:70:VAL:HG22	2.54	0.43
43:m:75:ILE:HG22	43:m:129:VAL:HG13	1.99	0.43
47:q:30:LYS:HD3	47:q:30:LYS:HA	1.85	0.43
53:w:30:LYS:HB2	53:w:30:LYS:HE3	1.81	0.43
1:1:372:G:HO2'	1:1:400:G:H1	1.65	0.43
1:1:667:U:H2'	1:1:668:A:O4'	2.18	0.43
1:1:2215:C:H2'	1:1:2216:G:C8	2.53	0.43
1:1:2292:U:H2'	1:1:2293:G:C8	2.54	0.43
2:2:255:G:H2'	2:2:256:U:C6	2.52	0.43
2:2:488:C:H2'	2:2:489:C:C6	2.53	0.43
2:2:539:A:H2'	2:2:540:G:H8	1.82	0.43
2:2:664:G:P	53:w:53:ARG:HH21	2.41	0.43
2:2:767:A:H2'	2:2:768:A:O4'	2.18	0.43
2:2:1144:G:N2	2:2:1146:A:H62	2.16	0.43
2:2:1187:G:H5'	44:n:115:LYS:HE3	2.01	0.43
12:F:86:LYS:HG2	12:F:132:VAL:HG22	2.01	0.43
41:k:20:GLY:O	41:k:23:GLU:HG3	2.19	0.43
42:l:20:SER:OG	42:l:23:LEU:HB3	2.19	0.43
52:v:13:VAL:O	52:v:55:ILE:HG23	2.19	0.43
56:z:59:LYS:HD2	56:z:59:LYS:C	2.44	0.43
1:1:248:G:H5'	1:1:250:G:N7	2.33	0.43
1:1:682:G:H5'	34:d:26:ASN:CG	2.44	0.43
1:1:1239:G:H2'	1:1:1240:U:O4'	2.18	0.43
1:1:1268:A:H2'	1:1:1269:A:O4'	2.19	0.43
1:1:1594:U:H2'	1:1:1595:C:C6	2.54	0.43
1:1:2109:U:C5'	59:1:3449:HOH:O	2.44	0.43
1:1:2842:G:H2'	1:1:2843:G:O4'	2.19	0.43
2:2:575:G:O2'	2:2:821:G:OP2	2.27	0.43
7:A:165:ASN:HD21	7:A:167:LYS:HE2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:106:ALA:O	8:B:196:GLY:N	2.50	0.43
13:G:101:ASP:HA	13:G:104:THR:OG1	2.18	0.43
45:o:81:GLU:OE2	45:o:81:GLU:N	2.47	0.43
1:1:175:G:H2'	1:1:176:A:C8	2.54	0.43
1:1:704:G:H1'	1:1:727:A:H61	1.83	0.43
1:1:1062:G:OP1	1:1:1070:A:H5'	2.19	0.43
1:1:1283:G:H22	1:1:1286:A:P	2.41	0.43
1:1:1721:G:H1'	1:1:1739:A:N6	2.34	0.43
1:1:2060:A:O2'	1:1:2061:G:OP2	2.37	0.43
1:1:2229:U:O2	28:X:34:HIS:HE1	2.01	0.43
1:1:2287:A:N7	1:1:2289:G:C8	2.87	0.43
1:1:2554:U:H2'	1:1:2555:U:C6	2.54	0.43
2:2:254:G:O3'	52:v:71:LYS:NZ	2.52	0.43
2:2:890:G:O2'	2:2:906:A:N6	2.52	0.43
2:2:1354:U:H2'	2:2:1355:G:H8	1.82	0.43
2:2:1521:C:H2'	2:2:1522:U:H6	1.82	0.43
6:6:40:ARG:HD3	59:6:201:HOH:O	2.18	0.43
6:6:90:PHE:HB2	7:A:141:LYS:HE2	1.99	0.43
6:6:115:VAL:HG23	6:6:125:VAL:HG22	2.00	0.43
6:6:139:ASP:O	6:6:140:PRO:C	2.61	0.43
7:A:9:ARG:NH1	7:A:10:VAL:HG22	2.34	0.43
15:K:123:LEU:HD12	15:K:123:LEU:HA	1.74	0.43
26:V:55:GLU:O	26:V:59:GLU:HG2	2.19	0.43
37:g:57:LEU:HD23	37:g:57:LEU:HA	1.88	0.43
45:o:15:HIS:O	45:o:18:ILE:HG22	2.19	0.43
1:1:84:A:H4'	1:1:85:G:O5'	2.18	0.43
1:1:548:G:H8	1:1:548:G:O5'	2.02	0.43
1:1:714:U:H5''	50:t:88:ARG:NH2	2.34	0.43
1:1:1028:A:N6	1:1:1125:G:H2'	2.33	0.43
1:1:1115:G:H2'	1:1:1116:G:H8	1.84	0.43
1:1:1273:U:H4'	1:1:1275:A:OP1	2.19	0.43
1:1:1773:A:N7	1:1:1829:A:H1'	2.34	0.43
1:1:1790:C:H2'	1:1:1791:A:C5	2.54	0.43
1:1:1818:U:O4	8:B:153:GLN:HG2	2.19	0.43
1:1:1954:G:O2'	1:1:1956:U:O4	2.26	0.43
1:1:2305:U:H5''	11:E:131:GLY:HA3	2.01	0.43
1:1:2638:G:O2'	1:1:2639:A:H8	2.01	0.43
1:1:2705:A:O2'	1:1:2852:G:OP1	2.29	0.43
1:1:2849:U:OP1	20:P:93:ARG:NH2	2.49	0.43
2:2:22:G:H2'	2:2:23:C:C6	2.54	0.43
2:2:154:U:H2'	2:2:155:A:H8	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:458:U:H3	2:2:474:G:H1	1.67	0.43
6:6:3:THR:HA	6:6:63:GLU:HA	2.00	0.43
8:B:160:THR:O	8:B:195:VAL:HG22	2.19	0.43
14:J:4:PHE:O	21:Q:64:ARG:NH2	2.51	0.43
25:U:9:ASP:O	25:U:25:VAL:HG12	2.18	0.43
28:X:12:PRO:HB3	28:X:30:LEU:HD23	2.00	0.43
37:g:4:VAL:HG11	37:g:212:LEU:HD21	2.01	0.43
37:g:31:ILE:HG21	37:g:39:HIS:CD2	2.46	0.43
38:h:59:ARG:HB3	38:h:64:ILE:HD13	2.00	0.43
41:k:2:ARG:HH11	41:k:68:GLN:NE2	2.17	0.43
45:o:59:LYS:HE2	45:o:62:ARG:NH2	2.30	0.43
1:1:192:C:O2	1:1:802:A:O2'	2.35	0.42
1:1:279:A:H2'	1:1:280:U:O4'	2.18	0.42
1:1:1329:U:HO2'	1:1:1330:C:P	2.39	0.42
2:2:174:A:C5	2:2:175:C:C5	3.07	0.42
2:2:1329:A:H2'	2:2:1330:U:O4'	2.19	0.42
3:3:29:A:H2'	3:3:30:C:C6	2.53	0.42
7:A:106:LYS:O	7:A:106:LYS:HG2	2.19	0.42
16:L:59:ARG:HA	35:e:13:ARG:NH2	2.34	0.42
27:W:33:ALA:N	27:W:64:ASP:OD1	2.52	0.42
28:X:77:LYS:HA	28:X:77:LYS:HD3	1.95	0.42
30:Z:12:SER:OG	30:Z:13:ALA:N	2.51	0.42
47:q:98:VAL:HG23	47:q:101:ALA:HB3	1.99	0.42
48:r:66:GLU:O	48:r:70:ARG:HG3	2.19	0.42
49:s:7:LYS:O	49:s:11:VAL:HG23	2.19	0.42
1:1:197:A:H2	1:1:2434:A:H62	1.67	0.42
1:1:849:A:H2'	1:1:850:U:C6	2.54	0.42
1:1:1047:G:H2'	1:1:1110:G:N2	2.34	0.42
1:1:1112:G:H2'	1:1:1113:U:C6	2.54	0.42
1:1:2079:U:C2	1:1:2080:A:C8	3.07	0.42
1:1:2102:G:H22	1:1:2187:U:HO2'	1.57	0.42
1:1:2345:G:N3	1:1:2381:A:H2'	2.33	0.42
1:1:2804:U:H2'	1:1:2805:C:C6	2.54	0.42
2:2:1039:G:H2'	2:2:1040:U:C6	2.54	0.42
2:2:1101:A:H4'	2:2:1102:A:O5'	2.19	0.42
2:2:1149:C:OP1	44:n:11:ARG:NH2	2.52	0.42
10:D:24:ASN:O	10:D:28:VAL:HG12	2.19	0.42
37:g:75:ALA:HB1	37:g:207:ILE:HG13	2.01	0.42
1:1:570:G:H2'	1:1:2030:A:N7	2.33	0.42
1:1:640:C:H2'	1:1:641:U:C6	2.54	0.42
1:1:700:G:O2'	1:1:1632:A:N3	2.41	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1619:G:C2	1:1:1620:G:C8	3.08	0.42
1:1:2104:U:N3	1:1:2186:G:C6	2.87	0.42
1:1:2783:U:H2'	1:1:2784:U:C6	2.54	0.42
2:2:430:A:OP1	39:i:9:LEU:HG	2.19	0.42
2:2:684:U:H2'	2:2:685:G:O4'	2.19	0.42
2:2:1171:A:H2'	2:2:1172:C:C6	2.53	0.42
3:3:18:G:H2'	3:3:19:C:C6	2.55	0.42
11:E:35:THR:HB	11:E:155:THR:OG1	2.18	0.42
11:E:40:VAL:HG23	11:E:43:ALA:HB2	2.01	0.42
21:Q:49:ASP:HA	21:Q:52:GLN:HB2	2.01	0.42
30:Z:31:ARG:HG3	30:Z:32:ILE:O	2.19	0.42
37:g:117:LEU:HD23	37:g:117:LEU:HA	1.77	0.42
39:i:9:LEU:HD13	39:i:32:CYS:HB3	2.02	0.42
46:p:18:ASP:HB3	46:p:81:ASN:HB2	2.01	0.42
47:q:94:ARG:HB2	47:q:95:TYR:CE2	2.53	0.42
50:t:8:THR:O	50:t:12:VAL:HG12	2.19	0.42
1:1:623:C:H2'	1:1:624:C:H6	1.84	0.42
1:1:804:A:H2'	1:1:806:C:C4	2.54	0.42
1:1:1255:U:C5	10:D:68:ALA:HA	2.53	0.42
1:1:1775:U:O4	1:1:1789:A:H2	2.02	0.42
1:1:2430:A:H5'	1:1:2431:U:OP2	2.19	0.42
1:1:2620:C:O2'	9:C:162:ALA:O	2.30	0.42
2:2:501:C:H1'	2:2:549:C:H1'	2.01	0.42
2:2:1060:U:H2'	2:2:1061:G:H8	1.84	0.42
18:N:98:LEU:HB2	18:N:112:TYR:HB2	2.00	0.42
22:R:37:GLU:HG3	22:R:53:PHE:CG	2.54	0.42
38:h:150:LYS:O	38:h:201:TRP:HD1	2.03	0.42
1:1:352:A:H2'	1:1:353:C:H6	1.85	0.42
1:1:1338:G:O2'	1:1:1393:A:N1	2.43	0.42
1:1:1664:A:C2	15:K:1:MET:HE1	2.54	0.42
1:1:1786:A:H1'	1:1:1938:A:N6	2.35	0.42
2:2:94:G:H4'	2:2:95:C:O5'	2.19	0.42
2:2:704:A:C4	2:2:705:G:C8	3.08	0.42
2:2:847:G:H2'	2:2:848:C:C6	2.55	0.42
2:2:865:A:H2'	2:2:866:C:C6	2.55	0.42
5:5:2:G:O2'	5:5:3:G:H8	2.01	0.42
7:A:208:TYR:CG	7:A:209:ILE:N	2.87	0.42
16:L:81:ASP:HB3	16:L:100:ILE:HD13	2.01	0.42
19:O:56:LYS:HE2	19:O:60:GLU:HG3	2.01	0.42
23:S:83:LYS:HG2	23:S:97:LEU:HD13	2.01	0.42
45:o:30:LYS:HE3	45:o:30:LYS:HB2	1.93	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:q:82:ILE:HG23	47:q:95:TYR:HB3	2.01	0.42
1:1:532:A:H2'	1:1:532:A:N3	2.35	0.42
1:1:592:A:H2	35:e:4:ILE:HD11	1.83	0.42
1:1:723:C:H2'	1:1:724:U:O4'	2.20	0.42
1:1:729:G:H5''	1:1:730:A:C5'	2.45	0.42
1:1:1614:A:C2	23:S:93:ALA:HB2	2.55	0.42
1:1:1726:C:N4	1:1:1735:A:H61	2.17	0.42
1:1:2037:A:H2'	1:1:2038:G:C8	2.54	0.42
1:1:2191:A:O2'	1:1:2192:U:O4'	2.16	0.42
1:1:2294:G:N1	1:1:2339:C:N3	2.68	0.42
2:2:80:A:H2'	2:2:81:A:C8	2.54	0.42
2:2:748:G:O6	2:2:749:A:N6	2.52	0.42
2:2:963:G:H21	45:o:57:VAL:HG11	1.85	0.42
6:6:134:GLU:HG2	6:6:135:ILE:N	2.34	0.42
8:B:157:SER:O	8:B:195:VAL:HG21	2.19	0.42
32:b:55:ILE:HG13	32:b:55:ILE:O	2.19	0.42
33:c:55:LYS:HD3	33:c:55:LYS:HA	1.87	0.42
37:g:70:VAL:HG13	37:g:163:VAL:HA	2.02	0.42
37:g:129:LEU:HB2	37:g:133:GLU:OE2	2.20	0.42
44:n:65:ILE:HD13	44:n:79:ILE:HG23	2.02	0.42
45:o:8:ILE:HD13	45:o:100:ILE:HA	2.01	0.42
46:p:64:GLN:HB3	46:p:95:SER:OG	2.20	0.42
49:s:98:LYS:HE2	49:s:98:LYS:HB3	1.84	0.42
50:t:24:SER:OG	50:t:27:VAL:HG23	2.20	0.42
1:1:77:G:H2'	1:1:78:U:C6	2.55	0.42
1:1:1675:C:O2	9:C:133:THR:HG22	2.20	0.42
1:1:1771:C:H2'	1:1:1772:A:H8	1.84	0.42
1:1:2193:G:O2'	1:1:2194:U:H5''	2.19	0.42
1:1:2220:U:H2'	1:1:2221:G:H8	1.85	0.42
1:1:2537:U:H2'	1:1:2538:C:C6	2.55	0.42
1:1:2591:C:H2'	1:1:2592:G:H8	1.83	0.42
1:1:2691:C:H2'	1:1:2692:G:H8	1.85	0.42
1:1:2723:C:OP1	9:C:114:LYS:NZ	2.36	0.42
2:2:1192:C:OP2	38:h:4:LYS:NZ	2.49	0.42
2:2:1473:G:H2'	2:2:1474:U:O4'	2.20	0.42
3:3:42:C:C6	11:E:66:LEU:HB2	2.54	0.42
9:C:73:VAL:HG12	9:C:74:GLU:O	2.19	0.42
11:E:58:ALA:HB2	11:E:65:PRO:HD3	2.01	0.42
13:G:40:THR:O	13:G:44:ILE:HG13	2.19	0.42
37:g:64:LYS:NZ	59:g:303:HOH:O	2.53	0.42
39:i:197:GLU:O	39:i:201:VAL:HG13	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:j:44:GLY:HA2	40:j:74:VAL:HB	2.01	0.42
42:l:72:THR:H	42:l:142:HIS:HE1	1.64	0.42
56:z:29:LEU:O	56:z:33:ARG:HG3	2.20	0.42
1:1:752:A:H3'	34:d:1:MET:SD	2.60	0.42
1:1:934:U:H2'	1:1:935:C:H6	1.85	0.42
1:1:1027:A:C6	1:1:1126:A:C4	3.08	0.42
1:1:1283:G:N2	1:1:1285:A:H3'	2.34	0.42
1:1:1536:C:H5''	1:1:1537:G:C2	2.54	0.42
1:1:2126:A:H3'	7:A:38:PHE:HB2	2.02	0.42
1:1:2333:A:P	27:W:77:ARG:HH22	2.43	0.42
1:1:2691:C:C4	1:1:2719:G:N2	2.88	0.42
1:1:2831:G:OP2	9:C:59:ARG:HD3	2.20	0.42
2:2:9:G:OP2	40:j:126:LYS:NZ	2.36	0.42
2:2:497:G:H2'	2:2:498:A:C8	2.54	0.42
2:2:590:U:H2'	2:2:591:U:C6	2.55	0.42
2:2:620:C:H1'	39:i:132:ILE:HG21	2.01	0.42
2:2:1250:A:OP1	44:n:69:GLY:N	2.46	0.42
2:2:1374:A:N1	2:2:1375:A:C2	2.88	0.42
3:3:73:A:H2'	3:3:74:U:C5	2.55	0.42
10:D:98:LYS:O	10:D:102:ARG:HG3	2.19	0.42
18:N:106:ASP:O	18:N:107:ASN:C	2.63	0.42
41:k:4:TYR:CE1	41:k:71:ILE:HG13	2.54	0.42
41:k:101:PRO:HA	41:k:104:LYS:NZ	2.34	0.42
49:s:73:PHE:CZ	49:s:78:GLY:HA2	2.55	0.42
52:v:49:GLU:C	52:v:51:ASN:N	2.77	0.42
53:w:13:PHE:HA	53:w:16:GLU:HG2	2.02	0.42
54:x:41:PHE:H	54:x:44:MET:HE3	1.83	0.42
1:1:1172:C:H2'	1:1:1173:U:O4'	2.20	0.42
1:1:1722:A:N6	1:1:1738:G:H1'	2.35	0.42
1:1:2190:G:O2'	1:1:2191:A:OP1	2.33	0.42
2:2:1077:G:N1	2:2:1080:A:OP2	2.52	0.42
2:2:1441:A:H2'	2:2:1441:A:N3	2.34	0.42
6:6:90:PHE:HB2	7:A:141:LYS:CE	2.50	0.42
9:C:186:LEU:HD21	20:P:4:ILE:HG21	2.02	0.42
17:M:21:ALA:HB1	17:M:100:LYS:HB2	2.02	0.42
17:M:49:ALA:O	17:M:53:MET:HG2	2.19	0.42
19:O:26:LEU:HD23	19:O:92:PHE:HD1	1.85	0.42
25:U:14:LEU:HD11	25:U:71:ALA:HB2	2.01	0.42
31:a:18:CYS:SG	31:a:40:CYS:HB3	2.60	0.42
51:u:18:GLN:OE1	51:u:35:ARG:NE	2.32	0.42
1:1:6:A:N3	14:J:135:GLN:NE2	2.64	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:181:A:H2'	1:1:182:A:H8	1.85	0.42
1:1:481:G:O2'	1:1:482:A:P	2.77	0.42
1:1:679:C:H2'	1:1:680:C:C6	2.55	0.42
1:1:1133:A:H4'	1:1:1134:A:H5''	2.02	0.42
1:1:1589:U:H2'	1:1:1590:A:C8	2.53	0.42
1:1:1591:A:H2'	1:1:1592:C:C6	2.54	0.42
1:1:2295:C:O2'	1:1:2296:U:H5'	2.19	0.42
1:1:2813:A:C4	1:1:2814:A:C8	3.08	0.42
2:2:202:G:O2'	2:2:468:A:H2'	2.19	0.42
2:2:844:G:H3'	2:2:844:G:N3	2.35	0.42
2:2:860:A:H2'	2:2:861:G:O4'	2.20	0.42
6:6:76:TYR:HE2	7:A:133:PRO:HB2	1.85	0.42
7:A:214:ILE:HA	7:A:223:ALA:O	2.20	0.42
10:D:196:VAL:HA	10:D:199:MET:HG2	2.02	0.42
13:G:32:PRO:HA	28:X:39:TRP:CD1	2.54	0.42
18:N:92:GLY:HA2	18:N:94:TYR:CZ	2.55	0.42
37:g:81:LYS:HD2	37:g:91:PHE:CE2	2.55	0.42
39:i:100:ASN:O	39:i:104:ARG:HG2	2.19	0.42
52:v:47:HIS:HB2	52:v:71:LYS:HD3	2.01	0.42
54:x:62:VAL:HA	54:x:66:MET:SD	2.59	0.42
56:z:7:ARG:HB2	56:z:10:GLU:HB2	2.02	0.42
56:z:69:ARG:CZ	56:z:69:ARG:HB3	2.48	0.42
1:1:704:G:C2	1:1:726:G:C2	3.08	0.41
1:1:1223:G:C6	1:1:1227:G:C6	3.08	0.41
1:1:1599:U:C2	1:1:1600:C:C5	3.08	0.41
1:1:2515:C:H2'	1:1:2516:A:H8	1.85	0.41
1:1:2574:G:H2'	1:1:2575:C:O4'	2.20	0.41
1:1:2745:C:H2'	1:1:2746:U:C6	2.54	0.41
1:1:2869:G:H2'	1:1:2870:C:O4'	2.20	0.41
1:1:2899:A:H2'	1:1:2900:A:H8	1.84	0.41
2:2:405:U:OP2	39:i:3:ARG:NH2	2.53	0.41
2:2:451:A:H4'	2:2:452:A:O4'	2.20	0.41
2:2:838:G:C5	2:2:849:G:N1	2.88	0.41
2:2:1087:G:H21	56:z:71:TYR:HA	1.84	0.41
6:6:165:PRO:HD2	6:6:168:VAL:CG2	2.50	0.41
28:X:5:CYS:HA	28:X:33:LEU:HD11	2.02	0.41
31:a:11:GLU:O	31:a:12:ILE:HD13	2.20	0.41
31:a:45:THR:O	31:a:49:ARG:NE	2.53	0.41
33:c:42:VAL:HG13	33:c:43:VAL:HG13	2.02	0.41
39:i:95:GLU:OE2	39:i:104:ARG:NH1	2.53	0.41
50:t:66:LEU:HA	50:t:66:LEU:HD23	1.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:w:34:THR:HG23	53:w:36:SER:N	2.32	0.41
1:1:5:A:H2'	1:1:6:A:H8	1.84	0.41
1:1:412:A:N7	1:1:2412:A:H1'	2.34	0.41
1:1:1086:A:O2'	1:1:1087:G:N7	2.51	0.41
1:1:1246:A:H4'	10:D:40:ARG:HH12	1.85	0.41
1:1:1992:G:N2	1:1:1996:C:O2'	2.52	0.41
1:1:2215:C:H2'	1:1:2216:G:H8	1.85	0.41
1:1:2290:G:H2'	1:1:2291:U:H6	1.85	0.41
2:2:1296:C:H4'	2:2:1302:C:H41	1.85	0.41
6:6:108:LEU:HD12	6:6:108:LEU:HA	1.87	0.41
7:A:71:ARG:NH1	7:A:73:VAL:O	2.53	0.41
8:B:21:ASN:HB3	8:B:24:LEU:HG	2.02	0.41
14:J:9:GLU:N	14:J:9:GLU:OE2	2.53	0.41
15:K:40:LYS:NZ	15:K:89:ASN:HD21	2.18	0.41
18:N:2:ARG:O	18:N:3:HIS:C	2.62	0.41
19:O:29:HIS:HA	19:O:97:PHE:HE2	1.86	0.41
21:Q:83:LEU:HD23	21:Q:83:LEU:HA	1.85	0.41
29:Y:37:LEU:HD12	29:Y:37:LEU:HA	1.86	0.41
48:r:9:ILE:CG2	48:r:18:ALA:HB1	2.50	0.41
49:s:34:VAL:HG23	49:s:35:ASN:ND2	2.35	0.41
54:x:51:VAL:CG1	54:x:75:ALA:HB2	2.50	0.41
1:1:24:G:H2'	1:1:25:U:H6	1.85	0.41
1:1:33:C:O2'	1:1:34:U:O5'	2.32	0.41
1:1:458:G:HO2'	1:1:469:G:H1	1.67	0.41
1:1:1061:U:H4'	1:1:1070:A:C4	2.55	0.41
1:1:1450:G:H21	1:1:1452:G:H1	1.66	0.41
1:1:2024:G:H2'	1:1:2025:C:O4'	2.20	0.41
1:1:2405:G:HO2'	1:1:2406:A:P	2.43	0.41
1:1:2792:A:H2'	1:1:2793:C:O4'	2.21	0.41
2:2:58:C:O2	2:2:58:C:H2'	2.20	0.41
2:2:352:C:O2'	2:2:354:G:OP1	2.31	0.41
2:2:560:A:H5'	2:2:566:G:N2	2.35	0.41
2:2:640:A:N6	2:2:641:U:O4	2.53	0.41
2:2:1055:A:C6	2:2:1206:G:C5	3.08	0.41
2:2:1477:U:H2'	2:2:1478:U:H6	1.85	0.41
2:2:1486:G:H2'	2:2:1487:G:O4'	2.20	0.41
7:A:55:SER:O	7:A:57:GLN:N	2.52	0.41
11:E:147:ASP:OD1	11:E:147:ASP:N	2.51	0.41
37:g:27:MET:HE3	37:g:27:MET:HB3	1.82	0.41
37:g:118:GLU:HG3	37:g:119:THR:N	2.35	0.41
40:j:148:ASN:HD22	40:j:152:MET:HE2	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:n:18:ARG:HG3	44:n:66:THR:HG23	2.03	0.41
53:w:43:ARG:HE	53:w:43:ARG:HB2	1.58	0.41
1:1:695:G:O6	1:1:767:U:C2	2.74	0.41
1:1:974:G:C6	1:1:1186:G:C6	3.09	0.41
1:1:1069:A:H4'	1:1:1070:A:H8	1.86	0.41
1:1:1499:C:C2	1:1:1500:G:C8	3.08	0.41
1:1:2305:U:C2	11:E:151:GLY:HA3	2.55	0.41
1:1:2578:G:H21	9:C:130:GLN:NE2	2.19	0.41
1:1:2619:C:O2'	9:C:161:MET:HE3	2.19	0.41
2:2:461:A:C4	2:2:462:G:C8	3.09	0.41
2:2:568:G:O2'	2:2:574:A:N1	2.49	0.41
2:2:594:U:H2'	2:2:595:A:O4'	2.20	0.41
2:2:838:G:H2'	2:2:839:C:C6	2.55	0.41
2:2:1111:A:N1	38:h:177:THR:OG1	2.53	0.41
2:2:1375:A:OP1	42:l:25:LYS:NZ	2.32	0.41
2:2:1518:MA6:H103	2:2:1519:MA6:H102	2.02	0.41
2:2:1532:U:H2'	2:2:1533:C:C6	2.56	0.41
3:3:29:A:H2'	3:3:30:C:O4'	2.20	0.41
5:5:9:A:O2'	5:5:10:G:N7	2.53	0.41
7:A:198:LYS:HD2	7:A:198:LYS:HA	1.84	0.41
10:D:28:VAL:O	10:D:32:VAL:HG23	2.20	0.41
13:G:75:LEU:H	13:G:75:LEU:HD23	1.85	0.41
23:S:66:ILE:H	23:S:66:ILE:HD12	1.85	0.41
26:V:48:MET:SD	26:V:86:LEU:HG	2.61	0.41
33:c:36:LEU:HD23	33:c:36:LEU:HA	1.95	0.41
39:i:13:ARG:NH2	39:i:38:PRO:HA	2.35	0.41
39:i:47:ARG:HG2	39:i:47:ARG:HH11	1.86	0.41
43:m:40:LEU:HD23	43:m:40:LEU:HA	1.90	0.41
44:n:12:ARG:NH2	44:n:109:ARG:HH21	2.15	0.41
44:n:60:LYS:O	44:n:61:LEU:HD23	2.20	0.41
49:s:96:LEU:HD23	49:s:97:LYS:N	2.34	0.41
1:1:3:U:H2'	1:1:4:U:C6	2.56	0.41
1:1:247:G:OP2	1:1:249:C:N4	2.50	0.41
1:1:679:C:H2'	1:1:680:C:H6	1.86	0.41
1:1:1060:U:H4'	59:1:3537:HOH:O	2.20	0.41
1:1:1182:G:H2'	1:1:1183:U:O4'	2.20	0.41
1:1:1447:C:H2'	1:1:1448:G:H8	1.86	0.41
1:1:1666:G:H4'	15:K:6:THR:HG23	2.02	0.41
1:1:2542:A:H5''	1:1:2766:A:O2'	2.21	0.41
2:2:352:C:O2	2:2:355:C:N4	2.50	0.41
7:A:47:ASN:HB2	7:A:212:VAL:HG22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:L:29:LYS:HG3	16:L:30:THR:HG23	2.01	0.41
29:Y:22:LEU:HD23	29:Y:22:LEU:HA	1.79	0.41
37:g:5:SER:OG	37:g:7:ARG:HG2	2.20	0.41
40:j:149:SER:O	40:j:153:VAL:HG23	2.21	0.41
46:p:58:SER:O	46:p:91:PRO:HG2	2.21	0.41
48:r:113:ARG:H	48:r:113:ARG:HG2	1.64	0.41
54:x:45:ILE:HA	54:x:62:VAL:HG12	2.03	0.41
1:1:163:C:H2'	1:1:164:C:C6	2.56	0.41
1:1:228:C:O2'	1:1:229:C:P	2.79	0.41
1:1:971:G:OP1	1:1:974:G:O2'	2.20	0.41
1:1:1281:G:H2'	1:1:1282:U:C6	2.56	0.41
1:1:2126:A:N1	1:1:2163:A:H1'	2.35	0.41
2:2:211:G:C5	2:2:212:G:H1'	2.56	0.41
2:2:438:U:C4	2:2:494:G:C5	3.08	0.41
7:A:201:PRO:HG2	7:A:203:GLN:OE1	2.20	0.41
9:C:21:SER:O	9:C:21:SER:OG	2.37	0.41
10:D:97:ASN:HB2	10:D:100:MET:HG3	2.01	0.41
21:Q:97:ASP:OD1	21:Q:98:ILE:N	2.54	0.41
26:V:34:LYS:HG2	59:V:204:HOH:O	2.19	0.41
38:h:7:PRO:HB3	38:h:182:ILE:HD11	2.03	0.41
41:k:3:HIS:CD2	41:k:65:GLU:HB2	2.56	0.41
44:n:116:VAL:HG21	45:o:62:ARG:HD2	2.03	0.41
52:v:26:GLU:HB3	52:v:41:THR:HG22	2.03	0.41
53:w:65:LEU:HD23	53:w:65:LEU:HA	1.92	0.41
1:1:271:G:C6	1:1:367:G:N1	2.88	0.41
1:1:935:C:H2'	1:1:936:A:C8	2.52	0.41
1:1:1419:A:C8	1:1:1579:A:N6	2.89	0.41
1:1:2114:A:N3	59:1:3422:HOH:O	2.36	0.41
1:1:2118:U:H5'	59:1:3460:HOH:O	2.19	0.41
2:2:113:G:H1'	2:2:354:G:H5'	2.02	0.41
2:2:375:U:O2'	51:u:6:LEU:O	2.38	0.41
2:2:459:A:H2'	2:2:460:A:H8	1.85	0.41
2:2:768:A:N3	2:2:1512:U:O2'	2.53	0.41
2:2:1299:A:N3	2:2:1299:A:H2'	2.36	0.41
2:2:1383:C:O2'	2:2:1384:C:OP1	2.34	0.41
5:5:2:G:H4'	5:5:3:G:OP1	2.20	0.41
7:A:47:ASN:HD22	7:A:211:LYS:HD2	1.84	0.41
11:E:175:PHE:HD2	11:E:177:PHE:HD1	1.69	0.41
11:E:175:PHE:HA	11:E:176:PRO:HD3	1.87	0.41
18:N:103:ARG:HD3	18:N:110:MET:HE2	2.02	0.41
20:P:111:LYS:HB2	20:P:111:LYS:HE2	1.78	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:R:6:GLN:HA	22:R:11:GLN:HA	2.03	0.41
31:a:8:LYS:HB3	31:a:8:LYS:HE2	1.86	0.41
37:g:60:ILE:HD12	37:g:60:ILE:HA	1.93	0.41
38:h:116:VAL:HG23	38:h:200:VAL:HG21	2.01	0.41
41:k:22:ILE:HG23	41:k:39:LEU:HD11	2.03	0.41
41:k:51:ILE:O	41:k:54:LEU:HG	2.20	0.41
51:u:40:ASN:HD22	51:u:43:ALA:HB2	1.85	0.41
1:1:5:A:H2'	1:1:6:A:C8	2.56	0.41
1:1:598:U:H2'	1:1:599:A:H8	1.86	0.41
1:1:741:U:H2'	1:1:742:A:C8	2.56	0.41
1:1:1071:G:H1	1:1:1092:C:H41	1.68	0.41
1:1:1079:C:C2	1:1:1080:A:C8	3.08	0.41
1:1:2040:G:H2'	1:1:2041:U:O4'	2.21	0.41
1:1:2321:U:H5''	1:1:2322:A:OP2	2.21	0.41
2:2:84:U:H2'	2:2:86:G:N2	2.36	0.41
2:2:469:C:H2'	2:2:470:C:O4'	2.21	0.41
2:2:1004:A:OP1	2:2:1024:G:N1	2.41	0.41
2:2:1120:C:C2	2:2:1121:U:C5	3.08	0.41
3:3:29:A:OP2	19:O:32:PRO:HD2	2.20	0.41
7:A:48:LEU:HD12	7:A:49:GLY:N	2.35	0.41
10:D:48:THR:HG23	10:D:86:ALA:HB3	2.02	0.41
12:F:69:ARG:NH1	12:F:73:ASN:HD22	2.18	0.41
13:G:30:LEU:HB3	13:G:36:ALA:HB3	2.02	0.41
29:Y:14:LEU:HD23	29:Y:14:LEU:HA	1.92	0.41
37:g:74:ARG:HA	37:g:74:ARG:HE	1.85	0.41
41:k:21:MET:HB3	41:k:24:ARG:NH2	2.36	0.41
43:m:32:LEU:O	43:m:36:ILE:HG12	2.21	0.41
1:1:62:U:O2	1:1:62:U:H2'	2.20	0.41
1:1:128:C:H2'	1:1:129:C:H6	1.86	0.41
1:1:217:A:H2'	1:1:218:A:C8	2.55	0.41
1:1:242:G:H5''	35:e:64:TYR:CE2	2.56	0.41
1:1:365:U:H2'	1:1:366:C:C6	2.56	0.41
1:1:743:A:OP1	9:C:135:GLY:HA2	2.20	0.41
1:1:753:A:H2'	1:1:754:U:C6	2.56	0.41
1:1:1005:C:C2	1:1:1006:C:C5	3.09	0.41
1:1:1198:U:C2	1:1:1199:U:C5	3.09	0.41
1:1:1278:C:H2'	1:1:1279:G:H8	1.84	0.41
1:1:1292:G:H2'	1:1:1293:C:H6	1.86	0.41
1:1:1387:A:H2'	1:1:1388:G:H8	1.85	0.41
1:1:1710:G:H2'	1:1:1711:A:H8	1.85	0.41
1:1:1932:A:H2'	1:1:1933:G:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2093:G:N7	1:1:2225:A:H2'	2.36	0.41
1:1:2108:A:H8	1:1:2108:A:OP2	2.04	0.41
1:1:2287:A:C8	1:1:2289:G:C8	3.09	0.41
1:1:2331:G:O2'	1:1:2336:A:N1	2.48	0.41
1:1:2341:G:H2'	1:1:2342:C:C6	2.56	0.41
1:1:2414:G:C2	1:1:2415:G:C8	3.09	0.41
1:1:2513:A:C6	1:1:2574:G:C6	3.09	0.41
2:2:186:C:C2	2:2:187:G:C8	3.09	0.41
2:2:193:C:H2'	2:2:194:C:H6	1.86	0.41
2:2:836:G:C5	2:2:851:G:C6	3.09	0.41
2:2:1248:A:H2	44:n:72:ILE:HD11	1.86	0.41
2:2:1490:U:H2'	2:2:1491:G:O4'	2.20	0.41
5:5:3:G:O2'	5:5:4:C:H2'	2.21	0.41
6:6:173:VAL:HB	6:6:187:VAL:HG13	2.02	0.41
7:A:57:GLN:HA	7:A:202:THR:HB	2.02	0.41
7:A:94:LEU:CD2	7:A:100:LEU:HB2	2.51	0.41
8:B:181:MET:HE3	8:B:181:MET:HB3	1.82	0.41
10:D:80:SER:O	10:D:80:SER:OG	2.31	0.41
10:D:188:MET:HE1	10:D:196:VAL:HG21	2.02	0.41
11:E:9:LYS:HE2	11:E:9:LYS:HB3	1.84	0.41
11:E:139:PRO:HB2	31:a:32:LEU:HD11	2.01	0.41
12:F:102:VAL:HG12	12:F:116:GLN:HG2	2.03	0.41
16:L:1:MET:HE2	16:L:1:MET:HB3	1.84	0.41
17:M:53:MET:HE1	17:M:103:TYR:HB3	2.03	0.41
18:N:73:ASN:HA	18:N:76:VAL:HG12	2.02	0.41
19:O:15:ARG:HG2	19:O:93:ASP:OD1	2.21	0.41
22:R:2:TYR:CD1	22:R:13:ARG:HD3	2.55	0.41
22:R:34:GLU:N	22:R:34:GLU:OE2	2.53	0.41
23:S:24:ILE:HD13	23:S:36:LEU:HD11	2.03	0.41
34:d:3:ARG:HD3	34:d:3:ARG:HA	1.70	0.41
35:e:15:LYS:HB2	35:e:23:LYS:HE3	2.03	0.41
37:g:73:LYS:C	37:g:75:ALA:H	2.29	0.41
38:h:114:LYS:HB2	38:h:185:ASN:ND2	2.36	0.41
39:i:4:TYR:O	39:i:5:LEU:HD23	2.21	0.41
39:i:99:ASP:OD1	39:i:99:ASP:N	2.53	0.41
40:j:82:GLN:HB2	40:j:83:HIS:HD2	1.86	0.41
40:j:91:GLY:O	40:j:130:SER:OG	2.37	0.41
41:k:69:GLU:O	41:k:73:GLU:HG2	2.20	0.41
42:l:14:PRO:HB2	42:l:19:GLY:HA2	2.02	0.41
51:u:54:LEU:O	51:u:57:ILE:HG22	2.20	0.41
53:w:71:THR:O	53:w:74:HIS:ND1	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:903:C:H2'	1:1:904:G:H8	1.86	0.41
1:1:1387:A:H2'	1:1:1388:G:C8	2.56	0.41
1:1:1442:U:H2'	1:1:1443:U:C6	2.56	0.41
1:1:2373:G:H2'	1:1:2374:C:H6	1.86	0.41
1:1:2590:A:H2'	1:1:2591:C:H6	1.86	0.41
1:1:2729:G:H5'	9:C:190:LYS:HE2	2.03	0.41
1:1:2848:G:H8	20:P:95:ALA:HB2	1.86	0.41
2:2:1013:G:N2	2:2:1015:G:H3'	2.36	0.41
2:2:1319:A:O2'	2:2:1323:G:N7	2.47	0.41
2:2:1340:A:H2'	2:2:1341:U:O4'	2.21	0.41
2:2:1493:A:H4'	4:4:19:C:H1'	2.02	0.41
7:A:66:PRO:HB2	7:A:67:HIS:CD2	2.50	0.41
7:A:205:LYS:HA	7:A:205:LYS:HD3	1.79	0.41
11:E:165:GLU:H	11:E:165:GLU:HG2	1.57	0.41
19:O:63:LYS:HE2	19:O:63:LYS:HB2	1.95	0.41
20:P:9:GLU:HA	20:P:55:LEU:HD22	2.03	0.41
37:g:170:HIS:HA	37:g:173:ILE:HG12	2.03	0.41
39:i:184:ARG:HD3	59:i:402:HOH:O	2.20	0.41
40:j:100:SER:O	40:j:103:THR:HG23	2.20	0.41
43:m:86:TYR:CE1	43:m:124:GLU:HG3	2.56	0.41
45:o:18:ILE:HD12	45:o:18:ILE:HA	1.81	0.41
48:r:69:LEU:HD12	48:r:69:LEU:HA	1.84	0.41
1:1:872:U:H2'	1:1:873:C:H6	1.85	0.40
1:1:880:G:H1	1:1:897:C:N4	2.03	0.40
1:1:1771:C:H2'	1:1:1772:A:C8	2.55	0.40
1:1:1790:C:H2'	1:1:1791:A:C8	2.55	0.40
1:1:2051:A:H8	1:1:2051:A:OP2	2.04	0.40
1:1:2813:A:H2'	1:1:2814:A:H8	1.86	0.40
2:2:33:A:H2'	2:2:34:C:C6	2.56	0.40
2:2:750:C:O2'	50:t:21:ASP:HB2	2.21	0.40
2:2:1207:2MG:C5	2:2:1208:C:C5	3.09	0.40
2:2:1250:A:O3'	44:n:69:GLY:HA2	2.22	0.40
8:B:201:MET:HG3	8:B:202:LEU:HD22	2.03	0.40
9:C:25:THR:OG1	9:C:191:GLY:O	2.38	0.40
38:h:21:THR:HG23	38:h:58:GLU:HB3	2.03	0.40
41:k:101:PRO:HA	41:k:104:LYS:HZ3	1.86	0.40
43:m:7:ILE:HB	43:m:77:ARG:NH1	2.36	0.40
43:m:50:LYS:NZ	43:m:52:GLU:HB2	2.37	0.40
44:n:11:ARG:HG3	44:n:15:SER:O	2.21	0.40
53:w:55:LEU:HD23	53:w:55:LEU:HA	1.87	0.40
1:1:301:G:OP2	25:U:82:ARG:NH1	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:302:C:H2'	1:1:303:G:H8	1.85	0.40
1:1:404:A:H1'	1:1:406:G:N9	2.36	0.40
1:1:537:G:H5''	14:J:5:THR:HG21	2.03	0.40
1:1:555:G:O2'	1:1:556:A:H8	2.04	0.40
1:1:569:U:H2'	1:1:570:G:O4'	2.20	0.40
1:1:851:C:H2'	1:1:852:U:H6	1.86	0.40
1:1:929:U:H4'	30:Z:38:ARG:NH2	2.36	0.40
1:1:934:U:H2'	1:1:935:C:C6	2.56	0.40
1:1:935:C:C2	1:1:936:A:C8	3.09	0.40
1:1:948:C:H2'	1:1:949:G:C8	2.56	0.40
1:1:1433:A:H2'	1:1:1434:A:O4'	2.21	0.40
1:1:1582:C:H2'	1:1:1583:A:O4'	2.21	0.40
1:1:2128:G:N2	1:1:2159:G:N7	2.69	0.40
1:1:2364:C:H2'	1:1:2365:G:O4'	2.20	0.40
2:2:464:U:H3	2:2:467:U:P	2.43	0.40
2:2:950:U:OP2	48:r:101:ARG:HD2	2.20	0.40
2:2:1095:U:H2'	2:2:1096:C:C6	2.56	0.40
2:2:1124:G:O2'	2:2:1127:G:O6	2.39	0.40
2:2:1312:G:H2'	2:2:1313:U:C6	2.56	0.40
2:2:1435:G:H2'	2:2:1436:U:C6	2.57	0.40
3:3:13:G:N2	3:3:16:G:N3	2.68	0.40
6:6:135:ILE:HA	6:6:156:LEU:HA	2.03	0.40
7:A:63:THR:HB	7:A:162:ARG:O	2.22	0.40
12:F:127:THR:HG22	12:F:128:GLN:N	2.36	0.40
12:F:148:LEU:HA	12:F:151:TYR:HD2	1.87	0.40
31:a:28:VAL:HG11	31:a:32:LEU:HD12	2.03	0.40
35:e:45:ARG:HH11	35:e:45:ARG:HD2	1.77	0.40
37:g:165:ASP:HB3	37:g:168:HIS:HB3	2.03	0.40
37:g:191:SER:OG	37:g:192:ASP:N	2.54	0.40
48:r:33:ILE:HD11	48:r:63:PHE:HD2	1.86	0.40
51:u:23:ASP:HB3	51:u:26:ASN:ND2	2.36	0.40
1:1:481:G:HO2'	1:1:482:A:P	2.44	0.40
1:1:1174:U:C5	59:1:3513:HOH:O	2.68	0.40
1:1:2117:A:C5	59:1:3466:HOH:O	2.73	0.40
2:2:361:G:H2'	2:2:362:G:O4'	2.22	0.40
2:2:476:U:H2'	2:2:477:C:C6	2.56	0.40
2:2:663:A:H5''	53:w:50:LYS:HE3	2.03	0.40
2:2:1219:A:H2'	2:2:1220:G:H8	1.86	0.40
2:2:1412:C:H2'	2:2:1413:A:H8	1.83	0.40
2:2:1513:A:H2'	2:2:1514:G:H8	1.87	0.40
13:G:84:ALA:HA	13:G:90:LEU:HA	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:J:109:LEU:HD23	14:J:109:LEU:HA	1.89	0.40
15:K:53:LYS:HE2	15:K:53:LYS:HB2	1.84	0.40
20:P:8:LEU:O	20:P:11:GLU:HG2	2.21	0.40
39:i:151:LYS:HB3	39:i:151:LYS:HE2	1.85	0.40
45:o:32:THR:HG23	45:o:33:GLY:N	2.36	0.40
45:o:85:ASP:OD1	45:o:86:ALA:N	2.54	0.40
47:q:7:LEU:HD23	52:v:34:TYR:CE1	2.57	0.40
50:t:7:ALA:O	50:t:11:ILE:HG12	2.22	0.40
1:1:18:U:P	21:Q:30:ARG:HH22	2.43	0.40
1:1:272:A:H2'	1:1:273:G:C8	2.57	0.40
1:1:397:U:OP2	28:X:10:LYS:NZ	2.47	0.40
1:1:598:U:H2'	1:1:599:A:C8	2.57	0.40
1:1:1295:C:C2	1:1:1296:G:C8	3.10	0.40
1:1:1422:G:C6	1:1:1577:C:N3	2.90	0.40
1:1:1565:C:O2'	1:1:1566:A:C8	2.74	0.40
1:1:2190:G:HO2'	1:1:2191:A:P	2.44	0.40
1:1:2446:G:N2	1:1:2449:U:O2	2.48	0.40
1:1:2579:C:H2'	1:1:2580:U:O2	2.22	0.40
1:1:2756:U:H1'	1:1:2757:A:H5''	2.03	0.40
2:2:79:G:C6	2:2:80:A:C5	3.10	0.40
2:2:151:A:C4	2:2:152:A:C8	3.10	0.40
2:2:414:A:C4	2:2:415:A:C8	3.10	0.40
2:2:849:G:H2'	2:2:850:U:O4'	2.21	0.40
2:2:909:A:N3	2:2:1413:A:O2'	2.40	0.40
2:2:946:A:C2	2:2:947:G:C5	3.10	0.40
2:2:1021:A:N3	2:2:1021:A:H2'	2.36	0.40
2:2:1216:A:H5''	49:s:5:SER:HB2	2.03	0.40
5:5:67:G:H2'	5:5:68:U:C6	2.57	0.40
13:G:42:LYS:O	13:G:45:GLU:HG3	2.21	0.40
13:G:56:ALA:O	13:G:60:GLU:HG2	2.22	0.40
26:V:65:VAL:HG22	26:V:66:ASP:OD2	2.21	0.40
39:i:62:ARG:HE	39:i:62:ARG:HB3	1.60	0.40
43:m:6:PRO:HB2	43:m:33:LYS:HE3	2.04	0.40
43:m:52:GLU:HB3	43:m:58:GLU:OE2	2.21	0.40
45:o:17:LEU:HD11	45:o:93:ALA:HB3	2.02	0.40
47:q:21:VAL:HG13	47:q:95:TYR:HE1	1.87	0.40
48:r:95:LEU:HB3	48:r:96:PRO:HD2	2.02	0.40
49:s:51:LEU:HD12	49:s:51:LEU:HA	1.96	0.40
49:s:64:CYS:HB2	49:s:80:SER:HB3	2.04	0.40
51:u:80:LYS:HE3	51:u:80:LYS:HB3	1.85	0.40
1:1:208:C:H2'	1:1:209:C:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:607:U:O2	1:1:608:A:C8	2.75	0.40
1:1:801:G:C8	10:D:50:ALA:HB2	2.57	0.40
1:1:1045:C:H4'	1:1:1047:G:H1'	2.04	0.40
1:1:1799:G:C2	8:B:154:LEU:HD23	2.56	0.40
1:1:2171:A:H1'	1:1:2172:U:C6	2.56	0.40
1:1:2516:A:O2'	1:1:2517:C:H5'	2.21	0.40
2:2:86:G:N2	59:2:1818:HOH:O	2.49	0.40
2:2:859:G:H2'	2:2:860:A:H8	1.84	0.40
2:2:1118:U:H2'	2:2:1119:C:H6	1.86	0.40
14:J:99:ARG:HA	14:J:99:ARG:HD2	1.90	0.40
16:L:127:VAL:HG11	16:L:142:ILE:HG21	2.03	0.40
18:N:6:SER:OG	18:N:7:GLY:N	2.54	0.40
35:e:55:LEU:HD23	35:e:55:LEU:HA	1.93	0.40
41:k:100:SER:O	41:k:103:VAL:HG12	2.21	0.40
43:m:35:ALA:O	43:m:39:VAL:HG23	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	6	185/188 (98%)	174 (94%)	10 (5%)	1 (0%)	24	57
7	A	222/224 (99%)	194 (87%)	26 (12%)	2 (1%)	14	44
8	B	269/273 (98%)	253 (94%)	16 (6%)	0	100	100
9	C	207/209 (99%)	193 (93%)	14 (7%)	0	100	100
10	D	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
11	E	175/179 (98%)	167 (95%)	8 (5%)	0	100	100
12	F	173/177 (98%)	163 (94%)	10 (6%)	0	100	100
13	G	147/149 (99%)	135 (92%)	12 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	J	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
15	K	121/123 (98%)	115 (95%)	5 (4%)	1 (1%)	16	47
16	L	142/144 (99%)	134 (94%)	8 (6%)	0	100	100
17	M	134/136 (98%)	126 (94%)	8 (6%)	0	100	100
18	N	117/127 (92%)	108 (92%)	9 (8%)	0	100	100
19	O	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
20	P	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
21	Q	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
22	R	101/103 (98%)	91 (90%)	10 (10%)	0	100	100
23	S	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
24	T	92/100 (92%)	90 (98%)	2 (2%)	0	100	100
25	U	101/104 (97%)	95 (94%)	6 (6%)	0	100	100
26	V	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
27	W	73/84 (87%)	69 (94%)	4 (6%)	0	100	100
28	X	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
29	Y	60/63 (95%)	60 (100%)	0	0	100	100
30	Z	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
31	a	64/70 (91%)	58 (91%)	6 (9%)	0	100	100
32	b	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
33	c	50/55 (91%)	48 (96%)	2 (4%)	0	100	100
34	d	44/46 (96%)	40 (91%)	4 (9%)	0	100	100
35	e	62/65 (95%)	57 (92%)	5 (8%)	0	100	100
36	f	36/38 (95%)	36 (100%)	0	0	100	100
37	g	223/241 (92%)	204 (92%)	18 (8%)	1 (0%)	30	61
38	h	206/233 (88%)	193 (94%)	13 (6%)	0	100	100
39	i	203/206 (98%)	194 (96%)	9 (4%)	0	100	100
40	j	154/167 (92%)	146 (95%)	8 (5%)	0	100	100
41	k	102/135 (76%)	96 (94%)	6 (6%)	0	100	100
42	l	149/179 (83%)	135 (91%)	14 (9%)	0	100	100
43	m	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
44	n	125/130 (96%)	116 (93%)	9 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	o	97/103 (94%)	88 (91%)	9 (9%)	0	100	100
46	p	115/129 (89%)	107 (93%)	8 (7%)	0	100	100
47	q	120/124 (97%)	112 (93%)	8 (7%)	0	100	100
48	r	114/118 (97%)	109 (96%)	5 (4%)	0	100	100
49	s	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
50	t	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
51	u	80/82 (98%)	78 (98%)	2 (2%)	0	100	100
52	v	78/84 (93%)	72 (92%)	6 (8%)	0	100	100
53	w	64/75 (85%)	61 (95%)	3 (5%)	0	100	100
54	x	81/92 (88%)	76 (94%)	5 (6%)	0	100	100
55	y	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
56	z	68/71 (96%)	68 (100%)	0	0	100	100
All	All	6014/6324 (95%)	5680 (94%)	329 (6%)	5 (0%)	49	78

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	A	56	ASP
37	g	128	LYS
6	6	165	PRO
7	A	135	GLY
15	K	120	PRO

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	
6	6	154/154 (100%)	142 (92%)	12 (8%)	11	38
7	A	173/173 (100%)	169 (98%)	4 (2%)	44	70
8	B	216/218 (99%)	214 (99%)	2 (1%)	70	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	C	164/164 (100%)	164 (100%)	0	100	100
10	D	165/165 (100%)	165 (100%)	0	100	100
11	E	148/150 (99%)	148 (100%)	0	100	100
12	F	136/138 (99%)	136 (100%)	0	100	100
13	G	114/114 (100%)	114 (100%)	0	100	100
14	J	116/116 (100%)	116 (100%)	0	100	100
15	K	104/104 (100%)	103 (99%)	1 (1%)	68	79
16	L	103/103 (100%)	103 (100%)	0	100	100
17	M	109/109 (100%)	109 (100%)	0	100	100
18	N	99/103 (96%)	97 (98%)	2 (2%)	48	72
19	O	86/87 (99%)	86 (100%)	0	100	100
20	P	99/100 (99%)	99 (100%)	0	100	100
21	Q	89/90 (99%)	88 (99%)	1 (1%)	65	78
22	R	84/84 (100%)	84 (100%)	0	100	100
23	S	93/93 (100%)	93 (100%)	0	100	100
24	T	81/84 (96%)	81 (100%)	0	100	100
25	U	84/85 (99%)	84 (100%)	0	100	100
26	V	78/78 (100%)	78 (100%)	0	100	100
27	W	57/62 (92%)	56 (98%)	1 (2%)	51	73
28	X	67/68 (98%)	66 (98%)	1 (2%)	57	75
29	Y	54/55 (98%)	54 (100%)	0	100	100
30	Z	48/49 (98%)	48 (100%)	0	100	100
31	a	59/62 (95%)	59 (100%)	0	100	100
32	b	47/48 (98%)	47 (100%)	0	100	100
33	c	47/49 (96%)	47 (100%)	0	100	100
34	d	38/38 (100%)	38 (100%)	0	100	100
35	e	51/52 (98%)	50 (98%)	1 (2%)	48	72
36	f	34/34 (100%)	34 (100%)	0	100	100
37	g	187/199 (94%)	187 (100%)	0	100	100
38	h	171/190 (90%)	169 (99%)	2 (1%)	63	78
39	i	172/173 (99%)	172 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	j	119/126 (94%)	118 (99%)	1 (1%)	73	81
41	k	91/116 (78%)	91 (100%)	0	100	100
42	l	124/147 (84%)	122 (98%)	2 (2%)	55	75
43	m	104/105 (99%)	104 (100%)	0	100	100
44	n	105/107 (98%)	104 (99%)	1 (1%)	68	79
45	o	86/90 (96%)	86 (100%)	0	100	100
46	p	90/99 (91%)	90 (100%)	0	100	100
47	q	102/103 (99%)	102 (100%)	0	100	100
48	r	94/96 (98%)	93 (99%)	1 (1%)	65	78
49	s	83/84 (99%)	82 (99%)	1 (1%)	63	78
50	t	76/77 (99%)	76 (100%)	0	100	100
51	u	65/65 (100%)	65 (100%)	0	100	100
52	v	74/78 (95%)	74 (100%)	0	100	100
53	w	57/65 (88%)	57 (100%)	0	100	100
54	x	72/79 (91%)	72 (100%)	0	100	100
55	y	65/66 (98%)	65 (100%)	0	100	100
56	z	60/61 (98%)	60 (100%)	0	100	100
All	All	4994/5155 (97%)	4961 (99%)	33 (1%)	73	82

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	6	67	VAL
6	6	100	ILE
6	6	105	LYS
6	6	135	ILE
6	6	138	THR
6	6	139	ASP
6	6	143	LYS
6	6	152	LYS
6	6	168	VAL
6	6	173	VAL
6	6	176	VAL
6	6	187	VAL
7	A	53	ARG
7	A	123	VAL

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Mol	Chain	Res	Type
7	A	124	VAL
7	A	126	GLN
8	B	17	VAL
8	B	143	ASN
15	K	123	LEU
18	N	50	PRO
18	N	106	ASP
21	Q	4	VAL
27	W	31	VAL
28	X	2	SER
35	e	29	LEU
38	h	55	ILE
38	h	156	ARG
40	j	70	ASN
42	l	92	ARG
42	l	113	ASP
44	n	128	SER
48	r	9	ILE
49	s	86	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (87) such sidechains are listed below:

Mol	Chain	Res	Type
6	6	87	ASN
6	6	103	ASN
6	6	110	GLN
6	6	119	ASN
6	6	169	GLN
7	A	67	HIS
7	A	80	GLN
7	A	126	GLN
7	A	139	ASN
7	A	148	ASN
8	B	53	HIS
8	B	86	ASN
8	B	134	ASN
8	B	143	ASN
9	C	32	ASN
9	C	49	GLN
10	D	24	ASN
10	D	92	HIS
10	D	115	GLN

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Mol	Chain	Res	Type
11	E	21	ASN
12	F	73	ASN
13	G	2	GLN
13	G	66	ASN
14	J	76	HIS
15	K	89	ASN
18	N	18	GLN
19	O	19	GLN
19	O	34	HIS
20	P	3	ASN
20	P	12	GLN
20	P	52	ASN
20	P	66	ASN
20	P	115	ASN
21	Q	44	GLN
23	S	15	GLN
23	S	60	HIS
23	S	61	ASN
24	T	59	ASN
26	V	49	ASN
26	V	78	GLN
27	W	12	ASN
29	Y	58	ASN
32	b	42	HIS
34	d	13	ASN
34	d	16	HIS
34	d	29	GLN
35	e	43	HIS
36	f	35	GLN
37	g	39	HIS
37	g	51	ASN
37	g	109	GLN
37	g	120	GLN
38	h	69	HIS
38	h	102	ASN
38	h	123	GLN
38	h	140	ASN
39	i	40	GLN
39	i	74	ASN
39	i	140	ASN
40	j	89	HIS
40	j	148	ASN

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Mol	Chain	Res	Type
41	k	3	HIS
41	k	63	ASN
42	l	9	GLN
42	l	68	ASN
43	m	38	ASN
44	n	37	GLN
44	n	75	GLN
44	n	110	GLN
45	o	58	ASN
45	o	99	GLN
46	p	101	ASN
47	q	5	ASN
47	q	46	ASN
48	r	14	HIS
49	s	35	ASN
49	s	43	ASN
49	s	49	GLN
50	t	40	GLN
50	t	46	HIS
51	u	26	ASN
52	v	45	HIS
52	v	50	ASN
54	x	52	HIS
55	y	13	GLN
55	y	78	ASN
55	y	84	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2865/2903 (98%)	516 (18%)	29 (1%)
2	2	1531/1540 (99%)	254 (16%)	6 (0%)
3	3	119/120 (99%)	20 (16%)	0
4	4	8/18 (44%)	3 (37%)	1 (12%)
5	5	76/77 (98%)	18 (23%)	5 (6%)
All	All	4599/4658 (98%)	811 (17%)	41 (0%)

All (811) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	A

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Mol	Chain	Res	Type
1	1	14	A
1	1	15	G
1	1	34	U
1	1	35	G
1	1	36	G
1	1	45	G
1	1	46	G
1	1	50	U
1	1	51	G
1	1	63	A
1	1	71	A
1	1	74	A
1	1	75	G
1	1	82	U
1	1	98	G
1	1	102	U
1	1	103	A
1	1	118	A
1	1	119	A
1	1	120	U
1	1	125	A
1	1	135	U
1	1	139	U
1	1	140	C
1	1	141	G
1	1	142	A
1	1	149	A
1	1	162	U
1	1	163	C
1	1	196	A
1	1	199	A
1	1	215	G
1	1	216	A
1	1	221	A
1	1	222	A
1	1	225	C
1	1	228	C
1	1	229	C
1	1	233	A
1	1	242	G
1	1	243	U
1	1	248	G

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Mol	Chain	Res	Type
1	1	255	A
1	1	265	A
1	1	267	C
1	1	276	U
1	1	278	A
1	1	279	A
1	1	285	G
1	1	311	A
1	1	323	C
1	1	324	A
1	1	329	G
1	1	330	A
1	1	345	A
1	1	361	G
1	1	362	A
1	1	367	G
1	1	371	A
1	1	373	U
1	1	386	G
1	1	387	U
1	1	395	U
1	1	396	G
1	1	404	A
1	1	405	U
1	1	406	G
1	1	411	G
1	1	412	A
1	1	417	C
1	1	422	A
1	1	424	G
1	1	448	U
1	1	456	C
1	1	458	G
1	1	459	U
1	1	481	G
1	1	482	A
1	1	489	G
1	1	491	G
1	1	505	A
1	1	508	A
1	1	509	C
1	1	518	G

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Mol	Chain	Res	Type
1	1	529	A
1	1	530	G
1	1	532	A
1	1	545	U
1	1	546	U
1	1	547	A
1	1	548	G
1	1	550	C
1	1	556	A
1	1	563	A
1	1	573	U
1	1	575	A
1	1	603	A
1	1	614	A
1	1	615	U
1	1	622	G
1	1	627	A
1	1	637	A
1	1	645	C
1	1	646	U
1	1	647	G
1	1	654	A
1	1	655	A
1	1	659	G
1	1	668	A
1	1	670	A
1	1	677	A
1	1	685	A
1	1	686	U
1	1	694	U
1	1	695	G
1	1	704	G
1	1	717	C
1	1	730	A
1	1	738	G
1	1	747	C
1	1	764	A
1	1	765	C
1	1	775	G
1	1	776	G
1	1	782	A
1	1	783	A

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Mol	Chain	Res	Type
1	1	784	G
1	1	785	G
1	1	792	A
1	1	805	G
1	1	806	C
1	1	812	C
1	1	819	A
1	1	827	U
1	1	828	U
1	1	845	A
1	1	846	U
1	1	847	U
1	1	858	G
1	1	859	G
1	1	878	A
1	1	879	G
1	1	883	G
1	1	885	C
1	1	886	A
1	1	891	G
1	1	892	A
1	1	897	C
1	1	907	G
1	1	910	A
1	1	914	G
1	1	941	A
1	1	945	A
1	1	946	C
1	1	961	C
1	1	973	A
1	1	974	G
1	1	975	A
1	1	983	A
1	1	995	C
1	1	996	A
1	1	999	U
1	1	1005	C
1	1	1012	U
1	1	1013	C
1	1	1021	A
1	1	1023	U
1	1	1026	G

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Mol	Chain	Res	Type
1	1	1033	U
1	1	1045	C
1	1	1046	A
1	1	1047	G
1	1	1054	A
1	1	1057	A
1	1	1059	G
1	1	1060	U
1	1	1061	U
1	1	1062	G
1	1	1063	G
1	1	1064	C
1	1	1065	U
1	1	1066	U
1	1	1067	A
1	1	1068	G
1	1	1069	A
1	1	1070	A
1	1	1071	G
1	1	1072	C
1	1	1073	A
1	1	1075	C
1	1	1076	C
1	1	1080	A
1	1	1088	A
1	1	1089	A
1	1	1090	A
1	1	1094	U
1	1	1096	A
1	1	1097	U
1	1	1099	G
1	1	1103	A
1	1	1104	C
1	1	1106	G
1	1	1111	A
1	1	1112	G
1	1	1120	G
1	1	1130	U
1	1	1132	U
1	1	1133	A
1	1	1135	C
1	1	1139	G

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Mol	Chain	Res	Type
1	1	1142	A
1	1	1169	A
1	1	1173	U
1	1	1174	U
1	1	1175	A
1	1	1176	U
1	1	1177	G
1	1	1180	U
1	1	1181	U
1	1	1204	A
1	1	1206	G
1	1	1211	C
1	1	1212	G
1	1	1236	G
1	1	1237	A
1	1	1250	G
1	1	1253	A
1	1	1256	G
1	1	1271	G
1	1	1272	A
1	1	1300	G
1	1	1301	A
1	1	1306	C
1	1	1311	G
1	1	1321	A
1	1	1329	U
1	1	1330	C
1	1	1341	G
1	1	1345	C
1	1	1352	U
1	1	1365	A
1	1	1368	G
1	1	1379	U
1	1	1383	A
1	1	1395	A
1	1	1397	U
1	1	1414	C
1	1	1416	G
1	1	1420	A
1	1	1421	G
1	1	1428	C
1	1	1434	A

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Mol	Chain	Res	Type
1	1	1453	A
1	1	1454	C
1	1	1458	U
1	1	1461	C
1	1	1475	G
1	1	1482	G
1	1	1490	A
1	1	1491	G
1	1	1494	A
1	1	1497	U
1	1	1504	A
1	1	1508	A
1	1	1509	A
1	1	1515	A
1	1	1524	G
1	1	1529	G
1	1	1530	G
1	1	1534	U
1	1	1535	A
1	1	1536	C
1	1	1538	G
1	1	1558	C
1	1	1559	U
1	1	1560	G
1	1	1569	A
1	1	1578	U
1	1	1583	A
1	1	1584	U
1	1	1585	C
1	1	1607	C
1	1	1608	A
1	1	1647	U
1	1	1648	U
1	1	1649	G
1	1	1651	G
1	1	1654	A
1	1	1667	G
1	1	1672	A
1	1	1674	G
1	1	1675	C
1	1	1694	C
1	1	1695	G

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Mol	Chain	Res	Type
1	1	1715	G
1	1	1729	U
1	1	1730	C
1	1	1735	A
1	1	1738	G
1	1	1744	A
1	1	1757	A
1	1	1758	U
1	1	1759	A
1	1	1764	C
1	1	1773	A
1	1	1780	A
1	1	1786	A
1	1	1800	C
1	1	1801	A
1	1	1802	A
1	1	1808	A
1	1	1811	G
1	1	1816	C
1	1	1827	U
1	1	1829	A
1	1	1833	C
1	1	1848	A
1	1	1858	A
1	1	1862	G
1	1	1870	C
1	1	1871	A
1	1	1872	A
1	1	1884	G
1	1	1906	G
1	1	1913	A
1	1	1914	C
1	1	1915	U
1	1	1929	G
1	1	1930	G
1	1	1931	U
1	1	1937	A
1	1	1938	A
1	1	1940	U
1	1	1941	C
1	1	1955	U
1	1	1960	A

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Mol	Chain	Res	Type
1	1	1963	U
1	1	1966	A
1	1	1967	C
1	1	1970	A
1	1	1971	U
1	1	1972	G
1	1	1991	U
1	1	1993	U
1	1	1996	C
1	1	1997	C
1	1	2022	U
1	1	2023	C
1	1	2031	A
1	1	2033	A
1	1	2043	C
1	1	2052	A
1	1	2055	C
1	1	2056	G
1	1	2060	A
1	1	2061	G
1	1	2062	A
1	1	2069	A
1	1	2093	G
1	1	2096	C
1	1	2105	U
1	1	2107	G
1	1	2108	A
1	1	2110	G
1	1	2111	U
1	1	2112	G
1	1	2114	A
1	1	2116	G
1	1	2117	A
1	1	2119	A
1	1	2123	G
1	1	2124	G
1	1	2125	G
1	1	2126	A
1	1	2127	G
1	1	2128	G
1	1	2160	C
1	1	2161	C

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Mol	Chain	Res	Type
1	1	2167	U
1	1	2169	A
1	1	2170	A
1	1	2172	U
1	1	2173	A
1	1	2174	C
1	1	2177	C
1	1	2178	C
1	1	2179	C
1	1	2180	U
1	1	2181	U
1	1	2187	U
1	1	2188	U
1	1	2189	U
1	1	2190	G
1	1	2191	A
1	1	2193	G
1	1	2198	A
1	1	2204	G
1	1	2211	A
1	1	2213	U
1	1	2214	C
1	1	2225	A
1	1	2226	C
1	1	2238	G
1	1	2239	G
1	1	2250	G
1	1	2251	G
1	1	2279	G
1	1	2283	C
1	1	2287	A
1	1	2288	A
1	1	2297	A
1	1	2300	C
1	1	2305	U
1	1	2309	A
1	1	2320	U
1	1	2321	U
1	1	2322	A
1	1	2325	G
1	1	2327	A
1	1	2333	A

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Mol	Chain	Res	Type
1	1	2335	A
1	1	2336	A
1	1	2345	G
1	1	2347	C
1	1	2350	C
1	1	2357	G
1	1	2361	G
1	1	2382	G
1	1	2383	G
1	1	2385	C
1	1	2400	G
1	1	2402	U
1	1	2403	C
1	1	2406	A
1	1	2424	C
1	1	2425	A
1	1	2429	G
1	1	2430	A
1	1	2434	A
1	1	2435	A
1	1	2441	U
1	1	2448	A
1	1	2449	U
1	1	2474	U
1	1	2476	A
1	1	2478	A
1	1	2492	U
1	1	2499	C
1	1	2502	G
1	1	2503	A
1	1	2504	U
1	1	2505	G
1	1	2506	U
1	1	2507	C
1	1	2518	A
1	1	2529	G
1	1	2535	G
1	1	2547	A
1	1	2554	U
1	1	2566	A
1	1	2567	G
1	1	2572	A

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Mol	Chain	Res	Type
1	1	2573	C
1	1	2578	G
1	1	2582	G
1	1	2585	U
1	1	2586	U
1	1	2602	A
1	1	2609	U
1	1	2613	U
1	1	2615	U
1	1	2629	U
1	1	2646	C
1	1	2655	G
1	1	2656	U
1	1	2682	A
1	1	2689	U
1	1	2690	U
1	1	2707	U
1	1	2714	G
1	1	2718	G
1	1	2722	G
1	1	2726	A
1	1	2732	G
1	1	2733	A
1	1	2744	G
1	1	2748	A
1	1	2764	A
1	1	2765	A
1	1	2769	U
1	1	2778	A
1	1	2779	U
1	1	2791	G
1	1	2793	C
1	1	2798	U
1	1	2799	A
1	1	2800	A
1	1	2807	U
1	1	2808	G
1	1	2809	A
1	1	2818	U
1	1	2820	A
1	1	2821	A
1	1	2833	U

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Mol	Chain	Res	Type
1	1	2849	U
1	1	2861	U
1	1	2867	G
1	1	2868	A
1	1	2873	A
1	1	2879	A
1	1	2880	C
1	1	2883	A
1	1	2891	U
1	1	2893	A
1	1	2901	C
2	2	4	U
2	2	5	U
2	2	9	G
2	2	32	A
2	2	39	G
2	2	47	C
2	2	48	C
2	2	51	A
2	2	52	C
2	2	54	C
2	2	70	U
2	2	71	A
2	2	72	A
2	2	73	C
2	2	74	A
2	2	75	G
2	2	83	C
2	2	84	U
2	2	85	U
2	2	86	G
2	2	87	C
2	2	88	U
2	2	108	G
2	2	120	A
2	2	121	U
2	2	126	G
2	2	127	G
2	2	130	A
2	2	131	A
2	2	141	G
2	2	144	G

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Mol	Chain	Res	Type
2	2	163	C
2	2	173	U
2	2	174	A
2	2	189	A
2	2	191	G
2	2	197	A
2	2	204	G
2	2	209	U
2	2	211	G
2	2	212	G
2	2	226	G
2	2	245	U
2	2	247	G
2	2	251	G
2	2	262	A
2	2	266	G
2	2	267	C
2	2	281	G
2	2	289	G
2	2	321	A
2	2	328	C
2	2	330	C
2	2	332	G
2	2	347	G
2	2	352	C
2	2	354	G
2	2	367	U
2	2	372	C
2	2	373	A
2	2	382	A
2	2	388	G
2	2	392	C
2	2	397	A
2	2	406	G
2	2	412	A
2	2	413	G
2	2	414	A
2	2	421	U
2	2	422	C
2	2	424	G
2	2	428	G
2	2	429	U

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Mol	Chain	Res	Type
2	2	452	A
2	2	456	A
2	2	457	G
2	2	463	U
2	2	464	U
2	2	465	A
2	2	467	U
2	2	468	A
2	2	478	A
2	2	479	U
2	2	481	G
2	2	482	A
2	2	484	G
2	2	486	U
2	2	495	A
2	2	496	A
2	2	511	C
2	2	517	G
2	2	518	C
2	2	519	C
2	2	521	G
2	2	527	G7M
2	2	532	A
2	2	533	A
2	2	537	G
2	2	547	A
2	2	559	A
2	2	564	C
2	2	572	A
2	2	573	A
2	2	576	C
2	2	577	G
2	2	579	A
2	2	588	G
2	2	596	A
2	2	633	G
2	2	650	G
2	2	653	U
2	2	665	A
2	2	687	A
2	2	688	G
2	2	700	G

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Mol	Chain	Res	Type
2	2	721	G
2	2	723	U
2	2	724	G
2	2	731	G
2	2	734	G
2	2	747	A
2	2	748	G
2	2	755	G
2	2	777	A
2	2	793	U
2	2	794	A
2	2	815	A
2	2	817	C
2	2	828	U
2	2	829	G
2	2	843	U
2	2	844	G
2	2	845	A
2	2	846	G
2	2	872	A
2	2	889	A
2	2	914	A
2	2	926	G
2	2	934	C
2	2	935	A
2	2	960	U
2	2	965	U
2	2	966	2MG
2	2	967	5MC
2	2	968	A
2	2	969	A
2	2	971	G
2	2	975	A
2	2	976	G
2	2	977	A
2	2	981	U
2	2	992	U
2	2	993	G
2	2	994	A
2	2	996	A
2	2	1004	A
2	2	1007	U

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Mol	Chain	Res	Type
2	2	1008	U
2	2	1009	U
2	2	1018	G
2	2	1019	A
2	2	1021	A
2	2	1022	A
2	2	1026	G
2	2	1027	C
2	2	1028	C
2	2	1030	U
2	2	1031	C
2	2	1034	G
2	2	1035	A
2	2	1036	A
2	2	1037	C
2	2	1043	G
2	2	1044	A
2	2	1064	G
2	2	1065	U
2	2	1085	U
2	2	1094	G
2	2	1095	U
2	2	1101	A
2	2	1108	G
2	2	1124	G
2	2	1133	G
2	2	1135	U
2	2	1136	C
2	2	1137	C
2	2	1139	G
2	2	1140	C
2	2	1141	C
2	2	1145	A
2	2	1158	C
2	2	1159	U
2	2	1168	U
2	2	1174	G
2	2	1175	G
2	2	1176	A
2	2	1184	G
2	2	1196	A
2	2	1197	A

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Mol	Chain	Res	Type
2	2	1214	C
2	2	1227	A
2	2	1228	C
2	2	1238	A
2	2	1239	A
2	2	1240	U
2	2	1241	G
2	2	1257	A
2	2	1258	G
2	2	1260	G
2	2	1261	A
2	2	1268	G
2	2	1275	A
2	2	1279	G
2	2	1280	A
2	2	1281	C
2	2	1285	A
2	2	1286	U
2	2	1287	A
2	2	1290	G
2	2	1299	A
2	2	1302	C
2	2	1305	G
2	2	1317	C
2	2	1320	C
2	2	1322	C
2	2	1323	G
2	2	1338	G
2	2	1363	A
2	2	1370	G
2	2	1379	G
2	2	1383	C
2	2	1384	C
2	2	1398	A
2	2	1400	C
2	2	1419	G
2	2	1429	A
2	2	1432	G
2	2	1441	A
2	2	1445	U
2	2	1446	A
2	2	1452	C

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Mol	Chain	Res	Type
2	2	1453	G
2	2	1487	G
2	2	1491	G
2	2	1492	A
2	2	1495	U
2	2	1497	G
2	2	1499	A
2	2	1503	A
2	2	1506	U
2	2	1517	G
2	2	1519	MA6
2	2	1529	G
2	2	1530	G
3	3	2	G
3	3	9	G
3	3	24	G
3	3	35	C
3	3	42	C
3	3	56	G
3	3	57	A
3	3	73	A
3	3	77	U
3	3	78	A
3	3	79	G
3	3	88	C
3	3	89	U
3	3	90	C
3	3	108	A
3	3	109	A
3	3	116	G
3	3	117	G
3	3	118	C
3	3	119	A
4	4	13	A
4	4	15	G
4	4	19	C
5	5	2	G
5	5	3	G
5	5	4	C
5	5	5	A
5	5	6	C
5	5	14	A

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Mol	Chain	Res	Type
5	5	16	C
5	5	17	C
5	5	20	U
5	5	21	A
5	5	22	G
5	5	46	G
5	5	48	C
5	5	49	G
5	5	56	C
5	5	73	A
5	5	74	C
5	5	76	A

All (41) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	227	A
1	1	228	C
1	1	242	G
1	1	372	G
1	1	404	A
1	1	421	C
1	1	455	C
1	1	458	G
1	1	481	G
1	1	549	G
1	1	555	G
1	1	774	G
1	1	784	G
1	1	1020	A
1	1	1022	G
1	1	1070	A
1	1	1111	A
1	1	1320	C
1	1	1847	G
1	1	1857	G
1	1	1930	G
1	1	1940	U
1	1	2190	G
1	1	2286	G
1	1	2308	G
1	1	2326	C

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Mol	Chain	Res	Type
1	1	2655	G
1	1	2808	G
1	1	2867	G
2	2	516	PSU
2	2	966	2MG
2	2	1109	C
2	2	1383	C
2	2	1397	C
2	2	1491	G
4	4	12	A
5	5	2	G
5	5	3	G
5	5	16	C
5	5	48	C
5	5	72	G

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	G7M	2	527	2	23,26,27	3.70	11 (47%)	34,39,42	1.71	7 (20%)
2	5MC	2	1407	2	19,22,23	3.54	8 (42%)	26,32,35	1.02	1 (3%)
2	UR3	2	1498	2	19,22,23	2.71	7 (36%)	26,32,35	1.67	3 (11%)
2	PSU	2	516	2,57	18,21,22	1.07	1 (5%)	21,30,33	1.93	3 (14%)
2	2MG	2	1207	2	23,26,27	2.83	9 (39%)	33,38,41	2.14	10 (30%)
2	2MG	2	966	2	23,26,27	2.86	8 (34%)	33,38,41	2.19	10 (30%)
2	MA6	2	1519	2	23,26,27	1.59	5 (21%)	33,38,41	2.91	11 (33%)
2	2MG	2	1516	2	23,26,27	2.70	9 (39%)	33,38,41	2.33	12 (36%)
2	MA6	2	1518	2	23,26,27	1.59	5 (21%)	33,38,41	2.84	11 (33%)
6	KEO	6	34	6	16,18,19	0.75	0	15,21,23	1.40	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	5MC	2	967	2	19,22,23	3.57	8 (42%)	26,32,35	1.00	1 (3%)
47	0TD	q	89	47	8,9,10	1.96	1 (12%)	6,11,13	1.15	0
2	4OC	2	1402	2	20,23,24	2.97	8 (40%)	25,32,35	0.96	2 (8%)

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
2	G7M	2	527	2	-	3/7/25/26	0/3/3/3
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
2	UR3	2	1498	2	-	1/7/25/26	0/2/2/2
2	PSU	2	516	2,57	-	3/7/25/26	0/2/2/2
2	2MG	2	1207	2	-	0/9/27/28	0/3/3/3
2	2MG	2	966	2	-	0/9/27/28	0/3/3/3
2	MA6	2	1519	2	-	2/11/29/30	0/3/3/3
2	2MG	2	1516	2	-	0/9/27/28	0/3/3/3
2	MA6	2	1518	2	-	0/11/29/30	0/3/3/3
6	KEO	6	34	6	-	7/19/20/22	-
2	5MC	2	967	2	-	2/7/25/26	0/2/2/2
47	0TD	q	89	47	-	3/7/12/14	-
2	4OC	2	1402	2	-	2/9/29/30	0/2/2/2

All (80) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	527	G7M	C8-N7	10.92	1.51	1.33
2	2	1407	5MC	C6-C5	8.76	1.48	1.34
2	2	967	5MC	C6-C5	8.63	1.48	1.34
2	2	966	2MG	C2-N3	7.27	1.45	1.32
2	2	1207	2MG	C2-N3	7.20	1.45	1.32
2	2	1498	UR3	C2-N1	7.06	1.48	1.38
2	2	1402	4OC	C4-N3	6.74	1.44	1.32
2	2	967	5MC	C4-N3	6.57	1.44	1.34
2	2	1516	2MG	C2-N3	6.50	1.44	1.32
2	2	1207	2MG	C4-N3	6.45	1.49	1.34
2	2	1407	5MC	C4-N3	6.43	1.44	1.34
2	2	966	2MG	C4-N3	6.42	1.48	1.34
2	2	1402	4OC	C6-C5	6.03	1.49	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1498	UR3	C6-C5	6.00	1.49	1.35
2	2	527	G7M	C2-N3	5.96	1.47	1.33
2	2	967	5MC	C2-N3	5.96	1.48	1.36
2	2	1407	5MC	C2-N3	5.93	1.48	1.36
2	2	1516	2MG	C4-N3	5.92	1.47	1.34
2	2	966	2MG	C2-N2	5.89	1.45	1.33
2	2	527	G7M	C8-N9	5.86	1.51	1.35
2	2	1207	2MG	C2-N2	5.73	1.45	1.33
2	2	1402	4OC	C2-N3	5.71	1.47	1.36
2	2	527	G7M	C5-N7	5.60	1.45	1.39
2	2	967	5MC	C5-C4	5.40	1.48	1.44
2	2	1516	2MG	C2-N2	5.40	1.44	1.33
2	2	527	G7M	C4-N3	5.33	1.46	1.34
2	2	1407	5MC	C5-C4	5.09	1.48	1.44
2	2	1498	UR3	C2-N3	4.54	1.47	1.39
2	2	1207	2MG	C2-N1	4.43	1.43	1.36
2	2	966	2MG	C2-N1	4.42	1.43	1.36
2	2	1516	2MG	C2-N1	4.41	1.43	1.36
2	2	967	5MC	C4-N4	4.31	1.45	1.34
2	2	1407	5MC	C4-N4	4.19	1.44	1.34
2	2	1402	4OC	C4-N4	4.16	1.44	1.36
2	2	967	5MC	C6-N1	4.09	1.45	1.38
2	2	1407	5MC	C6-N1	4.07	1.44	1.38
47	q	89	0TD	CB-CA	-4.03	1.53	1.54
2	2	1407	5MC	C2-N1	3.71	1.47	1.40
2	2	967	5MC	C2-N1	3.68	1.47	1.40
2	2	1402	4OC	C2-N1	3.62	1.47	1.40
2	2	1518	MA6	C6-N6	3.61	1.46	1.36
2	2	1519	MA6	C5-C4	-3.55	1.32	1.39
2	2	1519	MA6	C6-N6	3.51	1.46	1.36
2	2	1207	2MG	C5-N7	-3.46	1.32	1.39
2	2	966	2MG	C5-N7	-3.45	1.32	1.39
2	2	1402	4OC	C5-C4	3.40	1.48	1.41
2	2	516	PSU	C6-C5	3.35	1.39	1.35
2	2	1518	MA6	C5-C4	-3.33	1.33	1.39
2	2	1516	2MG	C5-N7	-3.33	1.32	1.39
2	2	527	G7M	C2-N1	3.32	1.45	1.37
2	2	527	G7M	O6-C6	-3.28	1.17	1.23
2	2	527	G7M	C6-N1	3.27	1.45	1.38
2	2	527	G7M	C2-N2	3.25	1.41	1.34
2	2	1518	MA6	C5-N7	-3.22	1.33	1.39
2	2	1402	4OC	O2-C2	-3.14	1.17	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1498	UR3	O2-C2	-3.08	1.16	1.22
2	2	1519	MA6	C5-N7	-3.08	1.33	1.39
2	2	967	5MC	O2-C2	-2.99	1.18	1.23
2	2	527	G7M	C5-C6	2.95	1.51	1.43
2	2	1407	5MC	O2-C2	-2.95	1.18	1.23
2	2	527	G7M	C4-N9	2.93	1.45	1.38
2	2	966	2MG	O6-C6	-2.89	1.18	1.23
2	2	1516	2MG	C4-N9	-2.88	1.30	1.38
2	2	1516	2MG	O6-C6	-2.88	1.18	1.23
2	2	1498	UR3	O4-C4	-2.88	1.17	1.23
2	2	1402	4OC	C6-N1	2.83	1.44	1.38
2	2	1207	2MG	O6-C6	-2.70	1.18	1.23
2	2	1518	MA6	C4-N9	-2.44	1.32	1.37
2	2	1519	MA6	C4-N9	-2.43	1.32	1.37
2	2	966	2MG	C4-N9	-2.39	1.32	1.38
2	2	1207	2MG	C4-N9	-2.31	1.32	1.38
2	2	1519	MA6	C8-N9	-2.30	1.33	1.37
2	2	1207	2MG	C5-C6	2.27	1.52	1.44
2	2	1498	UR3	C6-N1	2.26	1.43	1.38
2	2	1518	MA6	C8-N9	-2.22	1.33	1.37
2	2	966	2MG	C5-C6	2.22	1.52	1.44
2	2	1516	2MG	C5-C6	2.17	1.52	1.44
2	2	1498	UR3	C5-C4	2.16	1.49	1.43
2	2	1207	2MG	C6-N1	2.11	1.42	1.38
2	2	1516	2MG	C6-N1	2.03	1.42	1.38

All (73) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1519	MA6	N1-C6-N6	-9.79	104.93	116.86
2	2	1518	MA6	N1-C6-N6	-9.34	105.48	116.86
2	2	1207	2MG	C2-N3-C4	6.48	120.11	112.00
2	2	966	2MG	C2-N3-C4	6.40	120.00	112.00
2	2	1516	2MG	C2-N3-C4	6.19	119.74	112.00
2	2	1519	MA6	C5-C6-N6	6.04	134.89	125.33
2	2	1518	MA6	C5-C6-N6	5.98	134.80	125.33
2	2	1498	UR3	C4-N3-C2	-5.81	119.90	124.58
2	2	1519	MA6	N1-C2-N3	-5.54	120.19	128.58
2	2	966	2MG	C5-C4-N3	-5.40	119.79	128.39
2	2	1518	MA6	N1-C2-N3	-5.39	120.42	128.58
2	2	1516	2MG	N1-C2-N2	5.35	122.03	116.56
2	2	1207	2MG	C5-C4-N3	-5.31	119.93	128.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1519	MA6	C5-C4-N3	-5.06	119.75	126.72
2	2	1518	MA6	C5-C4-N3	-4.89	119.98	126.72
2	2	516	PSU	C4-N3-C2	-4.86	119.67	126.37
2	2	516	PSU	N1-C2-N3	4.84	120.28	115.17
2	2	1516	2MG	C5-C4-N3	-4.81	120.73	128.39
2	2	1516	2MG	C2-N1-C6	-4.71	118.86	124.55
2	2	527	G7M	C2-N3-C4	4.56	120.15	112.30
2	2	1518	MA6	C4-C5-C6	4.49	120.55	115.91
2	2	966	2MG	C2-N1-C6	-4.46	119.16	124.55
2	2	1207	2MG	C2-N1-C6	-4.35	119.29	124.55
2	2	1519	MA6	C4-C5-C6	4.27	120.32	115.91
2	2	527	G7M	C5-C4-N3	-4.09	120.43	128.15
2	2	1519	MA6	N9-C8-N7	-3.99	108.28	113.94
2	2	527	G7M	C5-C6-N1	3.92	119.94	111.84
2	2	1518	MA6	N9-C8-N7	-3.92	108.38	113.94
2	2	1498	UR3	C5-C4-N3	3.77	120.00	115.04
2	2	1519	MA6	C2-N3-C4	3.35	120.02	111.83
2	2	527	G7M	O6-C6-C5	-3.31	120.61	128.01
6	6	34	KEO	CB-CA-C	-3.31	105.89	110.99
2	2	1518	MA6	C2-N1-C6	3.25	119.77	111.83
2	2	1516	2MG	CM2-N2-C2	-3.24	116.69	123.65
2	2	1518	MA6	C2-N3-C4	3.17	119.56	111.83
2	2	1519	MA6	C2-N1-C6	3.16	119.54	111.83
2	2	1407	5MC	C5-C6-N1	-3.15	119.89	123.31
2	2	966	2MG	N9-C4-N3	3.13	132.21	125.95
2	2	1207	2MG	N9-C4-N3	3.11	132.18	125.95
2	2	966	2MG	N1-C2-N2	3.09	119.72	116.56
2	2	1518	MA6	N3-C4-N9	3.05	132.35	127.17
2	2	527	G7M	C2-N1-C6	-3.01	119.65	125.11
2	2	1519	MA6	N3-C4-N9	3.01	132.28	127.17
2	2	1516	2MG	N9-C8-N7	-3.00	107.84	113.40
2	2	966	2MG	N9-C8-N7	-2.96	107.92	113.40
2	2	967	5MC	C5-C6-N1	-2.93	120.13	123.31
2	2	1207	2MG	N1-C2-N2	2.93	119.55	116.56
2	2	1207	2MG	N9-C8-N7	-2.89	108.04	113.40
2	2	966	2MG	C5-C6-N1	2.74	120.22	113.25
2	2	1207	2MG	C5-C6-N1	2.73	120.20	113.25
2	2	1516	2MG	C5-C6-N1	2.71	120.15	113.25
2	2	1516	2MG	N2-C2-N3	-2.61	117.18	120.51
2	2	1516	2MG	O6-C6-C5	-2.61	119.64	126.53
2	2	527	G7M	N9-C8-N7	-2.59	106.18	112.48
2	2	1519	MA6	C5-N7-C8	2.58	107.51	103.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1518	MA6	C5-N7-C8	2.57	107.49	103.45
2	2	516	PSU	C6-N1-C2	-2.55	120.32	122.69
2	2	966	2MG	O6-C6-C5	-2.53	119.85	126.53
2	2	1207	2MG	O6-C6-C5	-2.52	119.88	126.53
6	6	34	KEO	C06-C05-NZ	2.41	119.69	115.97
2	2	1402	4OC	CM4-N4-C4	-2.38	117.80	122.45
2	2	1498	UR3	C1'-N1-C2	2.28	120.78	117.04
2	2	1516	2MG	N9-C4-N3	2.17	130.29	125.95
2	2	527	G7M	C5-C4-N9	2.12	110.40	105.88
2	2	966	2MG	C8-N7-C5	2.09	107.99	104.26
2	2	1518	MA6	C4-N9-C8	2.05	107.89	105.74
2	2	1207	2MG	C8-N7-C5	2.04	107.89	104.26
2	2	966	2MG	CM2-N2-C2	-2.04	119.27	123.65
2	2	1402	4OC	C6-C5-C4	2.02	119.44	117.00
2	2	1207	2MG	CM2-N2-C2	-2.01	119.32	123.65
2	2	1516	2MG	C4-C5-N7	-2.01	107.48	110.67
2	2	1519	MA6	C4-N9-C8	2.01	107.85	105.74
2	2	1516	2MG	C8-N7-C5	2.01	107.84	104.26

There are no chirality outliers.

All (23) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	2	516	PSU	C2'-C1'-C5-C4
2	2	516	PSU	O4'-C1'-C5-C4
2	2	516	PSU	O4'-C1'-C5-C6
2	2	967	5MC	O4'-C4'-C5'-O5'
2	2	1519	MA6	O4'-C4'-C5'-O5'
6	6	34	KEO	CE-CD-CG-CB
6	6	34	KEO	CE-CD-CG-O01
6	6	34	KEO	CG-CD-CE-NZ
6	6	34	KEO	C05-C06-C07-C08
6	6	34	KEO	C05-C06-C07-N02
47	q	89	0TD	O-C-CA-CB
6	6	34	KEO	C06-C05-NZ-CE
2	2	527	G7M	C3'-C4'-C5'-O5'
2	2	967	5MC	C3'-C4'-C5'-O5'
6	6	34	KEO	O02-C05-NZ-CE
2	2	527	G7M	O4'-C4'-C5'-O5'
2	2	1402	4OC	O4'-C4'-C5'-O5'
2	2	1519	MA6	C3'-C4'-C5'-O5'
2	2	1402	4OC	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
47	q	89	0TD	CG-CB-SB-CSB
47	q	89	0TD	SB-CB-CG-OD1
2	2	527	G7M	C4'-C5'-O5'-P
2	2	1498	UR3	O4'-C4'-C5'-O5'

There are no ring outliers.

6 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	516	PSU	2	0
2	2	1207	2MG	1	0
2	2	966	2MG	1	0
2	2	1519	MA6	1	0
2	2	1518	MA6	2	0
6	6	34	KEO	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 587 ligands modelled in this entry, 586 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
58	LYS	5	101	5	7,8,9	0.62	0	3,8,10	0.17	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
58	LYS	5	101	5	-	0/6/7/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

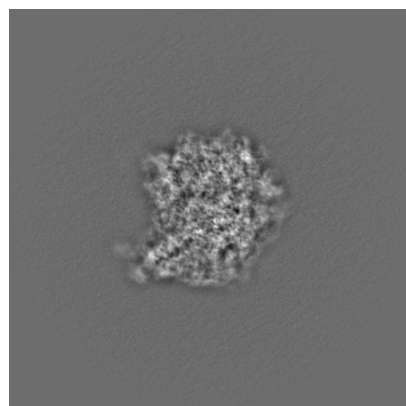
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43594. These allow visual inspection of the internal detail of the map and identification of artifacts.

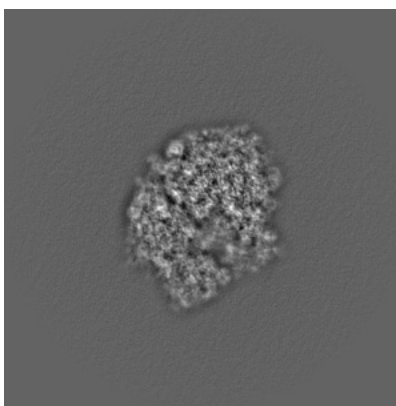
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

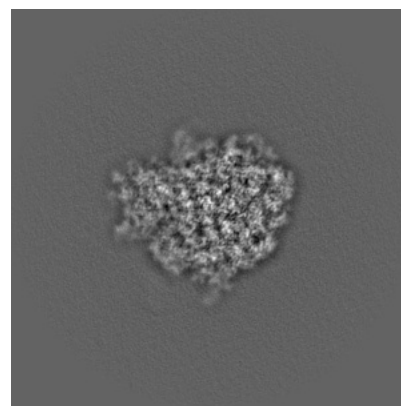
6.1.1 Primary map



X

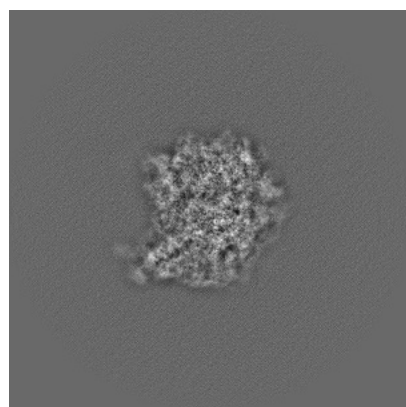


Y

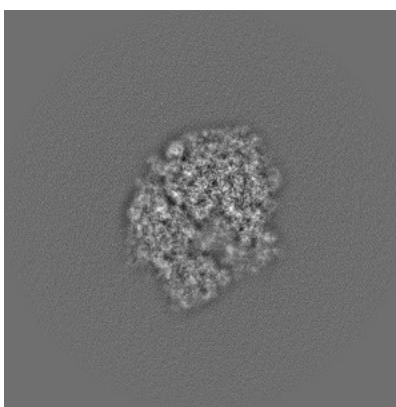


Z

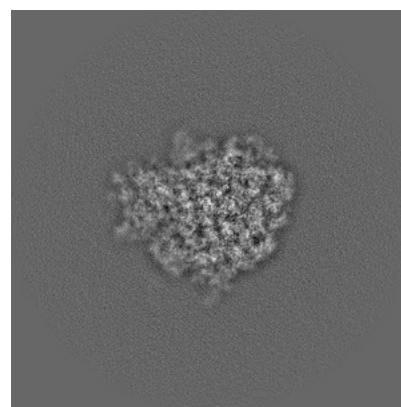
6.1.2 Raw map



X



Y

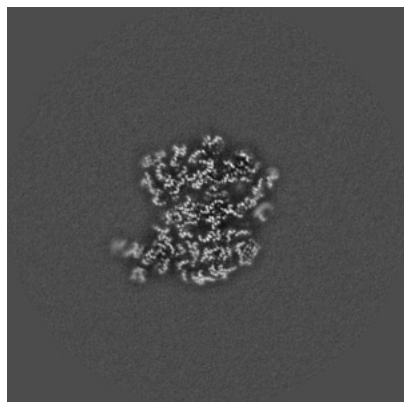


Z

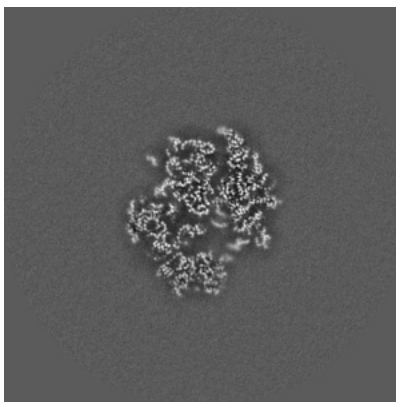
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

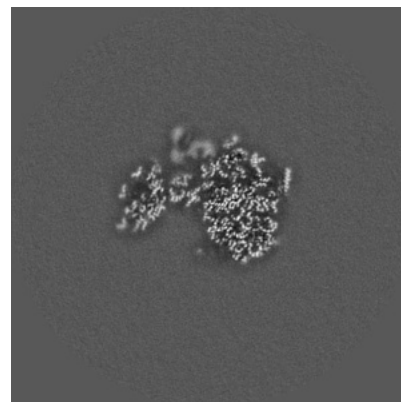
6.2.1 Primary map



X Index: 256

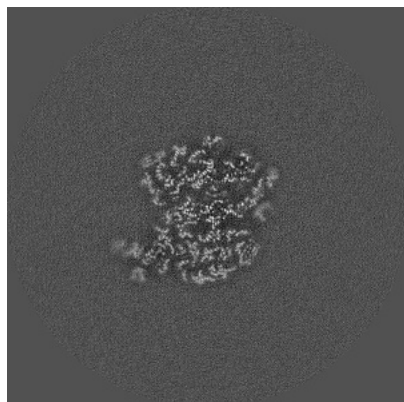


Y Index: 256

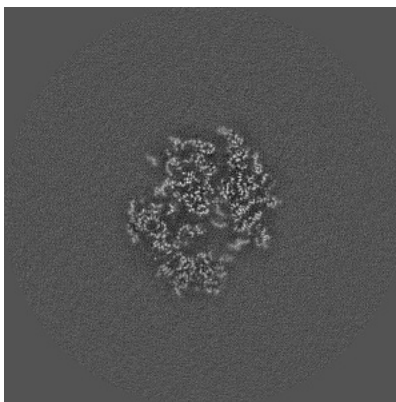


Z Index: 256

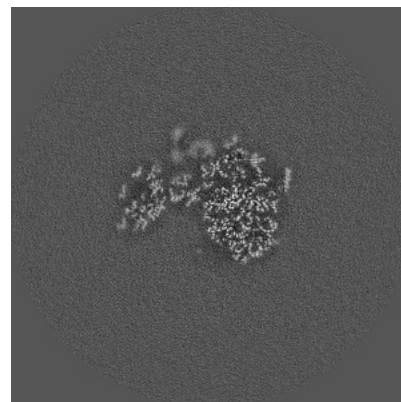
6.2.2 Raw map



X Index: 256



Y Index: 256

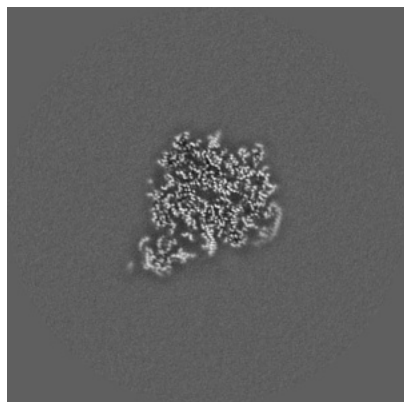


Z Index: 256

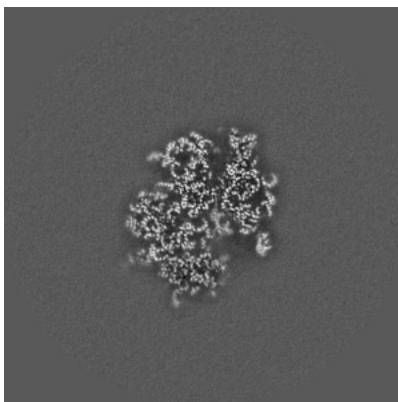
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

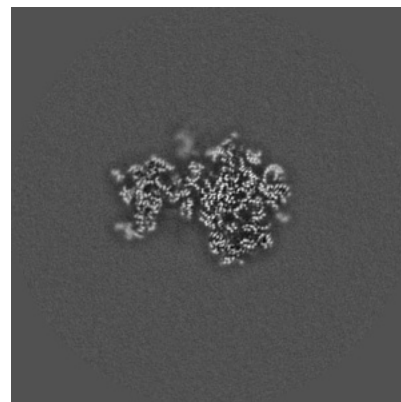
6.3.1 Primary map



X Index: 284

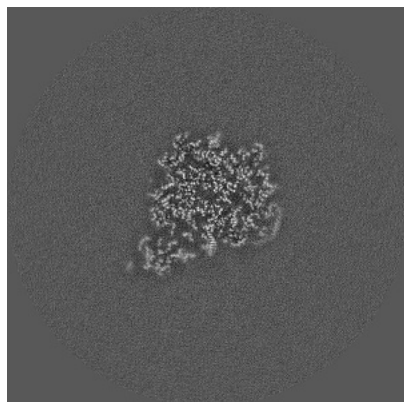


Y Index: 263

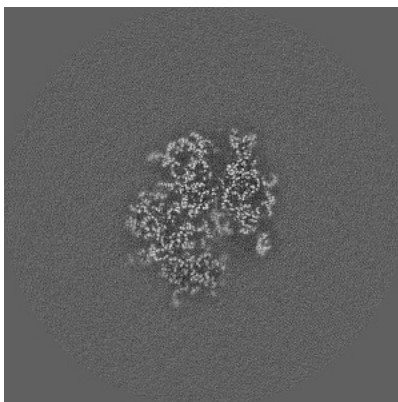


Z Index: 242

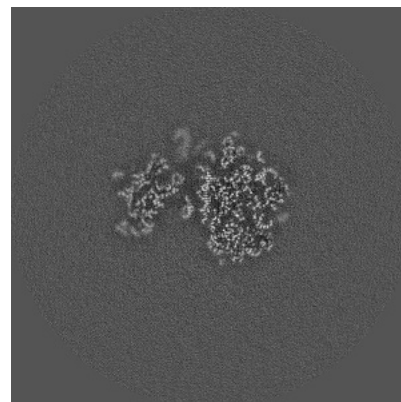
6.3.2 Raw map



X Index: 283



Y Index: 263

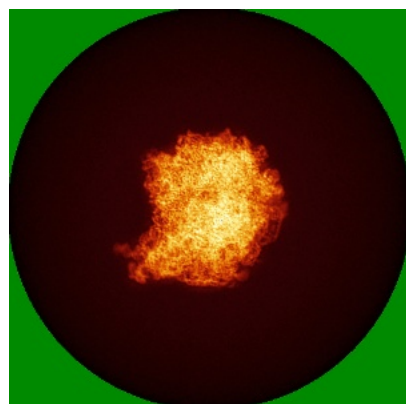


Z Index: 247

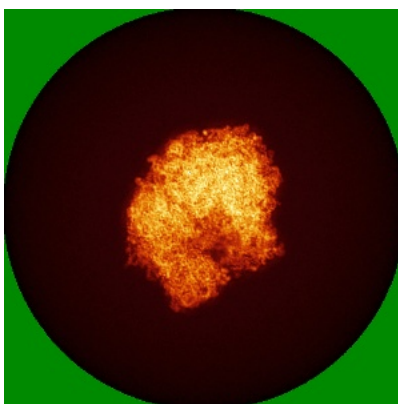
The images above show the largest variance slices of the map in three orthogonal directions.

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

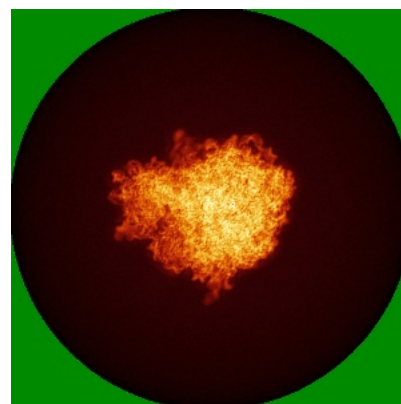
6.4.1 Primary map



X

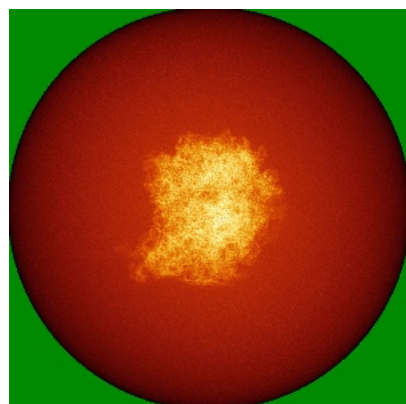


Y

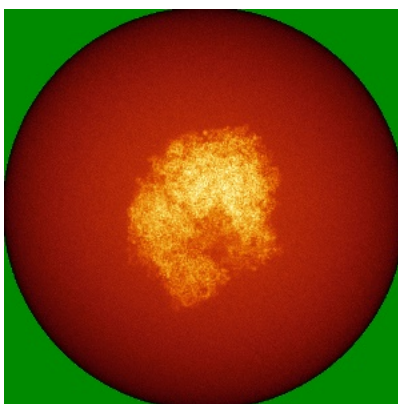


Z

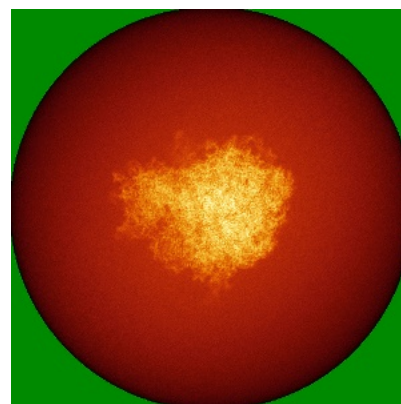
6.4.2 Raw map



X



Y

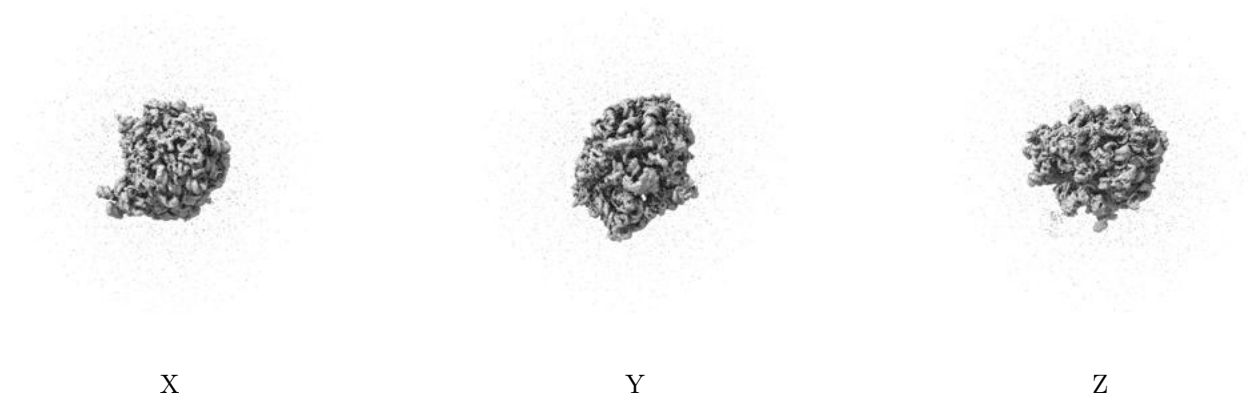


Z

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

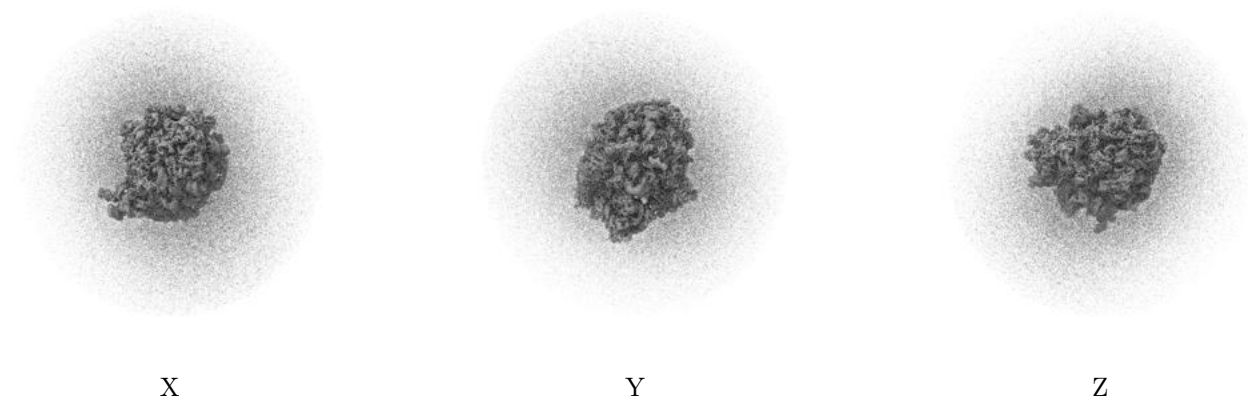
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0023. 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.

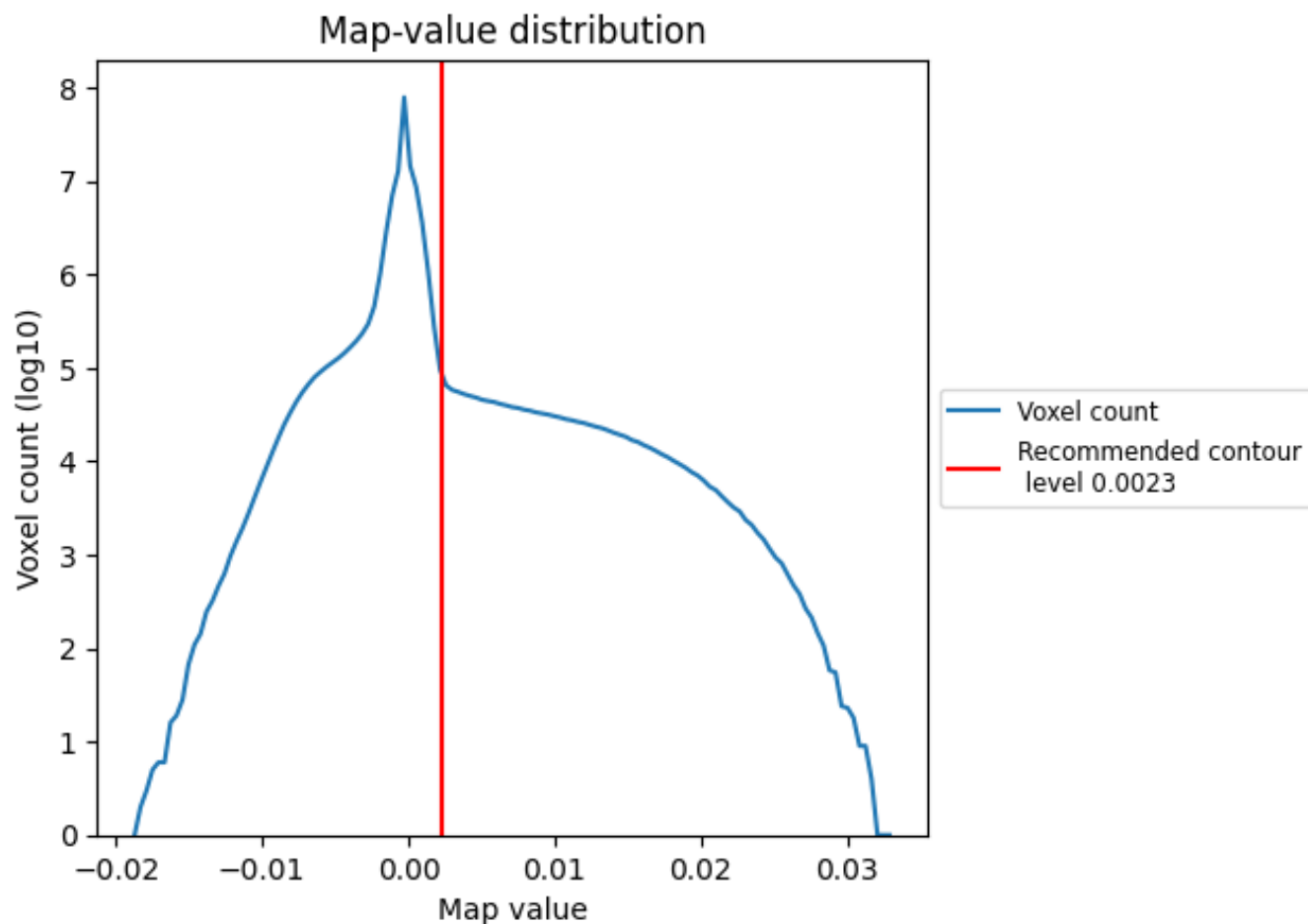
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

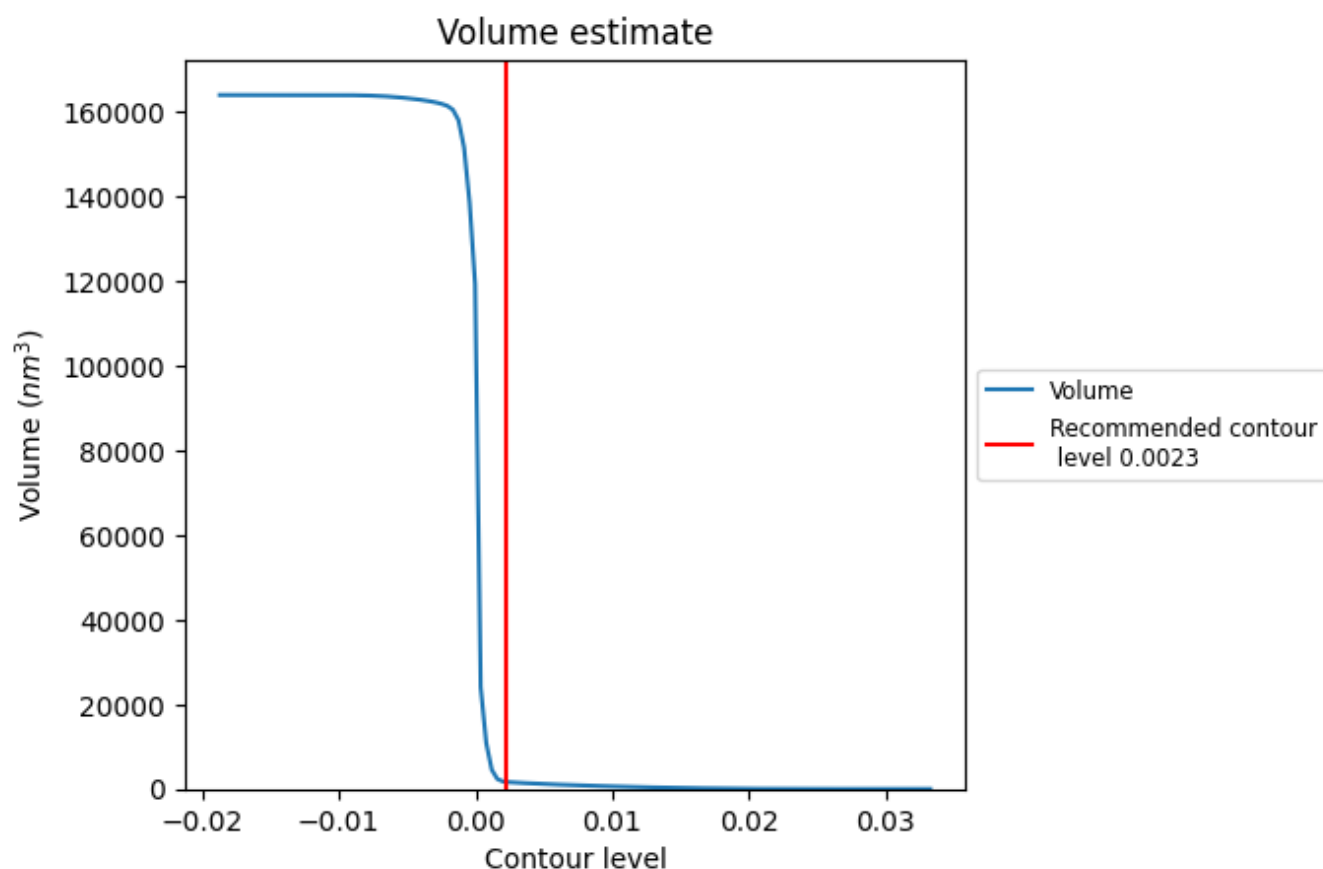
This section contains the results of statistical analysis of the map.

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.

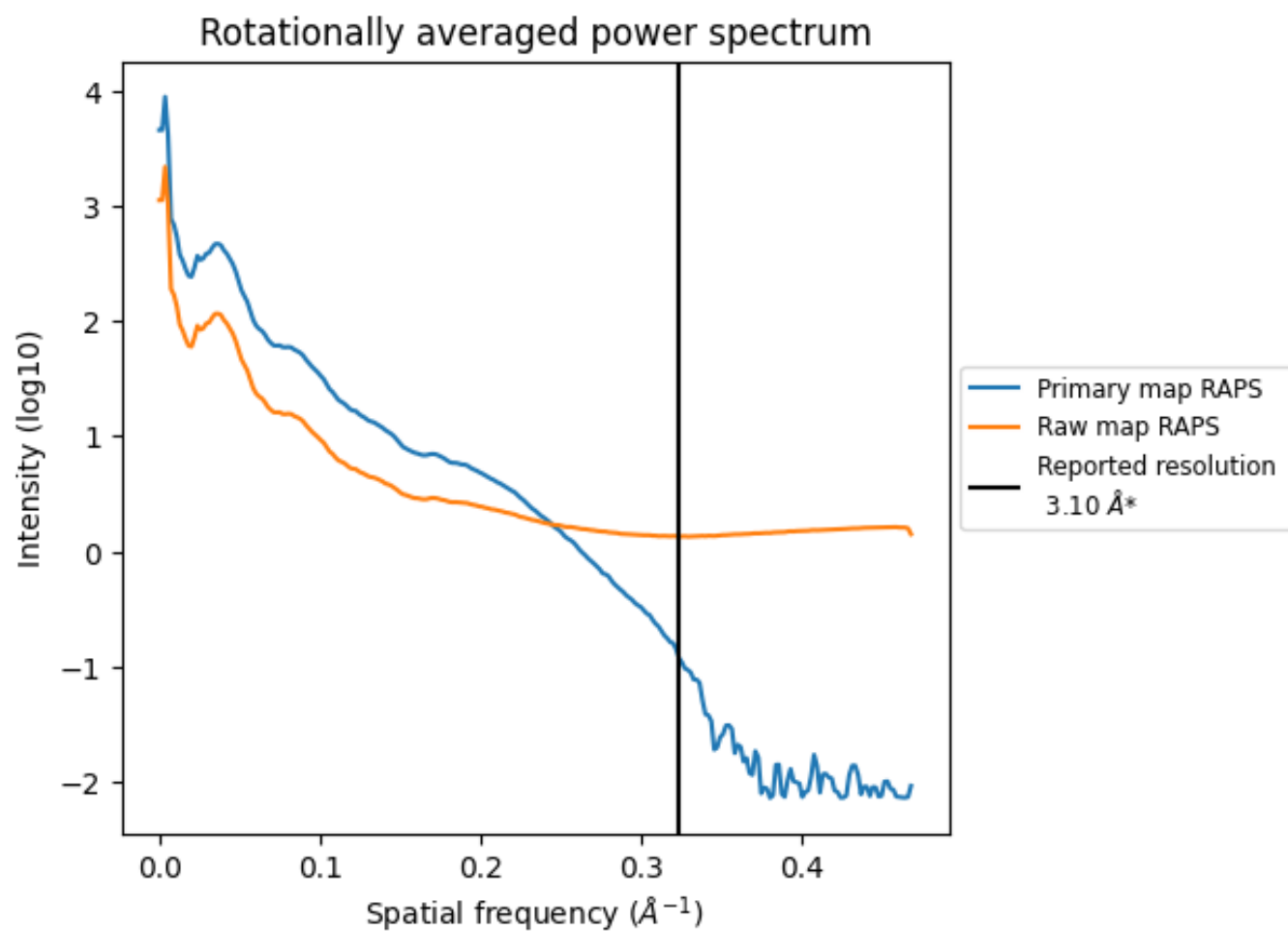
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1656 nm^3 ; this corresponds to an approximate mass of 1496 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 ⓘ

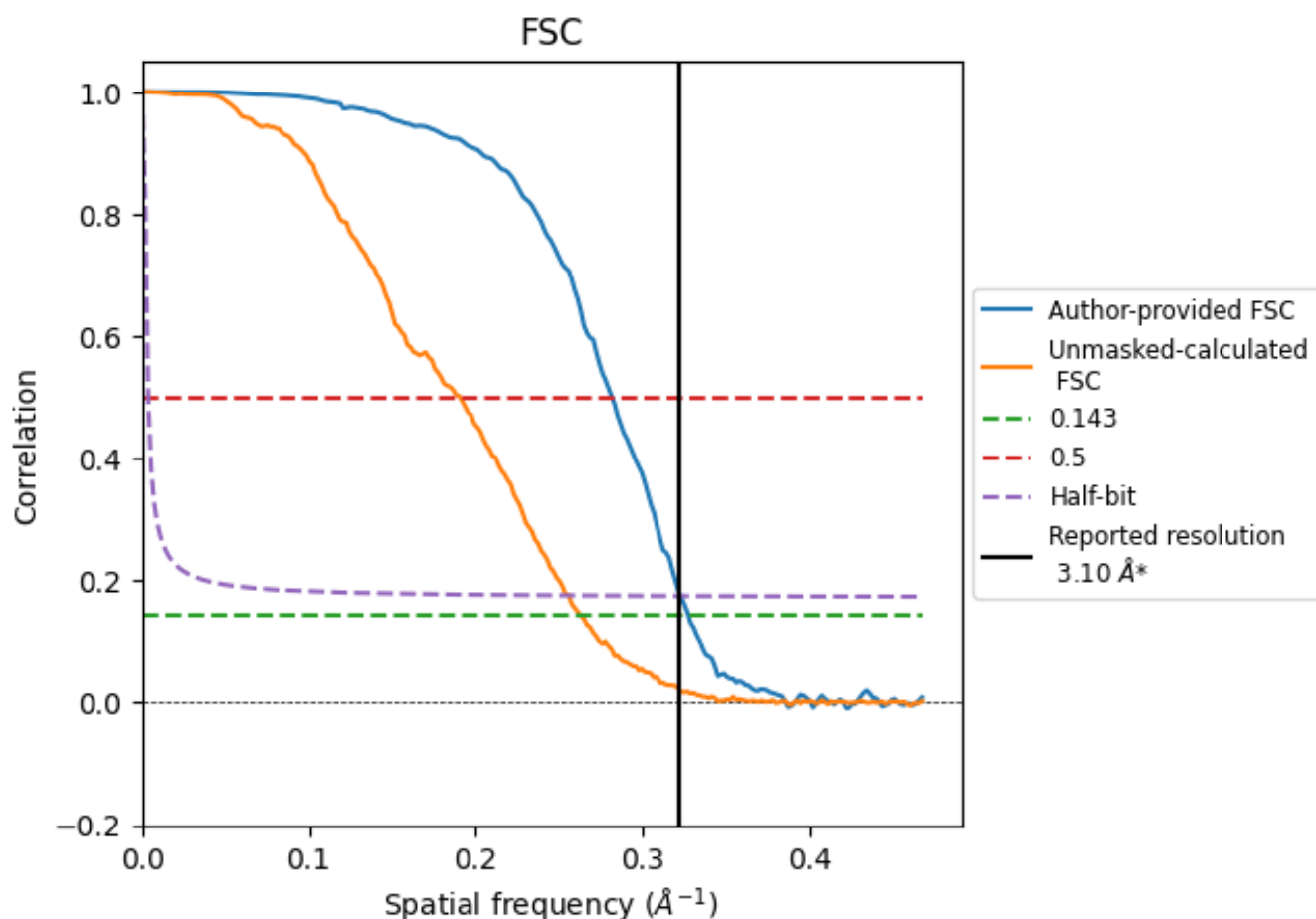


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

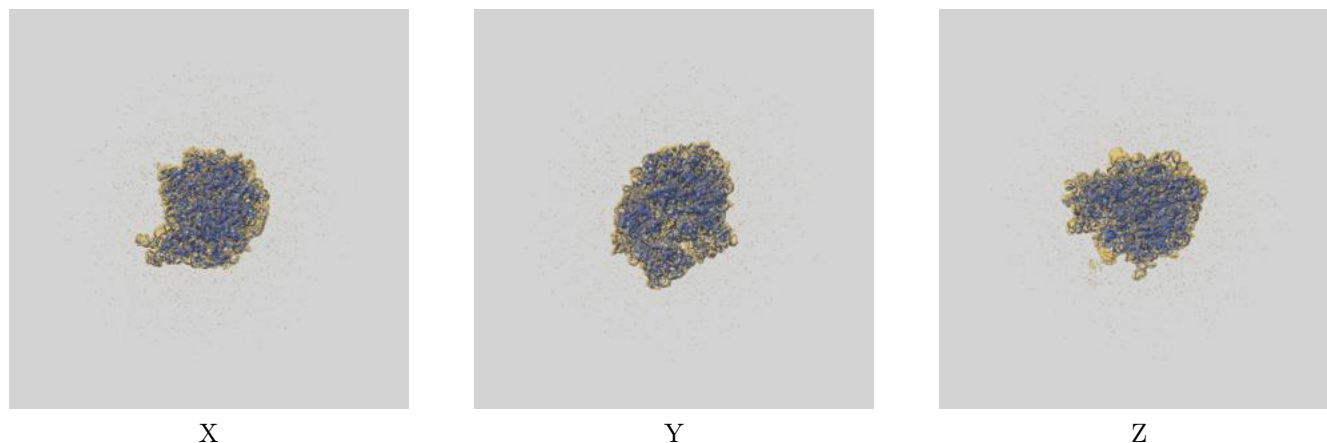
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.05	3.55	3.10
Unmasked-calculated*	3.80	5.25	3.91

*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 3.80 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

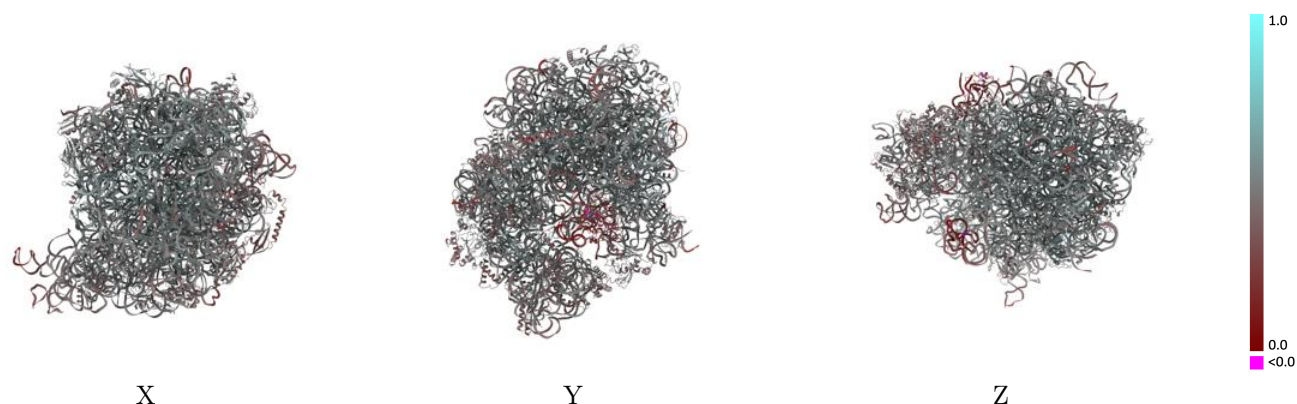
This section contains information regarding the fit between EMDB map EMD-43594 and PDB model 8VWQ. Per-residue inclusion information can be found in section [3](#) on page [19](#).

9.1 Map-model overlay [i](#)



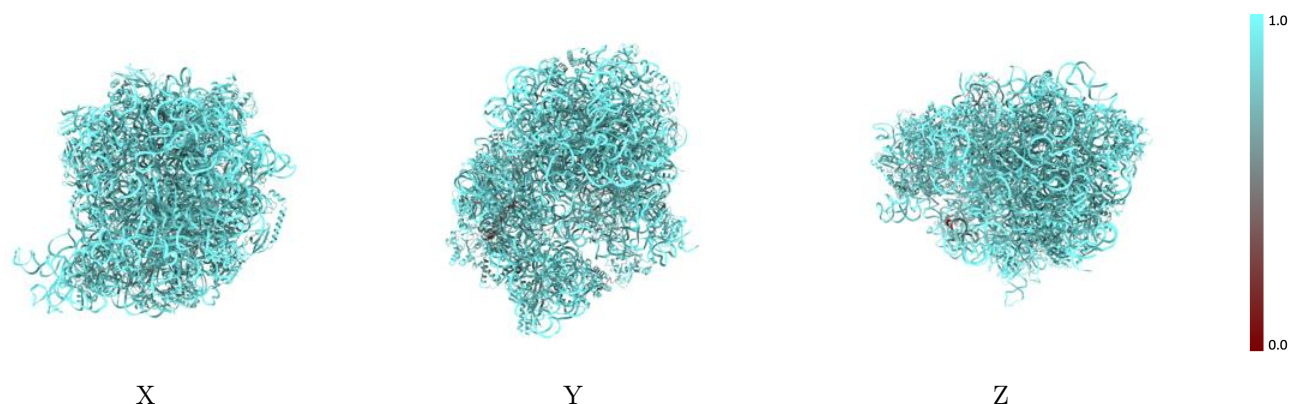
The images above show the 3D surface view of the map at the recommended contour level 0.0023 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



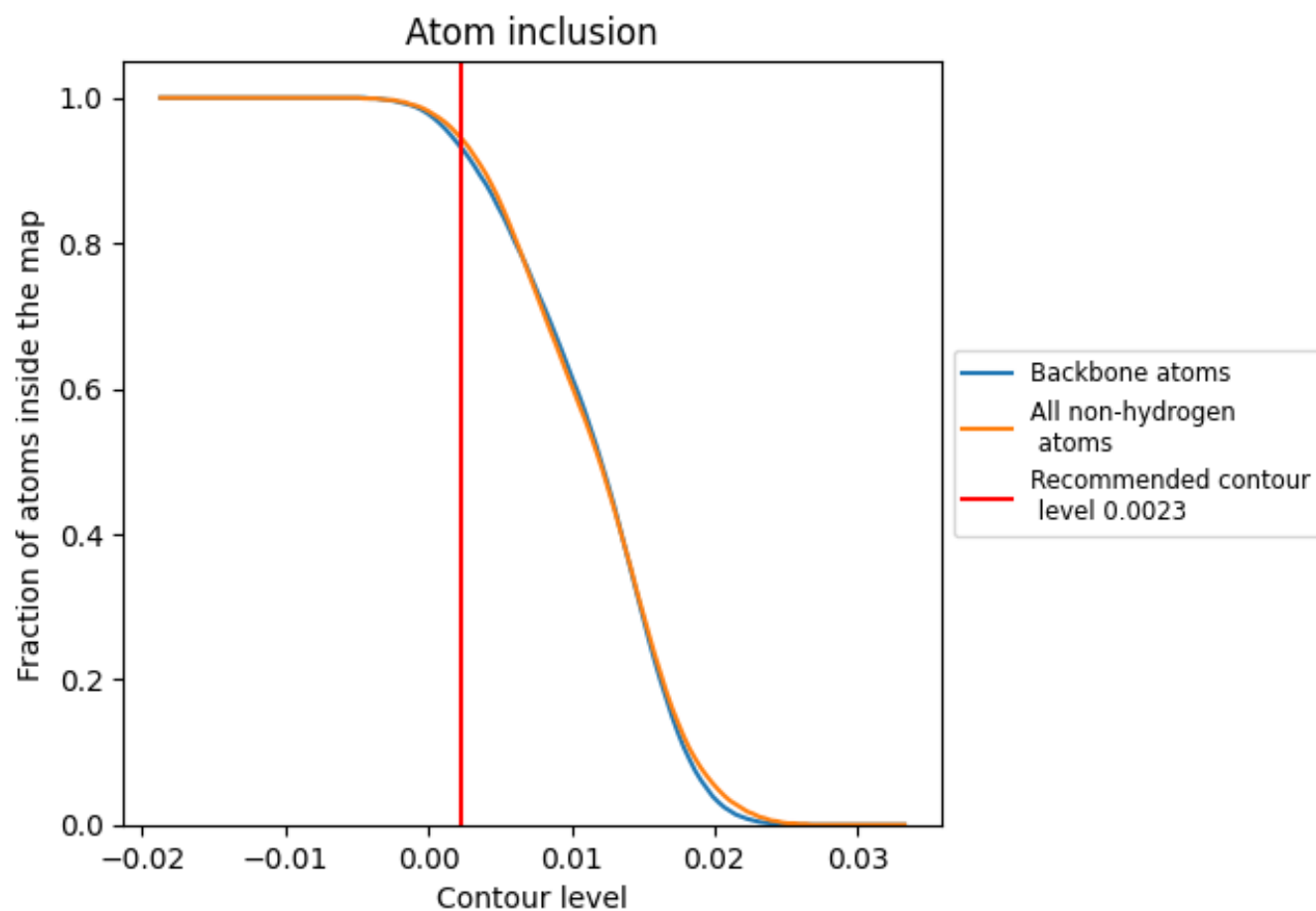
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0023).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 94% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.0023) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9440	 0.4750
1	 0.9790	 0.4840
2	 0.9850	 0.4730
3	 0.9850	 0.4610
4	 0.9100	 0.4850
5	 0.9730	 0.4640
6	 0.8240	 0.4480
A	 0.7380	 0.2340
B	 0.8930	 0.5280
C	 0.9100	 0.5210
D	 0.9090	 0.4940
E	 0.8720	 0.4350
F	 0.9250	 0.4600
G	 0.9080	 0.3910
J	 0.9050	 0.5090
K	 0.8940	 0.5170
L	 0.9040	 0.5120
M	 0.9000	 0.5140
N	 0.8990	 0.5160
O	 0.9000	 0.4650
P	 0.8970	 0.5120
Q	 0.8830	 0.4990
R	 0.9150	 0.5120
S	 0.8780	 0.5100
T	 0.8610	 0.4930
U	 0.9120	 0.4860
V	 0.9270	 0.4810
W	 0.8770	 0.5150
X	 0.8970	 0.5050
Y	 0.9060	 0.4420
Z	 0.9130	 0.5070
a	 0.7500	 0.3880
b	 0.8880	 0.5120
c	 0.8990	 0.4940
d	 0.8620	 0.5250



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Chain	Atom inclusion	Q-score
e	 0.8600	 0.5320
f	 0.8430	 0.5120
g	 0.8460	 0.4180
h	 0.9000	 0.4680
i	 0.8520	 0.4550
j	 0.8900	 0.4890
k	 0.8990	 0.4500
l	 0.8870	 0.4360
m	 0.9020	 0.4870
n	 0.8610	 0.4590
o	 0.8680	 0.4450
p	 0.9110	 0.4710
q	 0.8830	 0.4950
r	 0.8910	 0.4470
s	 0.8710	 0.4530
t	 0.8960	 0.4550
u	 0.9000	 0.4900
v	 0.9000	 0.4660
w	 0.8110	 0.4290
x	 0.8860	 0.4480
y	 0.8400	 0.4320
z	 0.5870	 0.4060