



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 12:41 PM UTC

PDB ID : 6WDC / pdb_00006wdc
EMDB ID : EMD-21631
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Cognate Structure IV-B)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 4.20 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

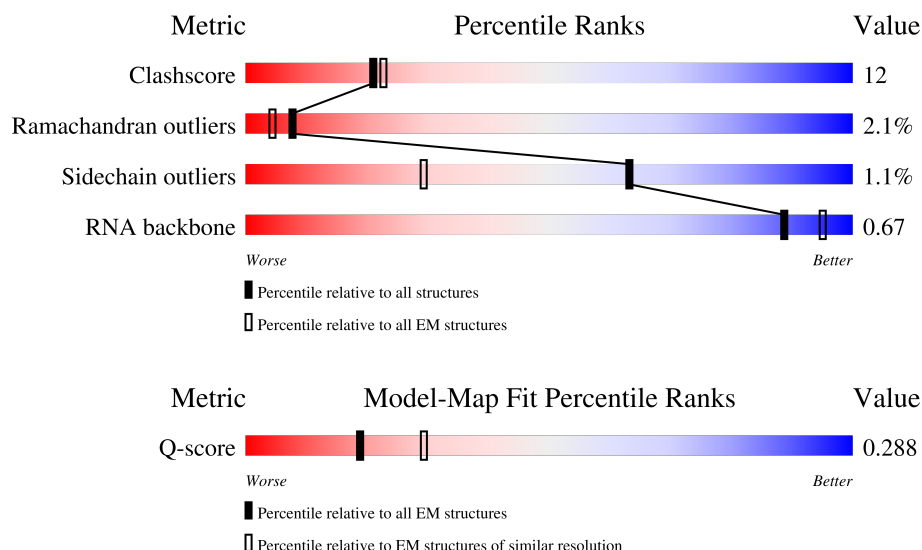
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 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.



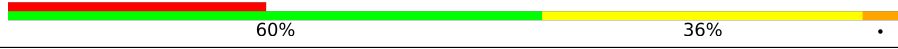
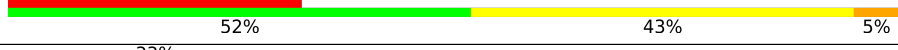
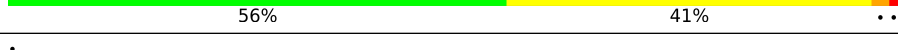
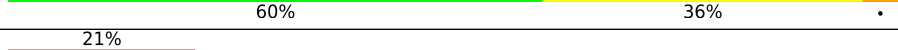
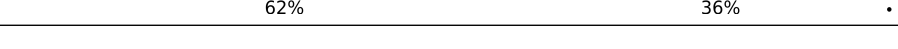
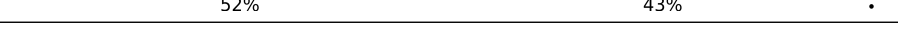
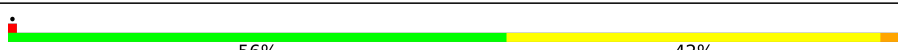
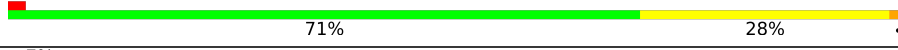
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	5410 (3.70 - 4.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	b	271	
2	c	209	
3	d	201	

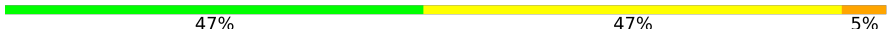
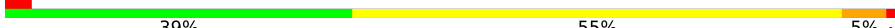
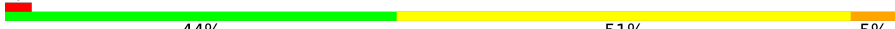
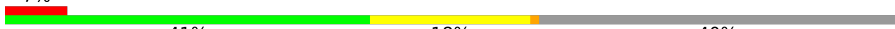
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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	B	56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

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Mol	Chain	Length	Quality of chain
29	E	64	
30	F	38	
31	G	225	
32	H	206	
33	I	205	
34	J	157	
35	K	100	
36	L	151	
37	M	129	
38	N	127	
39	O	98	
40	P	116	
41	Q	123	
42	R	114	
43	S	100	
44	T	88	
45	U	82	
46	V	80	
47	W	65	
48	X	79	
49	Y	85	
50	Z	65	
51	a	223	
52	3	1539	
53	1	2903	

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Mol	Chain	Length	Quality of chain
54	2	120	52% 41% 8%
55	5	77	61% 32% 6%
55	6	77	5% 66% 32%
56	4	18	56% 39% 6%
57	7	76	72% 14% 9%

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 150149 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 802133627

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

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	120	A	-	insertion	GB 1266961702

- Molecule 55 is a RNA chain called tRNA^fMet.

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

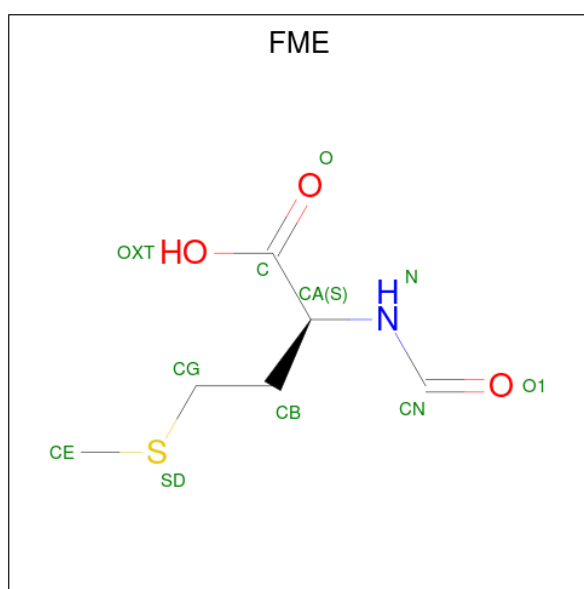
- Molecule 56 is a RNA chain called mRNA.

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

- Molecule 57 is a RNA chain called tRNA^{Phe}.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	7	73	Total	C	N	O	P	0	0
			1557	695	279	511	72		

- Molecule 58 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C₆H₁₁NO₃S).

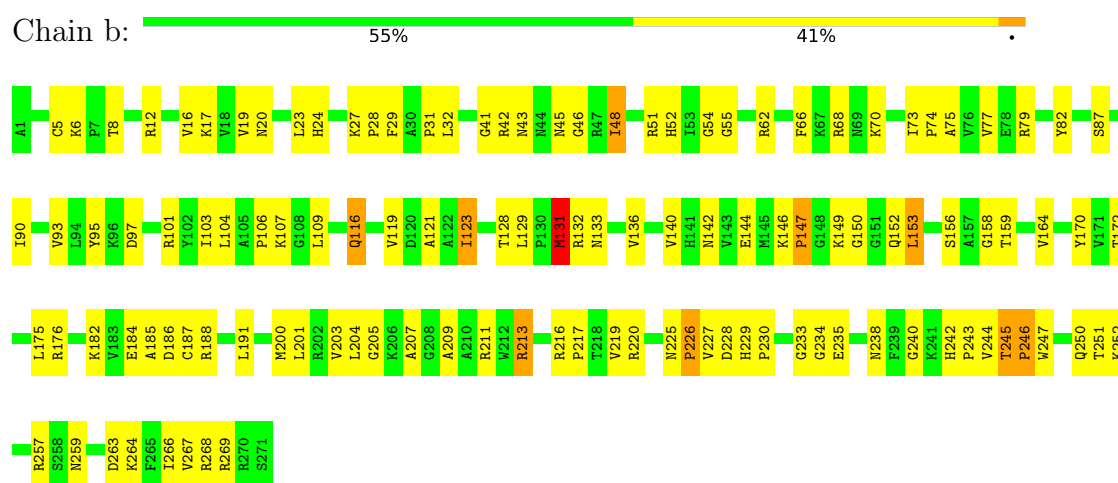


Mol	Chain	Residues	Atoms					AltConf
58	5	1	Total	C	N	O	S	0
			10	6	1	2	1	

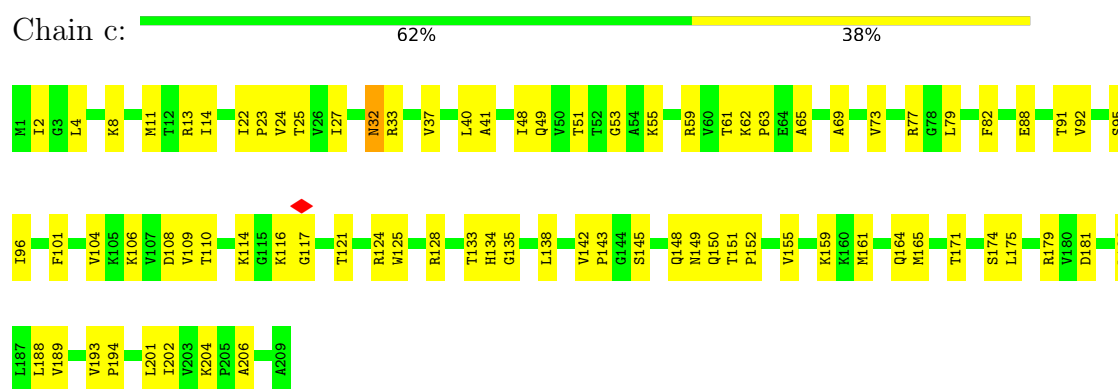
3 Residue-property plots

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

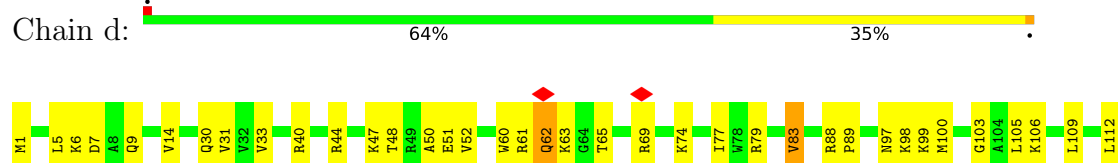
• Molecule 1: 50S ribosomal protein L2



• Molecule 2: 50S ribosomal protein L3

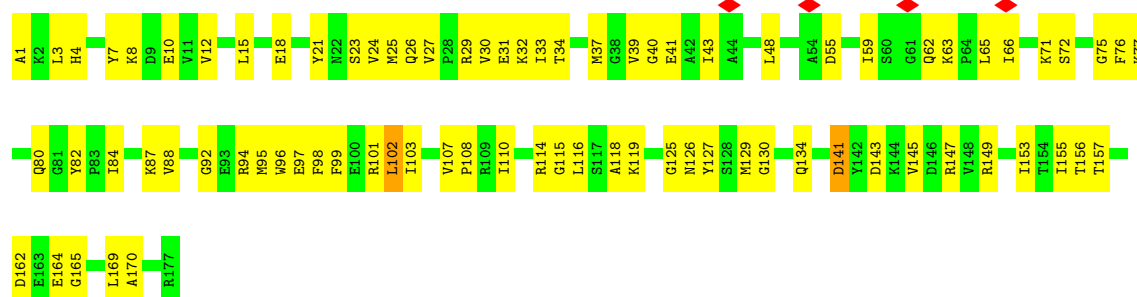


• Molecule 3: 50S ribosomal protein L4

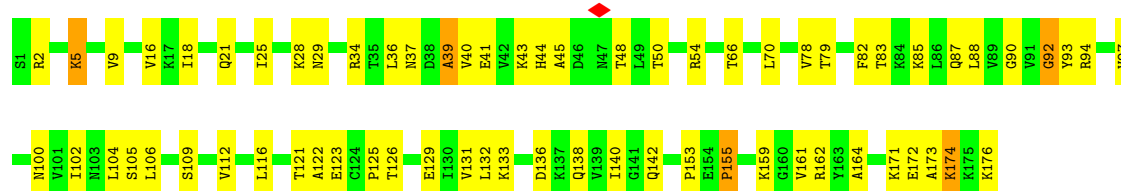




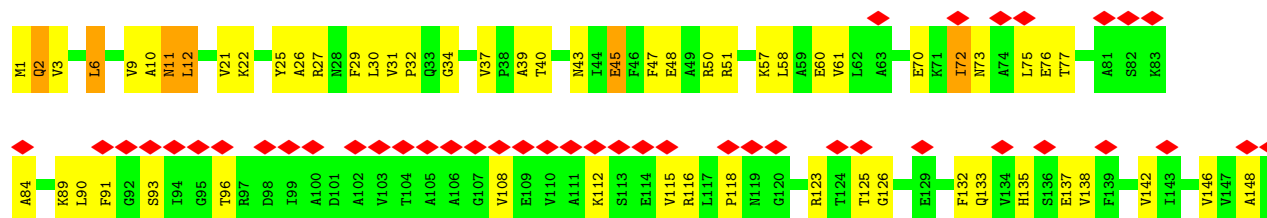
• Molecule 4: 50S ribosomal protein L5



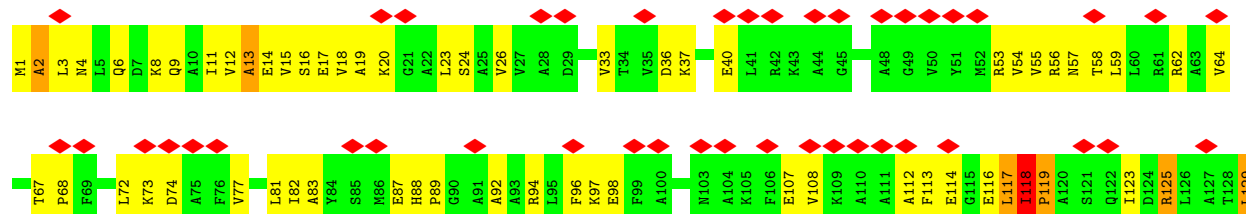
• Molecule 5: 50S ribosomal protein L6



• Molecule 6: 50S ribosomal protein L9

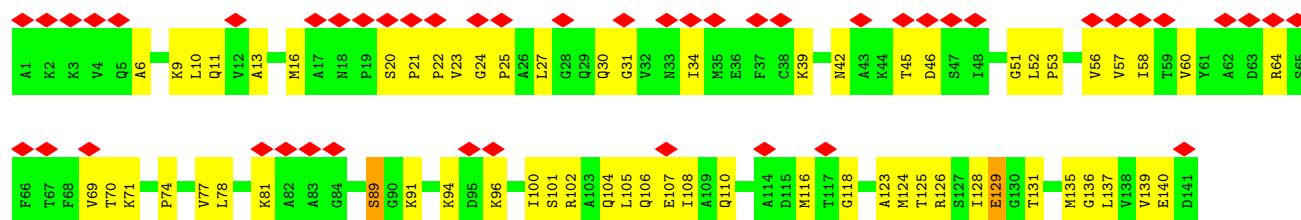


• Molecule 7: 50S ribosomal protein L10

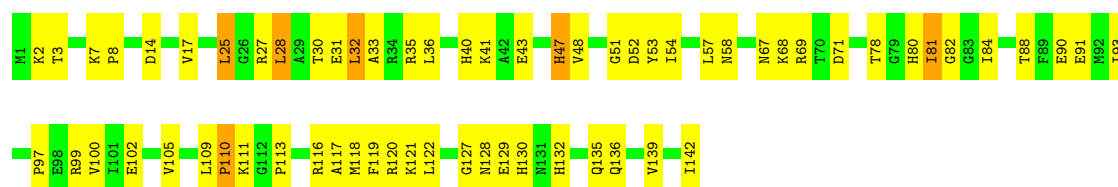




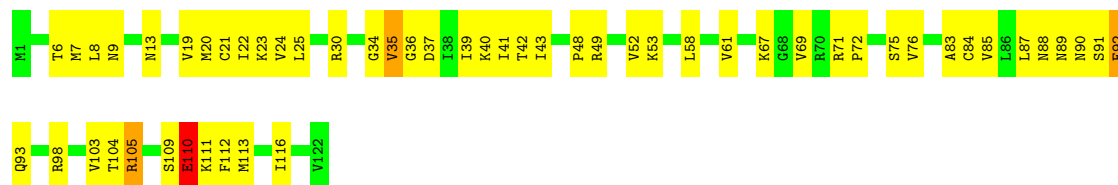
- Molecule 8: 50S ribosomal protein L11



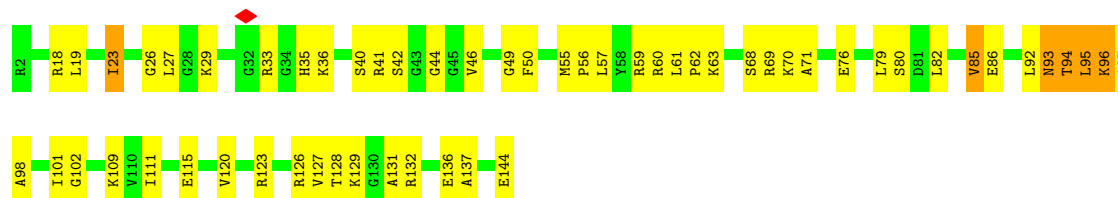
- Molecule 9: 50S ribosomal protein L13



- Molecule 10: 50S ribosomal protein L14

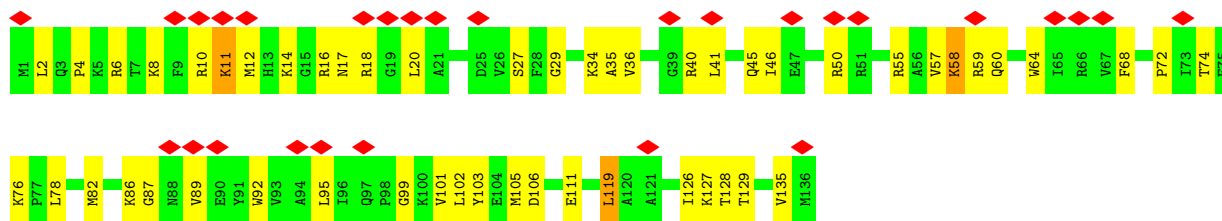


- Molecule 11: 50S ribosomal protein L15



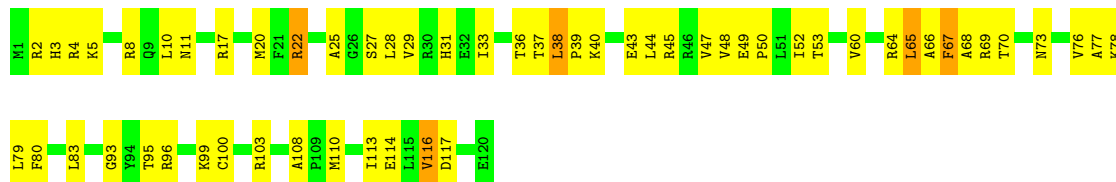
- Molecule 12: 50S ribosomal protein L16





• Molecule 13: 50S ribosomal protein L17

Chain n: 52% 43% .



• Molecule 14: 50S ribosomal protein L18

Chain o: 61% 34% .



• Molecule 15: 50S ribosomal protein L19

Chain p: 69% 27% .



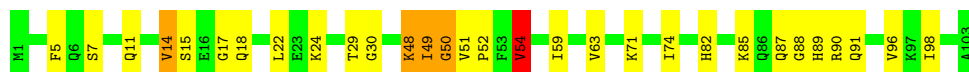
• Molecule 16: 50S ribosomal protein L20

Chain q: 71% 26% .

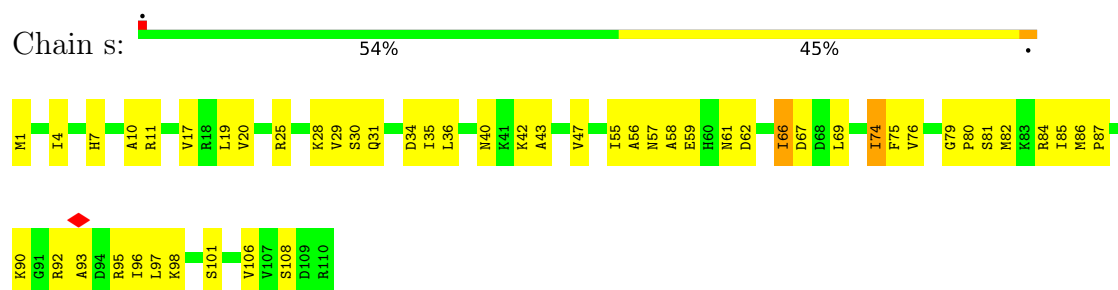


• Molecule 17: 50S ribosomal protein L21

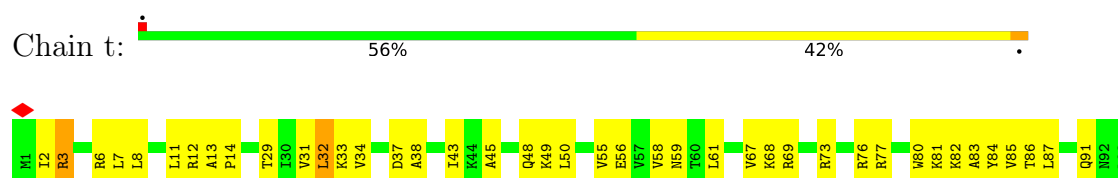
Chain r: 71% 24% . .



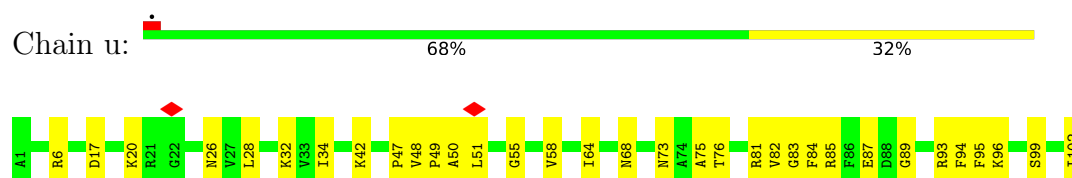
- Molecule 18: 50S ribosomal protein L22



- Molecule 19: 50S ribosomal protein L23



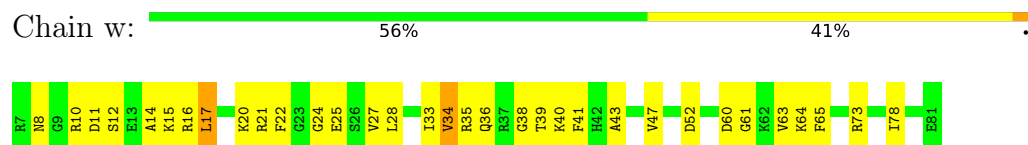
- Molecule 20: 50S ribosomal protein L24



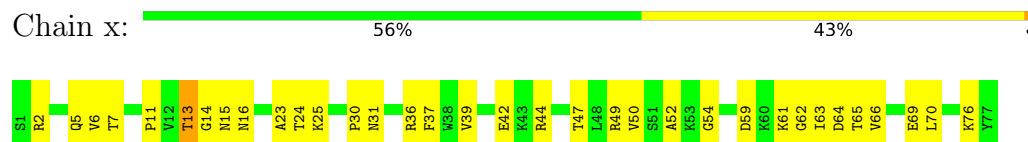
- Molecule 21: 50S ribosomal protein L25



- Molecule 22: 50S ribosomal protein L27



- Molecule 23: 50S ribosomal protein L28



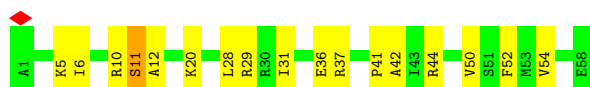
- Molecule 24: 50S ribosomal protein L29

Chain y:  71% 25%



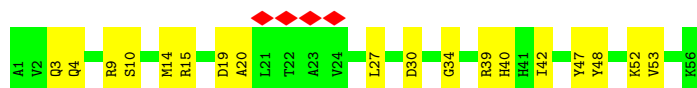
- Molecule 25: 50S ribosomal protein L30

Chain z:  71% 28%



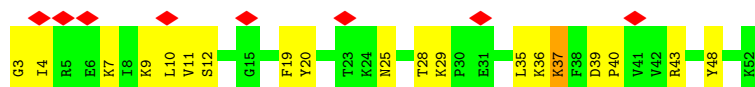
- Molecule 26: 50S ribosomal protein L32

Chain B:  7% 68% 32%



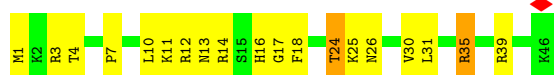
- Molecule 27: 50S ribosomal protein L33

Chain C:  16% 62% 36%



- Molecule 28: 50S ribosomal protein L34

Chain D:  59% 37%



- Molecule 29: 50S ribosomal protein L35

Chain E:  64% 30% 6%

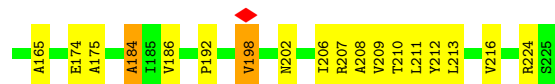
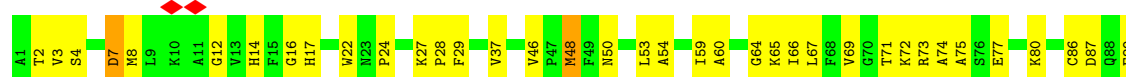


- Molecule 30: 50S ribosomal protein L36

Chain F:  47% 47% 5%



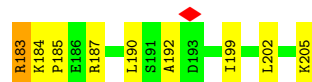
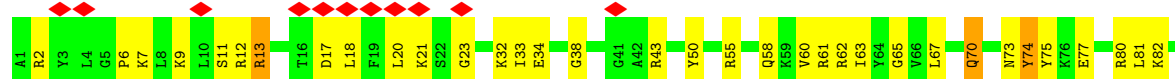
• Molecule 31: 30S ribosomal protein S2



• Molecule 32: 30S ribosomal protein S3

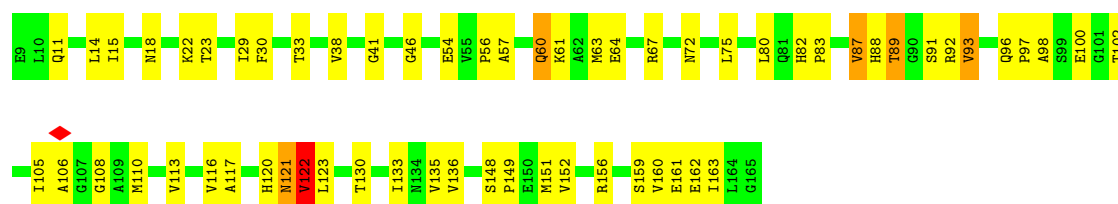


• Molecule 33: 30S ribosomal protein S4



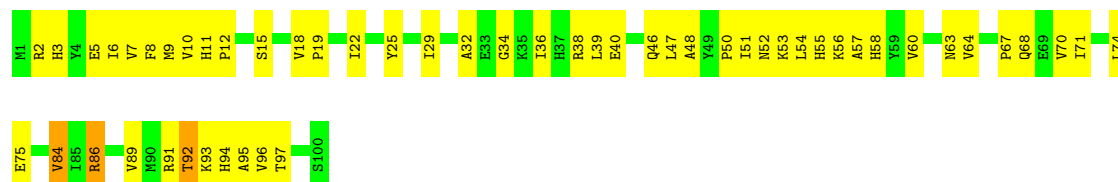
• Molecule 34: 30S ribosomal protein S5





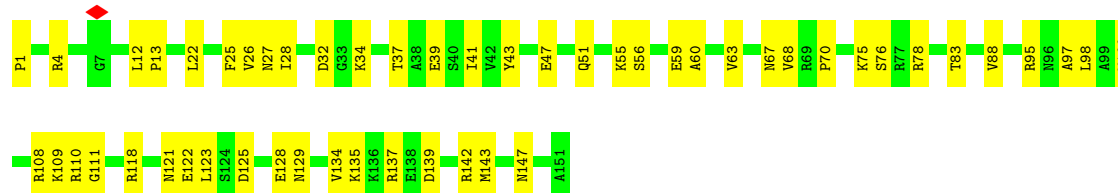
- Molecule 35: 30S ribosomal protein S6

Chain K: 47% 50% .



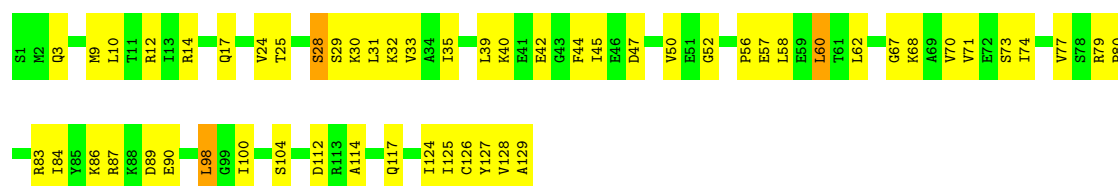
- Molecule 36: 30S ribosomal protein S7

Chain L: 66% 34% .



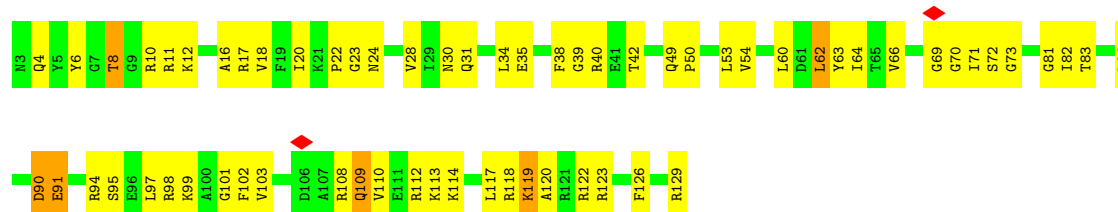
- Molecule 37: 30S ribosomal protein S8

Chain M: 57% 40% .

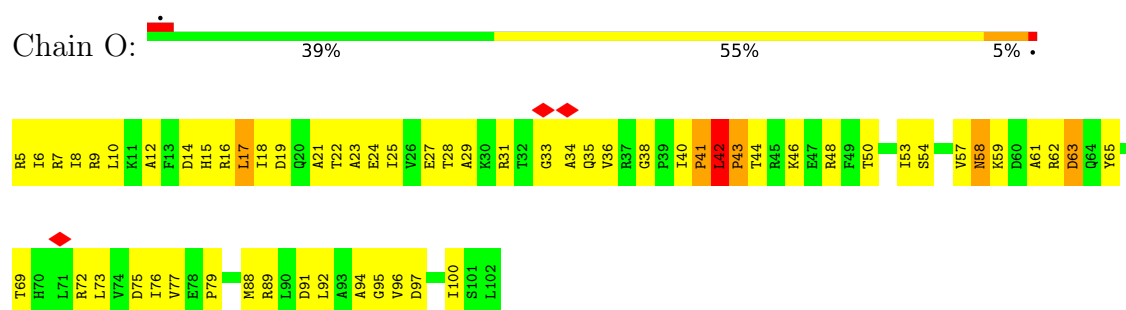


- Molecule 38: 30S ribosomal protein S9

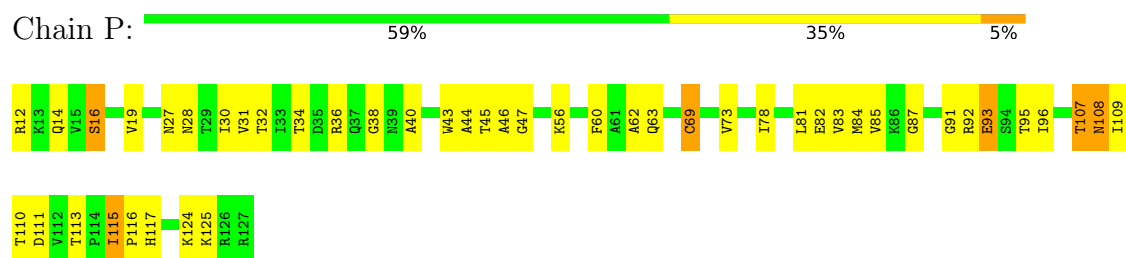
Chain N: 50% 46% 5% .



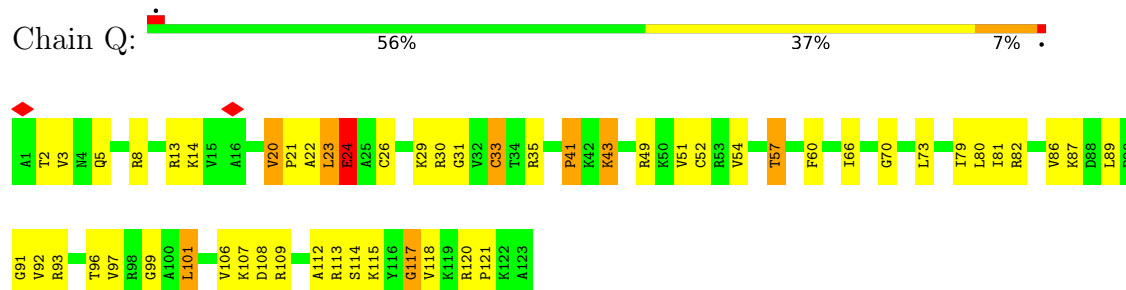
- Molecule 39: 30S ribosomal protein S10



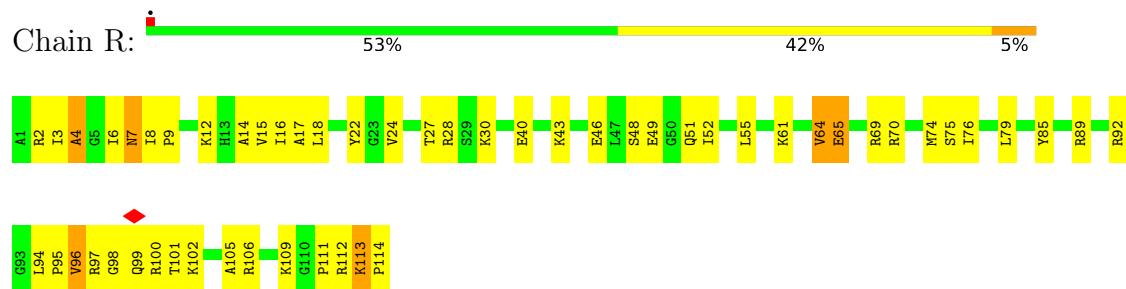
- Molecule 40: 30S ribosomal protein S11



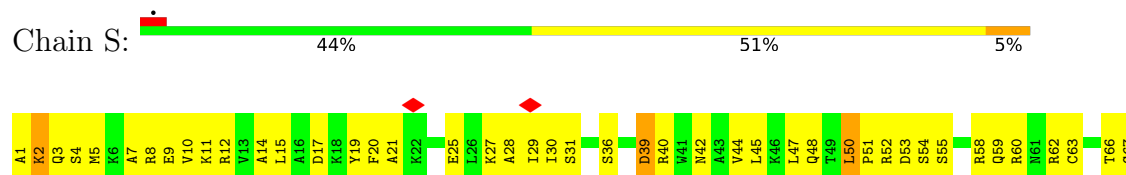
- Molecule 41: 30S ribosomal protein S12

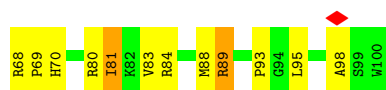


- Molecule 42: 30S ribosomal protein S13

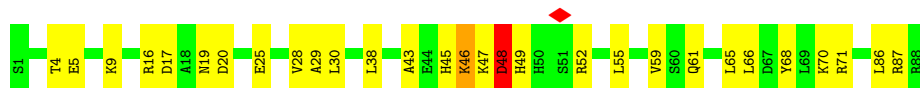


- Molecule 43: 30S ribosomal protein S14





- Molecule 44: 30S ribosomal protein S15



- Molecule 45: 30S ribosomal protein S16



- Molecule 46: 30S ribosomal protein S17



- Molecule 47: 30S ribosomal protein S18

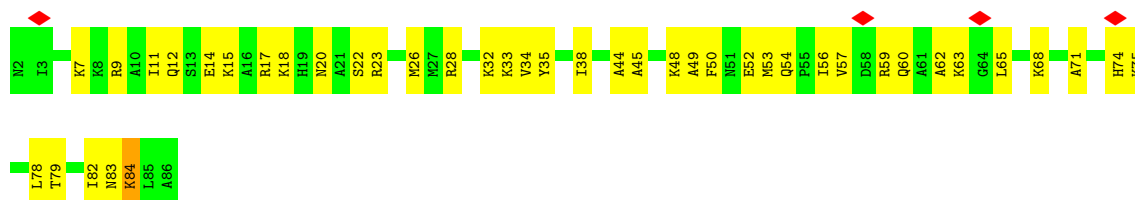


- Molecule 48: 30S ribosomal protein S19



- Molecule 49: 30S ribosomal protein S20

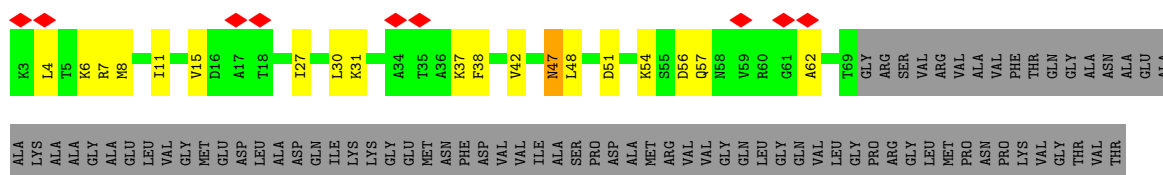




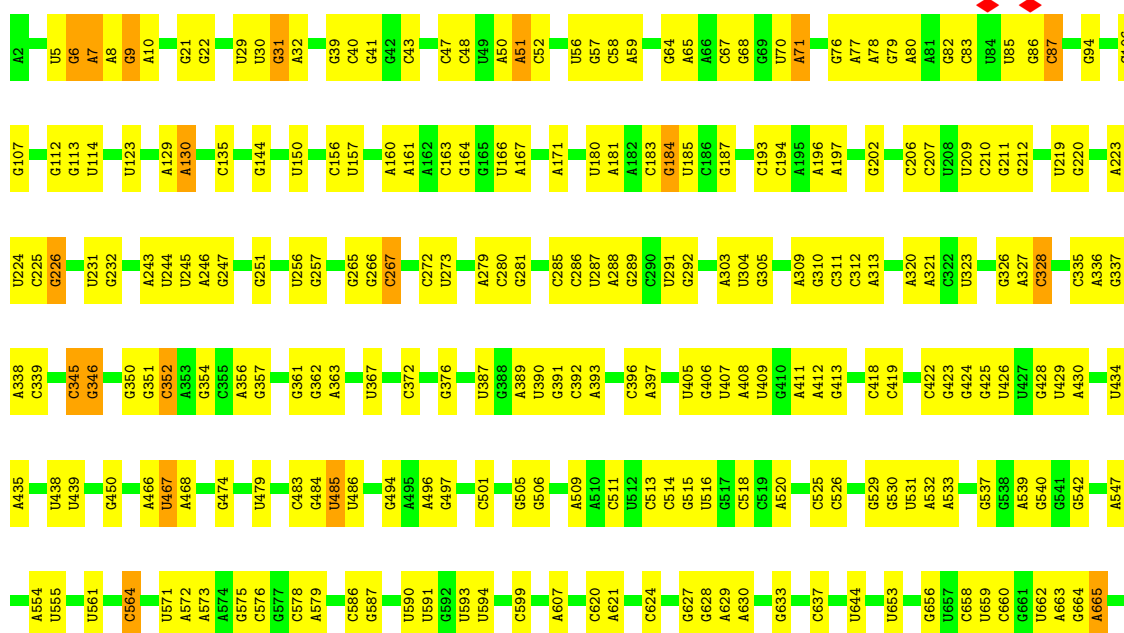
- Molecule 50: 30S ribosomal protein S21

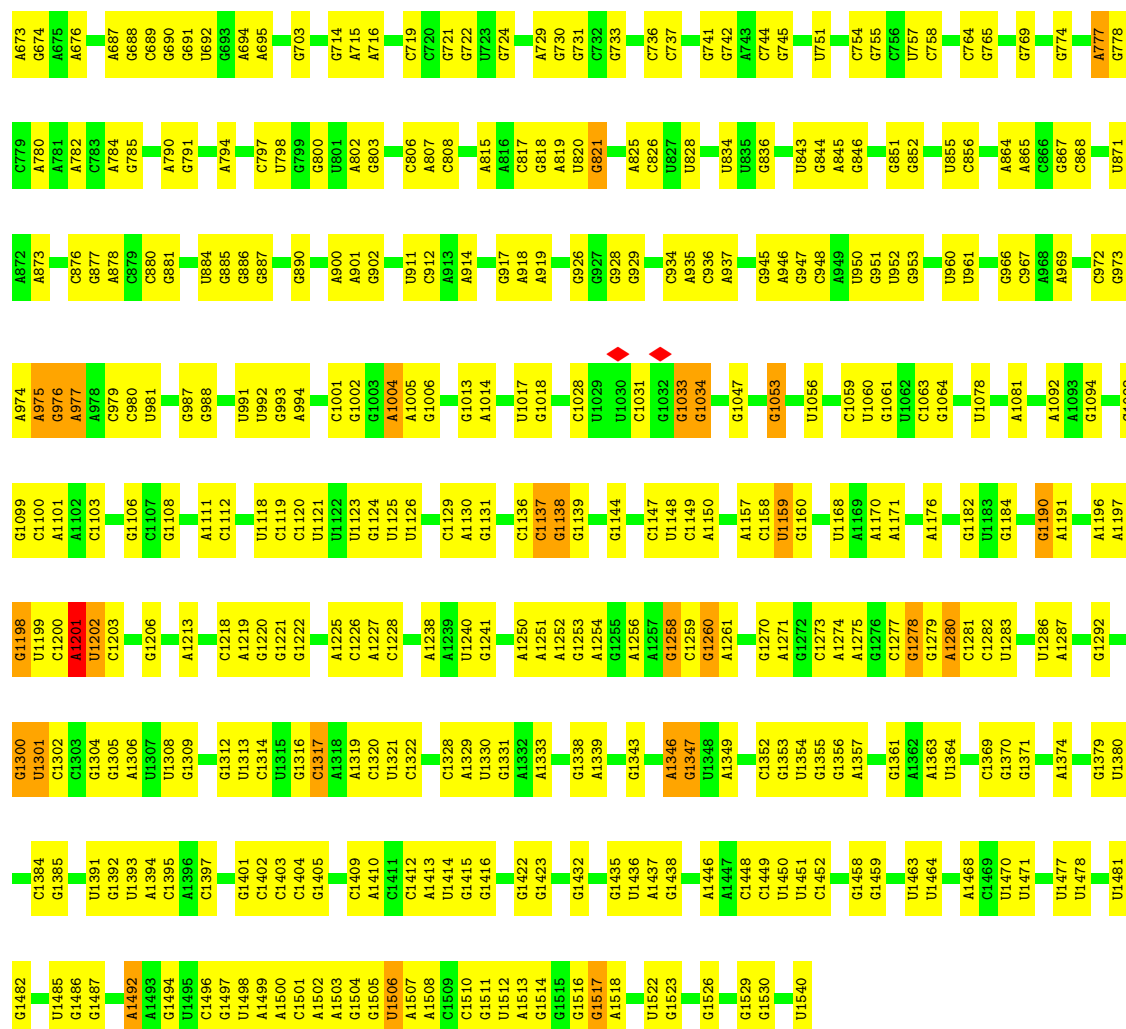


- Molecule 51: 50S ribosomal protein L1



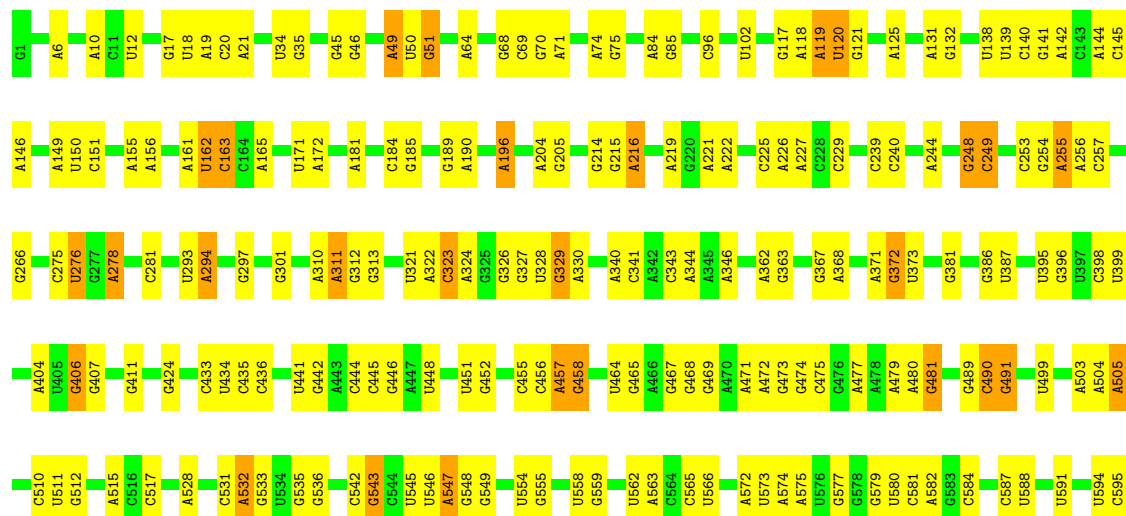
- Molecule 52: 16S ribosomal RNA



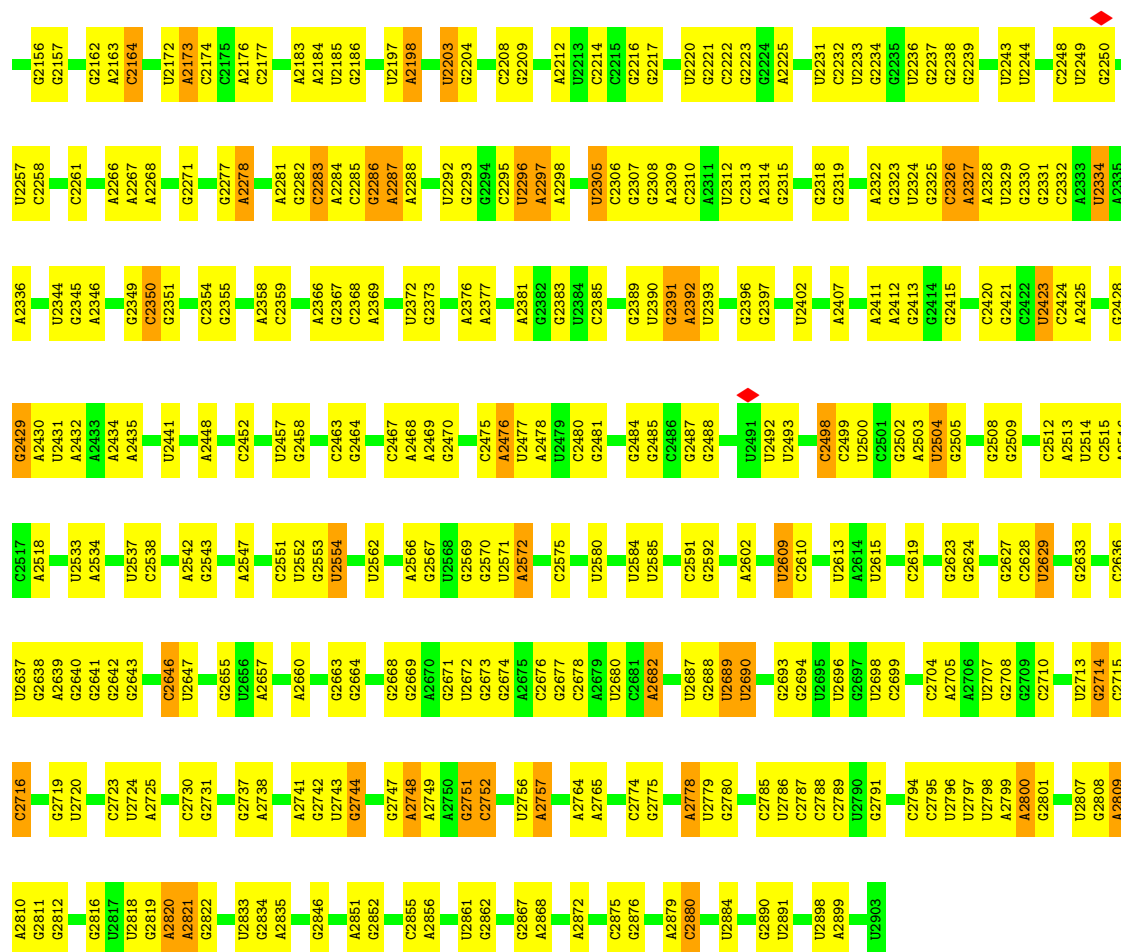


• Molecule 53: 23S ribosomal RNA

Chain 1: 60% 35% 5%

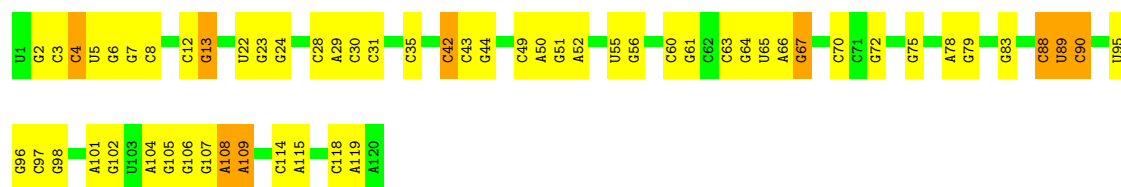


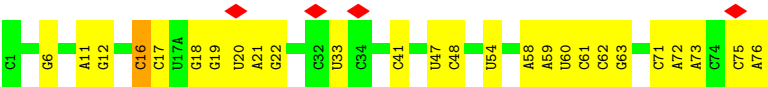
G2061	G1962	G1873	G1764	U1636	A1528	A1413	A1301	U1180	U1082	G994	U894	A781	U896
A2062	U1963	C1874	A1772	A1637	G1529	C1414	C1306	U1181	U1083	C995	U895	A782	G597
C2063	C1967	G1875	A1773	C1638	A1535	U1415	A1307	G1182	A1084	A996	A896	A783	G651
G2066	A1970	A1876	C1774	G1645	C1536	C1416	A1308	U1183	A1085	G997	A910	A785	A603
U2068	U1971	G1877	A1780	G1646	G1537	C1418	G1309	G1186	A1088	C1005	A911	A792	U606
G2069	G1972	A1878	U1781	U1647	G1538	A1419	U1313	G1187	A1089	C1006	C912	A793	U607
A2070	U1973	U1882	A1786	U1648	U1539	A1420	U1314	U1201	A1090	C1007	G913	A796	C611
A2071	A1977	U1883	U1786	G1651	C1540	G1421	C1320	G1202	G1093	U1012	C914	C796	G612
C2072	A1978	A1884	A1652	U1652	U1542	G1424	A1322	G1203	A1094	C1013	G915	G797	A613
U2082	U1979	A1885	C1790	G1653	G1543	G1425	A1323	A1205	A1095	A1014	A917	G798	A614
G2083	A1980	U1682	A1791	U1662	C1547	G1430	C1323	G1212	A1098	U1019	A918	G799	U615
U2086	A1890	G1663	U1682	A1664	A1548	A1431	U1326	U1216	C1104	A1020	C922	A800	A616
G2087	G1891	A1665	U1667	A1666	A1549	A1432	C1327	G1216	U1105	A1021	G923	A801	G617
A2088	C1892	G1666	G1674	G1667	C1550	A1433	A1328	U1224	G1106	U1022	G924	A806	G618
G2093	C1893	G1669	G1674	G1670	U1554	A1434	C1330	U1231	G1110	G1026	U929	A807	G619
A2094	C1894	G1671	G1677	G1678	G1555	A1435	C1331	G1232	A1111	A1027	U932	A808	G620
C2095	A1900	U1677	U1680	U1681	C1558	U1438	G1332	G1233	G1112	A1028	C937	A818	A621
G2096	A1901	U1681	U1682	U1683	G1560	A1439	C1333	U1234	G1122	A1029	G938	A819	G622
C2104	G1906	G1806	C1806	G1807	U1563	U1442	U1344	A1246	G1125	G1030	G940	A819	A631
U2105	G1907	A1807	A1808	U1699	C1564	U1443	U1345	A1247	U1130	A1032	G941	A820	A632
G2110	C1908	A1809	U1700	G1700	C1565	C1454	G1346	G1248	U1131	U1033	G942	A821	A633
U2111	G1909	A1810	G1701	U1701	C1566	C1455	G1347	U1249	U1132	G1034	A943	A822	G634
U2112	C1910	G1811	G1702	U1702	C1567	C1456	A1353	G1250	U1133	U1035	C946	A823	C635
U2113	U1911	G1812	G1703	G1703	A1569	A1469	A1354	G1251	U1134	G1036	C947	A824	C636
G2118	A1912	C1813	C1704	U1704	G1581	A1470	C1357	G1252	U1135	G1037	C948	A825	A637
A2119	A1913	U1814	A1705	U1705	U1582	A1471	G1358	A1253	G1138	G1038	C949	A826	G638
G2120	U1914	A1815	G1715	G1715	U1583	U1472	A1359	A1254	U1139	C1045	G952	A827	U639
G2121	U1915	A1816	U1720	U1720	G1587	U1473	G1360	G1255	U1140	A1046	G953	A828	C640
A2122	A1916	U1825	G1721	G1721	A1590	G1482	A1365	G1256	U1141	A1047	U955	A829	A643
G2123	C1920	G1826	U1729	U1729	A1591	G1483	A1366	G1257	U1142	G1047	U956	A830	A644
G2124	G1921	U1827	C1730	C1730	A1592	U1484	A1367	G1258	A1143	G1051	U957	A831	G645
U2127	U1922	G1828	U1736	U1736	A1597	A1490	A1368	U1264	G1149	C1052	U958	A832	U646
G2128	C1923	A1829	U1737	U1737	A1598	G1491	A1373	A1268	U1150	C1053	C961	A833	C650
U2130	U1924	C1837	G1738	G1738	G1601	C1493	U1375	A1269	U1151	A1054	G962	A834	A654
U2131	G1929	G1846	U1742	U1742	U1602	U1496	A1376	A1270	C1152	G1055	C963	A835	A655
U2132	G1930	A1947	G1743	G1743	A1603	U1497	U1377	A1271	C1153	U1060	C964	A836	G656
G2133	A1936	U1947	U1744	U1744	C1604	C1498	A1378	A1272	U1156	U1061	C965	A837	C660
A2134	A1937	U1851	A1745	A1745	C1605	C1507	U1379	A1273	G1157	G1062	U970	A838	A661
U2139	A1938	U1852	U1746	U1746	C1606	A1508	A1383	A1274	G1161	G1063	G971	A839	G662
G2140	U1943	A1853	A1747	A1747	C1607	A1509	A1384	A1275	U1162	U1066	A973	A840	G663
G2141	U1944	U1854	G1753	G1753	A1608	A1510	C1386	C1278	G1163	A1067	C974	A841	G669
C2145	A1952	U1855	U1754	U1754	A1609	G1511	A1387	G1279	U1170	A1070	C975	A842	C672
A2147	A1953	G1857	A1755	A1755	C1611	G1512	G1388	C1280	G1171	G1071	G976	A843	C673
G2148	G1954	A1858	G1756	G1756	A1614	A1513	G1389	C1281	U1172	A1072	G977	A844	G674
U2149	U1955	U1859	A1757	A1757	C1615	G1524	U1394	G1282	U1173	U1077	C987	A845	A675
C2150	U1956	G1863	U1758	U1758	A1616	A1525	C1398	C1297	G1174	U1078	A988	A846	A676
U2151	A2060	A1871	C1760	C1760	A1635	G1527	U1412	G1300	G1175	C1079	U993	A847	A677



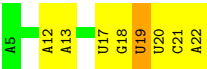
• Molecule 54: 5S ribosomal RNA

Chain 2: 52% 41% 8%

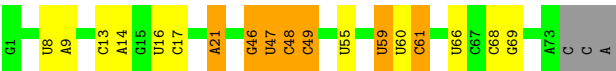




● Molecule 56: mRNA



● Molecule 57: tRNAPhe



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	1707	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	20.917	Depositor
Minimum map value	-11.939	Depositor
Average map value	0.125	Depositor
Map value standard deviation	0.927	Depositor
Recommended contour level	1	Depositor
Map size (Å)	383.904, 383.904, 383.904	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.333, 1.333, 1.333	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	b	0.31	0/2122	0.99	14/2852 (0.5%)
2	c	0.30	0/1586	0.91	2/2134 (0.1%)
3	d	0.30	0/1571	0.96	7/2113 (0.3%)
4	e	0.31	0/1435	0.91	3/1926 (0.2%)
5	f	0.30	0/1343	0.92	3/1816 (0.2%)
6	g	0.31	0/1122	0.99	7/1515 (0.5%)
7	h	0.33	0/1002	1.00	4/1350 (0.3%)
8	i	0.34	0/1046	1.02	4/1410 (0.3%)
9	j	0.30	0/1152	1.00	7/1551 (0.5%)
10	k	0.30	0/948	1.00	4/1268 (0.3%)
11	l	0.30	0/1054	1.05	6/1403 (0.4%)
12	m	0.32	0/1093	0.96	4/1460 (0.3%)
13	n	0.32	0/974	1.06	8/1301 (0.6%)
14	o	0.29	0/902	0.99	5/1209 (0.4%)
15	p	0.30	0/929	0.89	4/1242 (0.3%)
16	q	0.29	0/960	1.00	6/1278 (0.5%)
17	r	0.29	0/829	0.97	5/1107 (0.5%)
18	s	0.27	0/864	0.93	3/1156 (0.3%)
19	t	0.30	0/745	0.89	2/994 (0.2%)
20	u	0.29	0/788	0.99	2/1051 (0.2%)
21	v	0.30	0/766	0.94	3/1025 (0.3%)
22	w	0.27	0/582	0.91	2/769 (0.3%)
23	x	0.29	0/635	0.96	2/848 (0.2%)
24	y	0.28	0/510	0.90	3/677 (0.4%)
25	z	0.29	0/453	0.89	1/605 (0.2%)
26	B	0.29	0/450	0.99	2/599 (0.3%)
27	C	0.34	0/417	0.99	4/554 (0.7%)
28	D	0.32	0/380	1.10	4/498 (0.8%)
29	E	0.29	0/513	0.96	0/676
30	F	0.31	0/303	1.04	2/397 (0.5%)
31	G	0.30	0/1788	1.00	12/2408 (0.5%)
32	H	0.31	0/1652	0.93	4/2225 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.30	0/1665	0.94	5/2227 (0.2%)
34	J	0.31	0/1170	1.02	8/1573 (0.5%)
35	K	0.31	0/836	0.98	2/1128 (0.2%)
36	L	0.29	0/1196	1.00	2/1602 (0.1%)
37	M	0.30	0/989	1.00	5/1326 (0.4%)
38	N	0.31	0/1034	0.87	0/1375
39	O	0.33	0/797	0.99	5/1077 (0.5%)
40	P	0.32	0/886	1.01	8/1195 (0.7%)
41	Q	0.32	0/969	1.16	10/1300 (0.8%)
42	R	0.31	0/893	0.94	1/1193 (0.1%)
43	S	0.31	0/817	0.96	6/1088 (0.6%)
44	T	0.29	0/722	0.92	2/964 (0.2%)
45	U	0.34	0/659	1.04	7/884 (0.8%)
46	V	0.31	0/658	0.90	1/881 (0.1%)
47	W	0.32	0/545	0.88	0/731
48	X	0.33	0/653	1.10	7/877 (0.8%)
49	Y	0.29	0/671	1.01	3/888 (0.3%)
50	Z	0.33	0/551	1.04	5/728 (0.7%)
51	a	0.30	0/1034	0.95	5/1387 (0.4%)
52	3	0.40	0/36963	0.51	4/57662 (0.0%)
53	1	0.40	0/69796	0.51	1/108888 (0.0%)
54	2	0.40	0/2872	0.51	0/4479
55	5	0.40	0/1832	0.50	0/2855
55	6	0.40	0/1832	0.51	0/2855
56	4	0.40	0/436	0.49	0/679
57	7	0.39	0/1740	0.49	0/2712
All	All	0.37	0/163130	0.66	226/243971 (0.1%)

There are no bond length outliers.

All (226) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	n	116	VAL	N-CA-C	11.17	118.17	106.21
41	Q	20	VAL	N-CA-C	10.90	119.78	107.89
28	D	4	THR	N-CA-C	10.23	124.39	112.93
51	a	31	LYS	N-CA-C	-9.92	101.18	113.28
1	b	87	SER	N-CA-C	-9.30	102.06	113.50
26	B	19	ASP	N-CA-C	-8.44	102.75	113.72
7	h	117	LEU	N-CA-C	8.37	122.17	107.61
8	i	24	GLY	CA-C-N	8.16	127.81	119.82
8	i	24	GLY	C-N-CA	8.16	127.81	119.82
35	K	68	GLN	N-CA-C	8.12	119.76	111.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	l	95	LEU	N-CA-C	-8.11	102.83	112.89
41	Q	23	LEU	N-CA-C	-8.09	100.54	111.54
40	P	69	CYS	N-CA-C	-7.94	103.72	113.41
51	a	185	LEU	N-CA-C	-7.90	103.09	112.89
48	X	27	LYS	N-CA-C	7.75	120.31	109.31
7	h	107	GLU	N-CA-C	-7.67	100.64	112.99
11	l	96	LYS	N-CA-C	-7.67	103.38	112.89
17	r	49	ILE	N-CA-C	7.61	118.82	106.72
21	v	52	ALA	N-CA-C	-7.58	103.48	112.89
10	k	105	ARG	N-CA-C	7.43	120.03	111.11
48	X	57	VAL	N-CA-C	7.43	115.26	107.76
32	H	67	ILE	N-CA-C	7.43	118.83	107.99
10	k	67	LYS	N-CA-C	-7.37	104.09	113.23
3	d	178	VAL	N-CA-C	7.32	118.96	110.62
1	b	213	ARG	N-CA-C	-7.19	102.84	111.69
20	u	89	GLY	N-CA-C	-7.16	105.94	115.32
9	j	69	ARG	N-CA-C	-7.12	104.59	113.20
16	q	17	LEU	N-CA-C	7.10	119.02	111.28
45	U	62	GLY	N-CA-C	-7.09	106.04	115.32
40	P	93	GLU	N-CA-C	-7.08	103.75	112.88
13	n	68	ALA	N-CA-C	-7.05	104.80	113.19
34	J	116	VAL	N-CA-C	-7.04	104.56	113.22
31	G	165	ALA	N-CA-C	7.03	119.55	111.11
49	Y	33	LYS	N-CA-C	-7.00	103.72	111.36
39	O	29	ALA	N-CA-C	-6.99	105.94	114.75
27	C	37	LYS	N-CA-C	6.82	117.48	108.07
51	a	186	LYS	N-CA-C	-6.78	103.97	111.36
27	C	39	ASP	CA-C-N	6.72	126.31	119.19
27	C	39	ASP	C-N-CA	6.72	126.31	119.19
6	g	10	ALA	N-CA-C	6.71	120.20	108.52
40	P	107	THR	N-CA-C	-6.70	103.91	111.14
14	o	85	LYS	N-CA-C	-6.67	105.17	113.38
30	F	30	GLU	CA-C-N	6.66	126.44	119.05
30	F	30	GLU	C-N-CA	6.66	126.44	119.05
49	Y	84	LYS	N-CA-C	-6.65	104.11	111.36
11	l	92	LEU	N-CA-C	-6.63	103.24	112.45
21	v	4	ILE	N-CA-C	6.62	117.43	108.17
35	K	22	ILE	N-CA-C	6.61	117.10	110.23
51	a	184	LYS	N-CA-C	-6.58	105.08	113.23
31	G	46	VAL	N-CA-C	6.56	122.13	112.61
48	X	17	LYS	N-CA-C	6.54	118.09	110.97
34	J	122	VAL	N-CA-C	6.52	122.91	109.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	d	142	ALA	N-CA-C	6.51	120.37	111.39
10	k	112	PHE	N-CA-C	-6.50	103.96	112.41
6	g	39	ALA	N-CA-C	6.49	119.39	108.23
31	G	92	ASN	N-CA-C	6.48	121.72	113.55
45	U	19	VAL	N-CA-C	-6.47	99.45	108.12
37	M	67	GLY	N-CA-C	-6.46	104.72	113.37
41	Q	43	LYS	N-CA-C	6.46	124.08	109.81
18	s	66	ILE	N-CA-C	-6.46	104.23	113.07
40	P	115	ILE	N-CA-C	6.45	113.94	107.55
1	b	131	MET	N-CA-C	6.42	124.47	110.80
33	I	141	VAL	N-CA-C	6.37	117.76	108.53
16	q	83	LYS	N-CA-C	-6.36	104.27	111.14
1	b	27	LYS	CA-C-N	6.36	127.79	119.84
1	b	27	LYS	C-N-CA	6.36	127.79	119.84
50	Z	9	GLU	N-CA-C	6.34	123.83	109.81
41	Q	60	PHE	N-CA-C	6.34	118.27	109.15
32	H	71	ARG	CA-C-N	6.31	126.06	119.05
32	H	71	ARG	C-N-CA	6.31	126.06	119.05
3	d	115	GLN	N-CA-C	-6.28	104.89	113.30
45	U	54	LEU	N-CA-C	6.27	118.91	111.33
15	p	89	GLY	N-CA-C	6.25	119.11	111.93
12	m	119	LEU	N-CA-C	-6.25	103.78	111.40
31	G	46	VAL	CB-CA-C	-6.23	107.75	114.35
36	L	123	LEU	N-CA-C	-6.21	104.61	111.82
13	n	65	LEU	N-CA-C	-6.20	104.42	112.23
17	r	24	LYS	N-CA-C	6.20	119.81	110.64
13	n	78	LYS	N-CA-C	-6.18	104.08	111.69
5	f	39	ALA	N-CA-C	-6.16	105.59	113.23
34	J	30	PHE	N-CA-C	6.12	119.58	110.52
16	q	53	LYS	N-CA-C	-6.11	105.31	112.89
43	S	81	ILE	N-CA-C	6.11	116.27	110.53
11	l	129	LYS	N-CA-C	-6.08	106.00	113.41
23	x	59	ASP	N-CA-C	-6.08	104.57	112.23
44	T	46	LYS	N-CA-C	6.08	123.74	110.80
22	w	52	ASP	N-CA-C	-6.06	105.47	112.92
41	Q	114	SER	N-CA-C	-6.05	104.81	111.82
45	U	55	ASP	N-CA-C	6.04	117.95	111.36
43	S	89	ARG	N-CA-C	-6.00	105.79	113.23
32	H	32	LEU	N-CA-C	6.00	117.82	111.28
34	J	161	GLU	N-CA-C	6.00	117.51	110.97
17	r	50	GLY	N-CA-C	-5.99	104.87	113.86
16	q	39	ILE	N-CA-C	-5.99	103.91	112.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	X	9	PHE	N-CA-C	5.98	118.94	109.96
18	s	40	ASN	N-CA-C	5.98	119.17	107.57
41	Q	86	VAL	N-CA-C	5.98	117.14	112.12
40	P	46	ALA	N-CA-C	-5.97	104.89	111.82
3	d	60	TRP	N-CA-C	5.95	116.28	108.07
50	Z	8	ASN	N-CA-C	5.93	123.42	110.80
1	b	123	ILE	N-CA-C	5.90	116.60	107.99
33	I	89	LEU	N-CA-C	-5.87	104.80	111.14
43	S	98	ALA	N-CA-C	5.84	118.19	109.25
4	e	170	ALA	N-CA-C	-5.84	105.05	111.82
9	j	3	THR	N-CA-C	5.84	117.43	110.19
42	R	96	VAL	N-CA-C	5.83	118.79	112.96
14	o	68	LYS	N-CA-C	5.83	118.11	111.11
21	v	50	MET	N-CA-C	-5.81	105.29	112.90
31	G	175	ALA	N-CA-C	-5.79	106.05	113.23
31	G	198	VAL	N-CA-C	5.78	116.52	108.89
45	U	81	ALA	N-CA-C	-5.75	106.80	113.88
15	p	68	GLY	N-CA-C	5.75	119.96	112.25
39	O	77	VAL	N-CA-C	5.72	118.25	111.09
46	V	50	ASN	N-CA-C	5.72	116.78	107.23
39	O	62	ARG	N-CA-C	5.71	118.79	110.17
45	U	69	ASP	N-CA-C	5.70	117.95	111.11
44	T	43	ALA	N-CA-C	-5.70	105.21	111.82
52	3	1201	A	C2'-C3'-O3'	5.66	118.00	109.50
41	Q	117	GLY	N-CA-C	5.65	121.72	113.48
11	l	137	ALA	N-CA-C	-5.64	105.89	112.89
6	g	6	LEU	N-CA-C	-5.62	106.77	113.97
15	p	74	GLN	N-CA-C	-5.62	99.36	108.41
20	u	58	VAL	N-CA-C	5.62	116.86	109.21
9	j	28	LEU	N-CA-C	-5.62	104.55	111.40
4	e	164	GLU	N-CA-C	-5.62	105.16	112.23
1	b	6	LYS	CA-C-N	5.61	126.85	119.84
1	b	6	LYS	C-N-CA	5.61	126.85	119.84
27	C	40	PRO	N-CA-C	5.61	120.91	113.57
41	Q	21	PRO	N-CA-C	-5.59	103.90	113.12
31	G	107	ARG	N-CA-C	-5.58	105.97	112.89
6	g	45	GLU	N-CA-C	-5.57	105.29	111.36
43	S	11	LYS	N-CA-C	-5.56	105.37	111.82
36	L	135	LYS	N-CA-C	-5.55	105.31	111.36
3	d	31	VAL	N-CA-C	5.55	116.32	110.72
26	B	53	VAL	N-CA-C	5.53	119.86	111.89
12	m	135	VAL	N-CA-C	5.51	115.25	106.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	d	88	ARG	N-CA-C	-5.51	102.83	109.83
43	S	2	LYS	N-CA-C	-5.50	104.14	111.02
33	I	13	ARG	N-CA-C	-5.48	105.46	111.82
1	b	201	LEU	N-CA-C	-5.47	106.77	113.50
45	U	61	VAL	N-CA-C	-5.45	104.92	112.50
48	X	28	LYS	N-CA-C	-5.44	103.18	109.93
5	f	5	LYS	N-CA-C	-5.43	106.43	113.16
37	M	70	VAL	N-CA-C	5.43	117.33	111.58
9	j	67	ASN	N-CA-C	-5.42	104.56	113.50
12	m	111	GLU	N-CA-C	5.42	116.87	111.07
34	J	160	VAL	N-CA-C	5.41	116.14	110.62
14	o	79	ALA	N-CA-C	5.41	116.87	110.97
6	g	72	ILE	N-CA-C	-5.40	105.23	110.42
40	P	73	VAL	N-CA-C	-5.40	107.86	113.10
41	Q	3	VAL	N-CA-C	5.40	116.77	110.62
24	y	47	ARG	N-CA-C	-5.38	105.58	111.82
2	c	65	ALA	N-CA-C	-5.37	105.51	111.36
25	z	42	ALA	N-CA-C	-5.35	105.53	111.36
6	g	34	GLY	N-CA-C	-5.33	107.67	115.72
28	D	24	THR	N-CA-C	5.33	117.40	110.53
28	D	35	ARG	N-CA-C	-5.32	105.15	111.69
13	n	66	ALA	N-CA-C	-5.32	106.75	113.18
31	G	54	ALA	N-CA-C	-5.31	106.31	112.89
7	h	98	GLU	N-CA-C	-5.31	106.31	112.89
37	M	40	LYS	N-CA-C	-5.30	105.08	112.45
52	3	1300	G	N9-C1'-C2'	5.29	119.94	112.00
50	Z	28	LEU	N-CA-C	-5.29	106.68	113.23
11	l	97	ALA	N-CA-C	-5.28	106.68	113.23
17	r	48	LYS	N-CA-C	5.28	118.14	110.17
33	I	74	TYR	N-CA-C	5.27	117.03	111.28
1	b	225	ASN	CA-C-N	5.27	126.42	119.84
1	b	225	ASN	C-N-CA	5.27	126.42	119.84
31	G	110	ILE	N-CA-C	-5.26	105.26	111.00
37	M	100	ILE	N-CA-C	5.26	115.48	108.11
9	j	84	ILE	N-CA-C	-5.26	100.88	108.87
41	Q	70	GLY	N-CA-C	-5.25	105.98	112.33
28	D	17	GLY	N-CA-C	5.24	118.91	112.14
39	O	42	LEU	CA-C-N	5.24	126.39	119.84
39	O	42	LEU	C-N-CA	5.24	126.39	119.84
33	I	183	ARG	N-CA-C	5.24	116.94	109.14
51	a	178	VAL	N-CA-C	-5.24	106.78	112.80
1	b	245	THR	N-CA-C	-5.23	102.60	110.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	i	71	LYS	N-CA-C	5.23	117.96	109.86
14	o	10	ARG	N-CA-C	-5.22	107.56	114.04
13	n	77	ALA	N-CA-C	-5.22	106.76	113.23
34	J	121	ASN	N-CA-C	5.21	121.89	110.80
34	J	87	VAL	N-CA-C	5.20	116.39	109.37
19	t	50	LEU	N-CA-C	5.20	116.94	111.28
31	G	184	ALA	N-CA-C	5.19	117.63	108.75
43	S	39	ASP	N-CA-C	-5.19	105.80	111.82
14	o	89	ASP	N-CA-C	5.19	117.70	109.24
9	j	32	LEU	N-CA-C	-5.19	105.54	111.14
13	n	22	ARG	N-CA-C	-5.19	105.71	111.36
48	X	22	VAL	N-CA-C	5.19	115.96	110.72
34	J	60	GLN	N-CA-C	-5.18	106.46	112.89
40	P	117	HIS	N-CA-C	-5.18	103.83	111.81
16	q	50	ARG	N-CA-C	-5.17	105.71	112.23
31	G	108	GLN	N-CA-C	-5.17	105.33	111.69
12	m	46	ILE	N-CA-C	-5.15	106.12	111.58
53	l	1020	A	C2'-C3'-O3'	5.15	117.23	109.50
15	p	25	VAL	N-CA-C	5.15	115.89	108.48
22	w	34	VAL	N-CA-C	5.14	116.06	108.45
6	g	2	GLN	N-CA-C	-5.13	106.61	112.92
18	s	95	ARG	N-CA-C	5.13	117.15	110.43
19	t	3	ARG	N-CA-C	-5.13	105.38	110.97
37	M	3	GLN	N-CA-C	5.12	117.26	111.11
10	k	110	GLU	N-CA-C	5.12	121.71	110.80
24	y	14	LEU	N-CA-C	-5.11	105.90	111.82
17	r	14	VAL	N-CA-C	5.10	115.61	108.17
9	j	71	ASP	N-CA-C	5.09	119.96	113.55
5	f	92	GLY	N-CA-C	-5.08	107.84	113.79
2	c	69	ALA	N-CA-C	-5.08	107.03	113.18
4	e	96	TRP	N-CA-C	-5.08	105.93	111.82
49	Y	7	LYS	N-CA-C	-5.08	106.92	113.01
24	y	24	GLU	N-CA-C	5.07	121.60	110.80
40	P	16	SER	N-CA-C	5.06	121.58	110.80
23	x	70	LEU	N-CA-C	-5.06	105.85	111.36
1	b	152	GLN	N-CA-C	5.05	119.89	113.18
48	X	12	LEU	N-CA-C	5.05	116.59	111.14
1	b	153	LEU	N-CA-C	5.04	117.95	110.14
7	h	13	ALA	N-CA-C	-5.03	105.89	112.23
52	3	1190	G	C2'-C3'-O3'	5.03	117.04	109.50
31	G	7	ASP	N-CA-C	-5.02	105.90	112.23
13	n	67	PHE	N-CA-C	-5.02	107.33	113.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	Z	58	LYS	N-CA-C	-5.02	106.67	112.89
52	3	1301	U	N1-C1'-C2'	5.02	119.52	112.00
3	d	114	ARG	N-CA-C	-5.01	107.11	113.18
8	i	129	GLU	N-CA-C	-5.01	106.01	111.82
16	q	47	ARG	N-CA-C	5.01	117.39	111.33
50	Z	49	ALA	N-CA-C	-5.01	106.01	111.82

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	b	2083	0	2157	100	0
2	c	1565	0	1616	71	0
3	d	1552	0	1619	49	0
4	e	1411	0	1447	71	0
5	f	1323	0	1374	53	0
6	g	1111	0	1148	39	0
7	h	989	0	1025	53	0
8	i	1032	0	1088	48	0
9	j	1129	0	1162	50	0
10	k	939	0	1012	42	0
11	l	1045	0	1117	49	0
12	m	1074	0	1157	53	0
13	n	961	0	1000	44	0
14	o	892	0	923	38	0
15	p	917	0	965	39	0
16	q	947	0	1022	28	0
17	r	816	0	839	22	0
18	s	857	0	922	39	0
19	t	739	0	807	44	0
20	u	780	0	834	19	0
21	v	753	0	780	29	0
22	w	575	0	592	31	0
23	x	625	0	655	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	y	509	0	543	18	0
25	z	449	0	491	13	0
26	B	444	0	461	14	0
27	C	410	0	440	15	0
28	D	377	0	418	16	0
29	E	504	0	574	20	0
30	F	302	0	343	23	0
31	G	1757	0	1787	71	0
32	H	1625	0	1699	65	0
33	I	1643	0	1710	75	0
34	J	1157	0	1199	45	0
35	K	818	0	808	43	0
36	L	1182	0	1240	32	0
37	M	979	0	1034	49	0
38	N	1022	0	1070	60	0
39	O	787	0	828	42	0
40	P	870	0	878	39	0
41	Q	955	0	1019	50	0
42	R	884	0	944	55	0
43	S	805	0	847	55	0
44	T	714	0	737	23	0
45	U	649	0	666	27	0
46	V	649	0	691	35	0
47	W	536	0	552	23	0
48	X	638	0	665	31	0
49	Y	665	0	714	41	0
50	Z	545	0	579	36	0
51	a	1027	0	1092	31	0
52	3	33012	0	16618	492	0
53	1	62317	0	31346	835	0
54	2	2568	0	1303	66	0
55	5	1640	0	836	22	0
55	6	1640	0	837	17	0
56	4	388	0	196	6	0
57	7	1557	0	789	12	0
58	5	10	0	10	1	0
All	All	150149	0	101225	2989	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 12.

All (2989) 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)
53:1:45:G:H5''	53:1:46:G:H5'	1.32	1.12
8:i:25:PRO:HB2	53:1:1095:A:H61	1.17	1.04
55:5:13:C:H2'	55:5:14:A:H5''	1.40	1.02
19:t:2:ILE:HD11	53:1:144:A:H4'	1.39	1.00
43:S:60:ARG:HH21	52:3:981:U:H1'	1.27	0.97
41:Q:109:ARG:HB2	41:Q:118:VAL:HG21	1.42	0.97
53:1:1906:G:H2'	53:1:1907:G:H5''	1.46	0.96
9:j:81:ILE:HG23	9:j:82:GLY:H	1.33	0.94
34:J:100:GLU:N	34:J:121:ASN:HD21	1.64	0.94
34:J:100:GLU:H	34:J:121:ASN:HD21	1.00	0.93
13:n:2:ARG:O	13:n:2:ARG:HD3	1.69	0.93
51:a:47:ASN:HB3	51:a:210:LYS:HE3	1.52	0.92
33:I:82:LYS:HD3	52:3:5:U:O4	1.69	0.91
51:a:174:THR:HB	53:1:2124:G:H5''	1.53	0.90
2:c:8:LYS:HB2	2:c:201:LEU:HD11	1.55	0.89
5:f:5:LYS:NZ	53:1:1111:A:H4'	1.88	0.89
36:L:110:ARG:HH22	36:L:121:ASN:HB2	1.39	0.88
7:h:94:ARG:HD3	7:h:97:LYS:HD2	1.54	0.87
18:s:42:LYS:HB2	53:1:2010:G:H5''	1.57	0.87
52:3:405:U:H3'	52:3:406:G:H5'	1.57	0.86
10:k:13:ASN:HD21	10:k:98:ARG:HB2	1.40	0.85
32:H:177:LEU:HD11	52:3:1112:C:H2'	1.58	0.85
23:x:25:LYS:HE3	53:1:190:A:OP2	1.76	0.85
31:G:87:ASP:HB2	31:G:224:ARG:HH22	1.42	0.85
4:e:63:LYS:O	54:2:42:C:H1'	1.75	0.84
36:L:12:LEU:HD12	36:L:13:PRO:HD2	1.59	0.84
13:n:17:ARG:HA	13:n:20:MET:HE2	1.58	0.84
19:t:67:VAL:HG22	19:t:76:ARG:HB2	1.60	0.84
1:b:116:GLN:HG2	1:b:121:ALA:HB2	1.60	0.84
49:Y:63:LYS:NZ	52:3:196:A:H5'	1.92	0.84
26:B:30:ASP:HB3	26:B:34:GLY:H	1.42	0.83
33:I:111:ALA:HA	33:I:114:ARG:HD2	1.58	0.83
50:Z:66:ARG:NH2	52:3:1099:G:H4'	1.93	0.83
35:K:86:ARG:HH12	52:3:673:A:H4'	1.43	0.83
50:Z:44:ARG:NH2	52:3:722:G:H5''	1.94	0.83
53:1:1020:A:H1'	53:1:1021:A:OP2	1.77	0.83
19:t:61:LEU:HD13	53:1:1341:G:H5'	1.60	0.83
49:Y:63:LYS:HZ1	52:3:196:A:H5'	1.43	0.83
52:3:484:G:H4'	52:3:485:U:H5''	1.60	0.83
1:b:216:ARG:NH2	53:1:691:C:H5'	1.94	0.82
6:g:50:ARG:HD2	6:g:51:ARG:HG3	1.60	0.82
49:Y:68:LYS:HE2	52:3:185:U:H4'	1.61	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2391:G:H4'	53:1:2392:A:OP1	1.81	0.81
7:h:56:ARG:HH21	7:h:83:ALA:HB2	1.45	0.81
46:V:18:LYS:HA	46:V:49:ASN:HA	1.62	0.80
52:3:1306:A:H61	52:3:1331:G:H1'	1.46	0.80
41:Q:30:ARG:NH1	41:Q:57:THR:HG21	1.96	0.80
47:W:57:ALA:HA	47:W:60:ARG:HD2	1.63	0.80
27:C:25:ASN:HD22	27:C:28:THR:HG22	1.46	0.80
38:N:20:ILE:HD11	38:N:60:LEU:HB3	1.63	0.80
53:1:2286:G:H5''	53:1:2287:A:OP1	1.81	0.80
52:3:1259:C:H3'	52:3:1260:G:H5''	1.63	0.79
9:j:111:LYS:H	9:j:111:LYS:HD2	1.45	0.79
50:Z:9:GLU:HB2	50:Z:10:PRO:HD3	1.64	0.79
31:G:96:LEU:H	31:G:99:MET:HE3	1.48	0.79
7:h:23:LEU:HD13	7:h:118:ILE:HG12	1.64	0.79
36:L:111:GLY:HA2	36:L:118:ARG:HD3	1.64	0.79
47:W:11:ARG:HG3	52:3:845:A:H4'	1.65	0.79
53:1:275:C:H2'	53:1:276:U:H4'	1.65	0.79
43:S:36:SER:HA	43:S:40:ARG:HD3	1.65	0.79
35:K:29:ILE:HG22	35:K:34:GLY:HA3	1.63	0.78
34:J:80:LEU:HD13	34:J:122:VAL:HG11	1.65	0.78
14:o:100:HIS:HA	14:o:104:GLN:HE21	1.48	0.78
53:1:1645:G:H5''	53:1:1646:C:H5'	1.64	0.78
18:s:56:ALA:HA	18:s:59:GLU:HG2	1.65	0.78
2:c:2:ILE:HG21	2:c:48:ILE:HD11	1.66	0.78
1:b:20:ASN:HD22	1:b:23:LEU:HG	1.47	0.77
11:l:101:ILE:HG13	11:l:102:GLY:H	1.49	0.77
41:Q:52:CYS:HB3	41:Q:66:ILE:HD11	1.65	0.77
10:k:35:VAL:HG23	10:k:36:GLY:H	1.49	0.77
50:Z:28:LEU:HA	50:Z:31:VAL:HG12	1.67	0.77
4:e:66:ILE:H	4:e:66:ILE:HD12	1.49	0.77
45:U:2:VAL:HG23	45:U:65:ALA:HA	1.67	0.76
22:w:73:ARG:HH22	53:1:2332:C:H5''	1.48	0.76
15:p:38:ARG:HH22	52:3:345:C:H5'	1.50	0.76
28:D:7:PRO:HB2	53:1:1309:G:H4'	1.68	0.76
42:R:97:ARG:HB2	42:R:99:GLN:HE22	1.51	0.76
48:X:28:LYS:HD3	48:X:29:PRO:HD2	1.68	0.76
43:S:58:ARG:NH1	52:3:979:C:H2'	2.01	0.76
55:5:13:C:C2'	55:5:14:A:H5''	2.15	0.76
16:q:61:ILE:HD11	16:q:91:ARG:HD3	1.68	0.76
43:S:15:LEU:HG	43:S:54:SER:HB3	1.65	0.76
11:l:18:ARG:HH22	53:1:1249:U:H2'	1.51	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:E:1:PRO:HD2	53:1:591:U:H1'	1.68	0.75
3:d:112:LEU:HD22	3:d:117:ARG:HD3	1.67	0.75
32:H:13:ILE:HG13	32:H:14:VAL:HG23	1.69	0.75
53:1:1300:G:H4'	53:1:1301:A:H5'	1.66	0.75
5:f:5:LYS:HZ2	53:1:1111:A:H4'	1.52	0.75
5:f:34:ARG:HH21	5:f:70:LEU:HD12	1.52	0.75
8:i:89:SER:HB3	53:1:1063:G:H1'	1.67	0.75
12:m:41:LEU:H	12:m:41:LEU:HD12	1.50	0.75
20:u:85:ARG:HD3	20:u:87:GLU:HG3	1.68	0.75
18:s:90:LYS:HB2	18:s:92:ARG:HH12	1.51	0.75
1:b:216:ARG:HH21	53:1:691:C:H5'	1.52	0.74
25:z:41:PRO:HA	25:z:44:ARG:HB2	1.68	0.74
13:n:100:CYS:HA	26:B:42:ILE:HG12	1.68	0.74
52:3:979:C:H1'	52:3:1317:C:H41	1.52	0.74
1:b:16:VAL:HB	1:b:203:VAL:HG22	1.69	0.74
4:e:62:GLN:OE1	54:2:43:C:H4'	1.86	0.74
8:i:25:PRO:HB2	53:1:1095:A:N6	2.00	0.74
52:3:1301:U:O2	52:3:1301:U:H2'	1.88	0.74
37:M:12:ARG:NH2	52:3:826:C:H5'	2.03	0.74
5:f:121:THR:HG23	5:f:133:LYS:HB3	1.69	0.74
1:b:257:ARG:HH12	1:b:259:ASN:HD22	1.35	0.74
2:c:148:GLN:HB2	2:c:152:PRO:HG2	1.68	0.74
11:l:70:LYS:HD2	53:1:633:A:H5''	1.70	0.73
1:b:55:GLY:H	53:1:692:C:P	2.11	0.73
42:R:24:VAL:HG23	42:R:28:ARG:HB3	1.69	0.73
43:S:60:ARG:NH2	52:3:981:U:H1'	2.03	0.73
34:J:89:THR:HB	52:3:864:A:H5''	1.71	0.73
42:R:48:SER:OG	42:R:51:GLN:HG3	1.88	0.73
54:2:3:C:H3'	54:2:4:C:H5''	1.71	0.73
53:1:1906:G:C2'	53:1:1907:G:H5''	2.18	0.73
19:t:8:LEU:HD21	24:y:22:LEU:HD23	1.69	0.73
31:G:53:LEU:HD21	31:G:216:VAL:HG12	1.71	0.73
53:1:572:A:H61	53:1:2029:G:H21	1.35	0.73
7:h:118:ILE:HG13	7:h:119:PRO:HD3	1.70	0.72
12:m:76:LYS:HG3	53:1:956:G:H5''	1.70	0.72
13:n:79:LEU:HD23	13:n:83:LEU:HB2	1.71	0.72
43:S:27:LYS:HE2	52:3:1317:C:OP2	1.89	0.72
53:1:1053:C:H2'	53:1:1054:A:H5''	1.71	0.72
31:G:72:LYS:HE2	31:G:74:ALA:HB3	1.70	0.72
42:R:64:VAL:HG12	42:R:65:GLU:H	1.55	0.72
5:f:173:ALA:O	5:f:174:LYS:HG3	1.90	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1133:A:H4'	53:1:1134:A:H5''	1.72	0.72
35:K:32:ALA:HB1	35:K:70:VAL:HG11	1.70	0.72
53:1:2553:G:H3'	53:1:2554:U:H5''	1.72	0.72
1:b:43:ASN:HD21	1:b:45:ASN:HB2	1.55	0.71
31:G:156:LEU:HD12	31:G:157:PRO:HD2	1.71	0.71
40:P:28:ASN:HD21	40:P:47:GLY:N	1.88	0.71
7:h:72:LEU:H	7:h:72:LEU:HD12	1.55	0.71
37:M:80:PRO:HG2	52:3:878:A:H5''	1.73	0.71
52:3:327:A:O2'	52:3:328:C:H4'	1.90	0.71
12:m:35:ALA:HA	12:m:128:THR:HG22	1.72	0.71
25:z:11:SER:H	25:z:31:ILE:HD11	1.54	0.71
2:c:133:THR:HG22	2:c:134:HIS:H	1.53	0.71
42:R:113:LYS:H	42:R:114:PRO:HD2	1.54	0.71
21:v:77:VAL:HG12	21:v:89:ILE:HG13	1.73	0.71
19:t:87:LEU:HB2	19:t:91:GLN:HE21	1.56	0.71
38:N:11:ARG:HH22	38:N:12:LYS:HE2	1.54	0.71
53:1:1801:A:H5''	53:1:2203:U:H2'	1.71	0.70
1:b:175:LEU:HD13	53:1:1799:G:C5	2.25	0.70
14:o:40:ILE:HD13	54:2:8:C:O2'	1.90	0.70
33:I:111:ALA:HB1	52:3:407:U:H5''	1.74	0.70
38:N:113:LYS:HA	38:N:120:ALA:H	1.56	0.70
14:o:49:VAL:HG22	14:o:85:LYS:HG3	1.73	0.70
22:w:33:ILE:HG22	22:w:34:VAL:HG23	1.73	0.70
34:J:162:GLU:HG2	34:J:163:ILE:HD12	1.74	0.70
37:M:87:ARG:H	37:M:90:GLU:HB2	1.56	0.70
17:r:15:SER:H	17:r:18:GLN:HE21	1.39	0.70
37:M:52:GLY:HA3	37:M:56:PRO:HA	1.72	0.70
40:P:28:ASN:HD21	40:P:47:GLY:H	1.37	0.70
24:y:41:HIS:CE1	53:1:96:C:H4'	2.27	0.70
32:H:6:PRO:HG2	32:H:200:TRP:HE1	1.57	0.70
9:j:78:THR:HB	53:1:2641:G:H5''	1.74	0.70
19:t:73:ARG:HH12	53:1:456:C:H2'	1.57	0.70
52:3:1201:A:H1'	52:3:1202:U:OP2	1.92	0.70
54:2:3:C:C3'	54:2:4:C:H5''	2.22	0.70
52:3:1306:A:N6	52:3:1331:G:H1'	2.07	0.69
55:6:54:U:H3	55:6:58:A:H62	1.40	0.69
3:d:98:LYS:NZ	53:1:607:U:H5''	2.07	0.69
6:g:1:MET:HB3	6:g:3:VAL:HG23	1.73	0.69
45:U:5:ARG:HB2	52:3:376:G:H5''	1.74	0.69
51:a:48:LEU:HD21	51:a:196:LEU:HD21	1.74	0.69
51:a:211:LYS:NZ	53:1:2177:C:H4'	2.07	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2747:G:H21	53:1:2757:A:H62	1.39	0.69
22:w:25:GLU:HG3	53:1:923:G:H4'	1.74	0.69
50:Z:44:ARG:CZ	52:3:722:G:H5''	2.21	0.69
2:c:8:LYS:HD3	2:c:193:VAL:HG13	1.75	0.69
38:N:53:LEU:HD12	38:N:54:VAL:HG13	1.74	0.69
44:T:30:LEU:HD21	52:3:658:C:H5'	1.73	0.69
52:3:1200:C:H5''	52:3:1201:A:H3'	1.74	0.69
1:b:153:LEU:HD13	1:b:175:LEU:HD21	1.74	0.69
18:s:90:LYS:HB2	18:s:92:ARG:NH1	2.07	0.69
37:M:28:SER:HB2	37:M:58:LEU:HD13	1.74	0.69
17:r:29:THR:HG23	17:r:30:GLY:H	1.57	0.69
38:N:11:ARG:HH21	38:N:73:GLY:HA2	1.58	0.69
3:d:163:ASN:HB2	53:1:322:A:OP2	1.91	0.69
32:H:141:MET:HE3	32:H:169:GLU:HG3	1.74	0.69
36:L:27:ASN:HB3	52:3:1374:A:O2'	1.93	0.69
39:O:9:ARG:HH22	52:3:1279:G:P	2.16	0.69
39:O:92:LEU:HD23	39:O:92:LEU:H	1.57	0.69
50:Z:39:LYS:HA	50:Z:42:THR:HG22	1.73	0.69
2:c:33:ARG:HD3	2:c:73:VAL:HB	1.74	0.69
2:c:149:ASN:ND2	53:1:2575:C:H5'	2.08	0.69
5:f:5:LYS:HZ3	53:1:1111:A:H4'	1.58	0.69
37:M:104:SER:HB2	37:M:125:ILE:HD11	1.76	0.68
52:3:202:G:H21	52:3:466:A:H61	1.42	0.68
6:g:75:LEU:HD12	6:g:77:THR:H	1.58	0.68
46:V:13:SER:H	46:V:21:VAL:HG23	1.59	0.68
1:b:146:LYS:HB2	1:b:149:LYS:HB2	1.74	0.68
41:Q:23:LEU:HB3	41:Q:26:CYS:HB2	1.74	0.68
1:b:159:THR:HG21	53:1:1819:A:H5''	1.76	0.68
8:i:42:ASN:HA	8:i:45:THR:HG22	1.74	0.68
13:n:38:LEU:HB3	13:n:39:PRO:HD3	1.75	0.68
32:H:65:VAL:HB	32:H:100:ILE:HG12	1.74	0.68
18:s:17:VAL:HB	18:s:76:VAL:HG11	1.76	0.68
22:w:43:ALA:HB1	22:w:47:VAL:O	1.92	0.68
23:x:61:LYS:HG2	23:x:62:GLY:H	1.58	0.68
28:D:11:LYS:HE2	53:1:686:U:H5''	1.76	0.68
36:L:1:PRO:HB3	36:L:4:ARG:HB2	1.76	0.68
11:l:85:VAL:HG23	11:l:86:GLU:H	1.59	0.68
45:U:13:LYS:HE3	52:3:392:C:H5'	1.75	0.68
53:1:1415:U:H2'	53:1:1416:G:H4'	1.75	0.68
33:I:131:ILE:H	33:I:131:ILE:HD12	1.59	0.67
53:1:489:G:H22	53:1:1320:C:H3'	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:a:221:GLY:N	53:1:2176:A:H5''	2.09	0.67
39:O:50:THR:HB	52:3:975:A:H62	1.59	0.67
37:M:28:SER:HB3	37:M:56:PRO:HB2	1.76	0.67
49:Y:28:ARG:NH1	52:3:1437:A:H5''	2.10	0.67
25:z:12:ALA:HB1	25:z:20:LYS:HG2	1.75	0.67
31:G:59:ILE:HG22	31:G:64:GLY:HA3	1.77	0.67
52:3:29:U:O2'	52:3:30:U:H5'	1.94	0.67
12:m:95:LEU:H	12:m:95:LEU:HD23	1.59	0.67
32:H:49:ALA:HB1	32:H:75:VAL:HG22	1.76	0.67
48:X:49:ALA:HB1	48:X:56:HIS:HB3	1.76	0.67
21:v:47:VAL:HA	21:v:50:MET:HB2	1.76	0.67
22:w:39:THR:HG21	53:1:2336:A:H61	1.59	0.67
35:K:96:VAL:HG12	35:K:97:THR:H	1.60	0.67
51:a:51:ASP:OD2	51:a:54:LYS:HG3	1.95	0.66
48:X:28:LYS:HD3	48:X:29:PRO:CD	2.25	0.66
53:1:310:A:O2'	53:1:311:A:H5''	1.96	0.66
20:u:73:ASN:ND2	20:u:75:ALA:HB3	2.11	0.66
23:x:15:ASN:OD1	53:1:381:G:H5'	1.95	0.66
41:Q:106:VAL:HG22	41:Q:107:LYS:H	1.60	0.66
49:Y:45:ALA:HA	49:Y:48:LYS:HD2	1.77	0.66
55:5:55:U:H2'	55:5:56:C:H5''	1.77	0.66
37:M:83:ARG:HB2	46:V:36:PHE:HE2	1.61	0.66
38:N:129:ARG:NH2	55:5:33:U:H6	1.92	0.66
4:e:32:LYS:HZ1	53:1:2314:A:H4'	1.61	0.66
53:1:310:A:C2'	53:1:311:A:H5''	2.26	0.66
39:O:57:VAL:O	39:O:58:ASN:HB2	1.96	0.66
40:P:78:ILE:HD11	40:P:81:LEU:HB3	1.77	0.66
53:1:1807:G:H2'	53:1:1808:A:H5'	1.78	0.66
5:f:92:GLY:H	5:f:94:ARG:HH12	1.43	0.65
2:c:11:MET:HG2	2:c:25:THR:HG23	1.77	0.65
25:z:11:SER:N	25:z:31:ILE:HD11	2.11	0.65
33:I:61:ARG:HH21	33:I:67:LEU:HA	1.61	0.65
33:I:171:GLU:HB3	33:I:180:THR:HG23	1.78	0.65
42:R:15:VAL:HG13	42:R:40:GLU:HB2	1.79	0.65
4:e:24:VAL:HG12	54:2:55:U:H4'	1.76	0.65
34:J:64:GLU:HA	34:J:67:ARG:NH1	2.11	0.65
38:N:118:ARG:HB2	38:N:122:ARG:HB3	1.77	0.65
41:Q:113:ARG:HB2	41:Q:118:VAL:O	1.96	0.65
27:C:3:GLY:N	53:1:2283:C:H5'	2.11	0.65
28:D:26:ASN:CG	53:1:682:G:H5'	2.22	0.65
6:g:84:ALA:HA	6:g:91:PHE:H	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:o:15:ARG:NH2	54:2:8:C:H5''	2.11	0.65
47:W:54:LEU:O	47:W:58:ILE:HG12	1.94	0.65
5:f:82:PHE:HB3	5:f:140:ILE:HD13	1.79	0.65
5:f:97:VAL:HG22	5:f:102:ILE:HG23	1.78	0.65
16:q:55:GLN:O	16:q:58:GLN:HG2	1.96	0.65
17:r:74:ILE:HG23	17:r:87:GLN:HB3	1.77	0.65
19:t:80:TRP:HZ3	19:t:82:LYS:HB3	1.62	0.65
1:b:106:PRO:HG2	1:b:109:LEU:HB2	1.79	0.65
2:c:149:ASN:HB3	53:1:2572:A:OP2	1.97	0.65
53:1:2508:G:H1	53:1:2580:U:H3	1.44	0.65
53:1:2715:C:H2'	53:1:2716:C:H5''	1.78	0.65
12:m:82:MET:HE1	53:1:956:G:H4'	1.78	0.65
14:o:29:HIS:HB3	14:o:36:TYR:HD2	1.62	0.65
2:c:2:ILE:HD13	2:c:48:ILE:HD11	1.79	0.64
18:s:28:LYS:HE2	18:s:67:ASP:O	1.98	0.64
37:M:14:ARG:HH12	52:3:876:C:H4'	1.62	0.64
42:R:24:VAL:HA	52:3:1329:A:H5''	1.80	0.64
49:Y:20:ASN:ND2	52:3:323:U:H5''	2.12	0.64
53:1:542:C:H2'	53:1:543:G:H5''	1.79	0.64
53:1:2475:C:H2'	53:1:2476:A:H5'	1.79	0.64
15:p:38:ARG:HH12	52:3:345:C:H3'	1.62	0.64
21:v:9:ARG:HG3	21:v:41:GLU:HB2	1.79	0.64
33:I:33:ILE:HG22	33:I:34:GLU:H	1.61	0.64
11:l:111:ILE:HG12	53:1:636:G:C6	2.33	0.64
14:o:51:ALA:HB2	14:o:81:ARG:HD2	1.78	0.64
20:u:28:LEU:HD12	20:u:32:LYS:HB2	1.79	0.64
36:L:75:LYS:HE3	36:L:88:VAL:HG11	1.80	0.64
42:R:64:VAL:HG12	42:R:65:GLU:HG3	1.80	0.64
43:S:8:ARG:HD3	43:S:12:ARG:HH22	1.63	0.64
52:3:112:G:H4'	52:3:389:A:H4'	1.79	0.64
49:Y:23:ARG:O	49:Y:26:MET:HG3	1.98	0.64
52:3:758:C:H4'	52:3:880:C:H4'	1.79	0.64
39:O:65:TYR:HB3	43:S:95:LEU:HD11	1.80	0.64
54:2:3:C:H2'	54:2:4:C:H5''	1.80	0.64
4:e:134:GLN:HE22	4:e:149:ARG:H	1.46	0.64
8:i:126:ARG:HH21	53:1:1081:U:H5'	1.62	0.64
33:I:190:LEU:HD12	33:I:192:ALA:H	1.62	0.64
37:M:9:MET:HE1	37:M:35:ILE:HG21	1.79	0.64
53:1:729:G:H4'	53:1:763:G:H5'	1.80	0.64
6:g:58:LEU:O	6:g:61:VAL:HG22	1.98	0.64
14:o:24:THR:HG23	14:o:40:ILE:O	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:s:56:ALA:HA	18:s:59:GLU:CG	2.28	0.64
19:t:8:LEU:HD11	24:y:22:LEU:HG	1.78	0.64
31:G:96:LEU:HD22	52:3:1103:C:H5''	1.80	0.64
32:H:162:ALA:HB2	52:3:1056:U:H4'	1.79	0.64
52:3:1432:G:H1'	52:3:1468:A:N6	2.13	0.64
1:b:251:THR:HG23	1:b:252:LYS:HG3	1.80	0.64
3:d:47:LYS:HE2	3:d:51:GLU:HB3	1.79	0.64
11:l:62:PRO:HB2	29:E:29:ARG:HH11	1.63	0.64
38:N:22:PRO:HA	38:N:60:LEU:HD23	1.80	0.64
23:x:6:VAL:HG23	23:x:7:THR:HG23	1.80	0.63
27:C:28:THR:HG23	27:C:29:LYS:HG2	1.80	0.63
37:M:114:ALA:O	37:M:117:GLN:HG2	1.98	0.63
52:3:245:U:O2'	52:3:246:A:H5'	1.99	0.63
53:1:215:G:H4'	53:1:216:A:H4'	1.80	0.63
53:1:729:G:H4'	53:1:763:G:C5'	2.28	0.63
3:d:6:LYS:HE2	3:d:141:MET:HE3	1.81	0.63
18:s:1:MET:HE3	18:s:62:ASP:HB3	1.81	0.63
53:1:2277:G:C3'	53:1:2278:A:H5''	2.28	0.63
2:c:116:LYS:HG3	2:c:165:MET:HE3	1.80	0.63
3:d:150:THR:HG22	3:d:152:GLU:H	1.64	0.63
40:P:124:LYS:NZ	52:3:780:A:H5''	2.13	0.63
52:3:1413:A:H2	52:3:1487:G:H22	1.47	0.63
18:s:93:ALA:HB2	53:1:1614:A:C2	2.33	0.63
50:Z:9:GLU:HB2	50:Z:10:PRO:CD	2.27	0.63
1:b:216:ARG:HH21	53:1:691:C:C5'	2.12	0.63
8:i:106:GLN:HE22	8:i:125:THR:HG21	1.64	0.63
19:t:68:LYS:HA	19:t:68:LYS:HE2	1.81	0.63
38:N:35:GLU:HA	38:N:39:GLY:HA3	1.81	0.63
51:a:6:LYS:HG3	51:a:7:ARG:H	1.63	0.63
8:i:126:ARG:HH21	53:1:1081:U:C5'	2.12	0.62
10:k:24:VAL:HA	10:k:39:ILE:HG22	1.81	0.62
11:l:93:ASN:O	11:l:94:THR:HG22	1.98	0.62
53:1:119:A:H4'	53:1:120:U:H5'	1.80	0.62
33:I:97:LEU:HB2	33:I:134:TYR:HB3	1.80	0.62
48:X:77:ARG:HD3	52:3:1222:G:H5''	1.80	0.62
4:e:71:LYS:HE3	4:e:72:SER:H	1.63	0.62
5:f:126:THR:HG23	5:f:129:GLU:H	1.63	0.62
20:u:50:ALA:O	20:u:51:LEU:HG	1.98	0.62
46:V:7:LEU:HD21	46:V:24:ILE:HG12	1.79	0.62
53:1:49:A:H5'	53:1:51:G:O4'	1.99	0.62
37:M:86:LYS:HE2	37:M:90:GLU:HB3	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:O:6:ILE:HB	39:O:76:ILE:HB	1.82	0.62
45:U:1:MET:HG3	52:3:135:C:C2	2.34	0.62
51:a:189:LEU:O	51:a:192:LEU:HG	2.00	0.62
46:V:3:LYS:HD3	52:3:637:C:H5''	1.81	0.62
48:X:45:GLY:H	48:X:61:VAL:HB	1.65	0.62
50:Z:44:ARG:HH21	52:3:722:G:H3'	1.64	0.62
51:a:165:ASN:ND2	51:a:166:ASP:H	1.97	0.62
51:a:172:HIS:HB2	53:1:2123:G:H4'	1.80	0.62
30:F:19:ARG:HA	53:1:2756:U:H5''	1.82	0.62
42:R:97:ARG:HB2	42:R:99:GLN:NE2	2.14	0.62
52:3:1130:A:H61	52:3:1144:G:H1'	1.64	0.62
53:1:1796:U:H2'	53:1:1797:G:H8	1.63	0.62
53:1:2298:A:H62	53:1:2318:G:H21	1.48	0.62
22:w:17:LEU:H	22:w:17:LEU:HD22	1.65	0.62
49:Y:18:LYS:HE3	52:3:1459:G:H4'	1.81	0.62
53:1:1373:A:H4'	53:1:2212:A:H1'	1.80	0.62
5:f:85:LYS:HB3	5:f:164:ALA:HB2	1.81	0.62
43:S:48:GLN:HB2	48:X:12:LEU:HD22	1.80	0.61
52:3:769:G:H4'	52:3:1513:A:H4'	1.82	0.61
53:1:2432:A:H1'	55:6:75:C:H5'	1.81	0.61
1:b:23:LEU:HD13	1:b:82:TYR:HB2	1.80	0.61
1:b:48:ILE:HD11	1:b:51:ARG:HA	1.81	0.61
12:m:76:LYS:H	53:1:957:C:P	2.23	0.61
16:q:36:GLN:O	16:q:39:ILE:HG22	1.99	0.61
33:I:119:HIS:CG	52:3:438:U:H4'	2.36	0.61
35:K:38:ARG:HH21	35:K:40:GLU:HB2	1.65	0.61
36:L:70:PRO:HG3	36:L:98:LEU:HD11	1.82	0.61
40:P:116:PRO:HB3	52:3:676:A:H1'	1.80	0.61
53:1:2475:C:C2'	53:1:2476:A:H5'	2.30	0.61
3:d:69:ARG:NH1	3:d:69:ARG:HA	2.15	0.61
8:i:20:SER:HB2	8:i:21:PRO:HD3	1.81	0.61
31:G:213:LEU:HA	31:G:216:VAL:HG22	1.82	0.61
53:1:546:U:H2'	53:1:547:A:H4'	1.82	0.61
55:5:6:G:O2'	55:5:7:G:H5'	2.00	0.61
7:h:118:ILE:HG13	7:h:119:PRO:CD	2.31	0.61
13:n:28:LEU:HD23	13:n:48:VAL:HG21	1.82	0.61
33:I:120:LYS:HE3	52:3:439:U:H5''	1.81	0.61
34:J:54:GLU:HG3	34:J:56:PRO:HD2	1.81	0.61
52:3:764:C:H2'	52:3:765:G:O4'	2.00	0.61
1:b:19:VAL:HG11	53:1:1565:C:OP1	2.00	0.61
5:f:94:ARG:HB2	5:f:105:SER:HB2	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:m:76:LYS:CG	53:1:956:G:H5''	2.30	0.61
16:q:80:ASN:OD1	53:1:1151:A:H4'	2.01	0.61
36:L:47:GLU:O	36:L:51:GLN:HG2	2.01	0.61
38:N:62:LEU:HD12	38:N:62:LEU:N	2.16	0.61
40:P:92:ARG:NH2	50:Z:24:LYS:HE2	2.15	0.61
53:1:615:U:H5''	53:1:616:A:OP2	2.00	0.61
54:2:72:G:H21	54:2:104:A:H62	1.48	0.61
1:b:77:VAL:HG22	1:b:93:VAL:HG22	1.83	0.61
33:I:2:ARG:HH22	33:I:65:GLY:HA3	1.65	0.61
34:J:149:PRO:HA	34:J:152:VAL:HG22	1.83	0.61
42:R:3:ILE:N	42:R:3:ILE:HD12	2.16	0.61
52:3:1379:G:O2'	52:3:1380:U:H5'	2.01	0.61
53:1:1023:U:O2'	53:1:1122:G:H5'	2.01	0.61
53:1:1026:G:H2'	53:1:1027:A:H8	1.64	0.61
54:2:78:A:H62	54:2:98:G:H21	1.48	0.61
2:c:33:ARG:HG3	2:c:51:THR:HG23	1.83	0.61
27:C:4:ILE:HG22	53:1:2284:A:OP1	2.01	0.61
35:K:86:ARG:HH12	52:3:673:A:C4'	2.13	0.61
36:L:111:GLY:HA2	36:L:118:ARG:HH11	1.66	0.61
52:3:1319:A:H4'	52:3:1320:C:H5	1.65	0.61
53:1:2039:U:H2'	53:1:2040:G:C8	2.35	0.61
6:g:132:PHE:HE2	6:g:142:VAL:HB	1.65	0.61
11:l:57:LEU:HA	11:l:60:ARG:HE	1.65	0.61
53:1:2277:G:H3'	53:1:2278:A:H5''	1.82	0.61
1:b:12:ARG:HH21	53:1:728:G:H4'	1.66	0.60
5:f:104:LEU:HG	5:f:106:LEU:HG	1.83	0.60
27:C:7:LYS:HD2	53:1:2420:C:H5''	1.83	0.60
32:H:116:ALA:O	32:H:119:ILE:HG22	2.00	0.60
37:M:73:SER:H	37:M:129:ALA:HB3	1.65	0.60
53:1:1141:U:H4'	53:1:1142:A:O4'	2.01	0.60
8:i:102:ARG:O	8:i:106:GLN:HG2	2.02	0.60
10:k:21:CYS:HA	10:k:41:ILE:HG22	1.83	0.60
4:e:40:GLY:HA2	4:e:84:ILE:HD11	1.83	0.60
38:N:8:THR:HG21	38:N:10:ARG:NH2	2.17	0.60
47:W:24:ASP:O	47:W:28:LEU:HD13	2.01	0.60
53:1:619:G:H3'	53:1:620:G:H21	1.66	0.60
53:1:2452:C:H42	53:1:2504:U:H3	1.48	0.60
8:i:56:VAL:HG12	8:i:70:THR:HA	1.83	0.60
36:L:139:ASP:HA	36:L:142:ARG:HB2	1.82	0.60
44:T:68:TYR:HB2	52:3:754:C:H4'	1.82	0.60
52:3:782:A:H62	52:3:800:G:H21	1.49	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:c:151:THR:HB	2:c:152:PRO:HD3	1.84	0.60
44:T:49:HIS:HA	44:T:52:ARG:HD2	1.83	0.60
50:Z:50:SER:O	50:Z:53:LYS:HG3	2.01	0.60
53:1:1053:C:C2'	53:1:1054:A:H5''	2.32	0.60
30:F:23:ILE:H	30:F:23:ILE:HD12	1.66	0.60
33:I:199:ILE:HA	33:I:202:LEU:HD12	1.83	0.60
37:M:12:ARG:CZ	52:3:826:C:H5'	2.31	0.60
47:W:37:LYS:HD2	52:3:719:C:O2'	2.01	0.60
53:1:2296:U:H5''	53:1:2297:A:OP1	2.02	0.60
12:m:86:LYS:HG3	12:m:87:GLY:H	1.65	0.60
32:H:39:ARG:HG3	32:H:54:ILE:HD11	1.82	0.60
21:v:5:ASN:HD22	21:v:46:LYS:NZ	2.00	0.60
38:N:12:LYS:HA	38:N:109:GLN:HE22	1.66	0.60
48:X:18:VAL:HG21	48:X:43:MET:HG2	1.84	0.60
50:Z:66:ARG:HD2	52:3:1099:G:O4'	2.02	0.60
32:H:13:ILE:HG23	32:H:14:VAL:H	1.66	0.60
44:T:65:LEU:HD23	52:3:754:C:O2'	2.02	0.60
15:p:52:ARG:HH22	53:1:2720:U:H5''	1.67	0.60
15:p:93:LYS:HD2	53:1:1754:A:OP1	2.01	0.60
51:a:183:ASP:O	51:a:186:LYS:HB3	2.00	0.60
9:j:53:TYR:CE1	9:j:121:LYS:HD2	2.36	0.59
19:t:58:VAL:HG13	19:t:85:VAL:HG22	1.84	0.59
49:Y:68:LYS:NZ	52:3:185:U:H5'	2.17	0.59
53:1:1919:A:H2'	53:1:1920:C:H5'	1.83	0.59
54:2:3:C:C2'	54:2:4:C:H5''	2.32	0.59
5:f:9:VAL:HA	5:f:48:THR:HG23	1.83	0.59
9:j:33:ALA:HA	9:j:36:LEU:HB2	1.84	0.59
1:b:5:CYS:SG	1:b:17:LYS:HE2	2.43	0.59
5:f:21:GLN:HE21	5:f:36:LEU:HB2	1.66	0.59
9:j:90:GLU:O	9:j:93:ILE:HG22	2.03	0.59
53:1:2048:G:C3'	53:1:2049:G:H5''	2.32	0.59
32:H:176:THR:HG22	52:3:1111:A:N1	2.17	0.59
34:J:57:ALA:O	34:J:61:LYS:HG2	2.02	0.59
38:N:129:ARG:NH2	55:5:33:U:C6	2.71	0.59
41:Q:80:LEU:HD22	41:Q:101:LEU:HD23	1.83	0.59
42:R:18:LEU:HD22	42:R:24:VAL:HG21	1.84	0.59
3:d:44:ARG:HD2	53:1:444:C:OP2	2.02	0.59
13:n:33:ILE:HG13	13:n:114:GLU:HB3	1.85	0.59
34:J:60:GLN:HA	34:J:63:MET:HE3	1.84	0.59
42:R:27:THR:HG21	52:3:1328:C:H5''	1.83	0.59
53:1:2638:G:HI'	53:1:2778:A:H61	1.65	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:v:16:ALA:HA	21:v:19:ARG:HB3	1.84	0.59
51:a:172:HIS:CB	53:1:2123:G:H4'	2.33	0.59
52:3:1497:G:O2'	52:3:1498:U:H5'	2.03	0.59
8:i:106:GLN:NE2	8:i:125:THR:HG21	2.18	0.59
18:s:55:ILE:HG23	18:s:66:ILE:HD12	1.85	0.59
47:W:22:TYR:HB3	47:W:57:ALA:HB1	1.83	0.59
53:1:713:G:H21	53:1:718:A:H62	1.49	0.59
2:c:40:LEU:HD12	2:c:41:ALA:N	2.18	0.59
2:c:138:LEU:HD11	53:1:745:G:OP2	2.03	0.59
6:g:73:ASN:O	6:g:76:GLU:HG3	2.03	0.59
10:k:22:ILE:HG13	10:k:23:LYS:H	1.68	0.59
44:T:66:LEU:HD13	44:T:87:ARG:HH21	1.66	0.59
6:g:112:LYS:HD2	53:1:2220:U:OP1	2.03	0.59
12:m:58:LYS:HB2	12:m:60:GLN:HG2	1.83	0.59
38:N:17:ARG:NH1	52:3:1129:C:H4'	2.18	0.59
43:S:63:CYS:HB3	43:S:67:GLY:H	1.68	0.59
44:T:48:ASP:O	44:T:52:ARG:HG3	2.02	0.59
48:X:62:THR:HG22	48:X:65:MET:HE3	1.84	0.59
52:3:1033:G:H2'	52:3:1034:G:H5''	1.83	0.59
52:3:1338:G:H21	55:5:42:G:H1'	1.67	0.59
53:1:1344:U:H3'	53:1:1345:C:H5'	1.84	0.59
4:e:129:MET:HG3	4:e:130:GLY:H	1.68	0.58
19:t:68:LYS:HG3	19:t:77:ARG:HH21	1.68	0.58
48:X:76:THR:HG21	52:3:1221:G:H4'	1.85	0.58
52:3:1218:C:H2'	52:3:1219:A:C8	2.38	0.58
7:h:118:ILE:H	7:h:119:PRO:HD2	1.67	0.58
33:I:38:GLY:HA3	52:3:542:G:H5'	1.86	0.58
35:K:53:LYS:HD2	35:K:54:LEU:N	2.18	0.58
50:Z:44:ARG:HH22	52:3:722:G:H21	1.48	0.58
18:s:19:LEU:HD12	26:B:20:ALA:HA	1.86	0.58
42:R:12:LYS:HB2	42:R:17:ALA:HB2	1.86	0.58
53:1:2698:U:H2'	53:1:2699:C:C6	2.38	0.58
2:c:2:ILE:HD11	2:c:96:ILE:HD13	1.83	0.58
46:V:76:ARG:HG2	46:V:77:VAL:H	1.66	0.58
48:X:35:ARG:HE	48:X:71:GLY:HA2	1.68	0.58
53:1:2628:C:H3'	53:1:2629:U:H5'	1.85	0.58
4:e:23:SER:OG	54:2:56:G:H5'	2.03	0.58
11:l:93:ASN:HB2	11:l:96:LYS:HZ2	1.67	0.58
12:m:86:LYS:HG3	12:m:87:GLY:N	2.19	0.58
31:G:24:PRO:HB3	52:3:828:U:H2'	1.83	0.58
32:H:146:LYS:HD3	32:H:203:LYS:HA	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:174:LEU:HB2	52:3:1108:G:OP1	2.03	0.58
33:I:80:ARG:HD2	33:I:80:ARG:O	2.04	0.58
42:R:113:LYS:N	42:R:114:PRO:HD2	2.19	0.58
53:1:1077:A:H2'	53:1:1078:U:H5'	1.84	0.58
4:e:4:HIS:O	4:e:8:LYS:HG3	2.03	0.58
4:e:87:LYS:HD2	53:1:2313:C:H5''	1.85	0.58
12:m:126:ILE:C	12:m:127:LYS:HE2	2.27	0.58
24:y:38:GLN:NE2	24:y:39:GLN:HG3	2.17	0.58
46:V:46:HIS:HB2	46:V:70:LYS:HE2	1.85	0.58
4:e:27:VAL:O	4:e:29:ARG:NH1	2.36	0.58
5:f:123:GLU:HB2	5:f:131:VAL:HG23	1.86	0.58
49:Y:17:ARG:HD2	49:Y:18:LYS:N	2.18	0.58
52:3:1308:U:H2'	52:3:1309:G:C8	2.39	0.58
53:1:2533:U:H2'	53:1:2534:A:O4'	2.04	0.58
14:o:16:ARG:O	14:o:19:GLN:HG2	2.04	0.58
15:p:63:ILE:HA	15:p:68:GLY:HA2	1.86	0.58
30:F:38:GLY:OXT	53:1:1031:G:H1'	2.03	0.58
49:Y:11:ILE:H	49:Y:11:ILE:HD12	1.67	0.58
1:b:264:LYS:HE2	53:1:2223:G:O2'	2.04	0.58
12:m:20:LEU:HD23	21:v:81:PRO:HG2	1.84	0.58
15:p:36:LYS:NZ	52:3:345:C:OP1	2.37	0.58
43:S:30:ILE:HG22	43:S:40:ARG:HA	1.85	0.58
52:3:1502:A:H5'	52:3:1504:G:N7	2.18	0.58
53:1:894:U:H2'	53:1:895:U:H5'	1.84	0.58
53:1:1786:A:H1'	53:1:1938:A:N6	2.18	0.58
1:b:170:TYR:HD2	1:b:182:LYS:HB3	1.69	0.58
13:n:5:LYS:HE2	53:1:2690:U:O4	2.03	0.58
21:v:76:ASP:HB2	21:v:90:ASP:HB2	1.86	0.58
22:w:28:LEU:HD12	53:1:2354:C:OP1	2.04	0.58
53:1:1614:A:H2'	53:1:1615:C:H5'	1.85	0.58
3:d:199:MET:HG3	3:d:200:LEU:HD12	1.84	0.57
10:k:13:ASN:ND2	10:k:98:ARG:HB2	2.17	0.57
11:l:61:LEU:O	29:E:12:ARG:NE	2.36	0.57
31:G:113:LEU:HD23	31:G:151:LYS:HD3	1.85	0.57
32:H:59:PRO:HB3	39:O:94:ALA:HB2	1.86	0.57
41:Q:107:LYS:HD2	41:Q:107:LYS:O	2.04	0.57
32:H:78:LYS:O	32:H:79:LYS:HG3	2.05	0.57
40:P:124:LYS:HZ2	52:3:780:A:H5''	1.69	0.57
53:1:745:G:O2'	53:1:748:G:H1'	2.04	0.57
54:2:65:U:H3'	54:2:108:A:H61	1.69	0.57
55:6:71:C:H2'	55:6:72:A:C8	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:m:78:LEU:HD12	12:m:78:LEU:H	1.69	0.57
20:u:93:ARG:HB2	20:u:102:ILE:HB	1.85	0.57
23:x:31:ASN:HD22	23:x:52:ALA:HB2	1.69	0.57
35:K:91:ARG:HG3	35:K:92:THR:H	1.69	0.57
40:P:124:LYS:HE3	52:3:1523:G:H5''	1.86	0.57
50:Z:38:GLU:HB2	52:3:1526:G:OP2	2.04	0.57
52:3:70:U:H5''	52:3:71:A:OP1	2.03	0.57
52:3:77:A:H2'	52:3:78:A:H8	1.68	0.57
52:3:1352:C:H2'	52:3:1353:G:C8	2.39	0.57
5:f:16:VAL:HG23	5:f:25:ILE:HG12	1.86	0.57
52:3:1158:C:H2'	52:3:1159:U:H4'	1.85	0.57
2:c:101:PHE:HD1	2:c:104:VAL:HG21	1.70	0.57
13:n:39:PRO:HG2	53:1:1651:G:H4'	1.85	0.57
19:t:43:ILE:HD12	19:t:43:ILE:H	1.69	0.57
53:1:2743:U:H2'	53:1:2744:G:H5''	1.87	0.57
27:C:12:SER:HA	27:C:48:TYR:HA	1.87	0.57
39:O:44:THR:HG23	39:O:69:THR:C	2.29	0.57
52:3:225:C:H2'	52:3:226:G:H5''	1.86	0.57
52:3:757:U:H2'	52:3:758:C:O4'	2.04	0.57
53:1:2156:G:H2'	53:1:2157:G:H5'	1.87	0.57
10:k:49:ARG:HH12	52:3:1423:G:H5'	1.70	0.57
12:m:29:GLY:HA2	12:m:106:ASP:HB2	1.86	0.57
35:K:48:ALA:HB1	47:W:68:PRO:HG3	1.86	0.57
38:N:69:GLY:H	52:3:1250:A:H4'	1.68	0.57
42:R:85:TYR:CE2	52:3:1321:U:H4'	2.40	0.57
55:5:35:A:H2'	55:5:36:U:C6	2.39	0.57
3:d:69:ARG:HA	3:d:69:ARG:HH11	1.70	0.57
8:i:11:GLN:HB3	8:i:56:VAL:HG22	1.85	0.57
31:G:147:LEU:HD22	31:G:150:ILE:HD11	1.86	0.57
53:1:1597:A:H5''	53:1:1598:A:H5'	1.86	0.57
53:1:2128:G:H21	53:1:2173:A:H1'	1.69	0.57
54:2:106:G:H2'	54:2:107:G:O4'	2.05	0.57
1:b:219:VAL:HG21	53:1:782:A:N7	2.19	0.57
13:n:73:ASN:HA	13:n:76:VAL:HG22	1.87	0.57
52:3:1305:G:H22	52:3:1331:G:H2'	1.70	0.57
53:1:161:A:H62	53:1:165:A:H61	1.52	0.57
2:c:109:VAL:HB	2:c:193:VAL:HG23	1.86	0.57
5:f:29:ASN:HB2	5:f:78:VAL:HA	1.86	0.57
8:i:104:GLN:O	8:i:107:GLU:HG3	2.04	0.57
21:v:9:ARG:C	21:v:10:LYS:HD2	2.30	0.57
47:W:60:ARG:O	47:W:64:LEU:HG	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2163:A:N3	53:1:2163:A:H2'	2.20	0.57
1:b:106:PRO:HD2	1:b:109:LEU:HD22	1.86	0.56
7:h:26:VAL:HG13	7:h:82:ILE:HG23	1.86	0.56
10:k:19:VAL:HG12	10:k:43:ILE:HA	1.87	0.56
30:F:7:VAL:C	30:F:8:LYS:HD3	2.29	0.56
38:N:113:LYS:HB2	38:N:119:LYS:HA	1.87	0.56
43:S:84:ARG:HH12	52:3:1059:C:H4'	1.70	0.56
52:3:1005:A:H2'	52:3:1006:G:O4'	2.05	0.56
2:c:82:PHE:HE1	2:c:204:LYS:HE2	1.70	0.56
8:i:21:PRO:HB2	8:i:22:PRO:HD3	1.87	0.56
32:H:8:GLY:HA2	32:H:11:LEU:HD12	1.85	0.56
33:I:43:ARG:NH1	52:3:511:C:OP1	2.38	0.56
43:S:80:ARG:HG3	43:S:81:ILE:N	2.20	0.56
2:c:194:PRO:HA	53:1:2680:U:H5'	1.86	0.56
7:h:94:ARG:HE	7:h:131:THR:HG21	1.70	0.56
15:p:48:ALA:HB3	15:p:59:THR:HG22	1.87	0.56
37:M:10:LEU:HD11	37:M:126:CYS:SG	2.46	0.56
39:O:44:THR:HG23	39:O:69:THR:O	2.06	0.56
41:Q:14:LYS:HE2	52:3:884:U:O2'	2.05	0.56
42:R:16:ILE:HD13	52:3:1302:C:C5	2.40	0.56
43:S:8:ARG:O	43:S:12:ARG:HG3	2.06	0.56
44:T:4:THR:HG21	52:3:660:C:OP2	2.06	0.56
52:3:265:G:H2'	52:3:267:C:H5	1.70	0.56
52:3:1501:C:H5''	52:3:1502:A:OP2	2.05	0.56
53:1:1772:A:H2'	53:1:1773:A:H4'	1.86	0.56
53:1:2657:A:H62	53:1:2664:G:H21	1.53	0.56
1:b:70:LYS:HB3	1:b:73:ILE:HD12	1.88	0.56
52:3:1160:G:H1	52:3:1176:A:H61	1.51	0.56
52:3:1346:A:H2'	52:3:1347:G:H4'	1.88	0.56
53:1:2724:U:H2'	53:1:2725:A:C8	2.41	0.56
1:b:43:ASN:ND2	1:b:45:ASN:H	2.04	0.56
3:d:149:ILE:HG12	3:d:170:ARG:HB2	1.88	0.56
4:e:127:TYR:HB3	4:e:155:ILE:HD11	1.87	0.56
10:k:71:ARG:HD2	10:k:72:PRO:HD2	1.86	0.56
15:p:30:TRP:CZ3	15:p:37:LYS:HG2	2.41	0.56
22:w:73:ARG:NH2	53:1:2332:C:OP1	2.38	0.56
39:O:100:ILE:HD12	39:O:100:ILE:N	2.21	0.56
45:U:31:ARG:CZ	52:3:311:C:OP1	2.54	0.56
52:3:1496:C:H1'	52:3:1517:G:H22	1.70	0.56
53:1:1796:U:H2'	53:1:1797:G:C8	2.41	0.56
4:e:125:GLY:HA2	4:e:162:ASP:HA	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:f:41:GLU:HA	5:f:54:ARG:HH21	1.70	0.56
10:k:87:LEU:HD22	10:k:92:GLU:O	2.05	0.56
13:n:103:ARG:HB3	13:n:108:ALA:H	1.71	0.56
42:R:7:ASN:ND2	42:R:9:PRO:HD3	2.19	0.56
42:R:22:TYR:CE1	52:3:1330:U:H4'	2.41	0.56
53:1:554:U:H2'	53:1:555:G:O4'	2.05	0.56
53:1:1367:A:H2'	53:1:1368:G:H5'	1.87	0.56
53:1:2487:G:H2'	53:1:2488:G:C8	2.40	0.56
54:2:114:C:H2'	54:2:115:A:C8	2.41	0.56
5:f:100:ASN:HA	5:f:116:LEU:HD12	1.88	0.56
5:f:176:LYS:HD3	53:1:2660:A:N6	2.21	0.56
9:j:81:ILE:HG23	9:j:82:GLY:N	2.12	0.56
43:S:52:ARG:NH1	52:3:979:C:O2'	2.38	0.56
49:Y:32:LYS:HE2	52:3:1438:G:O3'	2.05	0.56
52:3:390:U:H2'	52:3:391:G:H8	1.71	0.56
53:1:2087:G:H2'	53:1:2088:A:H8	1.71	0.56
31:G:24:PRO:CB	52:3:828:U:H2'	2.36	0.56
34:J:96:GLN:HG3	34:J:97:PRO:HD2	1.88	0.56
34:J:100:GLU:N	34:J:121:ASN:ND2	2.44	0.56
35:K:2:ARG:HB3	35:K:92:THR:HG22	1.88	0.56
53:1:1053:C:C3'	53:1:1054:A:H5''	2.36	0.56
19:t:13:ALA:HB1	24:y:33:ALA:HB2	1.88	0.56
47:W:25:ILE:HA	47:W:28:LEU:HB2	1.86	0.56
52:3:70:U:H2'	52:3:94:G:O6	2.06	0.56
2:c:32:ASN:HD22	2:c:32:ASN:N	2.02	0.56
5:f:97:VAL:HG11	5:f:122:ALA:HB3	1.88	0.56
6:g:40:THR:OG1	6:g:43:ASN:ND2	2.39	0.56
9:j:2:LYS:HE2	9:j:2:LYS:HA	1.87	0.56
13:n:44:LEU:HB3	13:n:113:ILE:HD13	1.87	0.56
19:t:3:ARG:NH1	19:t:7:LEU:HD11	2.20	0.56
33:I:38:GLY:HA3	52:3:542:G:C5'	2.36	0.56
33:I:58:GLN:O	33:I:62:ARG:HG2	2.06	0.56
53:1:1547:C:H2'	53:1:1548:A:H8	1.69	0.56
53:1:1872:A:H2'	53:1:1873:G:O4'	2.05	0.56
54:2:55:U:H2'	54:2:56:G:C8	2.41	0.56
1:b:41:GLY:C	1:b:42:ARG:HD2	2.30	0.55
6:g:126:GLY:H	6:g:146:VAL:HB	1.70	0.55
33:I:33:ILE:HG22	33:I:34:GLU:N	2.21	0.55
34:J:156:ARG:HD3	37:M:42:GLU:HG3	1.88	0.55
35:K:10:VAL:HB	35:K:58:HIS:HB3	1.88	0.55
52:3:730:G:H2'	52:3:731:G:H5'	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:828:U:H2'	53:1:829:A:C8	2.40	0.55
53:1:1810:A:H2'	53:1:1811:G:O4'	2.06	0.55
3:d:52:VAL:HB	3:d:74:LYS:HG3	1.88	0.55
5:f:82:PHE:O	5:f:133:LYS:HD2	2.06	0.55
7:h:58:THR:HG21	7:h:82:ILE:H	1.71	0.55
7:h:114:GLU:HA	7:h:123:ILE:HD13	1.89	0.55
31:G:72:LYS:HG3	31:G:75:ALA:H	1.71	0.55
42:R:92:ARG:HA	53:1:888:C:N3	2.21	0.55
52:3:312:C:H2'	52:3:313:A:C8	2.41	0.55
53:1:2048:G:H2'	53:1:2049:G:H5''	1.87	0.55
2:c:121:THR:HG21	2:c:143:PRO:HB3	1.88	0.55
4:e:107:VAL:HB	4:e:108:PRO:HD3	1.89	0.55
9:j:31:GLU:HB3	9:j:142:ILE:HG13	1.88	0.55
10:k:22:ILE:HD11	10:k:40:LYS:HG3	1.88	0.55
38:N:98:ARG:HH12	38:N:103:VAL:HG11	1.71	0.55
38:N:123:ARG:HB2	52:3:1343:G:H4'	1.89	0.55
40:P:109:ILE:HD11	50:Z:16:ARG:HB3	1.88	0.55
42:R:111:PRO:HB2	42:R:113:LYS:HZ1	1.71	0.55
43:S:25:GLU:HA	43:S:28:ALA:HB3	1.89	0.55
53:1:655:A:H4'	53:1:656:G:H5'	1.88	0.55
53:1:894:U:C2'	53:1:895:U:H5'	2.36	0.55
34:J:75:LEU:HD23	34:J:75:LEU:H	1.71	0.55
42:R:49:GLU:OE2	42:R:52:ILE:HD12	2.07	0.55
42:R:111:PRO:HB2	42:R:113:LYS:NZ	2.20	0.55
49:Y:60:GLN:HB3	49:Y:65:LEU:HB3	1.89	0.55
16:q:10:ARG:HH21	53:1:1216:G:C5'	2.19	0.55
23:x:13:THR:OG1	23:x:14:GLY:N	2.40	0.55
53:1:2047:C:H2'	53:1:2048:G:H8	1.72	0.55
7:h:33:VAL:HG12	53:1:1055:G:H5''	1.89	0.55
48:X:44:ILE:HD13	48:X:63:ASP:HA	1.87	0.55
49:Y:28:ARG:HH12	52:3:1437:A:H5''	1.71	0.55
52:3:231:U:H2'	52:3:232:G:H8	1.70	0.55
53:1:2646:C:H2'	53:1:2647:U:O4'	2.06	0.55
1:b:176:ARG:NH2	52:3:774:G:H4'	2.21	0.55
14:o:15:ARG:HH21	54:2:8:C:H5''	1.70	0.55
31:G:94:ARG:HD3	52:3:1100:C:OP2	2.07	0.55
32:H:56:ILE:HG22	32:H:63:ILE:HD11	1.88	0.55
33:I:32:LYS:NZ	52:3:425:G:H5''	2.22	0.55
34:J:133:ILE:O	34:J:136:VAL:HG12	2.06	0.55
45:U:5:ARG:HD2	52:3:376:G:H4'	1.89	0.55
53:1:635:C:H2'	53:1:636:G:C8	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:s:31:GLN:O	18:s:35:ILE:HG13	2.07	0.55
21:v:72:VAL:HG12	21:v:93:ARG:HA	1.89	0.55
22:w:39:THR:HG21	53:1:2336:A:N6	2.21	0.55
31:G:67:LEU:HB3	31:G:160:LEU:HD13	1.89	0.55
39:O:10:LEU:HD11	39:O:22:THR:HG22	1.89	0.55
40:P:31:VAL:HG23	40:P:44:ALA:HB3	1.88	0.55
40:P:85:VAL:HG21	50:Z:16:ARG:HH22	1.72	0.55
53:1:2514:U:H2'	53:1:2515:C:C6	2.42	0.55
53:1:2800:A:H3'	53:1:2801:G:H5'	1.88	0.55
46:V:76:ARG:HG2	46:V:77:VAL:N	2.22	0.55
1:b:228:ASP:CG	53:1:780:G:H1	2.14	0.55
12:m:45:GLN:NE2	53:1:2485:G:H5''	2.22	0.55
13:n:79:LEU:HG	13:n:83:LEU:HD12	1.88	0.55
14:o:81:ARG:HA	14:o:84:GLU:HB2	1.89	0.55
21:v:83:LYS:O	21:v:85:LYS:N	2.37	0.55
39:O:50:THR:HB	52:3:975:A:N6	2.21	0.55
41:Q:113:ARG:HH21	52:3:501:C:P	2.30	0.55
9:j:47:HIS:CE1	9:j:48:VAL:HG23	2.42	0.54
12:m:72:PRO:HD3	12:m:92:TRP:CZ3	2.42	0.54
15:p:2:ASN:ND2	53:1:2876:G:H4'	2.21	0.54
18:s:93:ALA:HB2	53:1:1614:A:N1	2.22	0.54
21:v:5:ASN:HD22	21:v:46:LYS:HZ1	1.53	0.54
33:I:13:ARG:HG3	33:I:55:ARG:NH1	2.22	0.54
34:J:18:ASN:O	34:J:33:THR:HG22	2.07	0.54
43:S:81:ILE:HG21	52:3:1202:U:H3	1.71	0.54
52:3:715:A:H2'	52:3:716:A:C8	2.43	0.54
53:1:2287:A:O2'	53:1:2288:A:H2'	2.06	0.54
55:6:16:C:H4'	55:6:60:U:H1'	1.88	0.54
5:f:97:VAL:HG13	5:f:102:ILE:HG12	1.88	0.54
6:g:73:ASN:ND2	6:g:76:GLU:HA	2.22	0.54
15:p:71:ARG:HD3	15:p:73:PHE:CE1	2.42	0.54
16:q:50:ARG:NH2	53:1:993:G:OP2	2.41	0.54
25:z:50:VAL:O	25:z:54:VAL:HG22	2.07	0.54
33:I:77:GLU:HB2	33:I:80:ARG:HH21	1.71	0.54
35:K:11:HIS:ND1	35:K:12:PRO:HD2	2.22	0.54
40:P:32:THR:HG23	40:P:43:TRP:HB3	1.90	0.54
42:R:95:PRO:HA	52:3:1308:U:OP1	2.07	0.54
42:R:106:ARG:HB2	42:R:112:ARG:HH21	1.71	0.54
52:3:1271:A:H5'	52:3:1314:C:H5''	1.89	0.54
53:1:871:U:H2'	53:1:872:U:C6	2.42	0.54
53:1:2749:A:OP2	53:1:2751:G:H5''	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:132:ARG:HG3	1:b:185:ALA:HB1	1.90	0.54
12:m:18:ARG:NH2	53:1:952:G:OP1	2.40	0.54
13:n:50:PRO:O	13:n:53:THR:HG22	2.07	0.54
19:t:34:VAL:HG23	19:t:81:LYS:HB3	1.90	0.54
38:N:95:SER:O	38:N:99:LYS:HG2	2.07	0.54
42:R:95:PRO:HB2	42:R:99:GLN:OE1	2.06	0.54
2:c:49:GLN:NE2	2:c:79:LEU:HD13	2.22	0.54
4:e:41:GLU:HB3	4:e:48:LEU:HD23	1.89	0.54
4:e:147:ARG:HB3	4:e:149:ARG:HG3	1.87	0.54
19:t:77:ARG:HG2	53:1:64:A:H5'	1.89	0.54
29:E:31:ILE:HG23	29:E:31:ILE:O	2.07	0.54
49:Y:28:ARG:CZ	52:3:1437:A:H5''	2.37	0.54
49:Y:54:GLN:O	49:Y:57:VAL:HG12	2.08	0.54
52:3:494:G:O2'	52:3:496:A:H1'	2.07	0.54
52:3:791:G:H22	52:3:1497:G:H4'	1.72	0.54
53:1:2087:G:H2'	53:1:2088:A:C8	2.41	0.54
1:b:176:ARG:HH22	52:3:774:G:H4'	1.72	0.54
3:d:98:LYS:HZ2	53:1:607:U:H5''	1.72	0.54
8:i:34:ILE:H	8:i:34:ILE:HD12	1.72	0.54
53:1:1111:A:H2'	53:1:1111:A:N3	2.22	0.54
54:2:88:C:H5''	54:2:89:U:OP1	2.08	0.54
1:b:77:VAL:HG21	1:b:109:LEU:HD21	1.89	0.54
2:c:124:ARG:HG2	2:c:125:TRP:CD1	2.43	0.54
4:e:116:LEU:HD12	4:e:116:LEU:H	1.73	0.54
11:l:56:PRO:HD2	11:l:59:ARG:HD3	1.90	0.54
19:t:80:TRP:CZ3	19:t:82:LYS:HB3	2.41	0.54
52:3:77:A:H2'	52:3:78:A:C8	2.43	0.54
53:1:1979:U:O2'	53:1:1980:G:H5'	2.08	0.54
53:1:2328:A:H2'	53:1:2329:U:C6	2.43	0.54
1:b:42:ARG:HH11	1:b:42:ARG:HG2	1.72	0.54
1:b:52:HIS:HA	1:b:216:ARG:HB3	1.89	0.54
7:h:118:ILE:H	7:h:119:PRO:CD	2.19	0.54
39:O:28:THR:HA	39:O:31:ARG:HH21	1.71	0.54
41:Q:99:GLY:HA3	41:Q:117:GLY:HA3	1.90	0.54
51:a:211:LYS:HZ3	53:1:2177:C:H4'	1.70	0.54
53:1:161:A:H3'	53:1:162:U:H5''	1.90	0.54
2:c:23:PRO:HB3	53:1:2682:A:C2	2.42	0.54
8:i:107:GLU:OE2	8:i:108:ILE:HG23	2.07	0.54
9:j:8:PRO:HG3	9:j:48:VAL:HG21	1.89	0.54
11:l:109:LYS:HG2	11:l:126:ARG:HB3	1.90	0.54
29:E:5:THR:HG23	29:E:61:LEU:HA	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:G:186:VAL:HG11	31:G:192:PRO:HB3	1.89	0.54
46:V:63:CYS:SG	46:V:64:ARG:N	2.80	0.54
53:1:2350:C:H2'	53:1:2351:G:O4'	2.07	0.54
3:d:103:GLY:HA2	3:d:106:LYS:HD3	1.89	0.54
4:e:40:GLY:HA2	4:e:84:ILE:CD1	2.38	0.54
9:j:35:ARG:HG2	9:j:40:HIS:CD2	2.43	0.54
10:k:71:ARG:HB3	10:k:75:SER:H	1.73	0.54
14:o:7:ARG:HA	14:o:10:ARG:HH11	1.73	0.54
15:p:38:ARG:HH22	52:3:345:C:C5'	2.19	0.54
21:v:23:ALA:O	21:v:25:LYS:HG3	2.07	0.54
48:X:35:ARG:NH1	52:3:1221:G:H5''	2.23	0.54
50:Z:49:ALA:O	50:Z:52:VAL:HG12	2.08	0.54
53:1:1509:A:H2'	53:1:1510:G:C8	2.42	0.54
6:g:27:ARG:HD2	23:x:37:PHE:HE1	1.73	0.54
36:L:76:SER:HB3	55:6:33:U:H5''	1.90	0.54
38:N:71:ILE:HG23	38:N:72:SER:H	1.72	0.54
52:3:422:C:H5'	52:3:423:G:C2	2.43	0.54
53:1:1856:U:H2'	53:1:1857:G:O4'	2.08	0.54
53:1:2233:U:H2'	53:1:2234:G:H8	1.73	0.54
1:b:204:LEU:HB3	1:b:209:ALA:CB	2.39	0.53
4:e:145:VAL:HG12	4:e:147:ARG:H	1.72	0.53
12:m:11:LYS:HD3	53:1:2277:G:O3'	2.08	0.53
32:H:32:LEU:HD12	32:H:33:ASP:N	2.23	0.53
34:J:22:LYS:HD3	34:J:29:ILE:HD11	1.90	0.53
53:1:1790:C:H2'	53:1:1791:A:C5	2.43	0.53
53:1:2063:C:H1'	58:5:101:FME:O1	2.08	0.53
53:1:2799:A:C2'	53:1:2800:A:H5'	2.38	0.53
2:c:128:ARG:HE	53:1:1996:C:H5''	1.74	0.53
6:g:29:PHE:HB2	53:1:2198:A:C2	2.43	0.53
8:i:100:ILE:HD12	8:i:105:LEU:HD21	1.91	0.53
20:u:17:ASP:HA	20:u:20:LYS:HE2	1.89	0.53
52:3:86:G:H4'	52:3:87:C:C5	2.43	0.53
52:3:505:G:H2'	52:3:506:G:C8	2.43	0.53
53:1:310:A:H2'	53:1:311:A:H5''	1.90	0.53
53:1:635:C:H2'	53:1:636:G:H8	1.72	0.53
53:1:2788:C:H2'	53:1:2789:C:C6	2.43	0.53
57:7:49:C:H6	57:7:49:C:H5'	1.73	0.53
1:b:68:ARG:O	1:b:188:ARG:NH1	2.41	0.53
1:b:229:HIS:CD2	1:b:246:PRO:HB3	2.43	0.53
3:d:148:ILE:HB	3:d:169:VAL:HG12	1.91	0.53
19:t:73:ARG:NH1	53:1:456:C:H2'	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:w:20:LYS:HD2	53:1:2355:G:H4'	1.90	0.53
29:E:24:LYS:HG3	29:E:25:HIS:N	2.24	0.53
38:N:49:GLN:N	38:N:50:PRO:HD2	2.23	0.53
41:Q:8:ARG:NH2	52:3:881:G:OP2	2.41	0.53
57:7:14:A:H61	57:7:21:A:H2	1.55	0.53
1:b:229:HIS:ND1	1:b:230:PRO:HD2	2.22	0.53
7:h:125:ARG:H	7:h:125:ARG:HD3	1.73	0.53
18:s:20:VAL:HG21	18:s:43:ALA:HB3	1.89	0.53
31:G:12:GLY:HA2	31:G:14:HIS:CE1	2.43	0.53
31:G:125:PHE:HA	31:G:128:LEU:HB2	1.89	0.53
31:G:162:VAL:HB	31:G:184:ALA:HB2	1.90	0.53
37:M:30:LYS:O	37:M:33:VAL:HG22	2.09	0.53
38:N:8:THR:HG23	52:3:1148:U:H5''	1.90	0.53
38:N:129:ARG:HH22	55:5:33:U:H3'	1.74	0.53
52:3:721:G:H4'	52:3:722:G:O4'	2.08	0.53
52:3:1330:U:H2'	52:3:1331:G:O4'	2.08	0.53
53:1:1275:A:N6	53:1:1296:G:H4'	2.23	0.53
13:n:22:ARG:HG3	13:n:70:THR:HA	1.89	0.53
15:p:38:ARG:NH1	52:3:346:G:OP1	2.42	0.53
33:I:70:GLN:HA	33:I:73:ASN:ND2	2.24	0.53
37:M:60:LEU:HD12	37:M:60:LEU:N	2.24	0.53
48:X:35:ARG:NH2	48:X:71:GLY:O	2.41	0.53
53:1:150:U:H2'	53:1:151:C:C6	2.44	0.53
53:1:644:A:H61	53:1:2349:G:H21	1.55	0.53
53:1:669:G:H2'	53:1:669:G:N3	2.23	0.53
53:1:995:C:H6	53:1:995:C:H5'	1.74	0.53
53:1:1020:A:C1'	53:1:1021:A:OP2	2.54	0.53
53:1:1674:G:H21	53:1:1677:A:H61	1.55	0.53
53:1:2048:G:H3'	53:1:2049:G:H5''	1.89	0.53
53:1:2818:U:H2'	53:1:2819:G:C8	2.44	0.53
14:o:39:VAL:HB	14:o:49:VAL:H	1.72	0.53
25:z:6:ILE:HG22	25:z:28:LEU:HD11	1.90	0.53
40:P:60:PHE:O	40:P:63:GLN:HB3	2.08	0.53
42:R:15:VAL:HG23	42:R:16:ILE:H	1.73	0.53
47:W:54:LEU:HD23	47:W:55:ALA:N	2.24	0.53
53:1:226:A:H2'	53:1:227:A:O4'	2.07	0.53
53:1:613:A:H2'	53:1:613:A:N3	2.21	0.53
53:1:955:U:H3	53:1:962:G:H1	1.57	0.53
53:1:1013:C:H2'	53:1:1014:A:H8	1.73	0.53
14:o:12:THR:HG21	53:1:2334:U:H5'	1.91	0.53
33:I:70:GLN:HA	33:I:73:ASN:HD22	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:167:PRO:HB2	33:I:170:LEU:CD2	2.38	0.53
40:P:31:VAL:HG21	40:P:69:CYS:HB2	1.90	0.53
1:b:62:ARG:HD3	1:b:90:ILE:HD11	1.90	0.53
22:w:17:LEU:HD22	22:w:17:LEU:N	2.23	0.53
25:z:10:ARG:HH21	25:z:10:ARG:HG3	1.74	0.53
33:I:9:LYS:HG3	33:I:12:ARG:HH21	1.74	0.53
37:M:83:ARG:HB2	46:V:36:PHE:CE2	2.42	0.53
41:Q:87:LYS:NZ	52:3:525:C:H5''	2.23	0.53
43:S:44:VAL:HG13	43:S:45:LEU:HD22	1.90	0.53
52:3:1352:C:H2'	52:3:1353:G:H8	1.72	0.53
53:1:441:U:O2'	53:1:442:G:H5'	2.08	0.53
53:1:1353:A:H1'	53:1:1569:A:H2	1.74	0.53
53:1:2467:C:H2'	53:1:2468:A:O4'	2.09	0.53
3:d:121:VAL:HG23	3:d:189:THR:HA	1.91	0.53
6:g:31:VAL:N	6:g:32:PRO:HD2	2.23	0.53
9:j:27:ARG:HH22	53:1:1142:A:H5'	1.73	0.53
9:j:97:PRO:HA	9:j:100:VAL:HG23	1.91	0.53
35:K:6:ILE:N	35:K:6:ILE:HD12	2.24	0.53
35:K:86:ARG:NH1	52:3:673:A:H4'	2.20	0.53
39:O:38:GLY:O	39:O:40:ILE:HD12	2.09	0.53
52:3:1502:A:H8	52:3:1505:G:H22	1.57	0.53
5:f:172:GLU:HG3	5:f:174:LYS:H	1.74	0.53
8:i:107:GLU:HA	8:i:110:GLN:HG2	1.91	0.53
14:o:100:HIS:HA	14:o:104:GLN:NE2	2.20	0.53
27:C:29:LYS:HD3	53:1:2286:G:OP1	2.08	0.53
31:G:116:LEU:HB3	31:G:140:LEU:HD13	1.91	0.53
33:I:123:MET:HG3	33:I:127:ARG:C	2.34	0.53
37:M:28:SER:CB	37:M:58:LEU:HD13	2.38	0.53
37:M:77:VAL:HG21	37:M:127:TYR:CD1	2.44	0.53
38:N:16:ALA:HA	38:N:66:VAL:HG12	1.91	0.53
42:R:64:VAL:HG12	42:R:65:GLU:N	2.23	0.53
50:Z:34:ARG:HB3	50:Z:36:PHE:CE2	2.44	0.53
52:3:309:A:H2'	52:3:310:G:H8	1.74	0.53
52:3:1516:G:H2'	52:3:1518:A:OP2	2.09	0.53
53:1:473:G:O2'	53:1:474:G:H5'	2.08	0.53
53:1:562:U:O4'	53:1:2036:C:H5'	2.09	0.53
9:j:53:TYR:HE1	9:j:121:LYS:HD2	1.74	0.52
10:k:35:VAL:HG12	10:k:69:VAL:HG13	1.90	0.52
20:u:84:PHE:HB2	53:1:297:G:H5''	1.91	0.52
22:w:15:LYS:HB2	22:w:17:LEU:HD21	1.91	0.52
27:C:36:LYS:HD3	53:1:2344:U:OP2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:J:41:GLY:HA2	34:J:117:ALA:C	2.34	0.52
36:L:55:LYS:HB3	36:L:59:GLU:HG2	1.91	0.52
42:R:92:ARG:HG2	53:1:888:C:N4	2.24	0.52
48:X:2:ARG:HG2	52:3:1312:G:N7	2.23	0.52
52:3:51:A:H4'	52:3:52:C:H5''	1.92	0.52
52:3:211:G:H2'	52:3:212:G:H5'	1.90	0.52
2:c:110:THR:HA	2:c:171:THR:HG22	1.91	0.52
12:m:86:LYS:HE2	53:1:955:U:H5''	1.91	0.52
14:o:29:HIS:ND1	54:2:7:G:H5'	2.25	0.52
42:R:6:ILE:HG22	42:R:8:ILE:HG13	1.90	0.52
51:a:7:ARG:HB3	51:a:8:MET:HE2	1.90	0.52
52:3:1227:A:H5'	52:3:1228:C:OP2	2.09	0.52
52:3:1494:G:H4'	53:1:1913:A:N7	2.25	0.52
53:1:1827:U:H2'	53:1:1828:G:O4'	2.09	0.52
53:1:2818:U:H2'	53:1:2819:G:H8	1.73	0.52
1:b:176:ARG:HG2	53:1:1820:U:OP1	2.10	0.52
3:d:98:LYS:HZ1	53:1:607:U:H5''	1.72	0.52
21:v:70:ILE:N	21:v:70:ILE:HD12	2.24	0.52
25:z:5:LYS:HA	25:z:36:GLU:HA	1.91	0.52
33:I:116:LEU:HB3	33:I:121:ALA:HB3	1.91	0.52
38:N:64:ILE:HD12	38:N:64:ILE:N	2.24	0.52
39:O:41:PRO:HG2	52:3:1150:A:C2	2.44	0.52
41:Q:13:ARG:NH1	41:Q:14:LYS:O	2.42	0.52
53:1:121:G:H4'	53:1:149:A:H5'	1.91	0.52
53:1:532:A:H2'	53:1:532:A:N3	2.23	0.52
7:h:57:ASN:ND2	7:h:62:ARG:HD3	2.24	0.52
41:Q:43:LYS:HD3	52:3:1492:A:H4'	1.91	0.52
52:3:1402:C:H2'	52:3:1403:C:O4'	2.10	0.52
53:1:395:U:H2'	53:1:396:G:H8	1.75	0.52
53:1:2639:A:H2'	53:1:2640:G:O4'	2.10	0.52
1:b:32:LEU:HD11	1:b:101:ARG:HA	1.92	0.52
1:b:235:GLU:H	1:b:238:ASN:ND2	2.07	0.52
3:d:52:VAL:HG13	53:1:452:G:OP1	2.10	0.52
7:h:23:LEU:HD21	7:h:96:PHE:HB2	1.90	0.52
7:h:96:PHE:HE2	7:h:125:ARG:HA	1.74	0.52
8:i:101:SER:HA	8:i:140:GLU:O	2.09	0.52
13:n:67:PHE:C	13:n:69:ARG:H	2.15	0.52
21:v:45:ASP:O	21:v:48:MET:HB3	2.10	0.52
32:H:185:THR:HG23	32:H:197:VAL:O	2.10	0.52
38:N:91:GLU:HA	38:N:94:ARG:HB3	1.90	0.52
40:P:81:LEU:HD12	40:P:81:LEU:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:S:58:ARG:HH12	52:3:979:C:H2'	1.74	0.52
53:1:639:U:H2'	53:1:640:C:C6	2.44	0.52
53:1:792:A:H3'	53:1:793:A:H5'	1.91	0.52
54:2:3:C:H3'	54:2:4:C:C5'	2.39	0.52
56:4:19:U:H2'	56:4:20:U:C6	2.44	0.52
9:j:41:LYS:HB3	9:j:43:GLU:OE1	2.09	0.52
16:q:10:ARG:HH21	53:1:1216:G:H5''	1.75	0.52
17:r:17:GLY:H	17:r:98:ILE:HB	1.74	0.52
18:s:82:MET:HB2	18:s:98:LYS:HB2	1.90	0.52
33:I:21:LYS:O	33:I:21:LYS:HG3	2.09	0.52
45:U:10:GLY:HA2	52:3:624:C:H4'	1.91	0.52
53:1:1664:A:H61	53:1:1996:C:H42	1.57	0.52
53:1:2267:A:H5''	53:1:2268:A:H5'	1.92	0.52
8:i:13:ALA:HB1	8:i:16:MET:HB3	1.90	0.52
11:l:111:ILE:N	11:l:111:ILE:HD12	2.25	0.52
24:y:14:LEU:O	24:y:18:LEU:HD23	2.09	0.52
29:E:3:ILE:HG21	29:E:62:PRO:HG2	1.91	0.52
31:G:69:VAL:HA	31:G:91:VAL:HG23	1.92	0.52
34:J:22:LYS:HG3	52:3:1081:A:H5'	1.92	0.52
51:a:166:ASP:HB3	53:1:2122:U:H4'	1.91	0.52
52:3:123:U:H5''	52:3:311:C:O2'	2.10	0.52
53:1:971:G:H2'	53:1:972:A:O4'	2.10	0.52
53:1:2515:C:H2'	53:1:2516:A:H8	1.75	0.52
1:b:211:ARG:HD3	1:b:217:PRO:HD3	1.91	0.52
7:h:73:LYS:HD2	7:h:117:LEU:HD13	1.92	0.52
10:k:42:THR:HG21	53:1:1952:A:OP1	2.10	0.52
34:J:38:VAL:HG22	34:J:46:GLY:O	2.10	0.52
38:N:4:GLN:HE22	52:3:1131:G:H5'	1.74	0.52
49:Y:68:LYS:HZ1	52:3:185:U:H5'	1.73	0.52
53:1:367:G:H2'	53:1:368:A:O4'	2.09	0.52
53:1:2512:C:H2'	53:1:2513:A:O4'	2.10	0.52
53:1:2687:U:H2'	53:1:2688:G:O4'	2.09	0.52
54:2:28:C:H2'	54:2:29:A:C8	2.45	0.52
54:2:65:U:H3'	54:2:108:A:N6	2.24	0.52
1:b:184:GLU:HG3	1:b:186:ASP:OD2	2.10	0.52
7:h:53:ARG:HB2	7:h:55:VAL:HG13	1.91	0.52
11:l:80:SER:HA	11:l:115:GLU:HB3	1.91	0.52
31:G:89:PHE:CD2	31:G:153:MET:HE3	2.45	0.52
42:R:101:THR:HG21	52:3:1226:C:OP2	2.09	0.52
53:1:1704:C:H2'	53:1:1705:A:C8	2.45	0.52
53:1:1882:U:H2'	53:1:1883:U:C6	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2376:A:H2'	53:1:2377:A:O4'	2.10	0.52
4:e:30:VAL:HA	4:e:157:THR:HA	1.92	0.52
44:T:45:HIS:O	44:T:47:LYS:N	2.40	0.52
51:a:211:LYS:HZ1	53:1:2177:C:H4'	1.75	0.52
1:b:216:ARG:HG3	1:b:217:PRO:HD2	1.92	0.51
19:t:14:PRO:HD2	24:y:33:ALA:CB	2.40	0.51
34:J:64:GLU:HA	34:J:67:ARG:HH12	1.75	0.51
34:J:123:LEU:HD22	52:3:7:A:N7	2.25	0.51
35:K:12:PRO:HG3	35:K:56:LYS:O	2.09	0.51
38:N:34:LEU:HD23	38:N:34:LEU:O	2.10	0.51
39:O:59:LYS:HD3	52:3:973:G:OP1	2.10	0.51
43:S:19:TYR:HB3	43:S:50:LEU:HD13	1.92	0.51
52:3:946:A:H2'	52:3:947:G:C8	2.44	0.51
53:1:528:A:N1	53:1:2042:A:H2'	2.24	0.51
53:1:575:A:H4'	53:1:2500:U:H5''	1.92	0.51
53:1:796:C:H2'	53:1:797:G:C8	2.46	0.51
53:1:1060:U:H4'	53:1:1061:U:H5'	1.93	0.51
53:1:1138:G:H2'	53:1:1139:G:O4'	2.10	0.51
53:1:2277:G:H2'	53:1:2278:A:H5''	1.92	0.51
54:2:13:G:N7	54:2:70:C:H4'	2.24	0.51
1:b:93:VAL:HG21	1:b:103:ILE:HD11	1.92	0.51
7:h:36:ASP:O	7:h:40:GLU:HG2	2.11	0.51
18:s:36:LEU:HD13	18:s:47:VAL:HG23	1.91	0.51
23:x:65:THR:O	23:x:69:GLU:HG3	2.11	0.51
33:I:23:GLY:HA3	52:3:409:U:OP1	2.11	0.51
53:1:1268:A:H2'	53:1:1269:A:O4'	2.10	0.51
53:1:1298:C:H2'	53:1:1299:G:O4'	2.11	0.51
53:1:1637:A:H5'	53:1:1760:C:O2'	2.10	0.51
12:m:4:PRO:HG3	12:m:68:PHE:HE2	1.74	0.51
28:D:14:ARG:HG3	53:1:771:G:OP1	2.11	0.51
31:G:96:LEU:HD22	52:3:1103:C:C5'	2.40	0.51
36:L:125:ASP:HA	36:L:128:GLU:OE2	2.10	0.51
38:N:17:ARG:CZ	52:3:1129:C:H4'	2.41	0.51
40:P:34:THR:HG22	40:P:40:ALA:HA	1.92	0.51
41:Q:30:ARG:HH12	41:Q:57:THR:HG21	1.71	0.51
49:Y:57:VAL:HG22	49:Y:71:ALA:HB1	1.92	0.51
52:3:514:C:H2'	52:3:515:G:H8	1.75	0.51
52:3:516:U:H3	52:3:533:A:H62	1.57	0.51
53:1:1590:A:H2'	53:1:1591:A:C8	2.46	0.51
8:i:102:ARG:HG3	8:i:139:VAL:HG11	1.91	0.51
15:p:38:ARG:NH1	52:3:345:C:H3'	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:q:2:ARG:HB2	53:1:1248:G:C5	2.45	0.51
33:l:50:TYR:CD2	52:3:509:A:H5'	2.46	0.51
37:M:28:SER:OG	37:M:29:SER:N	2.43	0.51
37:M:74:ILE:HD13	37:M:128:VAL:HG22	1.92	0.51
38:N:12:LYS:HA	38:N:109:GLN:NE2	2.25	0.51
43:S:68:ARG:NH1	43:S:70:HIS:HB2	2.26	0.51
45:U:47:GLU:HG3	45:U:48:GLU:N	2.24	0.51
52:3:352:C:H4'	52:3:354:G:OP1	2.10	0.51
1:b:140:VAL:HG12	1:b:191:LEU:HA	1.92	0.51
12:m:11:LYS:HG3	53:1:2277:G:H4'	1.93	0.51
13:n:39:PRO:HB2	53:1:1651:G:H5'	1.92	0.51
38:N:70:GLY:HA3	52:3:1371:G:O3'	2.10	0.51
53:1:974:G:H1'	53:1:975:A:C8	2.45	0.51
53:1:1547:C:H2'	53:1:1548:A:C8	2.45	0.51
53:1:2423:U:O2'	53:1:2425:A:H2'	2.09	0.51
56:4:17:U:H2'	56:4:18:G:C8	2.46	0.51
2:c:194:PRO:HA	53:1:2680:U:C5'	2.40	0.51
7:h:6:GLN:O	7:h:9:GLN:HG2	2.11	0.51
22:w:39:THR:H	53:1:2331:G:H4'	1.76	0.51
23:x:76:LYS:HD2	23:x:76:LYS:O	2.10	0.51
53:1:2553:G:C3'	53:1:2554:U:H5''	2.38	0.51
7:h:125:ARG:HD3	7:h:125:ARG:N	2.25	0.51
11:l:101:ILE:HG13	11:l:102:GLY:N	2.21	0.51
14:o:49:VAL:CG2	14:o:85:LYS:HG3	2.39	0.51
28:D:12:ARG:O	28:D:16:HIS:HB2	2.10	0.51
52:3:1497:G:C2'	52:3:1498:U:H5'	2.41	0.51
53:1:1758:U:C5	53:1:2696:U:H5'	2.46	0.51
57:7:47:U:H3'	57:7:48:C:H5''	1.93	0.51
2:c:181:ASP:HB3	2:c:186:LEU:H	1.75	0.51
6:g:96:THR:HG23	6:g:115:VAL:HB	1.92	0.51
10:k:103:VAL:HG12	10:k:104:THR:H	1.76	0.51
12:m:50:ARG:HD3	12:m:50:ARG:C	2.36	0.51
17:r:7:SER:HB2	17:r:22:LEU:HD22	1.93	0.51
43:S:25:GLU:O	43:S:30:ILE:HD12	2.10	0.51
43:S:80:ARG:O	43:S:83:VAL:HG12	2.11	0.51
48:X:5:LYS:HZ3	48:X:6:LYS:HE3	1.75	0.51
53:1:118:A:OP2	53:1:119:A:H2'	2.11	0.51
53:1:1051:G:H4'	53:1:2752:C:O2'	2.11	0.51
55:5:29:G:H2'	55:5:30:G:C8	2.46	0.51
10:k:71:ARG:CD	10:k:72:PRO:HD2	2.40	0.51
11:l:41:ARG:HB2	11:l:44:GLY:HA3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:F:16:ILE:N	30:F:16:ILE:HD12	2.26	0.51
31:G:192:PRO:HB2	31:G:198:VAL:HG11	1.93	0.51
33:I:99:ASN:O	33:I:103:ARG:HG2	2.10	0.51
37:M:33:VAL:HG12	37:M:58:LEU:HD21	1.92	0.51
43:S:15:LEU:HD21	43:S:51:PRO:HG2	1.93	0.51
45:U:20:VAL:HG22	45:U:21:VAL:N	2.26	0.51
45:U:23:ASP:OD2	45:U:25:ARG:HB2	2.10	0.51
52:3:181:A:N6	52:3:194:C:H2'	2.26	0.51
52:3:1259:C:H3'	52:3:1260:G:C5'	2.37	0.51
53:1:1528:A:H2'	53:1:1529:G:O4'	2.10	0.51
1:b:200:MET:HE2	53:1:1820:U:C4	2.46	0.51
6:g:31:VAL:HG23	6:g:32:PRO:HD3	1.93	0.51
16:q:56:PHE:CZ	53:1:536:G:H4'	2.46	0.51
17:r:51:VAL:HG12	17:r:52:PRO:HD2	1.92	0.51
24:y:17:GLU:OE2	24:y:54:LYS:HD3	2.11	0.51
52:3:337:G:H2'	52:3:338:A:C8	2.45	0.51
53:1:704:G:H2'	53:1:726:G:N2	2.25	0.51
53:1:1434:A:H2'	53:1:1435:G:C8	2.46	0.51
53:1:2799:A:H2'	53:1:2800:A:H5'	1.93	0.51
2:c:188:LEU:HD21	15:p:7:LEU:HD21	1.94	0.50
52:3:979:C:H1'	52:3:1317:C:N4	2.25	0.50
53:1:2322:A:H2'	53:1:2323:G:O4'	2.11	0.50
2:c:133:THR:HG22	2:c:134:HIS:N	2.25	0.50
6:g:116:ARG:O	6:g:118:PRO:HD3	2.10	0.50
9:j:78:THR:CB	53:1:2641:G:H5''	2.41	0.50
21:v:16:ALA:HB1	21:v:20:LEU:HD13	1.93	0.50
26:B:10:SER:OG	26:B:14:MET:HE2	2.12	0.50
31:G:71:THR:HA	31:G:92:ASN:O	2.11	0.50
53:1:1110:G:H2'	53:1:1111:A:H8	1.76	0.50
53:1:1912:A:H62	53:1:1917:U:H3	1.57	0.50
53:1:2757:A:H2'	53:1:2757:A:N3	2.26	0.50
3:d:50:ALA:HB2	53:1:801:G:C8	2.46	0.50
4:e:25:MET:HE1	54:2:30:C:O2	2.10	0.50
31:G:192:PRO:HB2	31:G:198:VAL:CG1	2.41	0.50
32:H:13:ILE:HG23	32:H:14:VAL:N	2.26	0.50
32:H:128:MET:HE3	32:H:130:ARG:H	1.77	0.50
33:I:123:MET:HG3	33:I:128:VAL:N	2.26	0.50
35:K:86:ARG:NH1	52:3:673:A:H5''	2.27	0.50
52:3:791:G:N2	52:3:1497:G:H4'	2.26	0.50
53:1:1357:C:H2'	53:1:1358:G:O4'	2.10	0.50
53:1:2480:C:H2'	53:1:2481:G:O4'	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:d:47:LYS:O	3:d:83:VAL:HG23	2.12	0.50
4:e:75:GLY:HA3	53:1:2310:C:N3	2.26	0.50
4:e:114:ARG:NH2	4:e:115:GLY:O	2.44	0.50
5:f:2:ARG:NH1	53:1:2751:G:OP2	2.44	0.50
9:j:36:LEU:HG	9:j:54:ILE:HD12	1.93	0.50
9:j:68:LYS:HD3	53:1:1022:G:N7	2.26	0.50
15:p:71:ARG:HD3	15:p:73:PHE:CZ	2.46	0.50
19:t:55:VAL:HA	19:t:87:LEU:HD23	1.93	0.50
32:h:168:ARG:NH2	52:3:1106:G:HI'	2.26	0.50
44:T:70:LYS:HG2	44:T:71:ARG:NH2	2.27	0.50
50:Z:36:PHE:HB2	50:Z:40:PRO:HD3	1.92	0.50
53:1:69:C:H2'	53:1:70:G:C8	2.46	0.50
53:1:575:A:H4'	53:1:2500:U:C5'	2.41	0.50
53:1:1909:C:H2'	53:1:1910:G:H8	1.76	0.50
4:e:84:ILE:HG21	53:1:2312:U:H5'	1.92	0.50
7:h:118:ILE:CG1	7:h:119:PRO:HD3	2.41	0.50
12:m:59:ARG:HD2	57:7:55:U:OP1	2.12	0.50
30:F:36:ARG:HG2	30:F:37:GLN:H	1.75	0.50
37:M:17:GLN:HE21	37:M:71:VAL:HB	1.77	0.50
52:3:335:C:H2'	52:3:336:A:C8	2.47	0.50
52:3:876:C:H2'	52:3:877:G:H8	1.76	0.50
52:3:1301:U:O2	52:3:1301:U:C2'	2.60	0.50
53:1:1161:C:H2'	53:1:1162:G:H8	1.75	0.50
1:b:24:HIS:HB2	1:b:79:ARG:HD2	1.93	0.50
11:l:93:ASN:HB2	11:l:96:LYS:NZ	2.26	0.50
21:v:25:LYS:HB3	21:v:41:GLU:OE2	2.12	0.50
26:B:42:ILE:HG22	26:B:48:TYR:HB2	1.94	0.50
48:X:69:LYS:HE2	52:3:1320:C:O5'	2.11	0.50
52:3:917:G:H2'	52:3:918:A:C8	2.46	0.50
53:1:937:C:H2'	53:1:938:G:H8	1.77	0.50
53:1:987:C:H2'	53:1:988:A:O4'	2.11	0.50
24:y:20:ASN:HA	24:y:24:GLU:OE2	2.12	0.50
35:K:3:HIS:CD2	35:K:94:HIS:HA	2.47	0.50
37:M:77:VAL:HG12	37:M:84:ILE:HD12	1.94	0.50
40:P:62:ALA:HB1	40:P:95:THR:HB	1.94	0.50
52:3:50:A:H4'	52:3:51:A:H5'	1.94	0.50
53:1:1417:C:H4'	53:1:1587:G:H21	1.75	0.50
53:1:1758:U:H5	53:1:2696:U:H5'	1.76	0.50
53:1:2104:C:H2'	53:1:2105:U:C6	2.46	0.50
57:7:47:U:H3'	57:7:48:C:C5'	2.41	0.50
20:u:94:PHE:HD2	20:u:99:SER:HB2	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:119:ILE:HD12	32:H:122:GLN:OE1	2.11	0.50
34:J:97:PRO:HA	34:J:122:VAL:HG12	1.94	0.50
35:K:12:PRO:O	35:K:15:SER:HB2	2.12	0.50
36:L:37:THR:O	36:L:41:ILE:HG13	2.11	0.50
36:L:55:LYS:HB2	36:L:60:ALA:HB2	1.93	0.50
41:Q:33:CYS:HB2	41:Q:54:VAL:HG22	1.93	0.50
42:R:100:ARG:HE	42:R:102:LYS:HB3	1.77	0.50
43:S:2:LYS:O	43:S:5:MET:N	2.38	0.50
45:U:42:ILE:HG12	52:3:450:G:H4'	1.92	0.50
52:3:407:U:H2'	52:3:408:A:C8	2.47	0.50
52:3:664:G:H22	52:3:741:G:H1	1.58	0.50
53:1:323:C:H2'	53:1:1205:A:H61	1.77	0.50
53:1:558:U:H2'	53:1:559:G:H8	1.77	0.50
53:1:1161:C:H2'	53:1:1162:G:C8	2.46	0.50
53:1:1742:U:H2'	53:1:1743:G:O4'	2.12	0.50
53:1:2396:G:H2'	53:1:2397:G:H8	1.75	0.50
53:1:2834:G:H2'	53:1:2879:A:H61	1.77	0.50
6:g:72:ILE:HB	6:g:108:VAL:HG22	1.93	0.50
7:h:54:VAL:HG22	7:h:83:ALA:HB1	1.93	0.50
32:H:7:ASN:O	32:H:11:LEU:HG	2.12	0.50
33:I:81:LEU:HD12	33:I:82:LYS:H	1.76	0.50
37:M:24:VAL:HG23	37:M:60:LEU:HD13	1.94	0.50
37:M:87:ARG:HD3	52:3:599:C:H5''	1.93	0.50
38:N:71:ILE:HG23	38:N:72:SER:N	2.27	0.50
46:V:39:ARG:HA	52:3:280:C:O2	2.11	0.50
52:3:64:G:H4'	52:3:65:A:H3'	1.94	0.50
53:1:2286:G:H4'	53:1:2287:A:O5'	2.12	0.50
1:b:8:THR:HG21	53:1:727:A:H2	1.76	0.49
1:b:123:ILE:HG23	1:b:191:LEU:HD13	1.92	0.49
5:f:66:THR:OG1	53:1:2748:A:H1'	2.12	0.49
5:f:104:LEU:HB3	5:f:112:VAL:HB	1.93	0.49
7:h:23:LEU:HD23	7:h:87:GLU:OE2	2.12	0.49
9:j:109:LEU:HD12	9:j:119:PHE:HD1	1.75	0.49
23:x:11:PRO:HG3	23:x:30:PRO:HD2	1.93	0.49
24:y:24:GLU:HA	24:y:27:ASN:HB2	1.94	0.49
29:E:48:MET:SD	53:1:650:C:H5''	2.51	0.49
32:H:4:VAL:O	32:H:6:PRO:HD3	2.12	0.49
36:L:63:VAL:O	36:L:67:ASN:ND2	2.44	0.49
46:V:32:ILE:HD11	52:3:564:C:N3	2.27	0.49
49:Y:74:HIS:O	49:Y:78:LEU:HB2	2.12	0.49
53:1:1780:A:O2'	53:1:1781:U:H2'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2149:U:H2'	53:1:2150:C:O4'	2.12	0.49
53:1:2715:C:C2'	53:1:2716:C:H5''	2.41	0.49
12:m:45:GLN:HG2	53:1:2485:G:H5'	1.94	0.49
13:n:110:MET:HE2	13:n:110:MET:HA	1.94	0.49
17:r:29:THR:HG23	17:r:30:GLY:N	2.26	0.49
28:D:10:LEU:HD23	53:1:770:G:H5''	1.93	0.49
31:G:67:LEU:HD23	31:G:160:LEU:HD11	1.94	0.49
34:J:130:THR:HG23	34:J:135:VAL:HG11	1.94	0.49
35:K:6:ILE:HG13	35:K:89:VAL:HG22	1.94	0.49
39:O:14:ASP:CG	39:O:17:LEU:HB2	2.37	0.49
45:U:8:ARG:HD3	45:U:17:TYR:CE1	2.47	0.49
45:U:19:VAL:HG23	45:U:19:VAL:O	2.12	0.49
47:W:62:ARG:HB3	47:W:69:TYR:CE1	2.47	0.49
52:3:820:U:H3'	52:3:821:G:C5'	2.42	0.49
53:1:467:G:O2'	53:1:468:G:H5'	2.12	0.49
53:1:1558:C:H4'	53:1:1560:G:OP2	2.12	0.49
5:f:136:ASP:OD2	5:f:138:GLN:HB3	2.11	0.49
28:D:26:ASN:OD1	53:1:682:G:H5'	2.12	0.49
34:J:106:ALA:HB1	34:J:110:MET:HG3	1.95	0.49
42:R:3:ILE:HG22	42:R:4:ALA:N	2.28	0.49
43:S:7:ALA:HA	43:S:10:VAL:HG12	1.93	0.49
44:T:25:GLU:O	44:T:28:VAL:HG12	2.13	0.49
52:3:1316:G:H2'	52:3:1317:C:H5''	1.94	0.49
53:1:215:G:C4'	53:1:216:A:H4'	2.42	0.49
53:1:1936:A:H2	53:1:1943:U:H3	1.60	0.49
53:1:2358:A:H2'	53:1:2359:C:O4'	2.11	0.49
1:b:29:PHE:CE2	1:b:31:PRO:HB2	2.47	0.49
3:d:97:ASN:HB2	3:d:100:MET:HG3	1.94	0.49
4:e:71:LYS:HA	4:e:80:GLN:HE22	1.77	0.49
5:f:142:GLN:HE22	53:1:2744:G:H21	1.59	0.49
7:h:33:VAL:HA	53:1:1055:G:H4'	1.94	0.49
12:m:59:ARG:CZ	57:7:55:U:H5''	2.42	0.49
22:w:16:ARG:HG3	53:1:2271:G:H5'	1.94	0.49
23:x:2:ARG:O	23:x:11:PRO:HD3	2.13	0.49
23:x:5:GLN:HG3	23:x:49:ARG:H	1.77	0.49
23:x:42:GLU:HG2	23:x:44:ARG:HE	1.77	0.49
34:J:60:GLN:O	34:J:64:GLU:HG3	2.13	0.49
41:Q:51:VAL:HG22	41:Q:52:CYS:H	1.76	0.49
41:Q:89:LEU:HD13	41:Q:92:VAL:HG21	1.95	0.49
42:R:69:ARG:HD2	42:R:69:ARG:O	2.12	0.49
46:V:7:LEU:HD11	46:V:26:ARG:NH2	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:Y:62:ALA:HB1	52:3:223:A:OP1	2.12	0.49
52:3:434:U:H2'	52:3:435:A:C8	2.48	0.49
52:3:1319:A:H61	52:3:1361:G:H21	1.59	0.49
52:3:1354:U:H2'	52:3:1355:G:H8	1.78	0.49
53:1:832:U:H2'	53:1:833:A:C8	2.47	0.49
53:1:1922:G:H2'	53:1:1923:U:O4'	2.11	0.49
53:1:2183:A:H2'	53:1:2184:A:C8	2.47	0.49
53:1:2282:G:H4'	53:1:2389:G:O2'	2.13	0.49
53:1:2515:C:H2'	53:1:2516:A:C8	2.47	0.49
34:J:92:ARG:O	34:J:93:VAL:O	2.31	0.49
37:M:12:ARG:NH2	52:3:825:A:O2'	2.45	0.49
38:N:122:ARG:HD3	52:3:1349:A:H5''	1.94	0.49
41:Q:91:GLY:O	41:Q:93:ARG:NH1	2.46	0.49
43:S:15:LEU:HD21	43:S:51:PRO:CG	2.42	0.49
52:3:1137:C:H4'	52:3:1138:G:N2	2.27	0.49
52:3:1409:C:H2'	52:3:1410:A:C8	2.48	0.49
53:1:253:C:H2'	53:1:254:G:O4'	2.12	0.49
53:1:962:G:H21	53:1:2250:G:H1	1.60	0.49
53:1:1893:C:H2'	53:1:1894:C:H5'	1.94	0.49
53:1:2636:C:H2'	53:1:2637:U:C6	2.47	0.49
4:e:76:PHE:HE1	53:1:2308:G:C6	2.31	0.49
11:l:61:LEU:HB2	29:E:12:ARG:HD3	1.94	0.49
33:I:190:LEU:HD12	33:I:192:ALA:N	2.26	0.49
36:L:129:ASN:HB2	36:L:134:VAL:HG21	1.94	0.49
39:O:23:ALA:O	39:O:27:GLU:HG2	2.12	0.49
41:Q:22:ALA:O	41:Q:23:LEU:C	2.56	0.49
43:S:9:GLU:HA	43:S:12:ARG:HH11	1.77	0.49
43:S:58:ARG:HH11	52:3:979:C:H2'	1.76	0.49
50:Z:13:VAL:HG13	50:Z:15:LEU:HG	1.95	0.49
53:1:2329:U:H2'	53:1:2330:G:C8	2.48	0.49
54:2:97:C:H2'	54:2:98:G:O4'	2.12	0.49
5:f:18:ILE:HD12	5:f:18:ILE:H	1.77	0.49
9:j:27:ARG:NH2	53:1:1141:U:H5''	2.28	0.49
29:E:31:ILE:HD11	29:E:34:LYS:HD2	1.94	0.49
32:H:19:SER:O	43:S:93:PRO:HG3	2.13	0.49
33:I:60:VAL:HA	33:I:63:ILE:HD12	1.95	0.49
33:I:169:TRP:NE1	33:I:170:LEU:HD22	2.28	0.49
52:3:514:C:H2'	52:3:515:G:C8	2.48	0.49
52:3:1201:A:C1'	52:3:1202:U:OP2	2.61	0.49
52:3:1522:U:H2'	52:3:1523:G:H8	1.77	0.49
53:1:340:A:H2'	53:1:341:C:O4'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:511:U:H2'	53:1:512:G:H5'	1.95	0.49
53:1:680:C:H2'	53:1:681:G:C8	2.47	0.49
53:1:948:C:H2'	53:1:949:G:H8	1.78	0.49
1:b:54:GLY:HA3	53:1:691:C:H5''	1.94	0.49
2:c:114:LYS:HG3	53:1:2680:U:OP1	2.12	0.49
23:x:63:ILE:HG23	23:x:64:ASP:H	1.78	0.49
38:N:126:PHE:HZ	52:3:967:C:H4'	1.77	0.49
49:Y:28:ARG:NH2	52:3:1437:A:H5''	2.28	0.49
52:3:78:A:H2'	52:3:79:G:O4'	2.12	0.49
52:3:350:G:H2'	52:3:351:G:C8	2.48	0.49
52:3:396:C:C3'	52:3:397:A:H5''	2.42	0.49
52:3:802:A:H2'	52:3:803:G:O4'	2.13	0.49
53:1:2048:G:C2'	53:1:2049:G:H5''	2.42	0.49
53:1:2185:U:H2'	53:1:2186:G:C8	2.47	0.49
55:5:38:A:H2'	55:5:39:C:O4'	2.13	0.49
4:e:62:GLN:OE1	4:e:94:ARG:NH2	2.46	0.49
4:e:141:ASP:C	4:e:143:ASP:H	2.20	0.49
6:g:11:ASN:O	6:g:12:LEU:HD12	2.13	0.49
36:L:142:ARG:NH1	55:6:41:C:H4'	2.27	0.49
40:P:91:GLY:C	40:P:93:GLU:H	2.21	0.49
47:W:12:PHE:CE1	47:W:46:THR:HG22	2.48	0.49
48:X:35:ARG:HH11	52:3:1221:G:H5''	1.78	0.49
53:1:244:A:H62	53:1:254:G:H21	1.61	0.49
53:1:457:A:O3'	53:1:458:G:H4'	2.13	0.49
53:1:479:A:H4'	53:1:480:A:H5'	1.95	0.49
53:1:1093:G:H21	53:1:1098:A:H62	1.59	0.49
53:1:2798:U:H4'	53:1:2799:A:C4	2.47	0.49
54:2:49:C:H2'	54:2:50:A:C8	2.47	0.49
13:n:2:ARG:O	13:n:2:ARG:CD	2.52	0.49
28:D:13:ASN:O	53:1:125:A:H4'	2.13	0.49
33:I:7:LYS:HG2	52:3:430:A:OP2	2.11	0.49
37:M:98:LEU:O	37:M:98:LEU:HD12	2.13	0.49
42:R:43:LYS:HB2	42:R:46:GLU:OE1	2.12	0.49
42:R:52:ILE:HA	42:R:55:LEU:HB2	1.94	0.49
52:3:1397:C:H42	56:4:22:A:H2'	1.78	0.49
53:1:2463:C:H2'	53:1:2464:G:H8	1.78	0.49
1:b:245:THR:C	1:b:247:TRP:H	2.20	0.48
7:h:74:ASP:O	7:h:77:VAL:HG22	2.13	0.48
8:i:9:LYS:HG2	8:i:57:VAL:HG22	1.95	0.48
9:j:110:PRO:HB3	53:1:1007:C:O3'	2.13	0.48
15:p:10:GLU:HG3	15:p:11:GLN:HG3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:t:73:ARG:N	19:t:73:ARG:HD2	2.28	0.48
32:H:72:PRO:O	32:H:76:ILE:HG12	2.13	0.48
33:I:169:TRP:CD1	33:I:185:PRO:HG3	2.48	0.48
43:S:2:LYS:O	43:S:4:SER:N	2.46	0.48
52:3:1118:U:H2'	52:3:1119:C:C6	2.48	0.48
52:3:1513:A:H2'	52:3:1514:G:C8	2.47	0.48
53:1:255:A:H2'	53:1:256:A:O4'	2.13	0.48
1:b:48:ILE:HG23	1:b:48:ILE:O	2.13	0.48
1:b:75:ALA:HB2	1:b:95:TYR:CD1	2.47	0.48
4:e:141:ASP:HB3	42:R:2:ARG:HH22	1.77	0.48
11:l:127:VAL:HG12	11:l:128:THR:H	1.78	0.48
19:t:29:THR:HG23	19:t:85:VAL:C	2.38	0.48
31:G:86:CYS:O	31:G:224:ARG:NH2	2.46	0.48
39:O:53:ILE:HD12	39:O:63:ASP:OD1	2.13	0.48
49:Y:44:ALA:O	49:Y:48:LYS:HG3	2.13	0.48
51:a:8:MET:HE3	53:1:2174:C:H4'	1.95	0.48
52:3:106:C:H2'	52:3:107:G:C8	2.48	0.48
52:3:163:C:H2'	52:3:164:G:O4'	2.11	0.48
52:3:945:G:H2'	52:3:945:G:N3	2.28	0.48
52:3:1437:A:H2'	52:3:1438:G:H8	1.78	0.48
53:1:226:A:H5'	53:1:257:C:H4'	1.95	0.48
53:1:471:A:H2'	53:1:472:A:O4'	2.12	0.48
53:1:577:G:OP1	53:1:2502:G:H2'	2.13	0.48
53:1:660:C:H2'	53:1:661:A:C8	2.48	0.48
53:1:2029:G:O6	53:1:2032:G:H5'	2.13	0.48
53:1:2047:C:H2'	53:1:2048:G:C8	2.48	0.48
53:1:2248:C:C2'	53:1:2249:U:H5'	2.43	0.48
2:c:124:ARG:HG2	2:c:125:TRP:NE1	2.28	0.48
8:i:131:THR:O	8:i:135:MET:HG2	2.13	0.48
9:j:129:GLU:HG3	9:j:130:HIS:O	2.13	0.48
19:t:43:ILE:HD12	19:t:43:ILE:N	2.28	0.48
23:x:63:ILE:HG23	23:x:64:ASP:N	2.29	0.48
34:J:110:MET:O	34:J:113:VAL:HG12	2.12	0.48
39:O:54:SER:HB3	39:O:61:ALA:HB3	1.96	0.48
40:P:84:MET:HG2	40:P:110:THR:OG1	2.13	0.48
43:S:62:ARG:NH1	43:S:69:PRO:HD3	2.28	0.48
52:3:291:U:H2'	52:3:292:G:C8	2.47	0.48
52:3:741:G:H2'	52:3:742:G:C8	2.48	0.48
52:3:1202:U:H2'	52:3:1203:C:H5'	1.95	0.48
52:3:1319:A:H4'	52:3:1320:C:C5	2.46	0.48
55:5:41:C:H2'	55:5:42:G:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:f:125:PRO:HG2	5:f:129:GLU:O	2.12	0.48
6:g:47:PHE:HA	6:g:51:ARG:HB2	1.95	0.48
7:h:14:GLU:O	7:h:18:VAL:HG23	2.12	0.48
28:D:39:ARG:NH2	53:1:469:G:O6	2.45	0.48
31:G:3:VAL:HG22	31:G:4:SER:N	2.28	0.48
39:O:16:ARG:HA	39:O:19:ASP:OD2	2.13	0.48
40:P:28:ASN:HD22	40:P:56:LYS:HD2	1.78	0.48
41:Q:109:ARG:HB2	41:Q:118:VAL:CG2	2.28	0.48
44:T:28:VAL:HG13	44:T:29:ALA:N	2.29	0.48
52:3:70:U:H4'	52:3:71:A:H8	1.78	0.48
53:1:225:C:H2'	53:1:226:A:O4'	2.13	0.48
53:1:503:A:H4'	53:1:505:A:H5''	1.94	0.48
53:1:1432:G:H2'	53:1:1433:A:C8	2.48	0.48
53:1:2004:G:H2'	53:1:2005:A:O4'	2.14	0.48
53:1:2243:U:H2'	53:1:2244:U:C6	2.48	0.48
1:b:42:ARG:HD2	1:b:42:ARG:N	2.28	0.48
2:c:149:ASN:CB	53:1:2572:A:OP2	2.61	0.48
3:d:117:ARG:HH21	3:d:184:ASP:HA	1.78	0.48
9:j:80:HIS:O	9:j:81:ILE:C	2.56	0.48
11:l:26:GLY:C	11:l:27:LEU:HD22	2.39	0.48
11:l:63:LYS:HA	29:E:12:ARG:HG2	1.95	0.48
13:n:100:CYS:SG	13:n:110:MET:HB3	2.54	0.48
22:w:8:ASN:HA	22:w:10:ARG:NH1	2.28	0.48
22:w:33:ILE:HD11	22:w:78:ILE:HD11	1.95	0.48
33:I:167:PRO:HB2	33:I:170:LEU:HD21	1.95	0.48
38:N:118:ARG:HD3	38:N:122:ARG:HG3	1.95	0.48
40:P:30:ILE:HG12	40:P:45:THR:HG22	1.96	0.48
43:S:84:ARG:HG2	43:S:88:MET:HE2	1.95	0.48
45:U:74:LEU:HA	45:U:77:GLU:HG2	1.96	0.48
50:Z:38:GLU:C	50:Z:40:PRO:HD2	2.39	0.48
53:1:2001:C:H4'	53:1:2689:U:H2'	1.96	0.48
53:1:2257:U:O2'	53:1:2258:C:H5'	2.14	0.48
1:b:158:GLY:HA3	53:1:1820:U:C4	2.49	0.48
3:d:62:GLN:OE1	53:1:676:A:H5'	2.14	0.48
5:f:18:ILE:HD12	5:f:18:ILE:N	2.29	0.48
17:r:5:PHE:HB3	17:r:59:ILE:HD12	1.96	0.48
21:v:35:GLU:HB2	21:v:93:ARG:HH11	1.78	0.48
30:F:36:ARG:HH21	30:F:37:GLN:NE2	2.11	0.48
52:3:326:G:H2'	52:3:327:A:H5'	1.94	0.48
53:1:937:C:H2'	53:1:938:G:C8	2.48	0.48
53:1:1278:C:H2'	53:1:1279:G:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1535:A:H3'	53:1:1536:C:H5'	1.96	0.48
53:1:2297:A:H62	53:1:2319:G:H1'	1.79	0.48
53:1:2313:C:H2'	53:1:2314:A:C8	2.48	0.48
1:b:95:TYR:HB3	1:b:97:ASP:OD1	2.14	0.48
4:e:39:VAL:HG22	4:e:41:GLU:H	1.78	0.48
9:j:25:LEU:HB3	53:1:1140:C:OP1	2.13	0.48
15:p:52:ARG:NH2	53:1:2720:U:H5''	2.27	0.48
20:u:26:ASN:OD1	20:u:34:ILE:HD12	2.14	0.48
33:I:131:ILE:HD12	33:I:131:ILE:N	2.28	0.48
36:L:55:LYS:HE3	36:L:59:GLU:HG3	1.96	0.48
36:L:108:ARG:HB2	36:L:109:LYS:HZ2	1.79	0.48
41:Q:54:VAL:HG21	41:Q:79:ILE:HD11	1.95	0.48
50:Z:66:ARG:HH21	52:3:1099:G:H4'	1.71	0.48
51:a:190:GLU:HA	51:a:193:LEU:HD12	1.96	0.48
52:3:1273:C:H2'	52:3:1274:A:O4'	2.14	0.48
52:3:1369:C:H2'	52:3:1370:G:C8	2.49	0.48
53:1:621:A:H2'	53:1:622:G:H5'	1.96	0.48
53:1:948:C:H2'	53:1:949:G:C8	2.49	0.48
53:1:974:G:N3	53:1:974:G:H2'	2.29	0.48
53:1:1956:U:H1'	53:1:2552:U:OP1	2.13	0.48
53:1:2238:G:H2'	53:1:2238:G:N3	2.28	0.48
5:f:28:LYS:HG2	5:f:79:THR:HA	1.96	0.48
19:t:11:LEU:HG	19:t:32:LEU:HD13	1.95	0.48
19:t:13:ALA:O	19:t:33:LYS:N	2.47	0.48
19:t:14:PRO:HD2	24:y:33:ALA:HB3	1.95	0.48
40:P:92:ARG:CZ	50:Z:24:LYS:HE2	2.43	0.48
50:Z:39:LYS:N	50:Z:40:PRO:CD	2.76	0.48
51:a:54:LYS:HD2	51:a:57:GLN:NE2	2.28	0.48
52:3:193:C:H2'	52:3:194:C:C6	2.49	0.48
52:3:673:A:H2'	52:3:674:G:C8	2.49	0.48
52:3:1261:A:H1'	52:3:1283:U:H5''	1.96	0.48
53:1:395:U:H2'	53:1:396:G:C8	2.49	0.48
53:1:475:C:H4'	53:1:510:C:H5'	1.95	0.48
53:1:2009:A:H2'	53:1:2010:G:H8	1.77	0.48
54:2:118:C:H2'	54:2:119:A:C8	2.48	0.48
1:b:43:ASN:HD21	1:b:45:ASN:CB	2.23	0.48
1:b:257:ARG:NH1	1:b:259:ASN:HD22	2.08	0.48
7:h:24:SER:O	7:h:116:GLU:HB2	2.14	0.48
28:D:7:PRO:CB	53:1:1309:G:H4'	2.43	0.48
30:F:23:ILE:HD12	30:F:23:ILE:N	2.29	0.48
36:L:4:ARG:HH22	52:3:1092:A:H5''	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:581:C:H2'	53:1:582:A:C8	2.48	0.48
53:1:1028:A:H2'	53:1:1029:A:C8	2.49	0.48
53:1:2281:A:O2'	53:1:2282:G:H5'	2.14	0.48
53:1:2432:A:H1'	55:6:75:C:C5'	2.43	0.48
53:1:2715:C:C3'	53:1:2716:C:H5''	2.43	0.48
3:d:1:MET:N	3:d:14:VAL:O	2.47	0.48
17:r:49:ILE:HG23	17:r:54:VAL:HG22	1.96	0.48
21:v:55:GLU:HG3	21:v:59:GLU:HB2	1.96	0.48
25:z:29:ARG:NH2	53:1:1183:U:H4'	2.29	0.48
31:G:27:LYS:N	31:G:28:PRO:CD	2.77	0.48
36:L:97:ALA:HA	36:L:100:MET:HE2	1.96	0.48
44:T:16:ARG:N	44:T:16:ARG:HD2	2.27	0.48
46:V:5:ARG:HG3	46:V:5:ARG:HH11	1.79	0.48
46:V:22:VAL:HG22	46:V:23:ALA:N	2.29	0.48
49:Y:50:PHE:HA	49:Y:53:MET:HE2	1.95	0.48
52:3:335:C:H2'	52:3:336:A:H8	1.79	0.48
52:3:784:A:H2'	52:3:785:G:C8	2.49	0.48
52:3:1219:A:H2'	52:3:1220:G:C8	2.49	0.48
53:1:996:A:H2'	53:1:997:G:H8	1.79	0.48
54:2:108:A:H5'	54:2:109:A:O5'	2.14	0.48
55:5:23:C:H2'	55:5:24:U:C6	2.49	0.48
9:j:117:ALA:HA	9:j:120:ARG:HH21	1.78	0.47
13:n:27:SER:O	13:n:31:HIS:HB2	2.14	0.47
32:H:55:VAL:HB	32:H:66:THR:HB	1.95	0.47
32:H:113:LYS:HE2	32:H:184:ASN:CG	2.39	0.47
38:N:38:PHE:HB2	38:N:71:ILE:HD11	1.96	0.47
44:T:61:GLN:NE2	52:3:656:G:H4'	2.29	0.47
52:3:180:U:H2'	52:3:181:A:O4'	2.13	0.47
52:3:1432:G:H1'	52:3:1468:A:H61	1.79	0.47
53:1:1078:U:H5''	53:1:1079:C:H5''	1.96	0.47
53:1:1438:U:H2'	53:1:1439:A:C8	2.49	0.47
53:1:2036:C:H2'	53:1:2037:A:C8	2.48	0.47
53:1:2537:U:H2'	53:1:2538:C:C6	2.48	0.47
1:b:119:VAL:HG23	1:b:133:ASN:OD1	2.14	0.47
1:b:128:THR:C	1:b:129:LEU:HD12	2.39	0.47
9:j:88:THR:HG23	9:j:91:GLU:H	1.79	0.47
10:k:69:VAL:HG21	10:k:104:THR:HG21	1.95	0.47
12:m:8:LYS:HE2	53:1:869:G:H1'	1.96	0.47
16:q:36:GLN:NE2	53:1:1252:G:H22	2.11	0.47
36:L:22:LEU:O	36:L:26:VAL:HG23	2.15	0.47
52:3:513:C:H2'	52:3:514:C:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1256:A:H1'	52:3:1258:G:N9	2.29	0.47
53:1:703:U:H2'	53:1:704:G:O4'	2.14	0.47
53:1:1846:G:H2'	53:1:1847:A:O4'	2.14	0.47
57:7:46:G:O2'	57:7:48:C:H5'	2.14	0.47
4:e:127:TYR:O	4:e:155:ILE:HG12	2.15	0.47
10:k:6:THR:HG23	53:1:1666:G:H4'	1.97	0.47
34:J:105:ILE:HG13	34:J:123:LEU:HA	1.95	0.47
42:R:30:LYS:HD3	42:R:40:GLU:OE1	2.14	0.47
47:W:12:PHE:HE1	47:W:46:THR:HG22	1.79	0.47
47:W:37:LYS:HB2	52:3:719:C:H1'	1.97	0.47
50:Z:7:GLU:HG3	50:Z:15:LEU:HD13	1.97	0.47
51:a:11:ILE:O	51:a:15:VAL:HG12	2.14	0.47
53:1:20:C:H2'	53:1:21:A:C8	2.49	0.47
53:1:818:G:C2'	53:1:819:A:H5''	2.45	0.47
53:1:947:A:H2'	53:1:948:C:C6	2.49	0.47
53:1:2118:U:H5	53:1:2149:U:H1'	1.79	0.47
53:1:2277:G:C2'	53:1:2278:A:H5''	2.44	0.47
53:1:2584:U:H2'	53:1:2585:U:H2'	1.95	0.47
53:1:2723:C:H2'	53:1:2724:U:O4'	2.14	0.47
4:e:10:GLU:OE2	4:e:10:GLU:N	2.42	0.47
11:l:19:LEU:HD13	53:1:587:C:O2'	2.14	0.47
12:m:34:LYS:HA	12:m:101:VAL:HA	1.96	0.47
14:o:101:GLY:HA3	54:2:49:C:OP1	2.14	0.47
27:C:35:LEU:CD2	27:C:37:LYS:HG3	2.44	0.47
40:P:28:ASN:HB2	40:P:56:LYS:HZ3	1.79	0.47
41:Q:30:ARG:CZ	41:Q:57:THR:HG21	2.45	0.47
52:3:256:U:H2'	52:3:257:G:C8	2.49	0.47
52:3:867:G:H2'	52:3:868:C:C6	2.49	0.47
52:3:1504:G:OP1	52:3:1507:A:H4'	2.15	0.47
53:1:515:A:H1'	53:1:581:C:H1'	1.95	0.47
53:1:660:C:H2'	53:1:661:A:H8	1.80	0.47
53:1:2139:U:H2'	53:1:2140:G:C8	2.49	0.47
54:2:66:A:H4'	54:2:67:G:C8	2.49	0.47
1:b:46:GLY:HA3	53:1:773:U:H5'	1.96	0.47
4:e:92:GLY:O	4:e:95:MET:HG2	2.14	0.47
5:f:88:LEU:HG	5:f:161:VAL:HG22	1.96	0.47
10:k:8:LEU:HD21	10:k:84:CYS:HB3	1.95	0.47
19:t:6:ARG:NH2	19:t:37:ASP:O	2.47	0.47
26:B:39:ARG:O	26:B:40:HIS:HB2	2.14	0.47
32:H:109:GLU:HG3	32:H:140:ALA:HB2	1.96	0.47
37:M:25:THR:HG22	37:M:57:GLU:OE1	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R:85:TYR:O	42:R:89:ARG:HG2	2.13	0.47
42:R:100:ARG:HH21	42:R:102:LYS:HD3	1.79	0.47
52:3:689:C:H2'	52:3:690:G:O4'	2.13	0.47
53:1:1874:C:H2'	53:1:1875:G:O4'	2.13	0.47
2:c:13:ARG:HA	2:c:24:VAL:HG12	1.95	0.47
3:d:99:LYS:HD2	53:1:606:U:OP2	2.14	0.47
7:h:56:ARG:NH2	7:h:83:ALA:HB2	2.22	0.47
12:m:102:LEU:HG	12:m:103:TYR:CE1	2.50	0.47
13:n:60:VAL:HG12	53:1:1454:C:O2'	2.14	0.47
13:n:69:ARG:O	13:n:70:THR:OG1	2.32	0.47
16:q:111:LYS:NZ	17:r:50:GLY:HA2	2.30	0.47
17:r:49:ILE:HG22	17:r:54:VAL:N	2.29	0.47
18:s:28:LYS:HD3	18:s:30:SER:HB3	1.95	0.47
21:v:13:GLY:O	21:v:17:SER:HB2	2.15	0.47
31:G:87:ASP:HB2	31:G:224:ARG:NH2	2.21	0.47
31:G:209:VAL:HA	31:G:212:TYR:CD2	2.49	0.47
39:O:10:LEU:N	39:O:10:LEU:HD23	2.30	0.47
50:Z:36:PHE:CE2	50:Z:39:LYS:HD2	2.50	0.47
51:a:27:ILE:HA	51:a:30:LEU:HG	1.95	0.47
51:a:214:ILE:HD12	51:a:214:ILE:N	2.30	0.47
52:3:304:U:O2'	52:3:305:G:H5'	2.14	0.47
52:3:361:G:H2'	52:3:362:G:O4'	2.14	0.47
52:3:405:U:C3'	52:3:406:G:H5'	2.38	0.47
53:1:1201:U:H2'	53:1:1202:G:C8	2.50	0.47
53:1:2128:G:H1'	53:1:2173:A:N3	2.29	0.47
2:c:142:VAL:HB	2:c:143:PRO:HD2	1.97	0.47
12:m:55:ARG:HG2	12:m:55:ARG:HH21	1.80	0.47
13:n:67:PHE:C	13:n:69:ARG:N	2.72	0.47
14:o:3:LYS:HE2	54:2:30:C:OP1	2.14	0.47
17:r:14:VAL:HA	17:r:18:GLN:NE2	2.30	0.47
21:v:10:LYS:HD2	21:v:10:LYS:N	2.29	0.47
31:G:129:THR:HG23	31:G:132:GLU:H	1.79	0.47
32:H:156:LEU:HD12	32:H:156:LEU:O	2.15	0.47
34:J:108:GLY:H	52:3:9:G:H5''	1.80	0.47
41:Q:106:VAL:HG22	41:Q:107:LYS:N	2.26	0.47
41:Q:113:ARG:HH22	41:Q:120:ARG:HH11	1.62	0.47
43:S:44:VAL:O	43:S:48:GLN:NE2	2.47	0.47
44:T:55:LEU:HD23	53:1:715:A:C2	2.50	0.47
45:U:12:LYS:HG2	45:U:13:LYS:HG2	1.95	0.47
48:X:38:THR:HG22	48:X:39:ILE:H	1.79	0.47
49:Y:63:LYS:HZ2	52:3:196:A:H5'	1.76	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:211:G:C2'	52:3:212:G:H5'	2.45	0.47
52:3:303:A:H2'	52:3:304:U:O4'	2.14	0.47
52:3:423:G:H2'	52:3:424:G:H5'	1.96	0.47
52:3:886:G:H2'	52:3:887:G:O4'	2.15	0.47
52:3:1346:A:C2'	52:3:1347:G:H4'	2.44	0.47
52:3:1397:C:N4	56:4:22:A:H2'	2.30	0.47
53:1:18:U:H2'	53:1:19:A:C8	2.49	0.47
53:1:1013:C:H2'	53:1:1014:A:C8	2.49	0.47
53:1:1231:U:H2'	53:1:1232:G:H8	1.80	0.47
53:1:1258:U:H2'	53:1:1259:G:C8	2.50	0.47
53:1:2131:U:OP1	53:1:2134:A:H5'	2.15	0.47
53:1:2834:G:O2'	53:1:2835:A:H5'	2.15	0.47
57:7:61:C:H5'	57:7:61:C:H6	1.79	0.47
2:c:53:GLY:HA3	2:c:77:ARG:CD	2.45	0.47
6:g:26:ALA:O	6:g:31:VAL:HG22	2.14	0.47
15:p:25:VAL:HG21	15:p:83:ILE:HG22	1.95	0.47
16:q:91:ARG:NH2	53:1:1153:C:OP1	2.47	0.47
34:J:148:SER:OG	34:J:151:MET:HG2	2.14	0.47
39:O:10:LEU:HD23	39:O:10:LEU:H	1.79	0.47
40:P:87:GLY:H	40:P:113:THR:HG22	1.79	0.47
52:3:243:A:H4'	52:3:244:U:H3'	1.97	0.47
52:3:1500:A:H5''	52:3:1508:A:H5''	1.97	0.47
53:1:278:A:H2'	53:1:278:A:N3	2.30	0.47
53:1:596:U:H2'	53:1:597:G:C8	2.49	0.47
53:1:680:C:H2'	53:1:681:G:H8	1.79	0.47
53:1:1438:U:H2'	53:1:1439:A:H8	1.80	0.47
53:1:2156:G:C2'	53:1:2157:G:H5'	2.45	0.47
53:1:2623:G:H2'	53:1:2624:G:H8	1.80	0.47
53:1:2633:G:H5'	53:1:2811:G:O2'	2.14	0.47
2:c:106:LYS:HD3	2:c:174:SER:HB3	1.97	0.47
8:i:51:GLY:C	8:i:52:LEU:HD12	2.40	0.47
9:j:40:HIS:NE2	9:j:41:LYS:HG3	2.30	0.47
11:l:127:VAL:HG12	11:l:128:THR:N	2.30	0.47
12:m:16:ARG:HD2	53:1:958:U:O2	2.15	0.47
16:q:56:PHE:CE2	53:1:536:G:H4'	2.50	0.47
31:G:27:LYS:HB3	31:G:28:PRO:HD3	1.97	0.47
31:G:73:ARG:NH1	31:G:73:ARG:O	2.47	0.47
49:Y:12:GLN:HA	49:Y:15:LYS:HB3	1.97	0.47
51:a:38:PHE:CE1	53:1:2127:G:H4'	2.49	0.47
52:3:396:C:H2'	52:3:397:A:H5''	1.97	0.47
52:3:1481:U:H2'	52:3:1482:G:C8	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:248:G:N3	53:1:2431:U:H4'	2.30	0.47
53:1:912:C:O2'	53:1:913:U:H5'	2.14	0.47
53:1:1201:U:H2'	53:1:1202:G:H8	1.80	0.47
22:w:24:GLY:H	22:w:63:VAL:HG23	1.79	0.47
31:G:7:ASP:HB3	31:G:8:MET:HE2	1.97	0.47
32:H:54:ILE:HG22	32:H:67:ILE:HG12	1.96	0.47
33:I:119:HIS:ND1	52:3:438:U:H4'	2.30	0.47
40:P:12:ARG:C	40:P:14:GLN:H	2.23	0.47
45:U:6:LEU:HD22	45:U:17:TYR:HB3	1.96	0.47
49:Y:79:THR:O	49:Y:82:ILE:HG22	2.15	0.47
53:1:239:C:H2'	53:1:240:C:O4'	2.14	0.47
53:1:1035:U:H2'	53:1:1036:G:H8	1.78	0.47
54:2:28:C:H2'	54:2:29:A:H8	1.80	0.47
1:b:235:GLU:H	1:b:238:ASN:HD22	1.64	0.46
3:d:77:ILE:HD13	53:1:673:C:H4'	1.97	0.46
3:d:127:GLU:CD	3:d:133:LEU:HD21	2.40	0.46
5:f:87:GLN:HB2	5:f:162:ARG:HG2	1.97	0.46
10:k:103:VAL:HG12	10:k:104:THR:N	2.30	0.46
21:v:6:ALA:HB1	21:v:40:ILE:HG23	1.97	0.46
21:v:29:ILE:HA	21:v:40:ILE:H	1.80	0.46
23:x:11:PRO:HG3	23:x:30:PRO:CD	2.45	0.46
27:C:11:VAL:HG22	27:C:12:SER:H	1.80	0.46
41:Q:41:PRO:HG3	41:Q:49:ARG:HE	1.80	0.46
52:3:662:U:H2'	52:3:663:A:C8	2.50	0.46
52:3:1354:U:H2'	52:3:1355:G:C8	2.50	0.46
53:1:145:C:H2'	53:1:146:A:C8	2.50	0.46
53:1:807:U:H2'	53:1:808:G:C8	2.50	0.46
53:1:1297:C:OP1	53:1:2710:C:H4'	2.15	0.46
53:1:1308:A:H2'	53:1:1309:G:O4'	2.14	0.46
1:b:244:VAL:HG12	1:b:250:GLN:HA	1.96	0.46
1:b:250:GLN:NE2	1:b:251:THR:O	2.48	0.46
6:g:57:LYS:O	6:g:60:GLU:HG3	2.14	0.46
7:h:67:THR:HG22	7:h:68:PRO:HD3	1.97	0.46
37:M:39:LEU:O	37:M:44:PHE:N	2.46	0.46
41:Q:101:LEU:HD22	41:Q:101:LEU:H	1.80	0.46
46:V:22:VAL:HG12	46:V:43:LEU:O	2.15	0.46
52:3:620:C:H2'	52:3:621:A:O4'	2.16	0.46
52:3:1137:C:H5'	52:3:1138:G:H5'	1.97	0.46
52:3:1308:U:H2'	52:3:1309:G:H8	1.78	0.46
53:1:704:G:H2'	53:1:726:G:H22	1.79	0.46
53:1:1077:A:C2'	53:1:1078:U:H5'	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1857:G:H1'	53:1:1885:A:N6	2.30	0.46
55:6:59:A:C2'	55:6:60:U:H5'	2.46	0.46
1:b:144:GLU:HG2	1:b:150:GLY:C	2.41	0.46
12:m:36:VAL:HG21	12:m:129:THR:HG23	1.97	0.46
12:m:74:THR:HA	12:m:89:VAL:HA	1.97	0.46
13:n:93:GLY:HA3	53:1:2880:C:O2	2.15	0.46
22:w:38:GLY:HA2	53:1:2330:G:H21	1.79	0.46
25:z:10:ARG:HG3	25:z:10:ARG:NH2	2.30	0.46
31:G:96:LEU:HD13	52:3:1103:C:H4'	1.98	0.46
35:K:6:ILE:HD12	35:K:6:ILE:H	1.79	0.46
41:Q:109:ARG:NH1	52:3:537:G:H5''	2.30	0.46
52:3:865:A:H5'	52:3:1078:U:O4	2.15	0.46
53:1:326:G:H2'	53:1:327:G:C8	2.51	0.46
53:1:362:A:H3'	53:1:363:G:H8	1.80	0.46
53:1:1300:G:H4'	53:1:1301:A:C5'	2.42	0.46
53:1:2743:U:C3'	53:1:2744:G:H5''	2.45	0.46
53:1:2875:C:H2'	53:1:2876:G:C8	2.50	0.46
2:c:51:THR:HB	2:c:79:LEU:HD23	1.97	0.46
18:s:81:SER:OG	18:s:97:LEU:HB3	2.14	0.46
22:w:12:SER:HB3	53:1:2261:C:C5	2.50	0.46
29:E:54:LEU:O	29:E:58:ILE:HG23	2.15	0.46
36:L:122:GLU:HA	36:L:125:ASP:HB2	1.96	0.46
38:N:113:LYS:HA	38:N:120:ALA:N	2.27	0.46
44:T:4:THR:HG22	52:3:659:U:OP1	2.15	0.46
52:3:113:G:H1'	52:3:354:G:H5'	1.95	0.46
52:3:987:G:H2'	52:3:988:G:H8	1.80	0.46
53:1:2737:G:H2'	53:1:2738:A:C8	2.50	0.46
1:b:74:PRO:HD2	53:1:1490:A:H61	1.81	0.46
2:c:106:LYS:HA	2:c:175:LEU:O	2.16	0.46
7:h:8:LYS:HA	7:h:11:ILE:HG22	1.96	0.46
7:h:19:ALA:HB3	7:h:20:LYS:NZ	2.29	0.46
11:l:128:THR:HG1	11:l:131:ALA:H	1.61	0.46
15:p:113:LEU:O	15:p:113:LEU:HD12	2.16	0.46
27:C:10:LEU:HB3	27:C:20:TYR:HB2	1.98	0.46
33:I:20:LEU:H	33:I:20:LEU:HD12	1.80	0.46
47:W:25:ILE:HG21	47:W:66:LEU:HD22	1.97	0.46
48:X:52:ASN:HD21	48:X:55:GLN:HB2	1.80	0.46
52:3:1252:A:H2'	52:3:1253:G:O4'	2.15	0.46
53:1:956:G:H2'	53:1:957:C:H2'	1.97	0.46
53:1:1313:U:H2'	53:1:1610:A:C2	2.51	0.46
53:1:1701:A:H2'	53:1:1702:G:O4'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1825:U:H2'	53:1:1826:G:C8	2.51	0.46
56:4:20:U:H2'	56:4:21:C:C6	2.51	0.46
5:f:34:ARG:NH2	5:f:70:LEU:HD12	2.27	0.46
7:h:13:ALA:O	7:h:17:GLU:HG2	2.15	0.46
8:i:69:VAL:O	8:i:69:VAL:HG13	2.15	0.46
12:m:40:ARG:NE	53:1:958:U:H5	2.13	0.46
15:p:2:ASN:HD22	53:1:2876:G:H4'	1.79	0.46
18:s:4:ILE:HG22	18:s:106:VAL:HG22	1.97	0.46
19:t:61:LEU:N	19:t:61:LEU:HD23	2.30	0.46
22:w:8:ASN:HA	22:w:10:ARG:HH12	1.80	0.46
25:z:37:ARG:HH21	53:1:929:U:H4'	1.81	0.46
31:G:66:ILE:H	31:G:66:ILE:HD12	1.80	0.46
32:H:51:VAL:HG21	32:H:54:ILE:HG23	1.98	0.46
37:M:80:PRO:HG2	52:3:878:A:C5'	2.44	0.46
43:S:1:ALA:N	43:S:66:THR:O	2.47	0.46
46:V:30:HIS:HD2	46:V:33:TYR:H	1.63	0.46
47:W:52:ARG:HB3	47:W:56:ARG:HH12	1.80	0.46
49:Y:79:THR:HG21	52:3:187:G:H4'	1.98	0.46
52:3:160:A:H2'	52:3:161:A:O4'	2.16	0.46
52:3:184:G:H4'	52:3:224:U:H4'	1.96	0.46
52:3:287:U:H2'	52:3:288:A:C8	2.51	0.46
53:1:631:A:H2	53:1:2415:G:H21	1.64	0.46
53:1:796:C:H2'	53:1:797:G:H8	1.80	0.46
53:1:1077:A:C3'	53:1:1078:U:H5'	2.46	0.46
53:1:1386:C:H2'	53:1:1387:A:C8	2.50	0.46
53:1:2066:C:O2'	53:1:2067:G:H5'	2.16	0.46
54:2:49:C:H2'	54:2:50:A:H8	1.81	0.46
2:c:128:ARG:NE	53:1:1996:C:H5''	2.31	0.46
3:d:44:ARG:HH12	16:q:1:ALA:H2	1.62	0.46
9:j:57:LEU:O	9:j:58:ASN:HB2	2.15	0.46
9:j:110:PRO:HG2	9:j:118:MET:HE1	1.98	0.46
11:l:57:LEU:HB2	11:l:60:ARG:HH11	1.81	0.46
12:m:41:LEU:HD21	12:m:126:ILE:HD13	1.96	0.46
15:p:92:ARG:HD3	53:1:1753:G:H5''	1.97	0.46
27:C:36:LYS:HD2	27:C:36:LYS:N	2.31	0.46
35:K:91:ARG:CG	35:K:92:THR:H	2.28	0.46
36:L:108:ARG:HB2	36:L:109:LYS:NZ	2.30	0.46
38:N:28:VAL:HG23	38:N:63:TYR:HA	1.97	0.46
38:N:83:THR:HB	38:N:97:LEU:HD21	1.97	0.46
43:S:20:PHE:CD2	43:S:55:SER:HB2	2.51	0.46
52:3:1001:C:H2'	52:3:1002:G:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1391:U:H2'	52:3:1392:G:C8	2.51	0.46
53:1:1053:C:H3'	53:1:1054:A:H5''	1.97	0.46
53:1:1474:U:C2'	53:1:1475:G:H5'	2.45	0.46
53:1:1858:A:C2	53:1:1885:A:H1'	2.50	0.46
53:1:2786:U:H2'	53:1:2787:C:C6	2.50	0.46
4:e:23:SER:HB2	54:2:56:G:C5'	2.46	0.46
4:e:23:SER:HB2	54:2:56:G:H5''	1.97	0.46
4:e:43:ILE:HA	4:e:82:TYR:CE2	2.51	0.46
4:e:114:ARG:HB3	42:R:70:ARG:HH22	1.80	0.46
11:l:60:ARG:NH2	53:1:2428:G:H21	2.13	0.46
11:l:60:ARG:HH21	53:1:2428:G:H21	1.64	0.46
11:l:123:ARG:HA	11:l:144:GLU:HA	1.97	0.46
14:o:13:ARG:O	14:o:17:LYS:HG2	2.15	0.46
18:s:7:HIS:CD2	18:s:10:ALA:HB2	2.50	0.46
29:E:55:GLY:O	29:E:58:ILE:HG12	2.16	0.46
37:M:83:ARG:NH2	52:3:644:U:H4'	2.31	0.46
52:3:1280:A:O2'	52:3:1281:C:H5'	2.15	0.46
53:1:828:U:H4'	53:1:831:G:N1	2.31	0.46
53:1:2297:A:N6	53:1:2319:G:H1'	2.31	0.46
53:1:2372:U:H2'	53:1:2373:G:H8	1.81	0.46
19:t:11:LEU:HD21	19:t:32:LEU:HD22	1.98	0.46
19:t:48:GLN:HG2	19:t:55:VAL:HG23	1.98	0.46
52:3:1339:A:H2	55:5:30:G:H1'	1.81	0.46
52:3:1506:U:O2'	52:3:1507:A:H5'	2.16	0.46
53:1:1071:G:OP1	53:1:1071:G:H3'	2.15	0.46
53:1:1442:U:H2'	53:1:1443:U:C6	2.51	0.46
53:1:2128:G:H2'	53:1:2129:C:O4'	2.16	0.46
53:1:2389:G:H5''	53:1:2390:U:O4'	2.15	0.46
3:d:131:THR:HG22	3:d:160:ALA:HA	1.96	0.46
18:s:25:ARG:NH2	18:s:74:ILE:O	2.49	0.46
26:B:9:ARG:HD2	53:1:517:C:OP2	2.16	0.46
38:N:63:TYR:C	38:N:64:ILE:HD12	2.41	0.46
44:T:55:LEU:O	44:T:59:VAL:HG23	2.16	0.46
46:V:43:LEU:HD11	46:V:72:TRP:CD1	2.51	0.46
52:3:1001:C:H2'	52:3:1002:G:H8	1.81	0.46
53:1:542:C:C2'	53:1:543:G:H5''	2.46	0.46
53:1:721:A:H2'	53:1:722:A:C8	2.51	0.46
53:1:1525:A:H2'	53:1:1526:C:O4'	2.15	0.46
53:1:2366:A:H2'	53:1:2367:G:O4'	2.16	0.46
56:4:17:U:H2'	56:4:18:G:H8	1.81	0.46
10:k:76:VAL:H	15:p:72:VAL:HG12	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:m:10:ARG:HH21	12:m:10:ARG:HG3	1.81	0.45
17:r:85:LYS:NZ	53:1:1187:G:OP1	2.48	0.45
24:y:1:MET:HE3	24:y:4:LYS:HB2	1.98	0.45
30:F:37:GLN:OE1	53:1:1125:G:H5'	2.16	0.45
31:G:131:LYS:O	31:G:135:MET:HG2	2.16	0.45
33:I:74:TYR:HA	33:I:77:GLU:OE2	2.16	0.45
33:I:187:ARG:HH12	33:I:192:ALA:HA	1.80	0.45
39:O:7:ARG:HD2	39:O:73:LEU:HD11	1.98	0.45
39:O:8:ILE:HG12	39:O:100:ILE:HG23	1.98	0.45
39:O:44:THR:HB	39:O:46:LYS:HE3	1.98	0.45
46:V:5:ARG:HH22	46:V:62:GLU:HG2	1.81	0.45
47:W:66:LEU:O	47:W:67:LEU:HD22	2.16	0.45
48:X:39:ILE:HD12	48:X:65:MET:HB2	1.98	0.45
52:3:59:A:H5''	52:3:387:U:H5''	1.98	0.45
53:1:616:A:H2'	53:1:617:G:O4'	2.15	0.45
53:1:1045:C:P	53:1:1047:G:H5'	2.56	0.45
53:1:1322:A:N6	53:1:1333:G:H21	2.13	0.45
53:1:2266:A:H4'	53:1:2267:A:N3	2.31	0.45
53:1:2719:G:H4'	53:1:2846:G:H4'	1.97	0.45
1:b:164:VAL:HB	1:b:172:THR:OG1	2.16	0.45
2:c:149:ASN:HB3	2:c:150:GLN:H	1.45	0.45
2:c:155:VAL:O	53:1:2619:C:H5'	2.16	0.45
2:c:161:MET:HE1	53:1:2050:C:O2	2.17	0.45
4:e:129:MET:HG3	4:e:130:GLY:N	2.29	0.45
18:s:28:LYS:HG2	18:s:29:VAL:N	2.32	0.45
18:s:34:ASP:HB3	26:B:27:LEU:HD13	1.98	0.45
32:H:114:LEU:HA	32:H:117:ASP:OD2	2.16	0.45
33:I:150:LYS:HD3	33:I:154:VAL:HB	1.98	0.45
33:I:177:MET:N	33:I:177:MET:SD	2.90	0.45
43:S:15:LEU:HD23	43:S:53:ASP:HB2	1.98	0.45
44:T:20:ASP:OD1	52:3:751:U:H5'	2.16	0.45
48:X:35:ARG:NH2	48:X:74:ALA:HB3	2.32	0.45
52:3:730:G:C2'	52:3:731:G:H5'	2.46	0.45
52:3:1415:G:H2'	52:3:1416:G:C8	2.51	0.45
53:1:1019:U:H2'	53:1:1020:A:H8	1.81	0.45
55:6:72:A:H2'	55:6:73:A:O4'	2.16	0.45
2:c:193:VAL:HG21	2:c:201:LEU:HD13	1.97	0.45
3:d:131:THR:HG23	53:1:321:U:H5''	1.97	0.45
16:q:111:LYS:HZ1	17:r:50:GLY:HA2	1.81	0.45
18:s:69:LEU:HD12	18:s:108:SER:O	2.16	0.45
18:s:79:GLY:H	18:s:101:SER:HA	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:F:3:VAL:HG22	30:F:3:VAL:O	2.16	0.45
40:P:27:ASN:ND2	52:3:691:G:OP2	2.47	0.45
42:R:92:ARG:NH1	53:1:886:A:O2'	2.50	0.45
50:Z:16:ARG:HB2	50:Z:19:LYS:HD3	1.97	0.45
52:3:665:A:O4'	52:3:733:G:H1'	2.17	0.45
52:3:918:A:H2'	52:3:919:A:O4'	2.15	0.45
53:1:818:G:O2'	53:1:819:A:H5''	2.16	0.45
53:1:2120:G:H2'	53:1:2121:G:H8	1.82	0.45
54:2:5:U:H2'	54:2:6:G:C8	2.52	0.45
3:d:98:LYS:HZ2	53:1:607:U:C5'	2.29	0.45
5:f:66:THR:HG23	53:1:2747:G:O2'	2.16	0.45
6:g:25:TYR:CD1	53:1:2094:A:H5'	2.51	0.45
12:m:59:ARG:NH2	57:7:55:U:H5''	2.31	0.45
16:q:24:TYR:HE1	53:1:17:G:H4'	1.81	0.45
19:t:38:ALA:HB1	19:t:43:ILE:HD11	1.97	0.45
31:G:65:LYS:HB3	31:G:89:PHE:HE2	1.81	0.45
31:G:89:PHE:CE2	31:G:153:MET:HE3	2.52	0.45
33:I:131:ILE:HG22	33:I:133:SER:H	1.81	0.45
39:O:46:LYS:HB2	39:O:48:ARG:HH12	1.81	0.45
43:S:8:ARG:HD3	43:S:12:ARG:NH2	2.30	0.45
52:3:1435:G:H2'	52:3:1436:U:C6	2.51	0.45
53:1:968:C:H2'	53:1:969:G:C8	2.52	0.45
53:1:1045:C:H5'	53:1:1046:A:H5''	1.98	0.45
53:1:1636:U:H2'	53:1:1637:A:C8	2.51	0.45
53:1:2412:A:H2'	53:1:2413:G:O4'	2.16	0.45
53:1:2855:C:H2'	53:1:2856:A:C8	2.51	0.45
54:2:2:G:H2'	54:2:3:C:C6	2.51	0.45
54:2:30:C:H2'	54:2:31:C:O4'	2.17	0.45
54:2:42:C:H2'	54:2:43:C:O4'	2.16	0.45
3:d:5:LEU:O	3:d:9:GLN:HG2	2.17	0.45
4:e:43:ILE:HA	4:e:82:TYR:HE2	1.82	0.45
16:q:82:LEU:HA	16:q:85:ALA:HB3	1.99	0.45
20:u:73:ASN:HD22	20:u:76:THR:HG23	1.82	0.45
38:N:82:ILE:O	38:N:86:LEU:HG	2.16	0.45
41:Q:101:LEU:H	41:Q:101:LEU:CD2	2.29	0.45
42:R:74:MET:SD	42:R:75:SER:N	2.89	0.45
48:X:72:GLU:HG2	52:3:1320:C:H4'	1.99	0.45
53:1:704:G:H1'	53:1:727:A:H61	1.81	0.45
53:1:2484:G:H2'	53:1:2485:G:O4'	2.17	0.45
55:5:29:G:H2'	55:5:30:G:H8	1.82	0.45
1:b:45:ASN:O	53:1:773:U:H5''	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:220:ARG:NH1	53:1:1827:U:OP2	2.50	0.45
4:e:7:TYR:OH	4:e:29:ARG:HG3	2.16	0.45
7:h:59:LEU:HB3	7:h:62:ARG:CB	2.47	0.45
16:q:88:GLU:CD	16:q:88:GLU:N	2.75	0.45
22:w:11:ASP:CG	22:w:12:SER:H	2.24	0.45
34:J:83:PRO:HB3	34:J:96:GLN:NE2	2.31	0.45
35:K:86:ARG:HH22	52:3:674:G:P	2.38	0.45
49:Y:23:ARG:HB3	49:Y:60:GLN:NE2	2.31	0.45
52:3:129:A:H1'	52:3:130:A:C8	2.51	0.45
52:3:393:A:H5'	52:3:483:C:O2'	2.16	0.45
53:1:885:C:H2'	53:1:886:A:H8	1.81	0.45
53:1:1005:C:H2'	53:1:1006:C:C6	2.52	0.45
53:1:1038:G:H2'	53:1:1039:A:C8	2.51	0.45
53:1:1326:U:H2'	53:1:1327:A:C8	2.52	0.45
53:1:1876:A:H2'	53:1:1877:A:O4'	2.17	0.45
53:1:2163:A:N3	53:1:2164:C:H5'	2.32	0.45
53:1:2208:C:H2'	53:1:2209:G:C8	2.51	0.45
53:1:2638:G:H1'	53:1:2778:A:N6	2.32	0.45
55:6:16:C:O2'	55:6:17:C:H5'	2.16	0.45
2:c:37:VAL:HG13	2:c:48:ILE:HG22	1.98	0.45
4:e:98:PHE:HA	4:e:101:ARG:HD3	1.99	0.45
7:h:2:ALA:HB3	7:h:6:GLN:HG3	1.99	0.45
8:i:106:GLN:O	8:i:110:GLN:HG2	2.16	0.45
11:l:18:ARG:NH2	53:1:1249:U:H2'	2.27	0.45
11:l:95:LEU:HA	11:l:98:ALA:HB3	1.97	0.45
18:s:56:ALA:CA	18:s:59:GLU:HG2	2.42	0.45
21:v:21:ARG:HA	21:v:25:LYS:O	2.16	0.45
23:x:31:ASN:ND2	23:x:52:ALA:HB2	2.32	0.45
29:E:53:ASP:OD1	53:1:2359:C:H4'	2.16	0.45
45:U:78:VAL:O	45:U:79:ASN:C	2.60	0.45
52:3:483:C:H2'	52:3:484:G:C8	2.51	0.45
52:3:1258:G:H2'	52:3:1259:C:C6	2.51	0.45
53:1:1825:U:H2'	53:1:1826:G:H8	1.82	0.45
53:1:2487:G:H2'	53:1:2488:G:H8	1.81	0.45
2:c:14:ILE:HA	15:p:11:GLN:HE22	1.82	0.45
2:c:24:VAL:HG22	2:c:25:THR:N	2.32	0.45
4:e:126:ASN:HD21	53:1:2315:G:H4'	1.82	0.45
10:k:30:ARG:HD2	53:1:2674:G:H4'	1.99	0.45
11:l:132:ARG:O	11:l:136:GLU:HG3	2.17	0.45
14:o:12:THR:CG2	53:1:2334:U:H5'	2.46	0.45
14:o:16:ARG:HA	14:o:19:GLN:HG2	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:J:121:ASN:HB3	34:J:122:VAL:H	1.26	0.45
42:R:98:GLY:HA2	52:3:1322:C:H5'	1.99	0.45
46:V:7:LEU:HD22	46:V:60:ILE:HD11	1.98	0.45
53:1:1378:A:H1'	53:1:1379:U:C5	2.52	0.45
53:1:2323:G:H2'	53:1:2324:U:O4'	2.16	0.45
53:1:2808:G:H2'	53:1:2890:G:C6	2.51	0.45
1:b:156:SER:OG	53:1:1818:U:H5'	2.17	0.45
6:g:73:ASN:HD22	6:g:76:GLU:HA	1.82	0.45
9:j:102:GLU:O	9:j:105:VAL:HG12	2.17	0.45
10:k:52:VAL:HG22	10:k:53:LYS:N	2.31	0.45
12:m:74:THR:HG21	12:m:86:LYS:HD2	1.99	0.45
16:q:45:ALA:O	16:q:49:ARG:HG3	2.16	0.45
20:u:47:PRO:HD3	20:u:55:GLY:HA2	1.99	0.45
30:F:4:ARG:HH22	53:1:2477:U:C2'	2.30	0.45
33:I:182:LYS:HG3	33:I:183:ARG:N	2.32	0.45
42:R:89:ARG:HB2	42:R:96:VAL:HG12	1.98	0.45
52:3:392:C:H2'	52:3:393:A:C8	2.52	0.45
52:3:1033:G:C2'	52:3:1034:G:H5''	2.47	0.45
52:3:1384:C:H2'	52:3:1385:G:H8	1.82	0.45
52:3:1415:G:H2'	52:3:1416:G:H8	1.82	0.45
53:1:1755:A:H2'	53:1:1756:G:H5'	1.99	0.45
53:1:2421:G:H2'	55:6:76:A:N6	2.32	0.45
53:1:2676:C:H2'	53:1:2677:G:C8	2.52	0.45
1:b:234:GLY:HA3	1:b:238:ASN:HB2	1.99	0.45
7:h:12:VAL:HA	7:h:15:VAL:HG12	1.98	0.45
8:i:27:LEU:HD21	8:i:58:ILE:HG21	1.97	0.45
9:j:58:ASN:ND2	9:j:128:ASN:HA	2.31	0.45
9:j:132:HIS:HD1	53:1:6:A:HO2'	1.63	0.45
13:n:65:LEU:HG	13:n:69:ARG:HH22	1.82	0.45
19:t:56:GLU:HB2	19:t:86:THR:HG23	1.98	0.45
30:F:11:CYS:HB3	30:F:33:HIS:HE1	1.81	0.45
35:K:46:GLN:HG2	35:K:47:LEU:O	2.17	0.45
40:P:19:VAL:HG23	40:P:36:ARG:HD2	1.99	0.45
45:U:9:HIS:CE1	45:U:18:GLN:HG3	2.52	0.45
52:3:390:U:H2'	52:3:391:G:C8	2.50	0.45
52:3:663:A:H5'	52:3:836:G:OP1	2.17	0.45
52:3:1219:A:H2'	52:3:1220:G:H8	1.82	0.45
52:3:1414:U:H2'	52:3:1415:G:H8	1.81	0.45
53:1:214:G:H2'	53:1:215:G:C8	2.52	0.45
53:1:1306:C:H41	53:1:1606:C:H2'	1.82	0.45
53:1:1539:U:H2'	53:1:1540:G:H8	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2286:G:H4'	53:1:2287:A:O4'	2.16	0.45
53:1:2345:G:H4'	53:1:2346:A:H3'	1.99	0.45
1:b:226:PRO:HD3	1:b:233:GLY:N	2.32	0.44
3:d:61:ARG:HG2	3:d:63:LYS:H	1.82	0.44
11:l:35:HIS:HB3	11:l:36:LYS:H	1.67	0.44
14:o:65:THR:HG22	14:o:65:THR:O	2.16	0.44
15:p:25:VAL:HG23	15:p:84:SER:C	2.43	0.44
16:q:52:ARG:HD3	53:1:535:G:O2'	2.17	0.44
17:r:71:LYS:HB2	17:r:90:ARG:NH1	2.32	0.44
18:s:42:LYS:HB2	53:1:2010:G:C5'	2.39	0.44
32:H:112:ALA:HB3	32:H:184:ASN:HD22	1.82	0.44
35:K:50:PRO:HG3	35:K:55:HIS:HE1	1.82	0.44
40:P:28:ASN:HB2	40:P:56:LYS:NZ	2.32	0.44
46:V:45:VAL:HG12	46:V:46:HIS:N	2.32	0.44
48:X:21:ALA:O	48:X:27:LYS:NZ	2.49	0.44
52:3:40:C:H2'	52:3:41:G:H8	1.82	0.44
52:3:900:A:H2'	52:3:901:A:C8	2.52	0.44
52:3:911:U:H2'	52:3:912:C:C6	2.52	0.44
52:3:950:U:H2'	52:3:951:G:C8	2.52	0.44
53:1:1367:A:C2'	53:1:1368:G:H5'	2.47	0.44
53:1:1542:U:H2'	53:1:1543:G:O4'	2.17	0.44
53:1:2305:U:H2'	53:1:2306:C:C6	2.52	0.44
5:f:90:GLY:HA3	5:f:93:TYR:HD2	1.82	0.44
5:f:155:PRO:HB2	5:f:171:LYS:HZ3	1.82	0.44
11:l:46:VAL:HG11	11:l:50:PHE:CD2	2.52	0.44
12:m:2:LEU:HB3	12:m:68:PHE:CE1	2.53	0.44
14:o:110:ALA:O	14:o:115:LEU:HB2	2.17	0.44
16:q:2:ARG:HA	53:1:1248:G:O2'	2.18	0.44
22:w:35:ARG:HD2	22:w:35:ARG:HA	1.88	0.44
30:F:25:VAL:HG21	30:F:35:GLN:HE21	1.82	0.44
33:I:17:ASP:C	33:I:18:LEU:HD22	2.41	0.44
35:K:67:PRO:HG2	35:K:70:VAL:HG22	2.00	0.44
39:O:36:VAL:HG13	39:O:76:ILE:HA	1.98	0.44
40:P:83:VAL:HG11	40:P:96:ILE:HG22	1.98	0.44
42:R:18:LEU:HD23	42:R:18:LEU:O	2.17	0.44
42:R:101:THR:HA	42:R:105:ALA:HB3	1.99	0.44
43:S:14:ALA:O	43:S:17:ASP:OD1	2.34	0.44
45:U:76:LYS:HE3	52:3:474:G:OP1	2.17	0.44
49:Y:28:ARG:HH12	52:3:1437:A:C5'	2.30	0.44
52:3:692:U:H2'	52:3:694:A:OP2	2.17	0.44
52:3:784:A:H2'	52:3:785:G:H8	1.80	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1130:A:N6	52:3:1144:G:H1'	2.30	0.44
53:1:464:U:H2'	53:1:465:G:O4'	2.17	0.44
53:1:1360:G:H22	53:1:2214:C:H42	1.64	0.44
53:1:2231:U:H2'	53:1:2232:C:C6	2.51	0.44
4:e:33:ILE:HD12	4:e:155:ILE:HA	2.00	0.44
5:f:132:LEU:HD12	5:f:132:LEU:O	2.17	0.44
9:j:109:LEU:HD13	9:j:118:MET:HG3	2.00	0.44
12:m:119:LEU:HA	53:1:2467:C:O2'	2.16	0.44
15:p:88:ARG:H	15:p:88:ARG:HG2	1.45	0.44
16:q:23:TYR:CD1	53:1:533:G:H5'	2.51	0.44
28:D:3:ARG:HD3	28:D:3:ARG:HA	1.67	0.44
31:G:106:VAL:O	31:G:110:ILE:HG13	2.17	0.44
31:G:117:GLU:O	31:G:121:GLN:HG2	2.16	0.44
31:G:213:LEU:H	31:G:213:LEU:HD12	1.82	0.44
39:O:18:ILE:O	39:O:22:THR:HG23	2.18	0.44
48:X:52:ASN:OD1	48:X:53:GLY:N	2.40	0.44
52:3:855:U:H2'	52:3:856:C:C6	2.53	0.44
52:3:1254:A:H4'	52:3:1356:G:O3'	2.18	0.44
52:3:1401:G:H2'	52:3:1402:C:O4'	2.17	0.44
53:1:765:C:H2'	53:1:766:U:C6	2.53	0.44
53:1:1322:A:H61	53:1:1333:G:H21	1.64	0.44
53:1:1936:A:H3'	53:1:1937:A:H5'	2.00	0.44
53:1:2082:A:H2'	53:1:2083:G:O4'	2.17	0.44
53:1:2329:U:H2'	53:1:2330:G:H8	1.81	0.44
53:1:2591:C:H2'	53:1:2592:G:C8	2.52	0.44
3:d:162:ARG:NH1	53:1:321:U:H1'	2.33	0.44
4:e:97:GLU:OE2	4:e:101:ARG:HD2	2.17	0.44
6:g:133:GLN:NE2	6:g:135:HIS:O	2.51	0.44
6:g:137:GLU:OE1	6:g:138:VAL:HG13	2.16	0.44
8:i:11:GLN:CB	8:i:56:VAL:HG22	2.47	0.44
9:j:93:ILE:HA	9:j:97:PRO:HB3	1.99	0.44
11:l:42:SER:OG	53:1:672:C:H5	1.99	0.44
11:l:69:ARG:HG2	11:l:69:ARG:HH11	1.83	0.44
13:n:114:GLU:N	13:n:114:GLU:OE2	2.50	0.44
14:o:7:ARG:HD2	14:o:97:PHE:CZ	2.52	0.44
15:p:29:VAL:C	15:p:39:LEU:HD12	2.43	0.44
17:r:89:HIS:HE1	17:r:91:GLN:HB2	1.82	0.44
31:G:90:PHE:O	31:G:149:GLY:HA3	2.18	0.44
33:I:2:ARG:NH1	33:I:65:GLY:O	2.47	0.44
34:J:100:GLU:H	34:J:121:ASN:ND2	1.85	0.44
35:K:36:ILE:HD12	35:K:64:VAL:HB	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:L:78:ARG:HB3	36:L:83:THR:HG23	1.98	0.44
38:N:112:ARG:HH12	38:N:114:LYS:HG3	1.82	0.44
52:3:56:U:H2'	52:3:57:G:H8	1.83	0.44
52:3:206:C:H2'	52:3:207:C:O4'	2.17	0.44
52:3:1449:C:H2'	52:3:1450:U:O4'	2.18	0.44
52:3:1477:U:H2'	52:3:1478:U:C6	2.52	0.44
53:1:184:C:H2'	53:1:185:G:C8	2.53	0.44
55:6:59:A:H2'	55:6:60:U:H5'	1.99	0.44
1:b:227:VAL:HG11	53:1:784:G:C4	2.53	0.44
1:b:257:ARG:NH1	53:1:1799:G:OP1	2.51	0.44
6:g:26:ALA:HA	6:g:30:LEU:HB2	1.99	0.44
6:g:125:THR:HG21	6:g:148:ALA:HB2	2.00	0.44
6:g:137:GLU:OE2	6:g:138:VAL:HG22	2.17	0.44
13:n:79:LEU:O	13:n:80:PHE:HB2	2.16	0.44
15:p:29:VAL:O	15:p:39:LEU:HD12	2.18	0.44
18:s:29:VAL:HG13	18:s:69:LEU:O	2.16	0.44
31:G:109:SER:HA	31:G:112:ARG:HB3	2.00	0.44
31:G:206:ILE:O	31:G:210:THR:HG23	2.18	0.44
35:K:91:ARG:HG3	35:K:92:THR:N	2.31	0.44
35:K:92:THR:OG1	35:K:93:LYS:N	2.51	0.44
37:M:29:SER:HB3	37:M:32:LYS:HG3	1.98	0.44
37:M:45:ILE:HG21	37:M:60:LEU:HB3	2.00	0.44
37:M:87:ARG:N	37:M:90:GLU:HB2	2.30	0.44
37:M:112:ASP:N	37:M:112:ASP:OD1	2.50	0.44
38:N:23:GLY:H	38:N:60:LEU:HA	1.83	0.44
46:V:22:VAL:HG22	46:V:23:ALA:H	1.81	0.44
50:Z:13:VAL:HG22	50:Z:14:ALA:N	2.31	0.44
50:Z:44:ARG:HH22	52:3:722:G:N2	2.15	0.44
52:3:113:G:H2'	52:3:114:U:C6	2.53	0.44
53:1:162:U:C2'	53:1:163:C:H5'	2.47	0.44
53:1:326:G:H2'	53:1:327:G:H8	1.83	0.44
53:1:687:C:H2'	53:1:688:U:O4'	2.17	0.44
53:1:940:G:H3'	53:1:941:A:H5''	2.00	0.44
53:1:1186:G:H2'	53:1:1187:G:O4'	2.17	0.44
53:1:1890:A:H2'	53:1:1891:G:O4'	2.17	0.44
53:1:2120:G:H2'	53:1:2121:G:C8	2.52	0.44
53:1:2248:C:H2'	53:1:2249:U:H5'	1.99	0.44
53:1:2469:A:H2'	53:1:2470:G:O4'	2.17	0.44
2:c:24:VAL:HG22	2:c:25:THR:H	1.82	0.44
2:c:108:ASP:OD2	2:c:206:ALA:HA	2.18	0.44
2:c:116:LYS:HG3	2:c:165:MET:CE	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:37:MET:HE1	53:1:2305:U:H3	1.83	0.44
8:i:118:GLY:HA2	53:1:1082:U:H5'	2.00	0.44
11:l:82:LEU:HD23	11:l:120:VAL:HG21	2.00	0.44
11:l:94:THR:H	11:l:96:LYS:HZ2	1.65	0.44
13:n:103:ARG:HH21	13:n:110:MET:HE1	1.83	0.44
15:p:63:ILE:HA	15:p:68:GLY:CA	2.47	0.44
29:E:33:THR:HG23	53:1:2420:C:OP1	2.18	0.44
30:F:36:ARG:HH21	30:F:37:GLN:HE21	1.66	0.44
32:H:45:GLU:HG3	32:H:46:LEU:CD1	2.47	0.44
33:I:11:SER:OG	33:I:17:ASP:HA	2.17	0.44
33:I:123:MET:HA	33:I:128:VAL:HA	1.99	0.44
35:K:9:MET:HA	35:K:58:HIS:O	2.18	0.44
39:O:48:ARG:NH1	52:3:1253:G:OP1	2.51	0.44
43:S:27:LYS:O	43:S:31:SER:HB2	2.17	0.44
52:3:1412:C:H2'	52:3:1413:A:C8	2.53	0.44
53:1:2372:U:H2'	53:1:2373:G:C8	2.53	0.44
53:1:2637:U:H2'	53:1:2638:G:O4'	2.18	0.44
2:c:145:SER:O	53:1:2512:C:H1'	2.18	0.44
9:j:116:ARG:O	9:j:120:ARG:HG3	2.18	0.44
10:k:13:ASN:ND2	52:3:339:C:OP2	2.50	0.44
16:q:9:ALA:O	16:q:13:HIS:ND1	2.51	0.44
16:q:51:GLN:HA	16:q:54:ARG:HD2	2.00	0.44
32:H:78:LYS:C	32:H:79:LYS:HG3	2.42	0.44
33:I:98:ASP:HB3	33:I:132:ALA:HB1	1.99	0.44
38:N:98:ARG:NH1	38:N:103:VAL:HG11	2.33	0.44
40:P:91:GLY:O	40:P:92:ARG:HB3	2.17	0.44
41:Q:97:VAL:HG13	41:Q:97:VAL:O	2.18	0.44
42:R:89:ARG:NH2	42:R:94:LEU:HB3	2.33	0.44
42:R:105:ALA:HA	52:3:948:C:OP1	2.18	0.44
50:Z:44:ARG:NH2	52:3:722:G:H21	2.15	0.44
52:3:22:G:P	52:3:885:G:H5'	2.57	0.44
52:3:744:C:H2'	52:3:745:G:H8	1.83	0.44
53:1:346:A:H2'	53:1:346:A:N3	2.32	0.44
4:e:65:LEU:HD22	54:2:42:C:C5	2.53	0.44
6:g:90:LEU:HD11	6:g:93:SER:HA	2.00	0.44
8:i:31:GLY:O	8:i:64:ARG:NH1	2.50	0.44
9:j:36:LEU:O	9:j:51:GLY:HA3	2.17	0.44
11:l:62:PRO:HA	53:1:2393:U:O3'	2.17	0.44
12:m:41:LEU:H	12:m:41:LEU:CD1	2.26	0.44
21:v:35:GLU:HB2	21:v:93:ARG:NH1	2.32	0.44
32:H:27:GLU:O	32:H:31:ASN:ND2	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:N:126:PHE:CZ	52:3:967:C:H4'	2.52	0.44
44:T:70:LYS:HG2	44:T:71:ARG:HH22	1.83	0.44
47:W:33:THR:HG23	47:W:35:SER:H	1.82	0.44
49:Y:34:VAL:O	49:Y:38:ILE:HG13	2.17	0.44
50:Z:16:ARG:O	50:Z:19:LYS:HB2	2.18	0.44
52:3:106:C:H2'	52:3:107:G:H8	1.83	0.44
52:3:554:A:H2'	52:3:555:U:C6	2.53	0.44
52:3:806:C:H2'	52:3:807:A:C8	2.53	0.44
52:3:1053:G:O6	52:3:1199:U:H2'	2.18	0.44
52:3:1123:U:O2'	52:3:1124:G:H5'	2.17	0.44
53:1:184:C:H2'	53:1:185:G:H8	1.82	0.44
53:1:189:G:H2'	53:1:205:G:N2	2.32	0.44
53:1:594:U:H2'	53:1:595:C:C6	2.53	0.44
53:1:1330:C:H2'	53:1:1331:G:C8	2.53	0.44
53:1:1638:C:H5''	53:1:2710:C:O2'	2.18	0.44
53:1:2368:C:H2'	53:1:2369:A:C8	2.52	0.44
1:b:267:VAL:HG12	1:b:268:ARG:NH1	2.32	0.44
4:e:7:TYR:O	4:e:12:VAL:HG23	2.17	0.44
5:f:142:GLN:NE2	53:1:2744:G:H21	2.16	0.44
8:i:96:LYS:HD3	8:i:136:GLY:O	2.18	0.44
12:m:102:LEU:HG	12:m:103:TYR:CD1	2.53	0.44
16:q:16:ILE:HG23	16:q:38:VAL:HG21	2.00	0.44
17:r:49:ILE:CG2	17:r:54:VAL:H	2.31	0.44
20:u:48:VAL:HA	20:u:49:PRO:HD3	1.87	0.44
20:u:82:VAL:HG22	20:u:83:GLY:N	2.32	0.44
31:G:213:LEU:HD12	31:G:213:LEU:N	2.32	0.44
32:H:79:LYS:HE3	32:H:81:GLU:HB3	1.99	0.44
33:I:169:TRP:CD1	33:I:170:LEU:HD22	2.53	0.44
37:M:79:ARG:HB3	52:3:878:A:OP1	2.18	0.44
38:N:6:TYR:HE1	38:N:17:ARG:HA	1.83	0.44
40:P:30:ILE:HD11	52:3:689:C:H5''	2.00	0.44
41:Q:22:ALA:C	41:Q:24:GLU:N	2.73	0.44
46:V:58:VAL:HG13	46:V:74:LEU:HG	2.00	0.44
52:3:82:G:H2'	52:3:83:C:H5'	1.99	0.44
53:1:155:A:H2'	53:1:156:A:C8	2.53	0.44
53:1:196:A:N3	53:1:196:A:H2'	2.33	0.44
53:1:1496:A:H2'	53:1:1498:C:N4	2.33	0.44
53:1:2185:U:H2'	53:1:2186:G:H8	1.83	0.44
53:1:2704:C:H2'	53:1:2705:A:O4'	2.18	0.44
54:2:95:U:H2'	54:2:96:G:C8	2.53	0.44
55:6:62:C:H2'	55:6:63:G:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:25:MET:SD	54:2:55:U:H1'	2.57	0.43
4:e:153:ILE:HG23	4:e:153:ILE:O	2.18	0.43
5:f:122:ALA:HA	5:f:132:LEU:HA	2.00	0.43
7:h:59:LEU:HD21	53:1:1047:G:H8	1.82	0.43
18:s:84:ARG:HE	53:1:1323:C:H5''	1.82	0.43
25:z:52:PHE:CD2	54:2:83:G:H4'	2.54	0.43
37:M:31:LEU:HD12	37:M:32:LYS:N	2.33	0.43
40:P:116:PRO:HB3	52:3:676:A:C1'	2.46	0.43
41:Q:51:VAL:HG22	41:Q:52:CYS:N	2.32	0.43
43:S:81:ILE:HD12	52:3:1202:U:C2	2.53	0.43
52:3:876:C:H2'	52:3:877:G:C8	2.53	0.43
52:3:987:G:H2'	52:3:988:G:C8	2.53	0.43
52:3:1063:C:H2'	52:3:1064:G:C8	2.53	0.43
52:3:1277:C:H2'	52:3:1278:G:H5''	2.00	0.43
53:1:1474:U:H2'	53:1:1475:G:H5'	1.99	0.43
53:1:1549:A:H2'	53:1:1550:C:C6	2.53	0.43
53:1:1827:U:O2'	53:1:1828:G:H5'	2.18	0.43
53:1:2368:C:H2'	53:1:2369:A:H8	1.83	0.43
1:b:207:ALA:HB2	53:1:1790:C:O2'	2.18	0.43
2:c:32:ASN:O	2:c:96:ILE:HG22	2.18	0.43
4:e:31:GLU:HB3	4:e:156:THR:HG22	1.99	0.43
6:g:21:VAL:HG22	6:g:22:LYS:N	2.32	0.43
8:i:126:ARG:HG3	53:1:1080:A:O2'	2.18	0.43
15:p:16:VAL:O	15:p:16:VAL:HG13	2.19	0.43
19:t:56:GLU:HB2	19:t:86:THR:O	2.17	0.43
31:G:98:GLY:N	31:G:174:GLU:OE2	2.51	0.43
32:H:4:VAL:HG22	32:H:5:HIS:N	2.33	0.43
32:H:119:ILE:O	32:H:123:LEU:HG	2.17	0.43
34:J:98:ALA:HB1	52:3:6:G:C6	2.54	0.43
41:Q:29:LYS:HA	41:Q:29:LYS:HD2	1.80	0.43
49:Y:84:LYS:HD3	49:Y:84:LYS:C	2.44	0.43
52:3:729:A:H2'	52:3:730:G:H8	1.83	0.43
53:1:480:A:H3'	53:1:481:G:H5''	2.00	0.43
53:1:1563:U:H2'	53:1:1564:C:C6	2.53	0.43
54:2:105:G:H2'	54:2:106:G:H8	1.83	0.43
55:5:43:A:H2'	55:5:44:A:C8	2.53	0.43
3:d:117:ARG:HA	3:d:185:LYS:HD2	2.00	0.43
7:h:4:ASN:O	7:h:8:LYS:HG2	2.18	0.43
12:m:12:MET:HG2	53:1:911:A:N6	2.34	0.43
19:t:13:ALA:HB1	24:y:33:ALA:CB	2.47	0.43
27:C:11:VAL:HG22	27:C:12:SER:N	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:F:3:VAL:O	30:F:3:VAL:HG13	2.17	0.43
30:F:32:LYS:HD3	53:1:2478:A:OP1	2.18	0.43
34:J:108:GLY:H	52:3:9:G:C5'	2.31	0.43
39:O:21:ALA:O	39:O:24:GLU:HG3	2.18	0.43
39:O:53:ILE:HG12	52:3:1060:U:H5''	1.99	0.43
40:P:96:ILE:HD13	50:Z:16:ARG:HH11	1.83	0.43
41:Q:73:LEU:HD12	41:Q:73:LEU:N	2.33	0.43
44:T:86:LEU:N	44:T:86:LEU:HD23	2.33	0.43
46:V:74:LEU:C	46:V:74:LEU:HD23	2.43	0.43
48:X:24:SER:HB3	48:X:27:LYS:NZ	2.33	0.43
52:3:9:G:H2'	52:3:10:A:C8	2.53	0.43
52:3:67:C:H2'	52:3:68:G:C8	2.54	0.43
52:3:166:U:H2'	52:3:167:A:C8	2.53	0.43
52:3:741:G:H2'	52:3:742:G:H8	1.82	0.43
52:3:851:G:H2'	52:3:852:G:C8	2.53	0.43
53:1:490:C:H4'	53:1:491:G:OP2	2.18	0.43
53:1:780:G:H2'	53:1:782:A:N7	2.34	0.43
53:1:940:G:C3'	53:1:941:A:H5''	2.48	0.43
53:1:1854:A:N6	53:1:1888:G:H1'	2.33	0.43
53:1:2236:U:H2'	53:1:2237:G:O4'	2.17	0.43
3:d:105:LEU:O	3:d:109:LEU:HD13	2.17	0.43
4:e:15:LEU:HD23	4:e:18:GLU:CD	2.44	0.43
8:i:11:GLN:OE1	8:i:56:VAL:HG13	2.19	0.43
8:i:39:LYS:HD2	8:i:39:LYS:C	2.43	0.43
9:j:99:ARG:NH1	53:1:2780:G:O6	2.52	0.43
10:k:61:VAL:HG23	10:k:85:VAL:HB	2.00	0.43
19:t:67:VAL:HA	19:t:76:ARG:HA	1.99	0.43
26:B:47:TYR:CZ	26:B:52:LYS:HD3	2.53	0.43
31:G:16:GLY:HA2	31:G:202:ASN:HD22	1.83	0.43
31:G:208:ALA:O	31:G:211:LEU:HG	2.18	0.43
33:I:144:ILE:N	33:I:144:ILE:HD12	2.33	0.43
39:O:42:LEU:HA	39:O:43:PRO:HD2	1.79	0.43
40:P:111:ASP:HB3	50:Z:3:ILE:CD1	2.48	0.43
42:R:51:GLN:O	42:R:55:LEU:HD23	2.17	0.43
47:W:28:LEU:HA	47:W:31:TYR:CD2	2.54	0.43
47:W:48:ALA:HB2	52:3:834:U:OP1	2.18	0.43
51:a:37:LYS:HG3	53:1:2127:G:H5'	2.00	0.43
52:3:70:U:H4'	52:3:71:A:C8	2.53	0.43
52:3:1033:G:C3'	52:3:1034:G:H5''	2.48	0.43
52:3:1157:A:H4'	52:3:1158:C:O5'	2.19	0.43
53:1:84:A:H4'	53:1:85:G:O5'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:742:A:H2'	53:1:743:A:C8	2.53	0.43
53:1:1149:G:H2'	53:1:1150:C:C6	2.53	0.43
53:1:1507:C:H2'	53:1:1508:A:O4'	2.19	0.43
54:2:6:G:H2'	54:2:7:G:H8	1.83	0.43
1:b:42:ARG:HG2	1:b:42:ARG:NH1	2.33	0.43
3:d:48:THR:C	3:d:50:ALA:H	2.27	0.43
3:d:63:LYS:O	3:d:65:THR:N	2.52	0.43
7:h:67:THR:N	7:h:68:PRO:CD	2.81	0.43
12:m:99:GLY:HA3	21:v:81:PRO:HB3	2.00	0.43
14:o:13:ARG:HB2	53:1:2334:U:O3'	2.18	0.43
18:s:86:MET:HE3	18:s:87:PRO:HD2	2.00	0.43
19:t:12:ARG:O	24:y:29:ARG:HG2	2.19	0.43
32:H:81:GLU:H	32:H:81:GLU:HG2	1.67	0.43
32:H:106:ARG:HH11	32:H:107:LYS:HE2	1.83	0.43
32:H:155:ARG:HH11	32:H:155:ARG:HG3	1.84	0.43
32:H:201:ILE:O	32:H:203:LYS:NZ	2.51	0.43
34:J:82:HIS:HB2	34:J:83:PRO:HD2	2.00	0.43
35:K:47:LEU:HD12	35:K:55:HIS:HA	2.01	0.43
46:V:16:MET:SD	46:V:20:ILE:HA	2.59	0.43
50:Z:8:ASN:HB3	50:Z:9:GLU:H	1.61	0.43
52:3:150:U:H3	52:3:171:A:H62	1.66	0.43
53:1:697:G:H2'	53:1:698:C:C6	2.53	0.43
53:1:1374:G:H2'	53:1:1375:U:O4'	2.19	0.43
53:1:1434:A:H2'	53:1:1435:G:H8	1.82	0.43
53:1:1476:U:H3	53:1:1515:A:H62	1.65	0.43
53:1:2030:A:N3	53:1:2499:C:H5''	2.33	0.43
54:2:66:A:H5''	54:2:67:G:OP1	2.18	0.43
1:b:216:ARG:HG3	1:b:217:PRO:CD	2.49	0.43
7:h:56:ARG:O	53:1:1106:G:H4'	2.18	0.43
9:j:35:ARG:HG2	9:j:40:HIS:CG	2.53	0.43
10:k:22:ILE:HG13	10:k:23:LYS:N	2.33	0.43
13:n:10:LEU:HD13	13:n:40:LYS:HG2	2.01	0.43
13:n:64:ARG:HH22	53:1:2852:G:H5'	1.82	0.43
14:o:10:ARG:HD3	53:1:2295:C:OP2	2.18	0.43
14:o:36:TYR:HD1	14:o:52:SER:HG	1.67	0.43
31:G:130:LYS:O	31:G:134:LEU:HD13	2.19	0.43
32:H:184:ASN:O	32:H:199:VAL:HG22	2.18	0.43
35:K:5:GLU:HG2	35:K:63:ASN:HA	2.01	0.43
35:K:18:VAL:N	35:K:19:PRO:CD	2.82	0.43
37:M:17:GLN:OE1	37:M:62:LEU:HD13	2.18	0.43
38:N:30:ASN:O	38:N:31:GLN:HB2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:S:80:ARG:HG3	43:S:81:ILE:H	1.83	0.43
43:S:80:ARG:HG3	43:S:81:ILE:HG13	1.99	0.43
46:V:30:HIS:HA	46:V:31:PRO:HD3	1.84	0.43
52:3:320:A:H2'	52:3:321:A:C8	2.54	0.43
52:3:407:U:H2'	52:3:408:A:H8	1.84	0.43
52:3:467:U:H5'	52:3:468:A:OP2	2.19	0.43
52:3:505:G:H2'	52:3:506:G:H8	1.84	0.43
52:3:1060:U:H2'	52:3:1061:G:H8	1.83	0.43
53:1:817:C:H2'	53:1:818:G:O4'	2.19	0.43
53:1:942:G:H2'	53:1:943:A:O4'	2.19	0.43
53:1:1182:G:H2'	53:1:1183:U:O4'	2.19	0.43
53:1:2296:U:C5'	53:1:2297:A:OP1	2.67	0.43
53:1:2671:G:H2'	53:1:2672:U:C6	2.54	0.43
53:1:2693:G:O2'	53:1:2694:G:H5'	2.18	0.43
54:2:51:G:H2'	54:2:52:A:O4'	2.18	0.43
2:c:61:THR:HB	2:c:63:PRO:HD2	1.99	0.43
4:e:88:VAL:HA	54:2:42:C:N3	2.33	0.43
7:h:67:THR:CG2	7:h:68:PRO:HD3	2.49	0.43
8:i:91:LYS:HD2	8:i:94:LYS:NZ	2.34	0.43
9:j:81:ILE:HG12	53:1:2515:C:OP1	2.18	0.43
10:k:8:LEU:HD21	10:k:84:CYS:SG	2.59	0.43
12:m:105:MET:HE3	12:m:106:ASP:N	2.34	0.43
13:n:69:ARG:HG3	13:n:69:ARG:HH21	1.83	0.43
16:q:32:ARG:HG3	53:1:581:C:OP1	2.17	0.43
24:y:18:LEU:O	24:y:22:LEU:HB2	2.19	0.43
30:F:1:MET:SD	30:F:24:ARG:NH2	2.92	0.43
30:F:19:ARG:NE	53:1:2756:U:OP2	2.49	0.43
31:G:142:LYS:HD3	52:3:1098:C:OP2	2.19	0.43
32:H:58:ARG:HB2	32:H:63:ILE:HD12	2.00	0.43
34:J:15:ILE:HD12	34:J:15:ILE:N	2.33	0.43
36:L:32:ASP:HB2	36:L:34:LYS:HG2	2.01	0.43
38:N:94:ARG:HH11	38:N:94:ARG:HG2	1.84	0.43
52:3:396:C:H3'	52:3:397:A:H5''	2.01	0.43
53:1:171:U:H2'	53:1:172:A:C8	2.53	0.43
53:1:1806:C:H2'	53:1:1807:G:O4'	2.18	0.43
53:1:2432:A:H1'	55:6:75:C:C4'	2.49	0.43
53:1:2463:C:H2'	53:1:2464:G:C8	2.54	0.43
53:1:2508:G:H2'	53:1:2509:G:C8	2.53	0.43
53:1:2623:G:H2'	53:1:2624:G:C8	2.53	0.43
53:1:2807:U:H3	53:1:2891:U:H3	1.67	0.43
54:2:60:C:H2'	54:2:61:G:H8	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:21:VAL:HG22	6:g:22:LYS:H	1.83	0.43
12:m:18:ARG:HG2	54:2:90:C:H5''	2.00	0.43
12:m:64:TRP:HZ3	12:m:106:ASP:HB3	1.83	0.43
13:n:11:ASN:ND2	53:1:1652:A:H62	2.17	0.43
13:n:36:THR:OG1	13:n:37:THR:N	2.52	0.43
14:o:75:GLY:HA3	14:o:109:ALA:HB3	1.99	0.43
14:o:111:ARG:NH2	14:o:117:PHE:OXT	2.52	0.43
21:v:7:GLU:HG2	21:v:41:GLU:O	2.18	0.43
24:y:41:HIS:NE2	53:1:96:C:H4'	2.33	0.43
26:B:4:GLN:O	53:1:2017:U:H4'	2.19	0.43
34:J:102:THR:HA	34:J:120:HIS:CE1	2.53	0.43
37:M:39:LEU:HD12	37:M:45:ILE:HD11	2.01	0.43
43:S:58:ARG:HH12	52:3:980:C:H5'	1.83	0.43
52:3:5:U:H4'	52:3:6:G:C5	2.54	0.43
52:3:1404:C:H2'	52:3:1405:G:C8	2.53	0.43
53:1:45:G:H5''	53:1:46:G:C5'	2.23	0.43
53:1:204:A:O3'	53:1:205:G:H4'	2.18	0.43
53:1:327:G:H2'	53:1:328:U:O4'	2.18	0.43
53:1:799:G:H5''	53:1:800:A:H2'	2.01	0.43
53:1:1045:C:OP1	53:1:1047:G:H5'	2.18	0.43
53:1:1590:A:H2'	53:1:1591:A:H8	1.84	0.43
53:1:1635:A:H2'	53:1:1636:U:O4'	2.19	0.43
53:1:1936:A:H5''	53:1:1937:A:O4'	2.18	0.43
53:1:2009:A:H2'	53:1:2010:G:C8	2.53	0.43
53:1:2861:U:H2'	53:1:2862:G:C8	2.54	0.43
1:b:104:LEU:HD23	1:b:104:LEU:H	1.83	0.43
1:b:257:ARG:NH2	1:b:266:ILE:HD12	2.34	0.43
8:i:30:GLN:HB3	8:i:60:VAL:HG21	2.00	0.43
9:j:135:GLN:O	9:j:136:GLN:HB2	2.19	0.43
25:z:36:GLU:O	25:z:37:ARG:NH1	2.48	0.43
31:G:29:PHE:CZ	31:G:48:MET:HE1	2.54	0.43
36:L:143:MET:HE3	36:L:147:ASN:HB3	2.00	0.43
38:N:18:VAL:HG21	38:N:81:GLY:HA3	2.01	0.43
46:V:12:VAL:HB	46:V:21:VAL:HG23	2.00	0.43
52:3:1510:C:H2'	52:3:1511:G:H8	1.84	0.43
53:1:917:A:H2'	53:1:918:A:O4'	2.17	0.43
53:1:1130:U:O2'	53:1:1131:G:OP1	2.29	0.43
53:1:1469:A:H2'	53:1:1470:A:C8	2.54	0.43
53:1:1680:U:H2'	53:1:1681:G:H5'	2.00	0.43
53:1:2809:A:H2'	53:1:2810:A:C8	2.54	0.43
5:f:43:LYS:HB2	5:f:50:THR:HG23	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:i:10:LEU:HD22	8:i:23:VAL:HG13	2.01	0.43
8:i:126:ARG:HA	8:i:129:GLU:HB2	2.00	0.43
18:s:96:ILE:O	18:s:96:ILE:HG13	2.19	0.43
20:u:42:LYS:HE2	53:1:499:U:H5''	1.99	0.43
31:G:77:GLU:O	31:G:80:LYS:HB3	2.19	0.43
33:I:75:TYR:HD2	33:I:89:LEU:HD13	1.83	0.43
36:L:25:PHE:O	36:L:28:ILE:HG22	2.18	0.43
38:N:40:ARG:CD	52:3:1292:G:H5'	2.49	0.43
49:Y:56:ILE:HA	49:Y:59:ARG:NH1	2.34	0.43
52:3:1485:U:H5'	53:1:1961:C:H5''	1.99	0.43
53:1:435:C:H2'	53:1:436:C:H5'	2.00	0.43
53:1:826:U:H5''	53:1:2429:G:P	2.58	0.43
53:1:1412:U:H2'	53:1:1413:A:C8	2.53	0.43
53:1:1909:C:H2'	53:1:1910:G:C8	2.54	0.43
53:1:2243:U:H2'	53:1:2244:U:H6	1.84	0.43
53:1:2633:G:H5''	53:1:2812:G:H5'	2.00	0.43
53:1:2677:G:H2'	53:1:2678:C:C6	2.53	0.43
2:c:27:ILE:HD11	2:c:189:VAL:CG1	2.49	0.42
3:d:30:GLN:O	3:d:33:VAL:HG12	2.19	0.42
4:e:21:TYR:HB3	4:e:26:GLN:HB3	2.00	0.42
7:h:59:LEU:HB3	7:h:62:ARG:HB2	2.01	0.42
7:h:112:ALA:O	7:h:113:PHE:C	2.62	0.42
11:l:19:LEU:HD12	11:l:19:LEU:N	2.33	0.42
11:l:29:LYS:HE3	53:1:566:U:H5''	2.01	0.42
14:o:29:HIS:HB3	14:o:36:TYR:CD2	2.49	0.42
15:p:89:GLY:O	15:p:112:ARG:NH1	2.51	0.42
18:s:86:MET:HB2	18:s:96:ILE:HD13	2.01	0.42
19:t:3:ARG:O	19:t:7:LEU:HG	2.19	0.42
31:G:66:ILE:HD12	31:G:66:ILE:N	2.34	0.42
32:H:38:VAL:O	32:H:42:LEU:HD23	2.19	0.42
33:I:131:ILE:HG21	52:3:620:C:O2	2.19	0.42
40:P:107:THR:O	40:P:108:ASN:HB3	2.19	0.42
46:V:16:MET:HG3	46:V:19:SER:O	2.19	0.42
52:3:530:G:H3'	52:3:531:U:C5'	2.48	0.42
52:3:952:U:H2'	52:3:953:G:H8	1.84	0.42
52:3:1170:A:H2'	52:3:1171:A:O4'	2.19	0.42
52:3:1510:C:H2'	52:3:1511:G:C8	2.53	0.42
53:1:859:G:C2'	53:1:860:U:OP2	2.66	0.42
53:1:2086:U:H2'	53:1:2087:G:C8	2.54	0.42
53:1:2141:G:H22	53:1:2151:U:H1'	1.84	0.42
53:1:2743:U:C2'	53:1:2744:G:H5''	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2795:C:H2'	53:1:2796:U:O4'	2.19	0.42
53:1:2821:A:H2'	53:1:2822:G:O4'	2.19	0.42
1:b:66:PHE:HB3	1:b:142:ASN:HD21	1.84	0.42
1:b:131:MET:CE	1:b:187:CYS:HB2	2.50	0.42
3:d:40:ARG:HH12	53:1:1246:A:H4'	1.83	0.42
3:d:118:LEU:HD12	3:d:186:VAL:O	2.19	0.42
4:e:39:VAL:HG13	4:e:40:GLY:N	2.33	0.42
13:n:3:HIS:CG	53:1:2820:A:H4'	2.54	0.42
17:r:88:GLY:O	53:1:1224:U:H4'	2.19	0.42
29:E:61:LEU:N	29:E:62:PRO:HD3	2.32	0.42
31:G:110:ILE:O	31:G:151:LYS:HE3	2.19	0.42
31:G:143:LEU:HA	31:G:146:SER:HB2	2.00	0.42
35:K:9:MET:HB3	35:K:57:ALA:HB1	2.00	0.42
39:O:15:HIS:HA	39:O:18:ILE:HG22	2.00	0.42
41:Q:20:VAL:HG23	41:Q:20:VAL:O	2.19	0.42
41:Q:81:ILE:HG22	41:Q:82:ARG:N	2.34	0.42
47:W:38:ILE:HG13	47:W:62:ARG:HH22	1.84	0.42
50:Z:34:ARG:HB3	50:Z:36:PHE:CZ	2.54	0.42
52:3:219:U:H2'	52:3:220:G:C8	2.54	0.42
52:3:356:A:H2'	52:3:357:G:O4'	2.19	0.42
53:1:189:G:H2'	53:1:205:G:H22	1.84	0.42
53:1:254:G:C2'	53:1:255:A:H5''	2.49	0.42
53:1:579:G:H4'	53:1:2018:G:H5''	2.01	0.42
53:1:940:G:H2'	53:1:941:A:C4'	2.49	0.42
55:5:10:G:C2	55:5:26:G:H1'	2.54	0.42
3:d:79:ARG:HH21	53:1:448:U:H4'	1.85	0.42
4:e:3:LEU:HD22	4:e:99:PHE:HD2	1.83	0.42
7:h:72:LEU:HD12	7:h:72:LEU:N	2.30	0.42
14:o:99:TYR:HA	14:o:103:VAL:HG11	2.00	0.42
19:t:11:LEU:O	24:y:29:ARG:NH1	2.52	0.42
23:x:36:ARG:HG2	23:x:47:THR:OG1	2.20	0.42
31:G:69:VAL:HA	31:G:91:VAL:CG2	2.49	0.42
39:O:22:THR:HA	39:O:25:ILE:HG22	2.02	0.42
43:S:58:ARG:HD2	52:3:979:C:O2	2.19	0.42
44:T:47:LYS:HE2	52:3:808:C:OP2	2.20	0.42
48:X:77:ARG:NH1	52:3:1222:G:H5''	2.33	0.42
52:3:40:C:H2'	52:3:41:G:C8	2.54	0.42
53:1:310:A:O2'	53:1:311:A:H2'	2.19	0.42
53:1:1028:A:N6	53:1:1125:G:H2'	2.34	0.42
54:2:22:U:H2'	54:2:23:G:C8	2.55	0.42
6:g:2:GLN:O	6:g:2:GLN:HG2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:k:34:GLY:H	10:k:37:ASP:CG	2.28	0.42
12:m:78:LEU:HD12	12:m:78:LEU:N	2.34	0.42
17:r:63:VAL:HG12	17:r:96:VAL:HG22	2.01	0.42
18:s:82:MET:HB3	18:s:84:ARG:NH2	2.34	0.42
20:u:81:ARG:NH2	20:u:96:LYS:HG3	2.34	0.42
31:G:114:LYS:HG2	31:G:151:LYS:HE2	2.00	0.42
32:H:191:THR:O	52:3:1206:G:H4'	2.19	0.42
33:I:116:LEU:HD22	33:I:116:LEU:N	2.35	0.42
35:K:7:VAL:HA	35:K:60:VAL:O	2.19	0.42
36:L:68:VAL:HA	36:L:137:ARG:HD3	2.02	0.42
39:O:12:ALA:HB2	39:O:96:VAL:HB	2.02	0.42
42:R:74:MET:SD	42:R:74:MET:C	3.03	0.42
48:X:17:LYS:HE2	52:3:1013:G:OP1	2.20	0.42
49:Y:11:ILE:HD12	49:Y:11:ILE:N	2.33	0.42
52:3:272:C:H2'	52:3:273:U:C6	2.54	0.42
52:3:629:A:H2'	52:3:630:A:O4'	2.20	0.42
52:3:974:A:H5'	52:3:976:G:OP1	2.20	0.42
52:3:1004:A:H2'	52:3:1005:A:O4'	2.19	0.42
52:3:1356:G:H2'	52:3:1357:A:C8	2.55	0.42
52:3:1512:U:H2'	52:3:1513:A:C8	2.54	0.42
53:1:343:C:O2'	53:1:344:A:H5'	2.19	0.42
53:1:1035:U:H2'	53:1:1036:G:C8	2.54	0.42
53:1:1854:A:H61	53:1:1888:G:H1'	1.85	0.42
53:1:2834:G:H2'	53:1:2879:A:N6	2.34	0.42
54:2:101:A:H2'	54:2:102:G:O4'	2.19	0.42
2:c:179:ARG:HB3	2:c:188:LEU:HD12	2.00	0.42
10:k:25:LEU:HD12	53:1:2562:U:H4'	2.00	0.42
12:m:14:LYS:NZ	53:1:956:G:N7	2.62	0.42
13:n:25:ALA:O	13:n:29:VAL:HG23	2.19	0.42
14:o:70:ALA:O	14:o:74:VAL:HG23	2.19	0.42
18:s:11:ARG:HD2	18:s:11:ARG:HA	1.87	0.42
20:u:95:PHE:CG	20:u:102:ILE:HD11	2.54	0.42
22:w:64:LYS:HG3	22:w:65:PHE:N	2.34	0.42
23:x:16:ASN:HB3	23:x:24:THR:HB	1.99	0.42
32:H:22:PHE:HB2	39:O:95:GLY:C	2.44	0.42
33:I:158:LEU:HD21	33:I:174:ALA:HB1	2.01	0.42
38:N:17:ARG:NH2	52:3:1129:C:H4'	2.35	0.42
41:Q:81:ILE:HD13	41:Q:96:THR:HG23	2.01	0.42
52:3:9:G:H2'	52:3:10:A:H8	1.84	0.42
53:1:293:U:H2'	53:1:294:A:H5''	2.01	0.42
53:1:406:G:H2'	53:1:407:G:C8	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:631:A:H2'	53:1:632:A:O4'	2.19	0.42
53:1:1054:A:H2'	53:1:1055:G:C8	2.54	0.42
53:1:1430:G:H2'	53:1:1431:A:C8	2.55	0.42
53:1:2285:C:O2'	53:1:2287:A:H1'	2.20	0.42
53:1:2484:G:O2'	53:1:2485:G:H5'	2.19	0.42
57:7:59:U:H2'	57:7:60:U:H5'	2.01	0.42
57:7:68:C:H2'	57:7:69:G:C8	2.55	0.42
3:d:178:VAL:O	3:d:182:ALA:N	2.47	0.42
5:f:153:PRO:HA	5:f:159:LYS:O	2.19	0.42
8:i:123:ALA:HA	8:i:126:ARG:CZ	2.50	0.42
10:k:113:MET:HA	10:k:116:ILE:HG12	2.00	0.42
18:s:57:ASN:O	18:s:61:ASN:HB2	2.19	0.42
23:x:61:LYS:HG2	23:x:62:GLY:N	2.29	0.42
31:G:206:ILE:O	31:G:209:VAL:HG12	2.20	0.42
34:J:14:LEU:HD12	34:J:14:LEU:O	2.20	0.42
35:K:8:PHE:C	35:K:9:MET:HE2	2.44	0.42
38:N:122:ARG:NH1	38:N:123:ARG:O	2.53	0.42
41:Q:31:GLY:HA3	41:Q:54:VAL:CG1	2.49	0.42
49:Y:9:ARG:HE	49:Y:12:GLN:NE2	2.17	0.42
53:1:452:G:N2	53:1:458:G:H1'	2.34	0.42
53:1:752:A:O2'	53:1:1781:U:H5'	2.20	0.42
53:1:1863:G:H4'	53:1:2411:A:H4'	2.01	0.42
53:1:2569:G:O2'	53:1:2570:G:H5'	2.20	0.42
53:1:2627:G:H2'	53:1:2628:C:O4'	2.20	0.42
54:2:5:U:H2'	54:2:6:G:H8	1.83	0.42
54:2:88:C:C4'	54:2:89:U:OP1	2.67	0.42
1:b:28:PRO:HG3	1:b:62:ARG:NH2	2.34	0.42
1:b:131:MET:HE1	1:b:184:GLU:O	2.20	0.42
3:d:171:ASP:OD2	3:d:173:THR:HG22	2.20	0.42
9:j:113:PRO:HD2	53:1:558:U:P	2.60	0.42
10:k:88:ASN:O	10:k:91:SER:N	2.53	0.42
11:l:49:GLY:HA2	29:E:56:LEU:HD11	2.02	0.42
15:p:38:ARG:NH2	52:3:345:C:H5'	2.27	0.42
18:s:82:MET:HB3	18:s:84:ARG:HH22	1.84	0.42
23:x:39:VAL:HG21	23:x:42:GLU:HB3	2.00	0.42
32:H:39:ARG:NH1	32:H:54:ILE:HG13	2.34	0.42
32:H:76:ILE:HG13	32:H:77:GLY:N	2.35	0.42
32:H:78:LYS:O	32:H:81:GLU:HG2	2.20	0.42
35:K:25:TYR:HB3	35:K:74:LEU:HD11	2.01	0.42
37:M:29:SER:OG	37:M:31:LEU:HG	2.19	0.42
37:M:68:LYS:HD2	37:M:68:LYS:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:M:124:ILE:HD12	37:M:124:ILE:N	2.34	0.42
40:P:115:ILE:HG12	50:Z:28:LEU:HD12	2.02	0.42
41:Q:113:ARG:NH1	41:Q:121:PRO:HD2	2.34	0.42
52:3:928:G:H2'	52:3:929:G:C8	2.55	0.42
52:3:1014:A:N3	52:3:1219:A:H1'	2.35	0.42
53:1:1053:C:H3'	53:1:1054:A:C5'	2.49	0.42
53:1:1388:G:H2'	53:1:1389:G:C8	2.55	0.42
1:b:132:ARG:HD3	6:g:123:ARG:CZ	2.50	0.42
4:e:23:SER:CB	54:2:56:G:H5'	2.50	0.42
21:v:9:ARG:CG	21:v:41:GLU:HB2	2.50	0.42
26:B:15:ARG:NH2	53:1:1264:A:H5''	2.34	0.42
29:E:38:LYS:HD2	53:1:2351:G:O6	2.19	0.42
29:E:61:LEU:C	29:E:63:TYR:H	2.27	0.42
38:N:22:PRO:CA	38:N:60:LEU:HD23	2.49	0.42
39:O:5:ARG:HG2	39:O:79:PRO:HD3	2.01	0.42
42:R:14:ALA:HB3	42:R:40:GLU:HA	2.01	0.42
44:T:17:ASP:OD2	44:T:19:ASN:HB2	2.20	0.42
52:3:56:U:H2'	52:3:57:G:C8	2.55	0.42
52:3:520:A:N6	52:3:529:G:H1'	2.35	0.42
52:3:593:U:H2'	52:3:594:U:C6	2.55	0.42
52:3:664:G:N2	52:3:741:G:H1	2.17	0.42
52:3:1463:U:H2'	52:3:1464:U:C6	2.55	0.42
53:1:662:G:H2'	53:1:663:G:H8	1.84	0.42
53:1:864:G:O2'	53:1:865:C:H5'	2.20	0.42
53:1:1083:U:H2'	53:1:1085:A:OP2	2.19	0.42
53:1:1255:U:H3	53:1:2060:A:H5''	1.84	0.42
53:1:1720:U:H2'	53:1:1721:G:O4'	2.19	0.42
53:1:2668:G:H2'	53:1:2669:G:H8	1.84	0.42
54:2:63:C:H2'	54:2:64:G:C8	2.55	0.42
54:2:88:C:C5'	54:2:89:U:OP1	2.66	0.42
55:5:41:C:H2'	55:5:42:G:H8	1.85	0.42
55:6:11:A:H2'	55:6:12:G:C8	2.54	0.42
1:b:269:ARG:HH22	53:1:1798:U:P	2.42	0.42
6:g:3:VAL:HG13	6:g:37:VAL:O	2.19	0.42
7:h:33:VAL:O	7:h:37:LYS:HG2	2.19	0.42
10:k:109:SER:O	10:k:110:GLU:HG3	2.19	0.42
13:n:45:ARG:HG2	13:n:95:THR:HG21	2.02	0.42
15:p:30:TRP:CE3	15:p:37:LYS:HG2	2.55	0.42
26:B:15:ARG:HH22	53:1:1264:A:H5''	1.84	0.42
28:D:31:LEU:O	28:D:35:ARG:HG3	2.20	0.42
29:E:61:LEU:HD13	29:E:64:ALA:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:F:30:GLU:HA	30:F:31:PRO:HD3	1.82	0.42
32:H:156:LEU:HD11	32:H:163:ARG:HE	1.84	0.42
35:K:71:ILE:O	35:K:75:GLU:HG2	2.20	0.42
38:N:108:ARG:HB3	52:3:1347:G:C5'	2.50	0.42
48:X:31:ARG:NH1	48:X:56:HIS:HB2	2.34	0.42
49:Y:79:THR:O	49:Y:83:ASN:ND2	2.52	0.42
52:3:806:C:H2'	52:3:807:A:H8	1.85	0.42
52:3:977:A:H3'	52:3:977:A:N3	2.34	0.42
53:1:372:G:O2'	53:1:373:U:H5	2.03	0.42
53:1:565:C:H4'	53:1:1253:A:N6	2.33	0.42
53:1:1420:A:H5'	53:1:1421:G:OP2	2.20	0.42
53:1:2112:G:H2'	53:1:2113:U:H5'	2.01	0.42
53:1:2713:U:H3'	53:1:2714:G:H5''	2.00	0.42
57:7:59:U:C2'	57:7:60:U:H5'	2.50	0.42
1:b:204:LEU:HD11	1:b:213:ARG:HH21	1.85	0.42
2:c:13:ARG:NH1	15:p:74:GLN:OE1	2.53	0.42
4:e:107:VAL:HA	4:e:110:ILE:HG13	2.01	0.42
5:f:37:ASN:HB3	5:f:40:VAL:HG23	2.02	0.42
5:f:121:THR:CG2	5:f:133:LYS:HB3	2.46	0.42
8:i:100:ILE:O	8:i:140:GLU:N	2.52	0.42
8:i:124:MET:O	8:i:128:ILE:HG12	2.19	0.42
10:k:48:PRO:HB3	52:3:1422:G:C5'	2.50	0.42
11:l:68:SER:HB3	11:l:71:ALA:HB3	2.02	0.42
13:n:49:GLU:O	13:n:52:ILE:HG22	2.20	0.42
20:u:51:LEU:O	20:u:51:LEU:HD12	2.20	0.42
23:x:50:VAL:HB	23:x:54:GLY:HA3	2.01	0.42
33:I:9:LYS:HE3	52:3:428:G:OP2	2.20	0.42
37:M:39:LEU:HD22	37:M:44:PHE:HD2	1.85	0.42
38:N:101:GLY:C	38:N:103:VAL:H	2.28	0.42
38:N:114:LYS:HB2	38:N:117:LEU:CD1	2.50	0.42
43:S:52:ARG:HH22	52:3:1220:G:P	2.43	0.42
45:U:10:GLY:C	52:3:624:C:H4'	2.45	0.42
48:X:5:LYS:HB3	52:3:1313:U:OP2	2.19	0.42
49:Y:22:SER:HA	52:3:1458:G:O3'	2.19	0.42
49:Y:68:LYS:HE2	52:3:185:U:C4'	2.41	0.42
50:Z:36:PHE:C	50:Z:38:GLU:H	2.28	0.42
52:3:1409:C:H2'	52:3:1410:A:H8	1.84	0.42
52:3:1499:A:O2'	52:3:1500:A:H5'	2.20	0.42
53:1:479:A:O2'	53:1:481:G:H5'	2.20	0.42
53:1:548:G:H2'	53:1:549:G:O4'	2.19	0.42
53:1:1345:C:H2'	53:1:1346:G:H8	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1837:C:H2'	53:1:1899:A:H61	1.85	0.42
53:1:2248:C:H2'	53:1:2249:U:O4'	2.19	0.42
53:1:2851:A:H2'	53:1:2852:G:O4'	2.20	0.42
54:2:60:C:H2'	54:2:61:G:C8	2.55	0.42
54:2:65:U:O4	54:2:108:A:H2'	2.20	0.42
2:c:88:GLU:H	2:c:88:GLU:CD	2.28	0.41
2:c:135:GLY:O	53:1:2580:U:H5''	2.20	0.41
5:f:109:SER:HB2	53:1:2668:G:H1'	2.02	0.41
5:f:172:GLU:HG3	5:f:174:LYS:N	2.33	0.41
6:g:75:LEU:O	6:g:77:THR:HG23	2.21	0.41
8:i:136:GLY:C	8:i:137:LEU:HD12	2.45	0.41
11:l:23:ILE:HD12	17:r:82:HIS:CD2	2.56	0.41
11:l:79:LEU:HD23	11:l:82:LEU:HD13	2.01	0.41
11:l:111:ILE:HG12	53:1:636:G:C5	2.54	0.41
15:p:109:ILE:C	15:p:110:LYS:HE2	2.44	0.41
17:r:51:VAL:CG1	17:r:52:PRO:HD2	2.50	0.41
18:s:85:ILE:HG21	18:s:93:ALA:HB1	2.02	0.41
30:F:36:ARG:NH2	30:F:37:GLN:HE21	2.18	0.41
31:G:2:THR:OG1	31:G:50:ASN:ND2	2.53	0.41
36:L:67:ASN:O	36:L:137:ARG:NH1	2.53	0.41
45:U:19:VAL:HG23	45:U:36:VAL:HG23	2.02	0.41
51:a:54:LYS:HD2	51:a:57:GLN:HE21	1.85	0.41
51:a:54:LYS:HB3	51:a:56:ASP:OD1	2.20	0.41
52:3:694:A:H2'	52:3:695:A:O4'	2.19	0.41
52:3:1197:A:H2'	52:3:1198:G:H5''	2.02	0.41
52:3:1304:G:H21	52:3:1333:A:H62	1.68	0.41
53:1:580:U:H2'	53:1:581:C:C6	2.54	0.41
53:1:893:C:H2'	53:1:894:U:O4'	2.20	0.41
53:1:1877:A:H2'	53:1:1878:G:O4'	2.19	0.41
53:1:2707:U:H2'	53:1:2708:G:H8	1.85	0.41
53:1:2730:C:H2'	53:1:2731:G:C8	2.55	0.41
2:c:55:LYS:HE3	2:c:59:ARG:HG2	2.02	0.41
4:e:41:GLU:HB3	4:e:48:LEU:CD2	2.48	0.41
4:e:118:ALA:C	4:e:119:LYS:HD3	2.44	0.41
8:i:21:PRO:CB	8:i:22:PRO:HD3	2.50	0.41
9:j:36:LEU:HD11	9:j:122:LEU:HD22	2.02	0.41
14:o:100:HIS:CA	14:o:104:GLN:HE21	2.27	0.41
19:t:59:ASN:HB2	19:t:84:TYR:HB2	2.02	0.41
21:v:64:VAL:HG13	21:v:64:VAL:O	2.21	0.41
22:w:15:LYS:HB2	22:w:17:LEU:CD2	2.50	0.41
31:G:17:HIS:O	31:G:37:VAL:HG13	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:4:VAL:HG22	32:H:5:HIS:H	1.84	0.41
33:I:120:LYS:CE	52:3:439:U:H5''	2.48	0.41
34:J:159:SER:HB3	34:J:162:GLU:OE1	2.20	0.41
48:X:79:TYR:CZ	52:3:1226:C:H4'	2.55	0.41
52:3:285:C:H2'	52:3:286:C:C6	2.55	0.41
52:3:309:A:H2'	52:3:310:G:C8	2.54	0.41
52:3:777:A:H2'	52:3:778:G:O4'	2.20	0.41
53:1:433:C:O2'	53:1:434:U:H5'	2.20	0.41
53:1:1005:C:H2'	53:1:1006:C:H6	1.85	0.41
53:1:1278:C:H2'	53:1:1279:G:H8	1.84	0.41
53:1:1601:G:C2'	53:1:1602:U:H5'	2.50	0.41
53:1:1736:U:H2'	53:1:1737:G:O4'	2.20	0.41
53:1:1801:A:H5''	53:1:2203:U:C2'	2.45	0.41
53:1:2432:A:N3	55:6:75:C:H5'	2.35	0.41
54:2:75:G:H1	54:2:101:A:H61	1.68	0.41
1:b:8:THR:HG21	53:1:727:A:C2	2.55	0.41
4:e:99:PHE:HA	4:e:102:LEU:HG	2.02	0.41
5:f:44:HIS:CG	5:f:45:ALA:H	2.37	0.41
7:h:3:LEU:HD23	7:h:6:GLN:HG2	2.02	0.41
22:w:73:ARG:HH22	53:1:2332:C:C5'	2.23	0.41
28:D:1:MET:SD	28:D:1:MET:C	3.03	0.41
28:D:26:ASN:O	28:D:30:VAL:HG23	2.20	0.41
30:F:4:ARG:HH22	53:1:2477:U:H2'	1.85	0.41
31:G:207:ARG:H	31:G:207:ARG:HG2	1.68	0.41
32:H:22:PHE:CD2	39:O:97:ASP:HB2	2.55	0.41
32:H:171:ARG:HG3	52:3:1106:G:O3'	2.20	0.41
33:I:7:LYS:HD2	33:I:21:LYS:HD3	2.02	0.41
33:I:131:ILE:HG12	52:3:620:C:N3	2.35	0.41
35:K:5:GLU:OE2	35:K:63:ASN:ND2	2.54	0.41
40:P:16:SER:O	40:P:78:ILE:HA	2.20	0.41
41:Q:112:ALA:HB1	41:Q:115:LYS:HE2	2.02	0.41
45:U:40:ASN:ND2	45:U:43:ALA:HB2	2.36	0.41
52:3:928:G:H2'	52:3:929:G:H8	1.86	0.41
52:3:1346:A:H2'	52:3:1346:A:N3	2.35	0.41
53:1:1893:C:C2'	53:1:1894:C:H5'	2.51	0.41
53:1:2570:G:H2'	53:1:2571:U:O4'	2.20	0.41
53:1:2774:C:H2'	53:1:2775:G:O4'	2.20	0.41
53:1:2785:C:H2'	53:1:2786:U:C6	2.55	0.41
53:1:2810:A:H2'	53:1:2811:G:O4'	2.19	0.41
2:c:159:LYS:O	2:c:161:MET:HG3	2.21	0.41
3:d:176:ASP:OD1	3:d:179:SER:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:k:23:LYS:HE2	10:k:23:LYS:HB2	1.88	0.41
10:k:105:ARG:HH22	15:p:33:GLU:HG2	1.85	0.41
12:m:18:ARG:HG2	54:2:90:C:C5'	2.50	0.41
14:o:29:HIS:CE1	54:2:7:G:H5'	2.55	0.41
14:o:38:GLN:HE21	14:o:40:ILE:HG12	1.84	0.41
18:s:58:ALA:HA	18:s:62:ASP:OD2	2.21	0.41
22:w:34:VAL:HG11	22:w:41:PHE:CD2	2.55	0.41
37:M:89:ASP:OD1	37:M:89:ASP:N	2.52	0.41
46:V:30:HIS:HB3	46:V:34:GLY:H	1.86	0.41
46:V:37:ILE:HD12	46:V:39:ARG:HH21	1.85	0.41
47:W:18:GLN:HG3	47:W:19:GLU:H	1.85	0.41
52:3:1384:C:H2'	52:3:1385:G:C8	2.55	0.41
52:3:1470:U:H2'	52:3:1471:U:C6	2.55	0.41
53:1:171:U:H2'	53:1:172:A:H8	1.86	0.41
53:1:441:U:H2'	53:1:442:G:C8	2.54	0.41
53:1:1301:A:H2'	53:1:1301:A:N3	2.36	0.41
53:1:2663:G:H2'	53:1:2664:G:O4'	2.19	0.41
55:5:47:U:H3'	55:5:48:C:C5'	2.51	0.41
1:b:219:VAL:HG21	53:1:782:A:C8	2.55	0.41
3:d:164:LEU:HB3	3:d:167:VAL:HG12	2.02	0.41
7:h:64:VAL:O	7:h:67:THR:HG22	2.20	0.41
9:j:40:HIS:CE1	9:j:41:LYS:HG3	2.55	0.41
11:l:33:ARG:HD3	11:l:40:SER:HA	2.02	0.41
11:l:76:GLU:CD	53:1:636:G:H1	2.28	0.41
13:n:8:ARG:HD2	13:n:43:GLU:HG2	2.02	0.41
21:v:60:VAL:HG12	21:v:71:LYS:HE3	2.02	0.41
22:w:22:PHE:CD2	53:1:922:C:H1'	2.55	0.41
24:y:22:LEU:HB3	24:y:23:ARG:HH11	1.85	0.41
30:F:12:ARG:NH2	53:1:1090:A:H1'	2.34	0.41
31:G:162:VAL:HB	31:G:184:ALA:CB	2.50	0.41
32:H:10:ARG:HH22	32:H:174:LEU:C	2.28	0.41
32:H:18:ASN:ND2	43:S:89:ARG:O	2.53	0.41
33:I:61:ARG:NH2	33:I:67:LEU:HA	2.31	0.41
33:I:115:GLN:HE21	33:I:119:HIS:CE1	2.37	0.41
33:I:205:LYS:HB3	52:3:8:A:C6	2.55	0.41
35:K:54:LEU:HD12	35:K:55:HIS:H	1.84	0.41
38:N:113:LYS:HD3	38:N:118:ARG:O	2.21	0.41
41:Q:113:ARG:NH1	41:Q:120:ARG:HA	2.35	0.41
43:S:25:GLU:O	43:S:29:ILE:HG22	2.19	0.41
52:3:225:C:C2'	52:3:226:G:H5''	2.51	0.41
52:3:590:U:H2'	52:3:591:U:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1148:U:H2'	52:3:1149:C:O4'	2.20	0.41
53:1:131:A:H2'	53:1:132:G:C8	2.55	0.41
53:1:673:C:H2'	53:1:674:G:C8	2.55	0.41
53:1:1027:A:C2	53:1:2488:G:H5'	2.55	0.41
53:1:1028:A:H61	53:1:1125:G:H2'	1.86	0.41
53:1:1954:G:N2	53:1:2551:C:H5'	2.36	0.41
53:1:2036:C:H2'	53:1:2037:A:H8	1.85	0.41
53:1:2542:A:H4'	53:1:2543:G:C8	2.55	0.41
53:1:2542:A:H4'	53:1:2543:G:H8	1.86	0.41
54:2:88:C:H4'	54:2:89:U:OP1	2.18	0.41
1:b:75:ALA:HA	1:b:95:TYR:HA	2.03	0.41
2:c:4:LEU:HD13	2:c:101:PHE:CE2	2.56	0.41
6:g:6:LEU:HD11	6:g:37:VAL:HG23	2.03	0.41
6:g:70:GLU:OE2	6:g:138:VAL:HB	2.21	0.41
7:h:8:LYS:HE3	7:h:11:ILE:HG21	2.01	0.41
7:h:92:ALA:HB1	7:h:129:LEU:HD22	2.03	0.41
8:i:116:MET:HB3	8:i:124:MET:SD	2.61	0.41
9:j:17:VAL:HG13	9:j:139:VAL:HA	2.03	0.41
9:j:28:LEU:O	9:j:32:LEU:HG	2.21	0.41
10:k:7:MET:HE2	10:k:20:MET:HE2	2.02	0.41
10:k:111:LYS:HB3	10:k:111:LYS:HE2	1.81	0.41
11:l:55:MET:HA	11:l:56:PRO:HD3	1.86	0.41
13:n:47:VAL:C	13:n:50:PRO:HD2	2.46	0.41
14:o:7:ARG:HH12	14:o:95:SER:HB3	1.86	0.41
15:p:36:LYS:HE3	15:p:38:ARG:HB2	2.02	0.41
31:G:102:ASN:O	31:G:106:VAL:HG22	2.20	0.41
33:I:100:VAL:O	33:I:104:MET:HG2	2.20	0.41
33:I:190:LEU:CD1	33:I:192:ALA:H	2.30	0.41
34:J:87:VAL:HA	34:J:91:SER:O	2.20	0.41
35:K:51:ILE:C	35:K:53:LYS:H	2.28	0.41
39:O:88:MET:O	39:O:89:ARG:HG2	2.21	0.41
39:O:91:ASP:OD1	39:O:91:ASP:N	2.52	0.41
44:T:38:LEU:HD23	44:T:55:LEU:HD22	2.02	0.41
49:Y:75:LYS:O	49:Y:79:THR:OG1	2.33	0.41
52:3:156:C:H2'	52:3:157:U:O4'	2.20	0.41
52:3:312:C:H2'	52:3:313:A:H8	1.82	0.41
52:3:389:A:H3'	52:3:390:U:C6	2.56	0.41
52:3:571:U:O5'	52:3:571:U:H6	2.04	0.41
52:3:972:C:O2'	52:3:973:G:H5'	2.21	0.41
52:3:1251:A:H2'	52:3:1252:A:O4'	2.20	0.41
53:1:398:C:H2'	53:1:399:U:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:581:C:H2'	53:1:582:A:H8	1.85	0.41
53:1:611:C:H2'	53:1:612:G:O4'	2.20	0.41
53:1:1745:A:H2'	53:1:1746:A:C8	2.55	0.41
53:1:2307:G:H4'	53:1:2308:G:O5'	2.21	0.41
53:1:2668:G:H2'	53:1:2669:G:C8	2.55	0.41
2:c:22:ILE:O	2:c:22:ILE:HG13	2.20	0.41
2:c:62:LYS:N	2:c:63:PRO:CD	2.83	0.41
2:c:110:THR:HB	2:c:202:ILE:HB	2.02	0.41
7:h:23:LEU:HD12	7:h:24:SER:N	2.35	0.41
8:i:78:LEU:HD23	8:i:81:LYS:HD3	2.03	0.41
12:m:12:MET:HA	53:1:910:A:H62	1.86	0.41
14:o:79:ALA:HB1	14:o:113:ALA:CB	2.50	0.41
19:t:31:VAL:HA	19:t:83:ALA:O	2.20	0.41
33:I:67:LEU:HB2	33:I:70:GLN:HG2	2.02	0.41
37:M:33:VAL:CG1	37:M:58:LEU:HD21	2.49	0.41
43:S:20:PHE:O	43:S:21:ALA:HB3	2.21	0.41
46:V:76:ARG:HG2	46:V:76:ARG:HH11	1.85	0.41
52:3:425:G:H2'	52:3:426:U:O4'	2.21	0.41
52:3:578:C:H2'	52:3:579:A:C8	2.56	0.41
52:3:722:G:H1	52:3:733:G:H1	1.68	0.41
52:3:1120:C:H2'	52:3:1121:U:C6	2.56	0.41
53:1:976:G:H4'	53:1:1156:A:N6	2.36	0.41
53:1:1021:A:N3	53:1:1021:A:H3'	2.36	0.41
53:1:2673:G:H2'	53:1:2674:G:H8	1.84	0.41
53:1:2898:U:H2'	53:1:2899:A:C8	2.56	0.41
54:2:78:A:H2'	54:2:79:G:O4'	2.21	0.41
2:c:32:ASN:O	2:c:96:ILE:N	2.54	0.41
4:e:34:THR:HA	4:e:88:VAL:O	2.20	0.41
4:e:55:ASP:O	4:e:59:ILE:HG13	2.20	0.41
4:e:165:GLY:O	4:e:169:LEU:HG	2.20	0.41
8:i:34:ILE:HD12	8:i:34:ILE:N	2.35	0.41
10:k:24:VAL:HG23	10:k:24:VAL:O	2.20	0.41
18:s:74:ILE:O	18:s:74:ILE:HG23	2.21	0.41
19:t:32:LEU:HD12	19:t:32:LEU:O	2.21	0.41
31:G:114:LYS:HD2	31:G:114:LYS:HA	1.93	0.41
35:K:8:PHE:HB2	35:K:84:VAL:HG23	2.03	0.41
37:M:87:ARG:HE	52:3:599:C:P	2.44	0.41
38:N:108:ARG:HB3	52:3:1347:G:O5'	2.20	0.41
40:P:78:ILE:HD13	40:P:81:LEU:HD23	2.03	0.41
41:Q:23:LEU:HD13	41:Q:29:LYS:NZ	2.36	0.41
41:Q:24:GLU:O	41:Q:24:GLU:CG	2.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:T:5:GLU:O	44:T:9:LYS:HG3	2.20	0.41
46:V:16:MET:HG3	46:V:19:SER:C	2.46	0.41
51:a:62:ALA:HA	51:a:162:ARG:HA	2.02	0.41
52:3:21:G:H21	52:3:914:A:H62	1.68	0.41
52:3:79:G:O2'	52:3:80:A:H5'	2.20	0.41
52:3:586:C:O2'	52:3:587:G:H5'	2.21	0.41
52:3:1393:U:H5'	52:3:1502:A:OP1	2.20	0.41
53:1:996:A:H2'	53:1:997:G:C8	2.56	0.41
53:1:1170:C:H2'	53:1:1171:G:C8	2.56	0.41
53:1:1234:U:H2'	53:1:1235:G:O4'	2.21	0.41
53:1:1326:U:H2'	53:1:1327:A:H8	1.86	0.41
53:1:1510:G:H2'	53:1:1511:G:O4'	2.20	0.41
53:1:2296:U:C4'	53:1:2297:A:OP1	2.69	0.41
53:1:2326:C:O2'	53:1:2327:A:P	2.79	0.41
1:b:140:VAL:HG12	1:b:191:LEU:HD23	2.02	0.41
1:b:147:PRO:HG2	1:b:186:ASP:HB2	2.02	0.41
2:c:33:ARG:HA	2:c:95:SER:HA	2.03	0.41
3:d:191:ASP:O	3:d:195:GLN:HG2	2.21	0.41
4:e:88:VAL:HG22	54:2:42:C:O2	2.21	0.41
8:i:74:PRO:HB2	8:i:77:VAL:HG23	2.02	0.41
14:o:77:ALA:O	14:o:81:ARG:HG2	2.21	0.41
15:p:102:ARG:NH1	15:p:102:ARG:HG2	2.36	0.41
19:t:12:ARG:O	19:t:13:ALA:HB2	2.21	0.41
20:u:64:ILE:HG12	20:u:68:ASN:OD1	2.21	0.41
22:w:14:ALA:O	22:w:16:ARG:NH1	2.54	0.41
22:w:21:ARG:HD2	22:w:27:VAL:HG12	2.02	0.41
27:C:9:LYS:HD3	27:C:19:PHE:CE2	2.55	0.41
32:H:53:ARG:HG3	32:H:68:HIS:HB2	2.03	0.41
33:I:101:VAL:HG13	33:I:113:ALA:HB1	2.02	0.41
33:I:131:ILE:HG12	52:3:620:C:C2	2.56	0.41
35:K:96:VAL:HG12	35:K:97:THR:N	2.31	0.41
42:R:109:LYS:HB3	42:R:109:LYS:HE2	1.92	0.41
43:S:39:ASP:HA	43:S:42:ASN:HD22	1.85	0.41
43:S:81:ILE:HG21	52:3:1202:U:N3	2.33	0.41
45:U:33:ILE:N	45:U:33:ILE:HD12	2.35	0.41
49:Y:14:GLU:HA	49:Y:17:ARG:HG3	2.03	0.41
51:a:200:LYS:HA	51:a:201:PRO:HD3	1.94	0.41
52:3:31:G:N2	52:3:47:C:H5''	2.36	0.41
52:3:714:G:H2'	52:3:715:A:C8	2.56	0.41
52:3:994:A:H61	52:3:1047:G:H1'	1.86	0.41
52:3:1125:U:H2'	52:3:1126:U:H2'	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1513:A:H2'	52:3:1514:G:H8	1.84	0.41
53:1:68:G:H2'	53:1:69:C:O4'	2.21	0.41
53:1:445:C:O2'	53:1:446:G:H5'	2.21	0.41
53:1:1028:A:H2'	53:1:1029:A:H8	1.86	0.41
53:1:1394:U:H5''	53:1:1604:C:OP1	2.20	0.41
53:1:1424:G:H2'	53:1:1425:G:O4'	2.21	0.41
53:1:1636:U:H2'	53:1:1637:A:H8	1.86	0.41
53:1:1662:U:H2'	53:1:1663:G:C8	2.55	0.41
53:1:1923:U:H2'	53:1:1924:C:C6	2.55	0.41
53:1:2055:C:H5'	53:1:2056:G:O5'	2.21	0.41
53:1:2345:G:N3	53:1:2381:A:H2'	2.36	0.41
53:1:2492:U:H2'	53:1:2493:U:C6	2.56	0.41
53:1:2498:C:O2'	53:1:2499:C:H5'	2.21	0.41
53:1:2609:U:H5'	53:1:2610:C:OP2	2.21	0.41
3:d:166:LYS:HE3	3:d:166:LYS:HB3	1.90	0.41
9:j:30:THR:HG21	53:1:1005:C:O2'	2.21	0.41
10:k:35:VAL:HG23	10:k:36:GLY:N	2.26	0.41
12:m:10:ARG:HG3	12:m:10:ARG:NH2	2.36	0.41
17:r:11:GLN:N	17:r:11:GLN:OE1	2.54	0.41
26:B:30:ASP:HB3	26:B:34:GLY:N	2.23	0.41
31:G:3:VAL:HG22	31:G:4:SER:H	1.86	0.41
41:Q:23:LEU:HD23	41:Q:26:CYS:SG	2.61	0.41
42:R:61:LYS:H	42:R:61:LYS:HG2	1.68	0.41
43:S:30:ILE:HG22	43:S:30:ILE:O	2.21	0.41
45:U:12:LYS:HE2	52:3:43:C:P	2.61	0.41
46:V:10:ARG:C	46:V:22:VAL:HG23	2.45	0.41
46:V:25:GLU:CD	46:V:25:GLU:H	2.28	0.41
52:3:5:U:H4'	52:3:6:G:C8	2.56	0.41
52:3:1138:G:N3	52:3:1138:G:H3'	2.36	0.41
52:3:1270:G:H2'	52:3:1271:A:C8	2.56	0.41
53:1:69:C:O2'	53:1:70:G:H5'	2.20	0.41
53:1:1680:U:C2'	53:1:1681:G:H5'	2.51	0.41
53:1:2741:A:H2'	53:1:2742:G:O4'	2.21	0.41
1:b:12:ARG:NH2	53:1:728:G:H4'	2.34	0.40
1:b:242:HIS:HA	1:b:243:PRO:HD3	1.93	0.40
6:g:45:GLU:HA	6:g:48:GLU:HG2	2.02	0.40
10:k:37:ASP:OD1	10:k:37:ASP:N	2.53	0.40
15:p:28:LYS:HD3	15:p:39:LEU:HD21	2.02	0.40
20:u:28:LEU:HB2	20:u:32:LYS:HB2	2.03	0.40
31:G:142:LYS:HE3	31:G:142:LYS:HB2	1.89	0.40
32:H:25:THR:HA	32:H:28:PHE:HB2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:45:GLU:HG3	32:H:46:LEU:HD12	2.03	0.40
39:O:10:LEU:HG	39:O:72:ARG:HB2	2.03	0.40
46:V:13:SER:HB2	46:V:21:VAL:HG21	2.03	0.40
48:X:32:THR:HG22	48:X:33:TRP:H	1.87	0.40
51:a:42:VAL:HB	51:a:175:ILE:HG13	2.03	0.40
51:a:47:ASN:HD22	51:a:47:ASN:HA	1.58	0.40
51:a:165:ASN:HD21	51:a:170:ILE:N	2.19	0.40
52:3:58:C:O2'	52:3:59:A:H5'	2.21	0.40
52:3:628:G:H2'	52:3:629:A:O4'	2.22	0.40
52:3:790:A:H5'	55:5:39:C:H5'	2.03	0.40
52:3:936:C:H2'	52:3:937:A:O4'	2.21	0.40
53:1:329:G:O4'	53:1:477:A:H1'	2.20	0.40
53:1:863:A:H2'	53:1:864:G:C8	2.56	0.40
53:1:1794:A:H2'	53:1:1795:C:C6	2.56	0.40
55:5:57:A:H2'	55:5:58:A:H5'	2.03	0.40
55:6:21:A:O2'	55:6:22:G:C8	2.73	0.40
2:c:37:VAL:HG22	2:c:48:ILE:HG22	2.03	0.40
2:c:91:THR:OG1	2:c:92:VAL:N	2.53	0.40
2:c:117:GLY:C	2:c:164:GLN:HG3	2.46	0.40
4:e:87:LYS:HD2	53:1:2313:C:C5'	2.51	0.40
9:j:7:LYS:HA	9:j:8:PRO:HD3	1.86	0.40
9:j:52:ASP:O	9:j:54:ILE:HG13	2.21	0.40
12:m:4:PRO:HG3	12:m:68:PHE:CE2	2.55	0.40
13:n:3:HIS:O	13:n:4:ARG:HB2	2.21	0.40
16:q:5:ARG:HG3	53:1:584:C:OP2	2.20	0.40
22:w:36:GLN:OE1	22:w:40:LYS:N	2.51	0.40
22:w:60:ASP:OD1	22:w:61:GLY:N	2.48	0.40
23:x:63:ILE:O	23:x:66:VAL:HG12	2.20	0.40
26:B:3:GLN:HA	53:1:2615:U:N3	2.36	0.40
30:F:36:ARG:O	30:F:37:GLN:O	2.38	0.40
32:H:61:LYS:HA	32:H:61:LYS:HD3	1.94	0.40
32:H:113:LYS:HE2	32:H:184:ASN:HB3	2.03	0.40
45:U:8:ARG:NH1	45:U:15:PRO:HB3	2.36	0.40
45:U:9:HIS:HE1	45:U:18:GLN:HG3	1.86	0.40
45:U:35:ARG:HH22	52:3:627:G:P	2.44	0.40
49:Y:32:LYS:HA	49:Y:35:TYR:HB2	2.03	0.40
52:3:1017:U:H2'	52:3:1018:G:C8	2.56	0.40
53:1:727:A:H2'	53:1:728:G:O4'	2.21	0.40
53:1:755:U:H2'	53:1:756:A:C8	2.56	0.40
53:1:1773:A:H2	53:1:1977:A:H61	1.68	0.40
53:1:2292:U:H2'	53:1:2293:G:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:245:THR:O	1:b:247:TRP:N	2.55	0.40
2:c:110:THR:HG23	2:c:171:THR:HG22	2.02	0.40
3:d:48:THR:O	3:d:52:VAL:HG23	2.21	0.40
4:e:39:VAL:O	53:1:2307:G:O6	2.39	0.40
5:f:37:ASN:HD22	5:f:39:ALA:HB3	1.86	0.40
5:f:83:THR:HA	5:f:132:LEU:O	2.20	0.40
5:f:173:ALA:C	5:f:174:LYS:HG3	2.45	0.40
7:h:88:HIS:N	7:h:89:PRO:HD2	2.37	0.40
8:i:52:LEU:HA	8:i:53:PRO:HD3	1.92	0.40
9:j:78:THR:HG23	9:j:80:HIS:HB2	2.04	0.40
10:k:9:ASN:O	10:k:83:ALA:HA	2.21	0.40
11:l:19:LEU:HD12	11:l:19:LEU:H	1.86	0.40
12:m:17:ASN:O	54:2:90:C:H5'	2.20	0.40
15:p:52:ARG:HD3	15:p:52:ARG:HA	1.79	0.40
19:t:69:ARG:C	19:t:69:ARG:HD2	2.46	0.40
27:C:43:ARG:NH2	53:1:643:A:H1'	2.36	0.40
28:D:18:PHE:HE2	53:1:117:G:H4'	1.86	0.40
31:G:60:ALA:HA	31:G:64:GLY:H	1.86	0.40
35:K:75:GLU:OE1	35:K:89:VAL:HG21	2.22	0.40
38:N:6:TYR:CE2	52:3:1147:C:H4'	2.57	0.40
41:Q:2:THR:HG23	41:Q:2:THR:O	2.22	0.40
41:Q:87:LYS:HZ2	52:3:525:C:H5''	1.86	0.40
42:R:76:ILE:HA	42:R:79:LEU:HD12	2.03	0.40
43:S:47:LEU:HD21	52:3:1317:C:H4'	2.03	0.40
43:S:52:ARG:HG3	43:S:58:ARG:CZ	2.52	0.40
52:3:76:G:H2'	52:3:77:A:O4'	2.21	0.40
52:3:736:C:H2'	52:3:737:C:C6	2.56	0.40
53:1:248:G:H3'	53:1:249:C:C5'	2.51	0.40
53:1:312:G:H2'	53:1:313:G:H8	1.87	0.40
53:1:870:U:O2'	53:1:871:U:H5'	2.20	0.40
53:1:1045:C:H5'	53:1:1046:A:C5'	2.51	0.40
53:1:1554:U:H3'	53:1:1555:G:H5'	2.02	0.40
53:1:2197:U:O2'	53:1:2198:A:H5''	2.21	0.40
53:1:2642:G:H2'	53:1:2643:G:H8	1.86	0.40
1:b:207:ALA:HB1	53:1:1790:C:H4'	2.04	0.40
4:e:1:ALA:H1	4:e:97:GLU:HA	1.86	0.40
7:h:16:SER:O	7:h:20:LYS:HG2	2.22	0.40
10:k:88:ASN:O	10:k:90:ASN:N	2.54	0.40
13:n:44:LEU:HD12	13:n:44:LEU:HA	1.92	0.40
13:n:96:ARG:HE	13:n:116:VAL:HG12	1.86	0.40
13:n:99:LYS:NZ	53:1:2816:G:O3'	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:q:24:TYR:CE1	53:1:17:G:H4'	2.56	0.40
19:t:45:ALA:O	19:t:49:LYS:HG2	2.22	0.40
28:D:24:THR:OG1	28:D:25:LYS:N	2.54	0.40
32:H:122:GLN:O	32:H:127:VAL:HG22	2.21	0.40
33:I:32:LYS:HZ2	52:3:425:G:H5''	1.87	0.40
34:J:92:ARG:O	34:J:93:VAL:C	2.64	0.40
34:J:93:VAL:O	34:J:93:VAL:HG13	2.20	0.40
41:Q:5:GLN:HA	41:Q:8:ARG:HG2	2.04	0.40
41:Q:24:GLU:O	41:Q:24:GLU:HG3	2.20	0.40
43:S:27:LYS:C	43:S:31:SER:HB2	2.46	0.40
47:W:15:GLU:HG2	52:3:845:A:OP1	2.21	0.40
49:Y:49:ALA:O	49:Y:52:GLU:HB3	2.21	0.40
52:3:525:C:H2'	52:3:526:C:C6	2.57	0.40
52:3:1486:G:H2'	52:3:1487:G:O4'	2.21	0.40
53:1:677:A:O2'	53:1:2071:A:H5'	2.22	0.40
4:e:33:ILE:HD11	4:e:153:ILE:HD11	2.04	0.40
4:e:141:ASP:HB3	42:R:2:ARG:NH2	2.37	0.40
31:G:213:LEU:HA	31:G:216:VAL:CG2	2.50	0.40
33:I:182:LYS:HG3	33:I:183:ARG:HG2	2.04	0.40
33:I:184:LYS:HA	33:I:185:PRO:HD3	1.84	0.40
34:J:88:HIS:C	34:J:89:THR:HG1	2.29	0.40
36:L:39:GLU:HB3	36:L:43:TYR:CE2	2.57	0.40
38:N:129:ARG:NH2	55:5:33:U:H3'	2.35	0.40
40:P:19:VAL:HG22	40:P:82:GLU:HB3	2.04	0.40
41:Q:30:ARG:HB3	52:3:363:A:OP2	2.21	0.40
52:3:418:C:H2'	52:3:419:C:C6	2.57	0.40
52:3:539:A:H2'	52:3:540:G:C8	2.57	0.40
52:3:797:C:H2'	52:3:798:U:C6	2.56	0.40
53:1:1181:U:H2'	53:1:1182:G:C8	2.56	0.40
53:1:1774:C:H4'	53:1:1979:U:O2	2.21	0.40
53:1:1851:U:H2'	53:1:1852:U:O4'	2.22	0.40
53:1:2040:G:H2'	53:1:2041:U:O4'	2.21	0.40
53:1:2216:G:H2'	53:1:2217:G:C8	2.56	0.40
53:1:2221:G:O2'	53:1:2222:C:H5'	2.21	0.40
53:1:2457:U:H2'	53:1:2458:G:O4'	2.21	0.40
53:1:2819:G:H2'	53:1:2821:A:N7	2.37	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	
1	b	269/271 (99%)	224 (83%)	36 (13%)	9 (3%)	3	21
2	c	207/209 (99%)	174 (84%)	33 (16%)	0	100	100
3	d	199/201 (99%)	171 (86%)	26 (13%)	2 (1%)	12	47
4	e	175/177 (99%)	150 (86%)	22 (13%)	3 (2%)	7	35
5	f	174/176 (99%)	159 (91%)	13 (8%)	2 (1%)	11	45
6	g	147/149 (99%)	124 (84%)	20 (14%)	3 (2%)	6	32
7	h	129/131 (98%)	96 (74%)	28 (22%)	5 (4%)	2	19
8	i	139/141 (99%)	125 (90%)	11 (8%)	3 (2%)	5	29
9	j	140/142 (99%)	121 (86%)	15 (11%)	4 (3%)	3	24
10	k	120/122 (98%)	99 (82%)	17 (14%)	4 (3%)	3	21
11	l	141/143 (99%)	117 (83%)	23 (16%)	1 (1%)	18	54
12	m	134/136 (98%)	114 (85%)	17 (13%)	3 (2%)	5	29
13	n	118/120 (98%)	103 (87%)	14 (12%)	1 (1%)	16	52
14	o	114/116 (98%)	102 (90%)	8 (7%)	4 (4%)	3	21
15	p	112/114 (98%)	89 (80%)	22 (20%)	1 (1%)	14	49
16	q	115/117 (98%)	103 (90%)	10 (9%)	2 (2%)	7	35
17	r	101/103 (98%)	80 (79%)	20 (20%)	1 (1%)	12	47
18	s	108/110 (98%)	91 (84%)	15 (14%)	2 (2%)	6	32
19	t	91/93 (98%)	75 (82%)	16 (18%)	0	100	100
20	u	100/102 (98%)	82 (82%)	17 (17%)	1 (1%)	12	47
21	v	92/94 (98%)	77 (84%)	13 (14%)	2 (2%)	5	29
22	w	73/75 (97%)	61 (84%)	12 (16%)	0	100	100
23	x	75/77 (97%)	67 (89%)	6 (8%)	2 (3%)	4	26
24	y	61/63 (97%)	55 (90%)	5 (8%)	1 (2%)	7	37
25	z	56/58 (97%)	54 (96%)	1 (2%)	1 (2%)	6	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	B	54/56 (96%)	47 (87%)	7 (13%)	0	100	100
27	C	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
28	D	44/46 (96%)	34 (77%)	10 (23%)	0	100	100
29	E	62/64 (97%)	50 (81%)	7 (11%)	5 (8%)	1	9
30	F	36/38 (95%)	26 (72%)	9 (25%)	1 (3%)	4	25
31	G	223/225 (99%)	207 (93%)	15 (7%)	1 (0%)	30	66
32	H	204/206 (99%)	186 (91%)	17 (8%)	1 (0%)	24	62
33	I	203/205 (99%)	174 (86%)	27 (13%)	2 (1%)	12	47
34	J	155/157 (99%)	126 (81%)	24 (16%)	5 (3%)	3	22
35	K	98/100 (98%)	77 (79%)	16 (16%)	5 (5%)	1	16
36	L	149/151 (99%)	123 (83%)	24 (16%)	2 (1%)	9	41
37	M	127/129 (98%)	113 (89%)	11 (9%)	3 (2%)	4	28
38	N	125/127 (98%)	101 (81%)	17 (14%)	7 (6%)	1	15
39	O	96/98 (98%)	70 (73%)	18 (19%)	8 (8%)	0	9
40	P	114/116 (98%)	91 (80%)	20 (18%)	3 (3%)	4	26
41	Q	121/123 (98%)	91 (75%)	23 (19%)	7 (6%)	1	14
42	R	112/114 (98%)	96 (86%)	12 (11%)	4 (4%)	2	21
43	S	98/100 (98%)	81 (83%)	16 (16%)	1 (1%)	12	47
44	T	86/88 (98%)	74 (86%)	10 (12%)	2 (2%)	5	29
45	U	80/82 (98%)	64 (80%)	14 (18%)	2 (2%)	4	27
46	V	78/80 (98%)	63 (81%)	13 (17%)	2 (3%)	4	26
47	W	63/65 (97%)	55 (87%)	6 (10%)	2 (3%)	3	22
48	X	77/79 (98%)	64 (83%)	12 (16%)	1 (1%)	9	41
49	Y	83/85 (98%)	75 (90%)	8 (10%)	0	100	100
50	Z	63/65 (97%)	42 (67%)	17 (27%)	4 (6%)	1	13
51	a	130/223 (58%)	122 (94%)	8 (6%)	0	100	100
All	All	5919/6112 (97%)	5009 (85%)	785 (13%)	125 (2%)	8	30

All (125) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	107	LYS
1	b	131	MET

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Mol	Chain	Res	Type
3	d	83	VAL
6	g	9	VAL
7	h	81	LEU
7	h	108	VAL
8	i	89	SER
9	j	81	ILE
10	k	35	VAL
10	k	89	ASN
10	k	110	GLU
12	m	58	LYS
17	r	54	VAL
23	x	23	ALA
24	y	24	GLU
25	z	11	SER
30	F	37	GLN
34	J	93	VAL
34	J	122	VAL
35	K	95	ALA
36	L	56	SER
39	O	35	GLN
40	P	125	LYS
41	Q	101	LEU
42	R	65	GLU
43	S	3	GLN
44	T	46	LYS
1	b	205	GLY
5	f	174	LYS
11	l	85	VAL
16	q	32	ARG
29	E	3	ILE
29	E	31	ILE
31	G	22	TRP
34	J	11	GLN
34	J	23	THR
35	K	39	LEU
35	K	52	ASN
37	M	47	ASP
38	N	8	THR
38	N	90	ASP
38	N	91	GLU
38	N	119	LYS
39	O	58	ASN

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Mol	Chain	Res	Type
39	O	75	ASP
41	Q	35	ARG
41	Q	57	THR
41	Q	108	ASP
42	R	7	ASN
44	T	48	ASP
46	V	17	GLU
50	Z	34	ARG
3	d	89	PRO
7	h	118	ILE
12	m	27	SER
15	p	75	THR
20	u	6	ARG
21	v	39	ALA
21	v	81	PRO
29	E	17	GLY
29	E	19	GLY
29	E	62	PRO
33	I	152	SER
38	N	24	ASN
39	O	33	GLY
40	P	108	ASN
41	Q	33	CYS
42	R	4	ALA
46	V	49	ASN
47	W	13	THR
48	X	53	GLY
50	Z	25	ALA
1	b	240	GLY
5	f	155	PRO
6	g	11	ASN
7	h	2	ALA
7	h	125	ARG
9	j	25	LEU
9	j	127	GLY
12	m	6	ARG
13	n	117	ASP
14	o	34	HIS
14	o	99	TYR
16	q	21	LYS
23	x	13	THR
34	J	89	THR

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Mol	Chain	Res	Type
37	M	28	SER
38	N	102	PHE
39	O	34	ALA
41	Q	24	GLU
45	U	79	ASN
1	b	246	PRO
4	e	102	LEU
4	e	103	ILE
8	i	6	ALA
8	i	46	ASP
14	o	9	ARG
32	H	79	LYS
35	K	86	ARG
35	K	92	THR
36	L	95	ARG
38	N	109	GLN
39	O	43	PRO
42	R	113	LYS
1	b	147	PRO
1	b	226	PRO
4	e	77	LYS
6	g	89	LYS
10	k	93	GLN
33	I	6	PRO
41	Q	41	PRO
50	Z	8	ASN
50	Z	9	GLU
18	s	80	PRO
9	j	110	PRO
14	o	114	GLY
39	O	42	LEU
40	P	38	GLY
1	b	136	VAL
18	s	74	ILE
45	U	30	GLY
47	W	20	ILE
1	b	48	ILE
37	M	50	VAL
39	O	41	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	
1	b	216/216 (100%)	214 (99%)	2 (1%)	70	75
2	c	164/164 (100%)	163 (99%)	1 (1%)	78	80
3	d	165/165 (100%)	163 (99%)	2 (1%)	63	73
4	e	148/148 (100%)	147 (99%)	1 (1%)	76	78
5	f	137/137 (100%)	137 (100%)	0	100	100
6	g	114/114 (100%)	113 (99%)	1 (1%)	70	75
7	h	100/100 (100%)	96 (96%)	4 (4%)	28	49
8	i	109/109 (100%)	109 (100%)	0	100	100
9	j	116/116 (100%)	114 (98%)	2 (2%)	53	67
10	k	103/103 (100%)	101 (98%)	2 (2%)	50	66
11	l	102/102 (100%)	99 (97%)	3 (3%)	37	58
12	m	109/109 (100%)	107 (98%)	2 (2%)	51	66
13	n	100/100 (100%)	99 (99%)	1 (1%)	68	75
14	o	86/86 (100%)	85 (99%)	1 (1%)	63	73
15	p	99/99 (100%)	99 (100%)	0	100	100
16	q	89/89 (100%)	88 (99%)	1 (1%)	65	73
17	r	84/84 (100%)	82 (98%)	2 (2%)	43	63
18	s	93/93 (100%)	92 (99%)	1 (1%)	65	73
19	t	80/80 (100%)	79 (99%)	1 (1%)	61	71
20	u	83/83 (100%)	83 (100%)	0	100	100
21	v	78/78 (100%)	77 (99%)	1 (1%)	61	71
22	w	57/57 (100%)	56 (98%)	1 (2%)	51	66
23	x	67/67 (100%)	67 (100%)	0	100	100
24	y	55/55 (100%)	54 (98%)	1 (2%)	51	66
25	z	48/48 (100%)	48 (100%)	0	100	100
26	B	47/47 (100%)	47 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	C	45/45 (100%)	45 (100%)	0	100	100
28	D	38/38 (100%)	38 (100%)	0	100	100
29	E	51/51 (100%)	50 (98%)	1 (2%)	48	65
30	F	34/34 (100%)	34 (100%)	0	100	100
31	G	186/186 (100%)	184 (99%)	2 (1%)	65	73
32	H	170/170 (100%)	169 (99%)	1 (1%)	78	80
33	I	172/172 (100%)	169 (98%)	3 (2%)	53	67
34	J	119/119 (100%)	118 (99%)	1 (1%)	73	77
35	K	87/87 (100%)	86 (99%)	1 (1%)	65	73
36	L	124/124 (100%)	124 (100%)	0	100	100
37	M	104/104 (100%)	102 (98%)	2 (2%)	50	66
38	N	105/105 (100%)	101 (96%)	4 (4%)	29	51
39	O	86/86 (100%)	84 (98%)	2 (2%)	44	64
40	P	89/89 (100%)	89 (100%)	0	100	100
41	Q	103/103 (100%)	102 (99%)	1 (1%)	68	75
42	R	92/92 (100%)	91 (99%)	1 (1%)	65	73
43	S	83/83 (100%)	81 (98%)	2 (2%)	43	63
44	T	76/76 (100%)	75 (99%)	1 (1%)	61	71
45	U	65/65 (100%)	65 (100%)	0	100	100
46	V	74/74 (100%)	73 (99%)	1 (1%)	59	70
47	W	56/56 (100%)	56 (100%)	0	100	100
48	X	70/70 (100%)	69 (99%)	1 (1%)	59	70
49	Y	65/65 (100%)	65 (100%)	0	100	100
50	Z	55/55 (100%)	55 (100%)	0	100	100
51	a	110/174 (63%)	108 (98%)	2 (2%)	51	66
All	All	4908/4972 (99%)	4852 (99%)	56 (1%)	63	73

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	b	116	GLN
1	b	263	ASP
2	c	32	ASN

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Mol	Chain	Res	Type
3	d	7	ASP
3	d	62	GLN
4	e	141	ASP
6	g	12	LEU
7	h	1	MET
7	h	118	ILE
7	h	119	PRO
7	h	129	LEU
9	j	14	ASP
9	j	47	HIS
10	k	58	LEU
10	k	92	GLU
11	l	23	ILE
11	l	93	ASN
11	l	94	THR
12	m	11	LYS
12	m	57	VAL
13	n	38	LEU
14	o	115	LEU
16	q	17	LEU
17	r	48	LYS
17	r	54	VAL
18	s	75	PHE
19	t	32	LEU
21	v	85	LYS
22	w	17	LEU
24	y	43	LEU
29	E	61	LEU
31	G	48	MET
31	G	139	GLU
32	H	156	LEU
33	I	70	GLN
33	I	168	THR
33	I	180	THR
34	J	72	ASN
35	K	84	VAL
37	M	60	LEU
37	M	98	LEU
38	N	42	THR
38	N	62	LEU
38	N	90	ASP
38	N	110	VAL

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Mol	Chain	Res	Type
39	O	17	LEU
39	O	63	ASP
41	Q	24	GLU
42	R	64	VAL
43	S	50	LEU
43	S	59	GLN
44	T	48	ASP
46	V	17	GLU
48	X	28	LYS
51	a	4	LEU
51	a	47	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (128) such sidechains are listed below:

Mol	Chain	Res	Type
1	b	14	HIS
1	b	20	ASN
1	b	43	ASN
1	b	44	ASN
1	b	45	ASN
1	b	52	HIS
1	b	85	ASN
1	b	116	GLN
1	b	142	ASN
1	b	238	ASN
1	b	259	ASN
2	c	126	ASN
2	c	140	HIS
2	c	148	GLN
2	c	149	ASN
2	c	185	ASN
3	d	30	GLN
3	d	46	GLN
3	d	97	ASN
3	d	136	GLN
4	e	51	ASN
4	e	80	GLN
4	e	126	ASN
5	f	19	ASN
5	f	21	GLN
5	f	29	ASN
5	f	47	ASN

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Mol	Chain	Res	Type
5	f	63	GLN
5	f	127	GLN
5	f	138	GLN
6	g	33	GLN
6	g	43	ASN
6	g	66	ASN
6	g	133	GLN
6	g	145	ASN
7	h	57	ASN
7	h	103	ASN
8	i	30	GLN
8	i	106	GLN
9	j	47	HIS
9	j	58	ASN
9	j	86	GLN
10	k	5	GLN
10	k	13	ASN
10	k	88	ASN
12	m	22	GLN
13	n	11	ASN
13	n	73	ASN
13	n	107	ASN
14	o	104	GLN
15	p	2	ASN
15	p	11	GLN
15	p	40	GLN
16	q	36	GLN
16	q	71	ASN
17	r	6	GLN
17	r	18	GLN
18	s	7	HIS
18	s	31	GLN
19	t	59	ASN
19	t	70	HIS
19	t	91	GLN
20	u	52	ASN
20	u	53	GLN
20	u	73	ASN
21	v	5	ASN
21	v	49	ASN
21	v	87	GLN
22	w	42	HIS

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Mol	Chain	Res	Type
22	w	46	ASN
22	w	53	HIS
24	y	27	ASN
24	y	38	GLN
26	B	5	ASN
27	C	25	ASN
28	D	6	GLN
28	D	26	ASN
28	D	29	GLN
30	F	35	GLN
30	F	37	GLN
31	G	14	HIS
31	G	18	GLN
31	G	38	HIS
31	G	50	ASN
32	H	31	ASN
32	H	68	HIS
32	H	184	ASN
33	I	40	HIS
33	I	73	ASN
33	I	88	ASN
33	I	135	GLN
33	I	151	GLN
33	I	163	GLN
34	J	81	GLN
34	J	121	ASN
35	K	55	HIS
36	L	85	GLN
36	L	121	ASN
37	M	66	GLN
37	M	117	GLN
38	N	4	GLN
38	N	109	GLN
38	N	125	GLN
40	P	28	ASN
40	P	63	GLN
40	P	100	ASN
41	Q	5	GLN
41	Q	19	ASN
41	Q	45	ASN
42	R	7	ASN
42	R	13	HIS

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Mol	Chain	Res	Type
43	S	42	ASN
43	S	59	GLN
43	S	70	HIS
44	T	19	ASN
44	T	39	GLN
44	T	50	HIS
45	U	9	HIS
45	U	26	ASN
45	U	29	ASN
45	U	59	HIS
47	W	51	GLN
48	X	51	HIS
49	Y	12	GLN
49	Y	69	ASN
51	a	47	ASN
51	a	67	HIS
51	a	165	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	139 (9%)	2 (0%)
53	1	2902/2903 (99%)	323 (11%)	9 (0%)
54	2	119/120 (99%)	12 (10%)	1 (0%)
55	5	76/77 (98%)	10 (13%)	0
55	6	76/77 (98%)	8 (10%)	0
56	4	17/18 (94%)	3 (17%)	0
57	7	72/76 (94%)	13 (18%)	0
All	All	4800/4810 (99%)	508 (10%)	12 (0%)

All (508) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	6	G
52	3	7	A
52	3	9	G
52	3	31	G
52	3	32	A
52	3	39	G
52	3	48	C
52	3	51	A

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Mol	Chain	Res	Type
52	3	71	A
52	3	85	U
52	3	87	C
52	3	130	A
52	3	144	G
52	3	183	C
52	3	184	G
52	3	197	A
52	3	209	U
52	3	210	C
52	3	226	G
52	3	247	G
52	3	251	G
52	3	266	G
52	3	267	C
52	3	279	A
52	3	281	G
52	3	289	G
52	3	328	C
52	3	345	C
52	3	346	G
52	3	352	C
52	3	367	U
52	3	372	C
52	3	411	A
52	3	412	A
52	3	413	G
52	3	429	U
52	3	467	U
52	3	479	U
52	3	485	U
52	3	486	U
52	3	497	G
52	3	518	C
52	3	532	A
52	3	547	A
52	3	561	U
52	3	564	C
52	3	572	A
52	3	573	A
52	3	575	G
52	3	576	C

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Mol	Chain	Res	Type
52	3	607	A
52	3	633	G
52	3	653	U
52	3	665	A
52	3	687	A
52	3	688	G
52	3	703	G
52	3	724	G
52	3	755	G
52	3	777	A
52	3	794	A
52	3	815	A
52	3	817	C
52	3	818	G
52	3	819	A
52	3	821	G
52	3	843	U
52	3	844	G
52	3	846	G
52	3	871	U
52	3	873	A
52	3	890	G
52	3	902	G
52	3	926	G
52	3	934	C
52	3	935	A
52	3	960	U
52	3	961	U
52	3	966	G
52	3	969	A
52	3	975	A
52	3	976	G
52	3	977	A
52	3	991	U
52	3	992	U
52	3	993	G
52	3	1004	A
52	3	1028	C
52	3	1031	C
52	3	1033	G
52	3	1034	G
52	3	1053	G

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Mol	Chain	Res	Type
52	3	1094	G
52	3	1101	A
52	3	1136	C
52	3	1137	C
52	3	1138	G
52	3	1139	G
52	3	1159	U
52	3	1168	U
52	3	1182	G
52	3	1184	G
52	3	1191	A
52	3	1196	A
52	3	1198	G
52	3	1201	A
52	3	1202	U
52	3	1213	A
52	3	1225	A
52	3	1238	A
52	3	1240	U
52	3	1241	G
52	3	1258	G
52	3	1260	G
52	3	1275	A
52	3	1278	G
52	3	1280	A
52	3	1282	C
52	3	1286	U
52	3	1287	A
52	3	1300	G
52	3	1317	C
52	3	1346	A
52	3	1347	G
52	3	1363	A
52	3	1364	U
52	3	1394	A
52	3	1395	C
52	3	1446	A
52	3	1448	C
52	3	1451	U
52	3	1452	C
52	3	1492	A
52	3	1503	A

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Mol	Chain	Res	Type
52	3	1506	U
52	3	1517	G
52	3	1529	G
52	3	1530	G
52	3	1540	U
53	1	10	A
53	1	12	U
53	1	34	U
53	1	35	G
53	1	49	A
53	1	50	U
53	1	51	G
53	1	71	A
53	1	74	A
53	1	75	G
53	1	102	U
53	1	119	A
53	1	120	U
53	1	138	U
53	1	139	U
53	1	140	C
53	1	141	G
53	1	142	A
53	1	162	U
53	1	163	C
53	1	181	A
53	1	196	A
53	1	216	A
53	1	219	A
53	1	221	A
53	1	222	A
53	1	229	C
53	1	248	G
53	1	249	C
53	1	255	A
53	1	266	G
53	1	276	U
53	1	278	A
53	1	281	C
53	1	294	A
53	1	301	G
53	1	311	A

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Mol	Chain	Res	Type
53	1	323	C
53	1	324	A
53	1	329	G
53	1	330	A
53	1	371	A
53	1	372	G
53	1	386	G
53	1	387	U
53	1	404	A
53	1	406	G
53	1	411	G
53	1	424	G
53	1	451	U
53	1	455	C
53	1	457	A
53	1	458	G
53	1	481	G
53	1	491	G
53	1	504	A
53	1	505	A
53	1	531	C
53	1	532	A
53	1	543	G
53	1	545	U
53	1	547	A
53	1	563	A
53	1	573	U
53	1	574	A
53	1	588	U
53	1	603	A
53	1	614	A
53	1	616	A
53	1	627	A
53	1	628	G
53	1	637	A
53	1	646	U
53	1	654	A
53	1	669	G
53	1	686	U
53	1	687	C
53	1	695	G
53	1	730	A

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Mol	Chain	Res	Type
53	1	747	C
53	1	752	A
53	1	764	A
53	1	776	G
53	1	782	A
53	1	784	G
53	1	785	G
53	1	805	G
53	1	812	C
53	1	819	A
53	1	827	U
53	1	828	U
53	1	830	G
53	1	845	A
53	1	846	U
53	1	847	U
53	1	860	U
53	1	878	A
53	1	886	A
53	1	887	U
53	1	888	C
53	1	895	U
53	1	896	A
53	1	910	A
53	1	915	C
53	1	932	U
53	1	941	A
53	1	946	C
53	1	961	C
53	1	974	G
53	1	975	A
53	1	983	A
53	1	995	C
53	1	996	A
53	1	1012	U
53	1	1013	C
53	1	1021	A
53	1	1022	G
53	1	1026	G
53	1	1033	U
53	1	1045	C
53	1	1046	A

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Mol	Chain	Res	Type
53	1	1047	G
53	1	1054	A
53	1	1060	U
53	1	1062	G
53	1	1066	U
53	1	1070	A
53	1	1071	G
53	1	1079	C
53	1	1084	A
53	1	1088	A
53	1	1104	C
53	1	1106	G
53	1	1111	A
53	1	1131	G
53	1	1132	U
53	1	1135	C
53	1	1143	A
53	1	1157	G
53	1	1175	A
53	1	1177	G
53	1	1178	C
53	1	1180	U
53	1	1212	G
53	1	1251	C
53	1	1253	A
53	1	1256	G
53	1	1271	G
53	1	1272	A
53	1	1275	A
53	1	1289	C
53	1	1300	G
53	1	1301	A
53	1	1329	U
53	1	1330	C
53	1	1332	G
53	1	1345	C
53	1	1365	A
53	1	1379	U
53	1	1383	A
53	1	1398	C
53	1	1416	G
53	1	1419	A

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Mol	Chain	Res	Type
53	1	1420	A
53	1	1454	C
53	1	1461	C
53	1	1482	G
53	1	1490	A
53	1	1491	G
53	1	1493	C
53	1	1498	C
53	1	1515	A
53	1	1524	G
53	1	1535	A
53	1	1536	C
53	1	1537	G
53	1	1555	G
53	1	1560	G
53	1	1569	A
53	1	1581	G
53	1	1584	U
53	1	1608	A
53	1	1611	C
53	1	1616	A
53	1	1647	U
53	1	1648	U
53	1	1674	G
53	1	1699	G
53	1	1715	G
53	1	1729	U
53	1	1730	C
53	1	1738	G
53	1	1758	U
53	1	1764	C
53	1	1773	A
53	1	1780	A
53	1	1800	C
53	1	1801	A
53	1	1808	A
53	1	1816	C
53	1	1829	A
53	1	1871	A
53	1	1901	A
53	1	1906	G
53	1	1907	G

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Mol	Chain	Res	Type
53	1	1913	A
53	1	1914	C
53	1	1929	G
53	1	1930	G
53	1	1937	A
53	1	1938	A
53	1	1944	U
53	1	1955	U
53	1	1963	U
53	1	1967	C
53	1	1970	A
53	1	1972	G
53	1	1991	U
53	1	1993	U
53	1	1997	C
53	1	2022	U
53	1	2023	C
53	1	2030	A
53	1	2031	A
53	1	2034	U
53	1	2036	C
53	1	2043	C
53	1	2049	G
53	1	2055	C
53	1	2056	G
53	1	2060	A
53	1	2061	G
53	1	2062	A
53	1	2069	G
53	1	2072	C
53	1	2093	G
53	1	2096	C
53	1	2110	G
53	1	2111	U
53	1	2112	G
53	1	2113	U
53	1	2118	U
53	1	2119	A
53	1	2132	U
53	1	2133	G
53	1	2145	C
53	1	2147	A

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Mol	Chain	Res	Type
53	1	2162	G
53	1	2164	C
53	1	2172	U
53	1	2173	A
53	1	2198	A
53	1	2203	U
53	1	2204	G
53	1	2225	A
53	1	2239	G
53	1	2278	A
53	1	2283	C
53	1	2287	A
53	1	2297	A
53	1	2305	U
53	1	2309	A
53	1	2325	G
53	1	2327	A
53	1	2334	U
53	1	2350	C
53	1	2383	G
53	1	2385	C
53	1	2392	A
53	1	2402	U
53	1	2407	A
53	1	2423	U
53	1	2424	C
53	1	2429	G
53	1	2430	A
53	1	2434	A
53	1	2435	A
53	1	2441	U
53	1	2448	A
53	1	2476	A
53	1	2498	C
53	1	2503	A
53	1	2504	U
53	1	2505	G
53	1	2518	A
53	1	2547	A
53	1	2554	U
53	1	2566	A
53	1	2567	G

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Mol	Chain	Res	Type
53	1	2572	A
53	1	2602	A
53	1	2609	U
53	1	2613	U
53	1	2629	U
53	1	2646	C
53	1	2655	G
53	1	2682	A
53	1	2689	U
53	1	2690	U
53	1	2714	G
53	1	2716	C
53	1	2744	G
53	1	2748	A
53	1	2751	G
53	1	2752	C
53	1	2757	A
53	1	2764	A
53	1	2765	A
53	1	2778	A
53	1	2779	U
53	1	2791	G
53	1	2794	C
53	1	2797	U
53	1	2800	A
53	1	2809	A
53	1	2820	A
53	1	2821	A
53	1	2833	U
53	1	2867	G
53	1	2868	A
53	1	2872	A
53	1	2880	C
53	1	2884	U
54	2	4	C
54	2	12	C
54	2	13	G
54	2	24	G
54	2	35	C
54	2	42	C
54	2	44	G
54	2	67	G

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Mol	Chain	Res	Type
54	2	89	U
54	2	90	C
54	2	108	A
54	2	109	A
55	5	8	U
55	5	9	G
55	5	14	A
55	5	19	G
55	5	20	U
55	5	47	U
55	5	48	C
55	5	56	C
55	5	57	A
55	5	61	C
55	6	6	G
55	6	16	C
55	6	18	G
55	6	19	G
55	6	20	U
55	6	47	U
55	6	48	C
55	6	61	C
56	4	12	A
56	4	13	A
56	4	19	U
57	7	8	U
57	7	9	A
57	7	13	C
57	7	16	U
57	7	17	C
57	7	21	A
57	7	46	G
57	7	47	U
57	7	48	C
57	7	49	C
57	7	59	U
57	7	61	C
57	7	66	U

All (12) RNA pucker outliers are listed below:

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Mol	Chain	Res	Type
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Mol	Chain	Res	Type
52	3	1190	G
52	3	1201	A
53	1	490	C
53	1	859	G
53	1	895	U
53	1	1020	A
53	1	1130	U
53	1	2286	G
53	1	2296	U
53	1	2326	C
53	1	2391	G
54	2	88	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
58	FME	5	101	55	8,9,10	0.50	0	8,9,11	1.05	1 (12%)

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	FME	5	101	55	-	0/7/9/11	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
58	5	101	FME	O-C-CA	-2.00	119.62	124.77

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	5	101	FME	1	0

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.

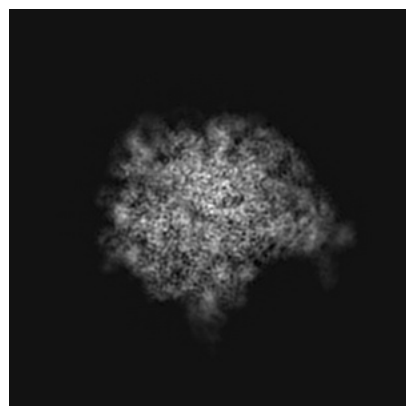
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21631. These allow visual inspection of the internal detail of the map and identification of artifacts.

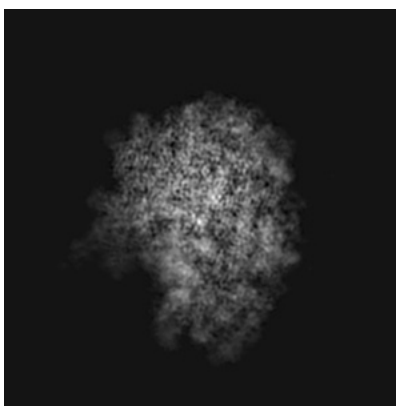
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

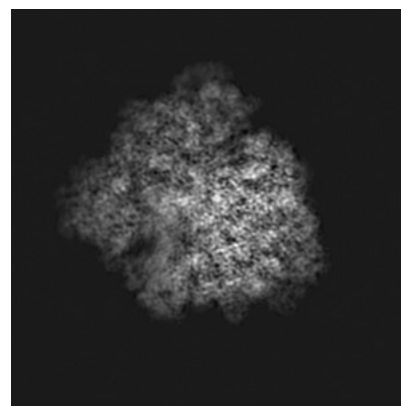
6.1.1 Primary map



X

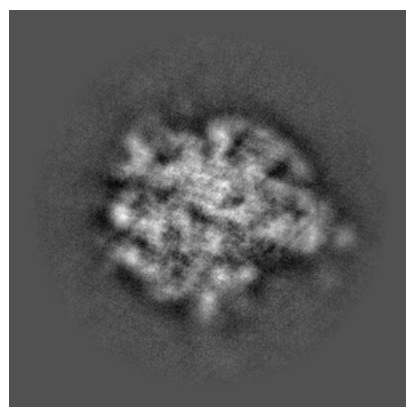


Y

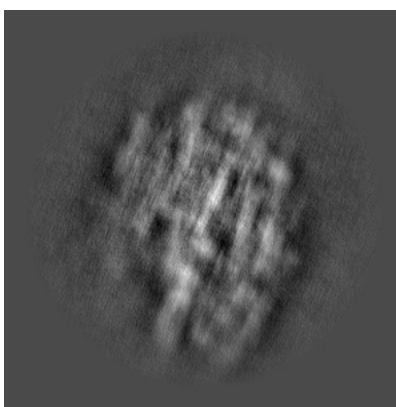


Z

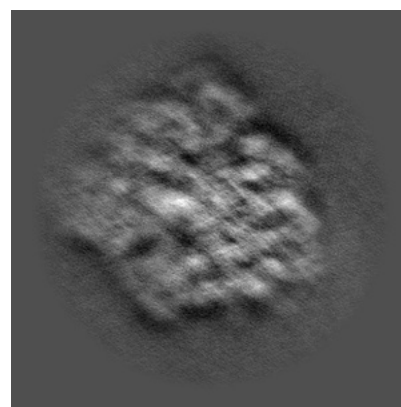
6.1.2 Raw map



X



Y

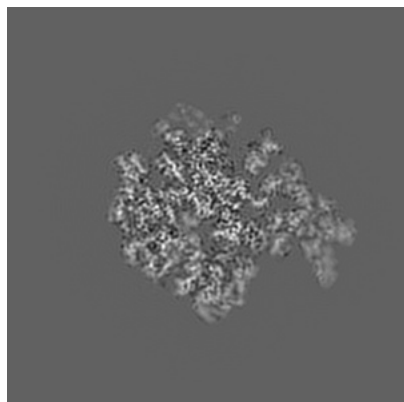


Z

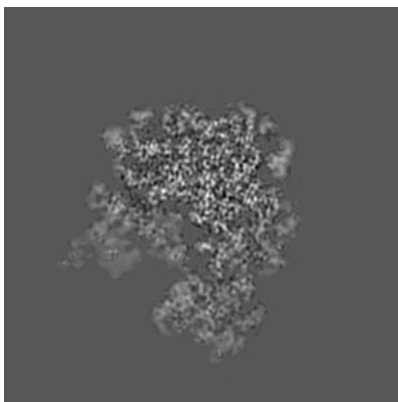
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

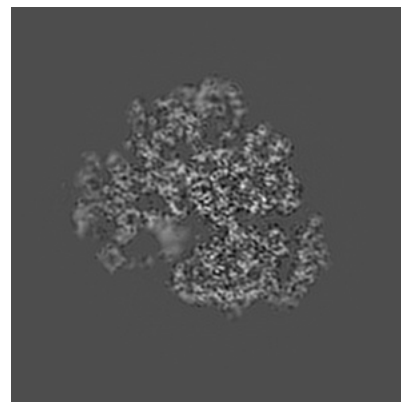
6.2.1 Primary map



X Index: 144

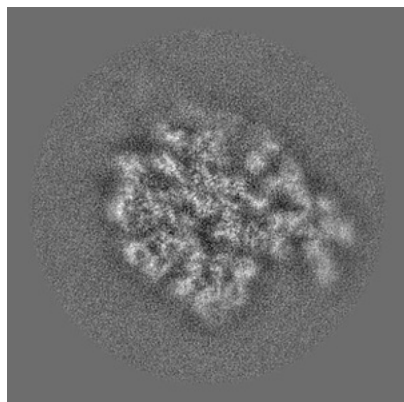


Y Index: 144

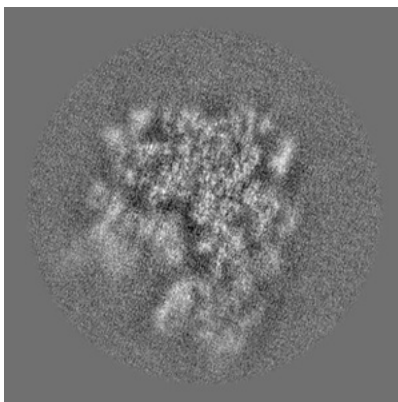


Z Index: 144

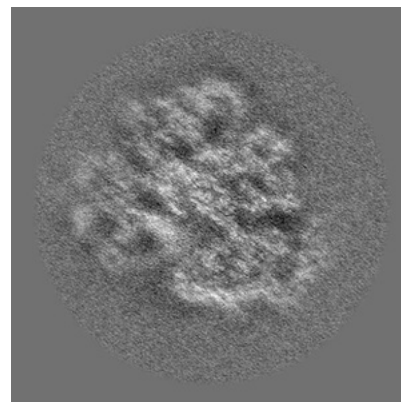
6.2.2 Raw map



X Index: 144



Y Index: 144

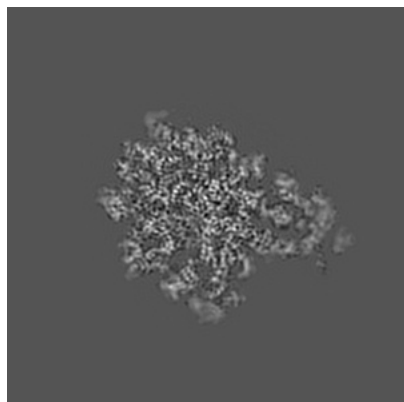


Z Index: 144

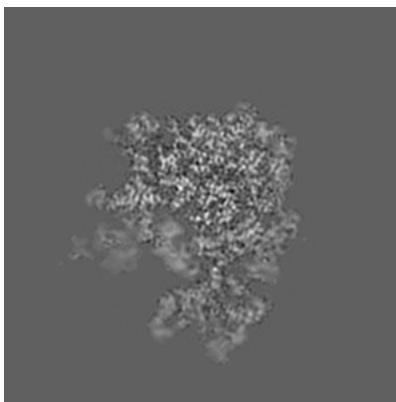
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

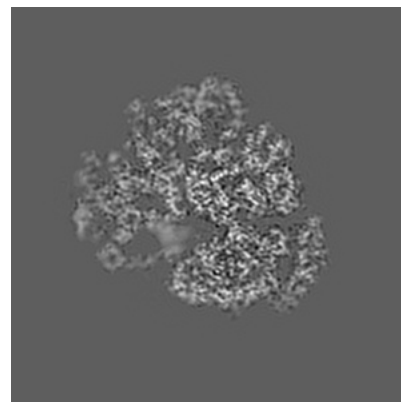
6.3.1 Primary map



X Index: 153

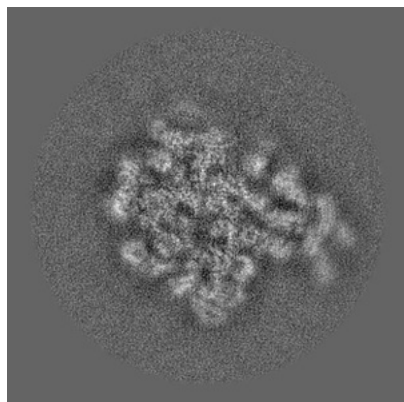


Y Index: 150

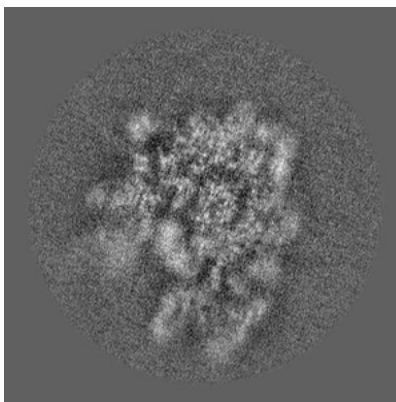


Z Index: 143

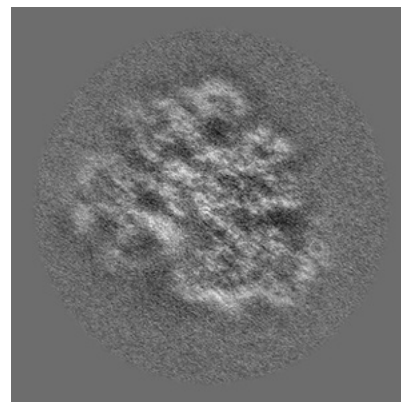
6.3.2 Raw map



X Index: 148



Y Index: 150

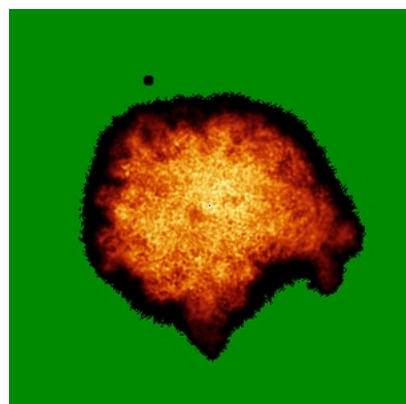


Z Index: 145

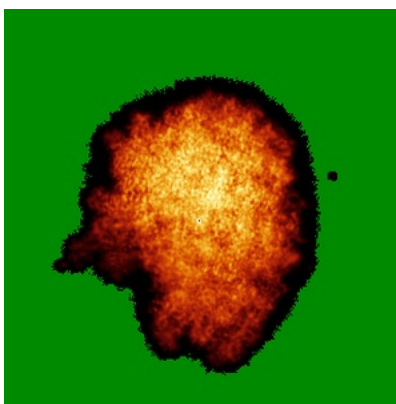
The images above show the largest variance slices of the map in three orthogonal directions.

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

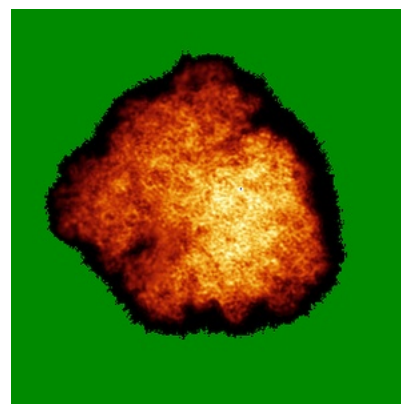
6.4.1 Primary map



X

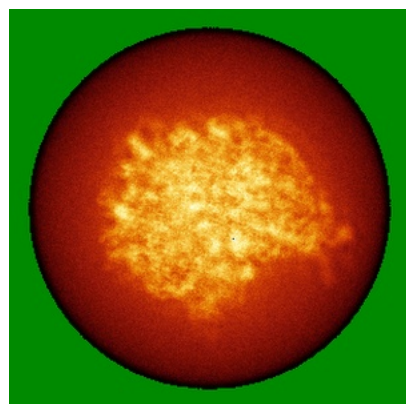


Y

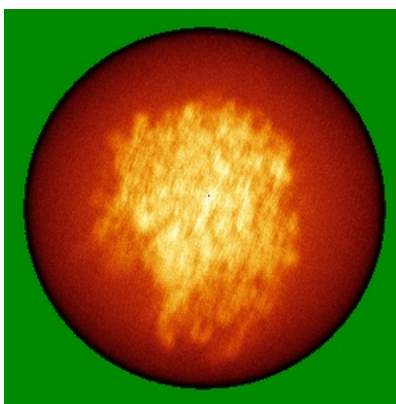


Z

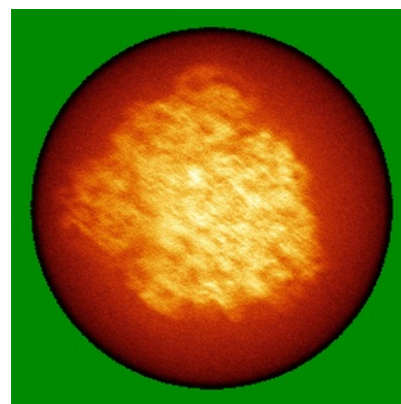
6.4.2 Raw map



X



Y

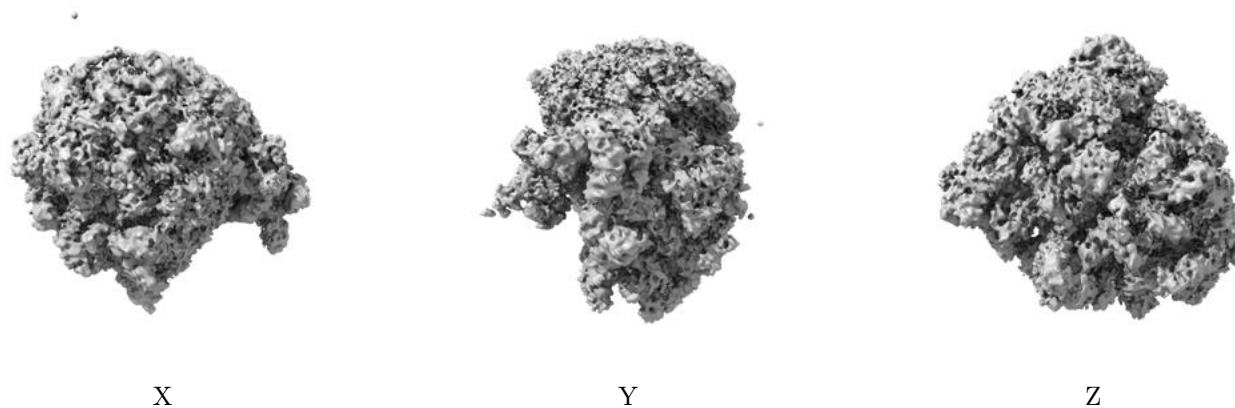


Z

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

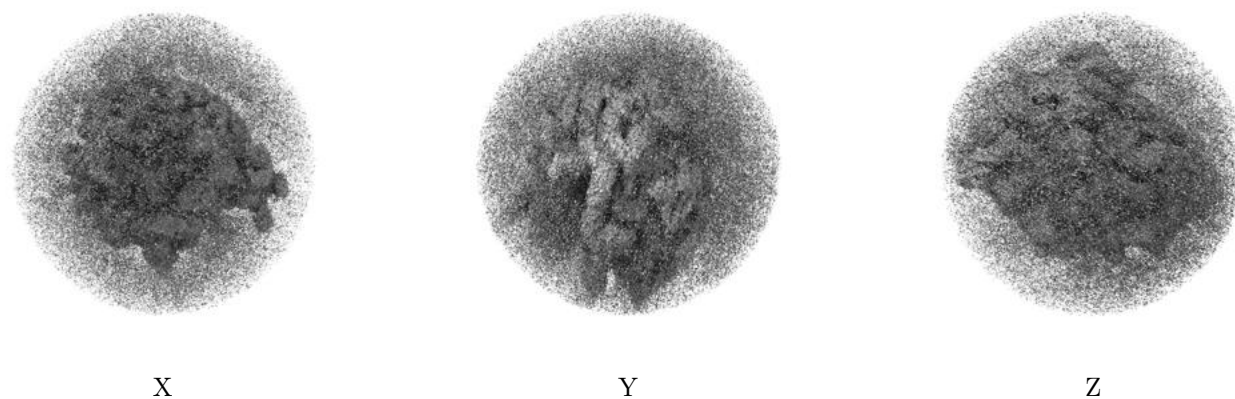
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

6.5.2 Raw map



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

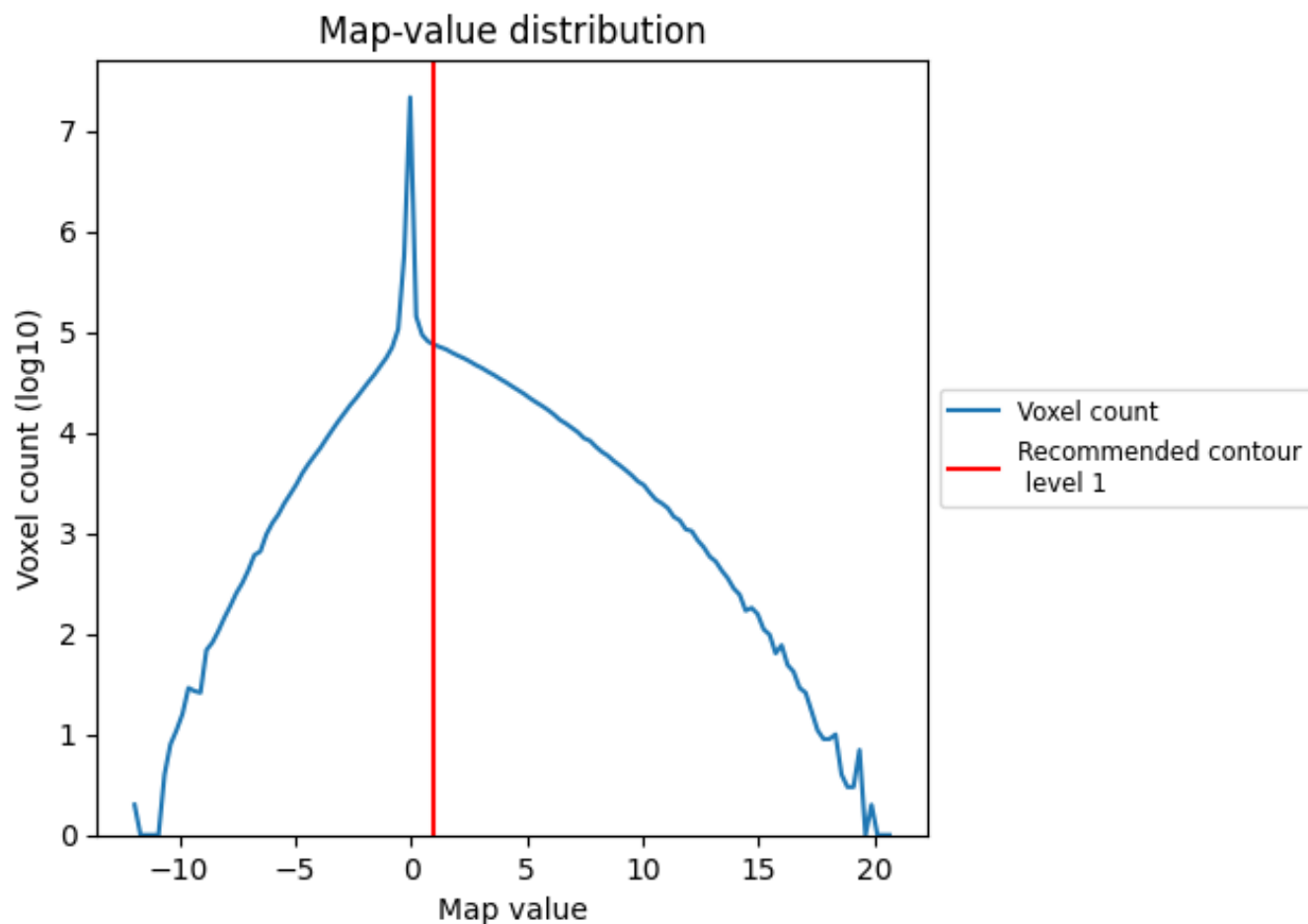
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

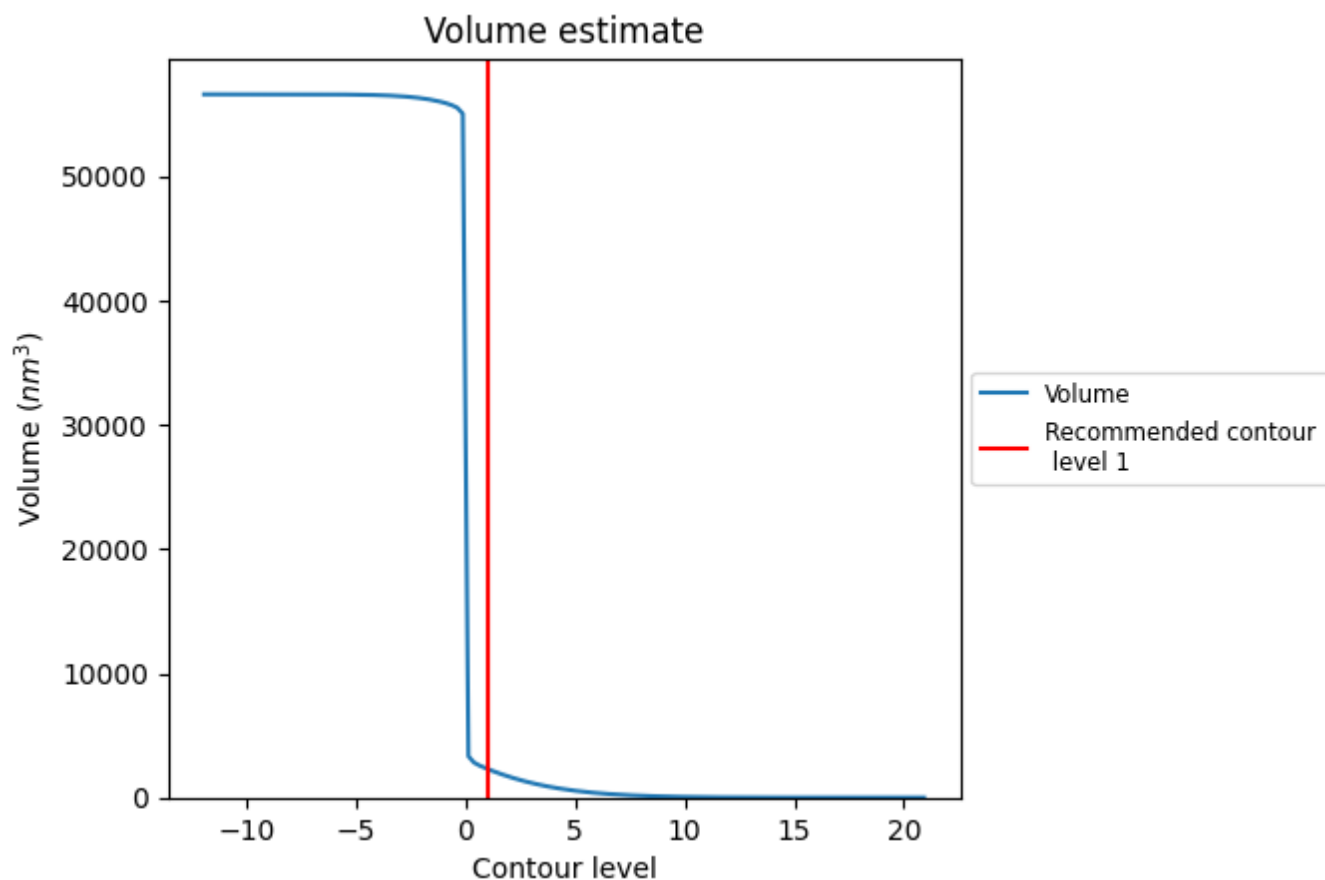
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

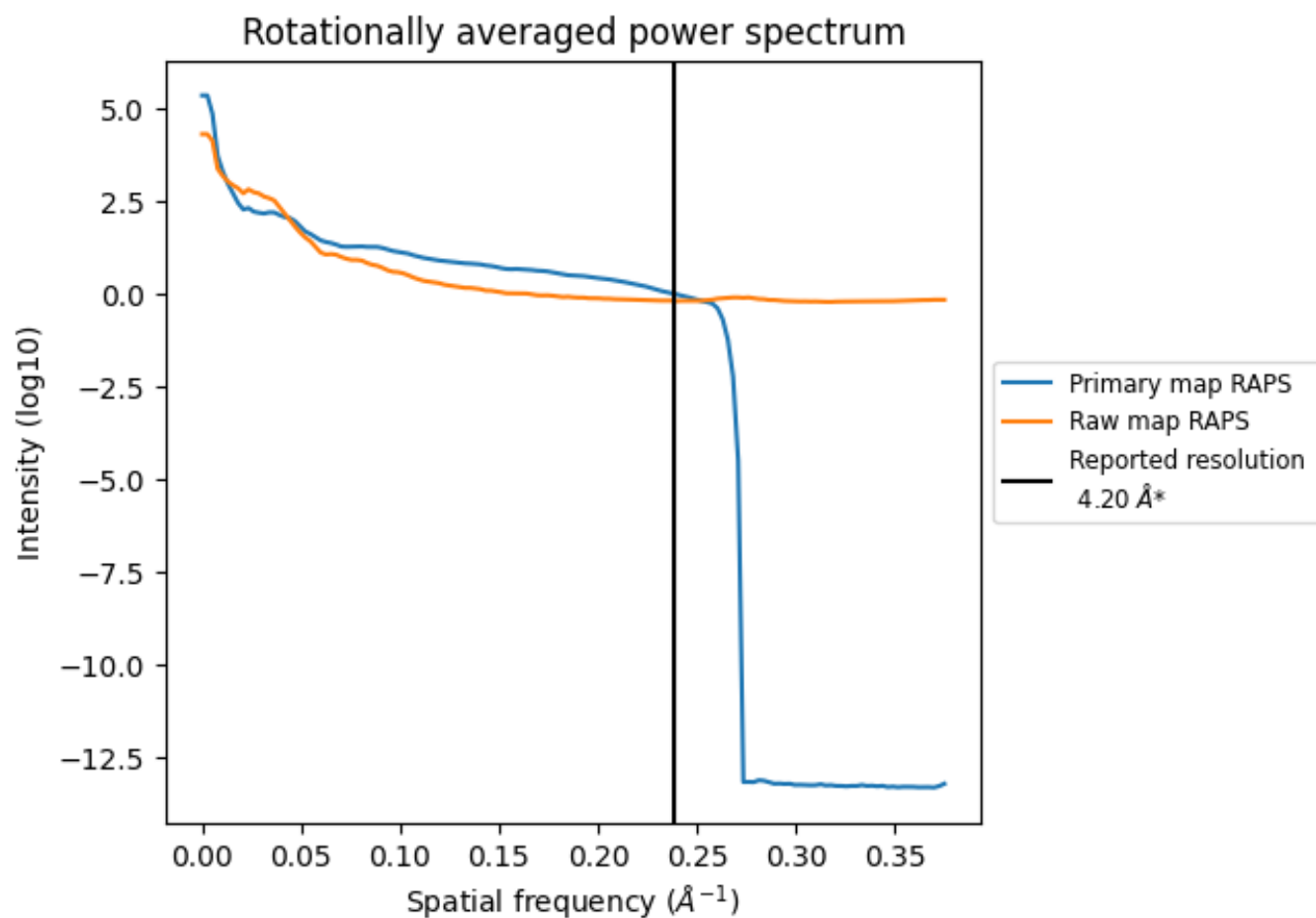
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2300 nm³; this corresponds to an approximate mass of 2077 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 ⓘ

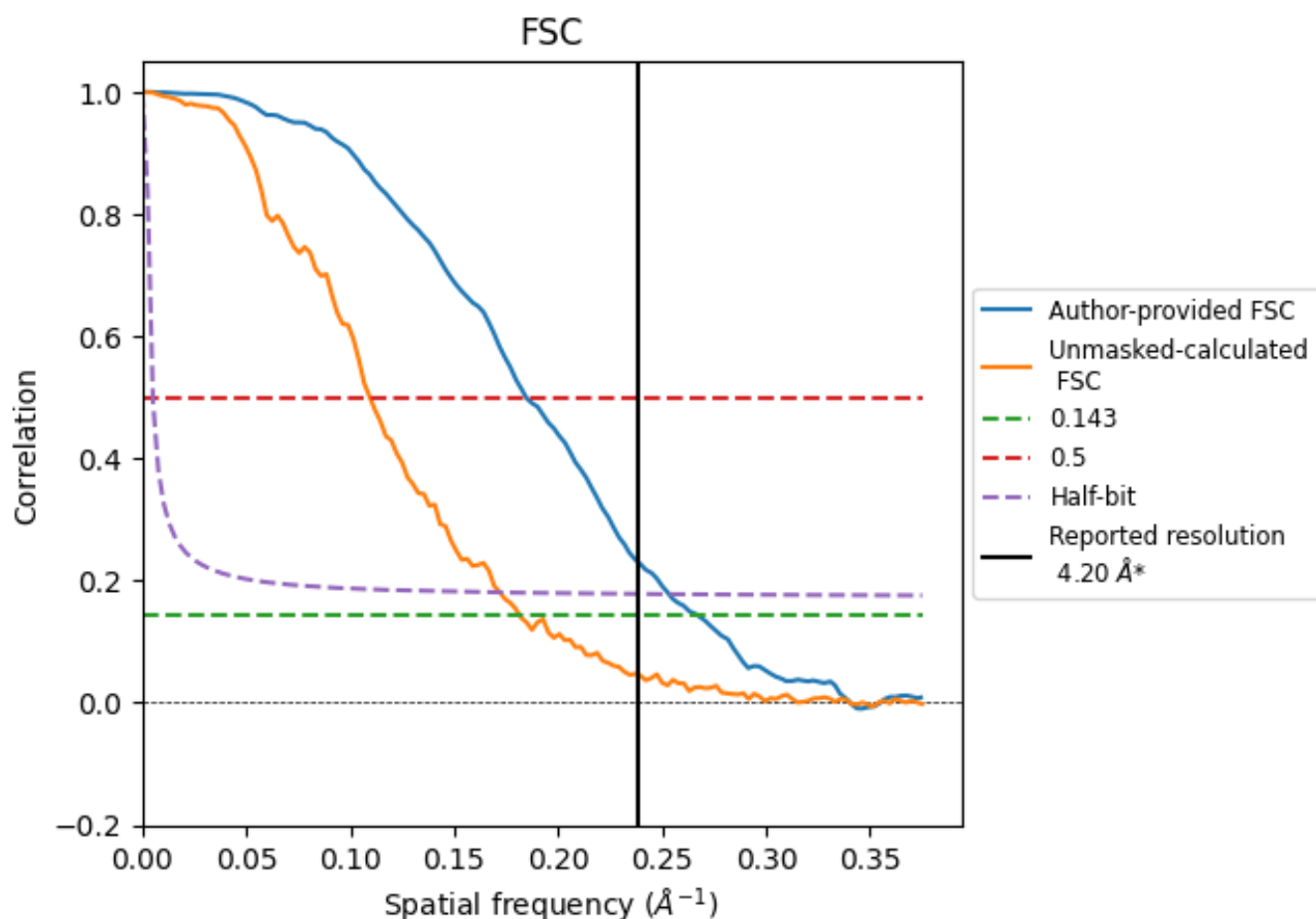


*Reported resolution corresponds to spatial frequency of 0.238 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.238 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.20	-	-
Author-provided FSC curve	3.74	5.42	3.95
Unmasked-calculated*	5.51	9.13	5.81

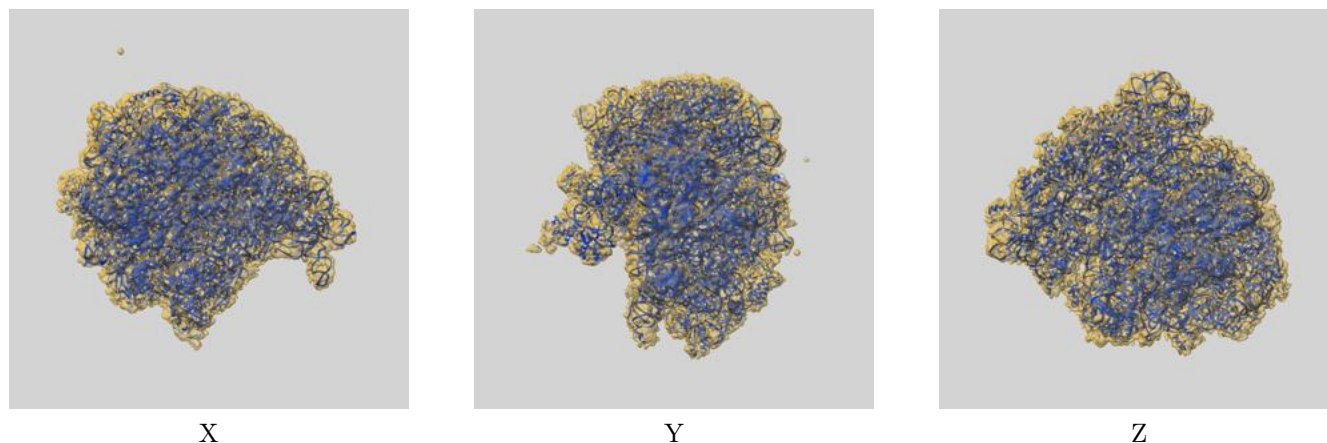
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.74 differs from the reported value 4.2 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.51 differs from the reported value 4.2 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21631 and PDB model 6WDC. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



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

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

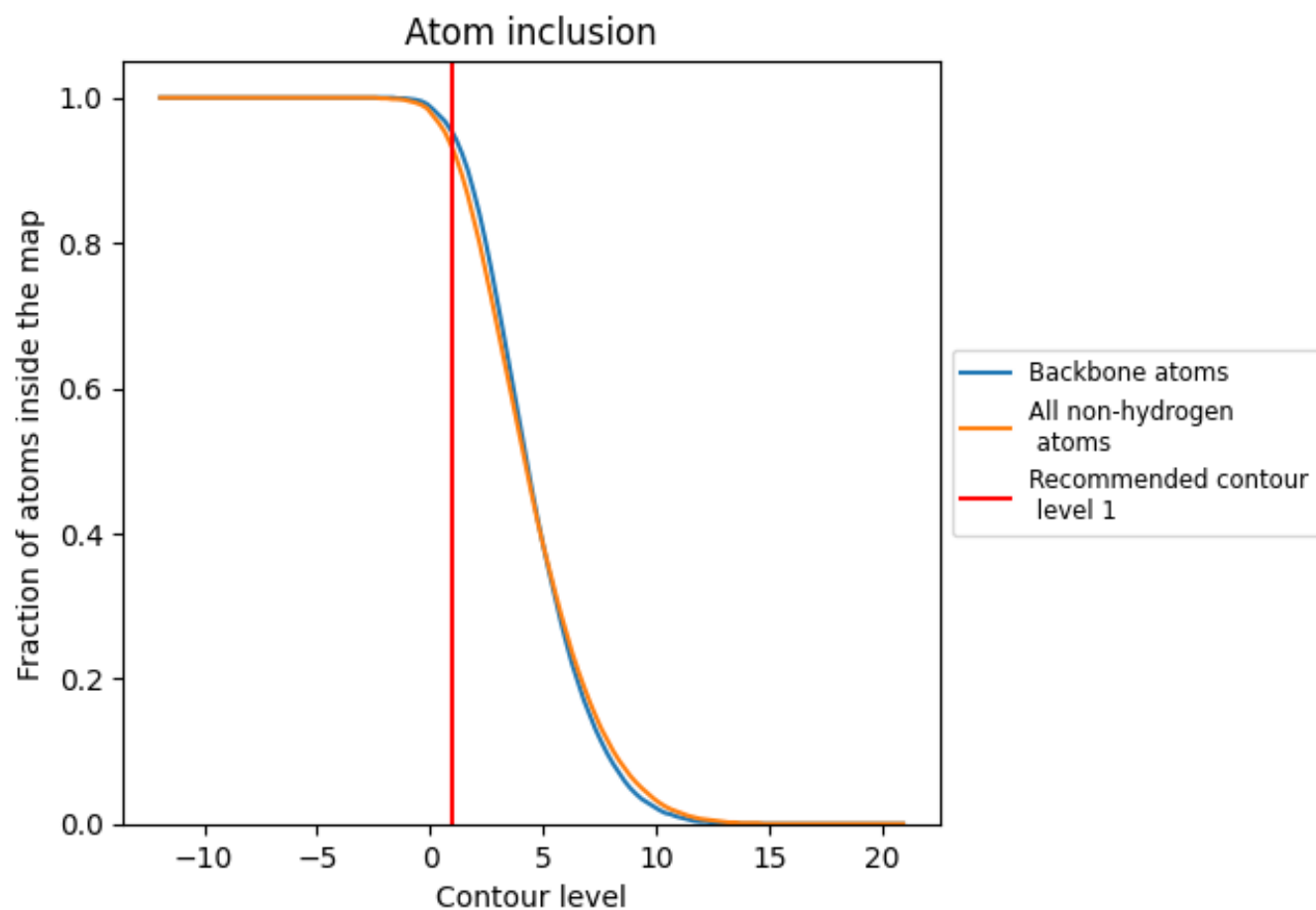


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 93% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9290	 0.2880
1	 0.9590	 0.3110
2	 0.9580	 0.2350
3	 0.9500	 0.2550
4	 0.9120	 0.2280
5	 0.8150	 0.1090
6	 0.7950	 0.1030
7	 0.8630	 0.1290
B	 0.8990	 0.3780
C	 0.6970	 0.2550
D	 0.9320	 0.4350
E	 0.9330	 0.4230
F	 0.8870	 0.3390
G	 0.8740	 0.2710
H	 0.8700	 0.2710
I	 0.8380	 0.2340
J	 0.9000	 0.3300
K	 0.9550	 0.2910
L	 0.9070	 0.2490
M	 0.9110	 0.3210
N	 0.8880	 0.2430
O	 0.8440	 0.2440
P	 0.9430	 0.3120
Q	 0.9140	 0.3400
R	 0.9080	 0.2370
S	 0.8510	 0.2620
T	 0.9460	 0.3070
U	 0.8820	 0.2750
V	 0.9340	 0.2890
W	 0.8830	 0.2620
X	 0.9200	 0.2390
Y	 0.8490	 0.2400
Z	 0.8730	 0.2710
a	 0.8180	 0.1550
b	 0.9370	 0.4110



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Chain	Atom inclusion	Q-score
c	 0.9400	 0.3970
d	 0.9180	 0.3440
e	 0.9240	 0.1990
f	 0.9410	 0.2530
g	 0.6250	 0.2100
h	 0.6030	 0.0930
i	 0.5900	 0.1090
j	 0.9460	 0.3960
k	 0.9340	 0.3970
l	 0.9300	 0.3550
m	 0.6530	 0.2910
n	 0.9210	 0.3930
o	 0.9270	 0.2960
p	 0.9400	 0.3570
q	 0.9370	 0.3900
r	 0.9490	 0.3650
s	 0.9270	 0.3790
t	 0.9310	 0.3680
u	 0.9400	 0.3310
v	 0.9050	 0.2830
w	 0.9430	 0.4090
x	 0.9420	 0.3800
y	 0.9520	 0.3090
z	 0.9500	 0.3710