



Full wwPDB EM Validation Report ⓘ

Jun 18, 2026 – 11:24 am BST

PDB ID : 6YSR / pdb_00006ysr
EMDB ID : EMD-10905
Title : Structure of the P+9 stalled ribosome complex
Authors : Chan, K.-H.; Petrychenko, V.; Mueller, C.; Maracci, C.; Holtkamp, W.; Wilson, D.N.; Fischer, N.; Rodnina, M.V.
Deposited on : 2020-04-23
Resolution : 3.10 Å (reported)
Based on initial models : 5AFI, 4RB7

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 : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

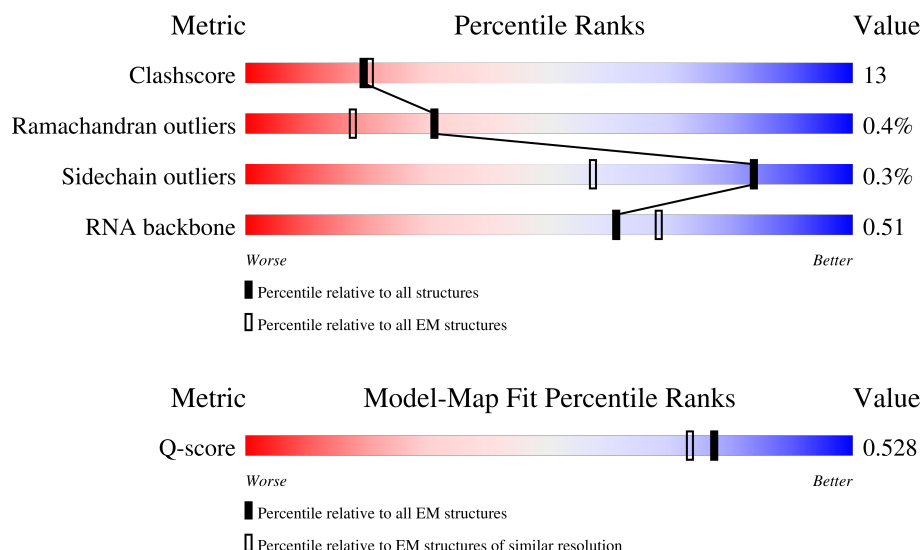
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



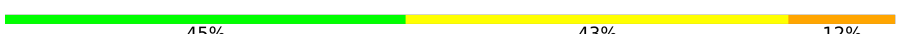
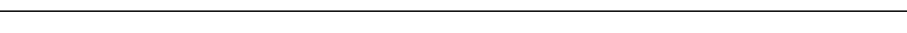
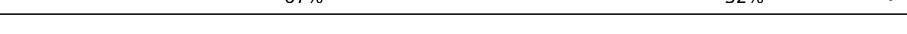
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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

Mol	Chain	Length	Quality of chain
1	0	57	
2	1	55	
3	2	46	

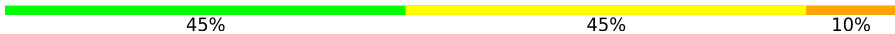
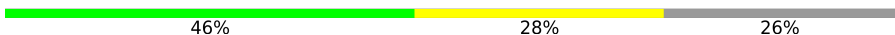
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Mol	Chain	Length	Quality of chain
4	3	65	
5	4	38	
6	5	165	
7	6	70	
8	A	2903	
9	B	120	
10	C	273	
11	D	209	
12	E	201	
13	F	179	
14	G	177	
15	H	149	
16	I	142	
17	J	142	
18	K	123	
19	L	144	
20	M	136	
21	N	127	
22	O	117	
23	P	115	
24	Q	118	
25	R	103	
26	S	110	
27	T	100	
28	U	104	

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Mol	Chain	Length	Quality of chain
29	V	94	
30	W	85	
31	X	78	
32	Y	63	
33	Z	59	
34	a	1542	
35	b	240	
36	c	233	
37	d	206	
38	e	167	
39	f	135	
40	g	179	
41	h	130	
42	i	130	
43	j	103	
44	k	129	
45	l	124	
46	m	118	
47	n	102	
48	o	89	
49	p	82	
50	q	84	
51	r	75	
52	s	92	
53	t	87	

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Mol	Chain	Length	Quality of chain
54	u	71	65% 25% 8%
55	v	2	50% 50%
56	w	76	42% 46% 8%
57	x	15	20% 47% 33%

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 145959 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 L32.

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

- Molecule 2 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 3 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 4 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 5 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 6 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	5	131	Total	C	N	O	0	0
			647	385	131	131		

- Molecule 7 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 8 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A	2903	Total	C	N	O	P	0	0
			62336	27815	11468	20150	2903		

- Molecule 9 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B	120	Total	C	N	O	P	0	0
			2570	1144	468	838	120		

- Molecule 10 is a protein called 50S ribosomal protein L2.

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

- Molecule 11 is a protein called 50S ribosomal protein L3.

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

- Molecule 12 is a protein called 50S ribosomal protein L4.

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

- Molecule 13 is a protein called 50S ribosomal protein L5.

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

- Molecule 14 is a protein called 50S ribosomal protein L6.

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

- Molecule 15 is a protein called 50S ribosomal protein L9.

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

- Molecule 16 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	I	141	Total	C	N	O	S	0	0
			693	411	141	141			

- Molecule 17 is a protein called 50S ribosomal protein L13.

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

- Molecule 18 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	K	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 19 is a protein called 50S ribosomal protein L15.

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

- Molecule 20 is a protein called 50S ribosomal protein L16.

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

- Molecule 21 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	N	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 22 is a protein called 50S ribosomal protein L18.

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

- Molecule 23 is a protein called 50S ribosomal protein L19.

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

- Molecule 24 is a protein called 50S ribosomal protein L20.

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

- Molecule 25 is a protein called 50S ribosomal protein L21.

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

- Molecule 26 is a protein called 50S ribosomal protein L22.

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

- Molecule 27 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	T	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 28 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	U	102	Total	C	N	O	0	0
			779	492	146	141		

- Molecule 29 is a protein called 50S ribosomal protein L25.

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

- Molecule 30 is a protein called 50S ribosomal protein L27.

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

- Molecule 31 is a protein called 50S ribosomal protein L28.

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

- Molecule 32 is a protein called 50S ribosomal protein L29.

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

- Molecule 33 is a protein called 50S ribosomal protein L30.

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

- Molecule 34 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	a	1539	Total	C	N	O	P	0	0
			33028	14738	6052	10699	1539		

- Molecule 35 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	b	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 36 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	c	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 37 is a protein called 30S ribosomal protein S4.

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

- Molecule 38 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	e	157	Total	C	N	O	S	0	0
			1141	709	218	208	6		

- Molecule 39 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	f	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 40 is a protein called 30S ribosomal protein S7.

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

- Molecule 41 is a protein called 30S ribosomal protein S8.

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

- Molecule 42 is a protein called 30S ribosomal protein S9.

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

- Molecule 43 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	j	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 44 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	k	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 45 is a protein called 30S ribosomal protein S12.

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

- Molecule 46 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	m	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 47 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	n	101	Total	C	N	O	S	0	0
			799	498	165	133	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	35	ALA	-	insertion	UNP C3SR07

- Molecule 48 is a protein called 30S ribosomal protein S15.

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

- Molecule 49 is a protein called 30S ribosomal protein S16.

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

- Molecule 50 is a protein called 30S ribosomal protein S17.

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

- Molecule 51 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	r	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 52 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	s	82	Total	C	N	O	S	0	0
			658	421	125	110	2		

- Molecule 53 is a protein called 30S ribosomal protein S20.

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

- Molecule 54 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	u	65	Total	C	N	O	S	0	0
			506	313	105	87	1		

- Molecule 55 is a protein called P-site fMet-Phe-tRNA(Phe).

Mol	Chain	Residues	Atoms					AltConf	Trace
55	v	2	Total	C	N	O	S	0	0
			19	14	2	2	1		

- Molecule 56 is a RNA chain called P-site fMet-Phe-tRNA(Phe).

Mol	Chain	Residues	Atoms						AltConf	Trace
56	w	76	Total	C	N	O	P	S	0	0
			1631	731	291	531	76	2		

- Molecule 57 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	x	15	Total	C	N	O	P	0	0
			314	141	49	109	15		

- Molecule 58 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
58	0	1	Total	Mg	0
			1	1	
58	6	1	Total	Mg	0
			1	1	
58	A	236	Total	Mg	0
			236	236	
58	B	5	Total	Mg	0
			5	5	
58	O	1	Total	Mg	0
			1	1	
58	Q	1	Total	Mg	0
			1	1	
58	T	1	Total	Mg	0
			1	1	
58	a	82	Total	Mg	0
			82	82	
58	g	1	Total	Mg	0
			1	1	
58	w	3	Total	Mg	0
			3	3	

- Molecule 59 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
59	4	1	Total	Zn	0
			1	1	
59	6	1	Total	Zn	0
			1	1	

- Molecule 60 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		AltConf
60	A	1	Total	Cl	0
			1	1	

- Molecule 61 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
61	A	1	Total	Na	0
			1	1	
61	V	1	Total	Na	0
			1	1	

- Molecule 62 is water.

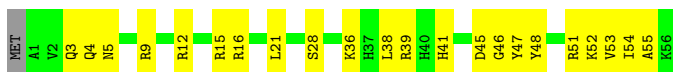
Mol	Chain	Residues	Atoms		AltConf
62	A	1	Total	O	0
			1	1	
62	a	1	Total	O	0
			1	1	

3 Residue-property plots [i](#)

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 L32

Chain 0: 



- Molecule 2: 50S ribosomal protein L33

Chain 1: 



- Molecule 3: 50S ribosomal protein L34

Chain 2: 



- Molecule 4: 50S ribosomal protein L35

Chain 3: 

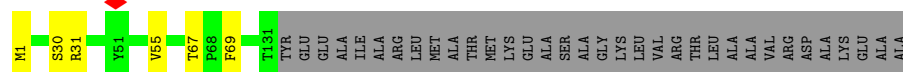
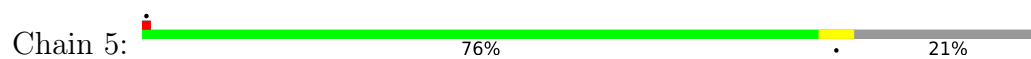


- Molecule 5: 50S ribosomal protein L36

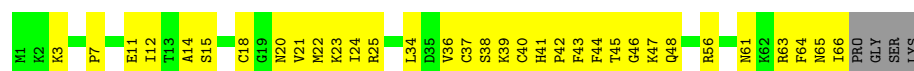
Chain 4: 



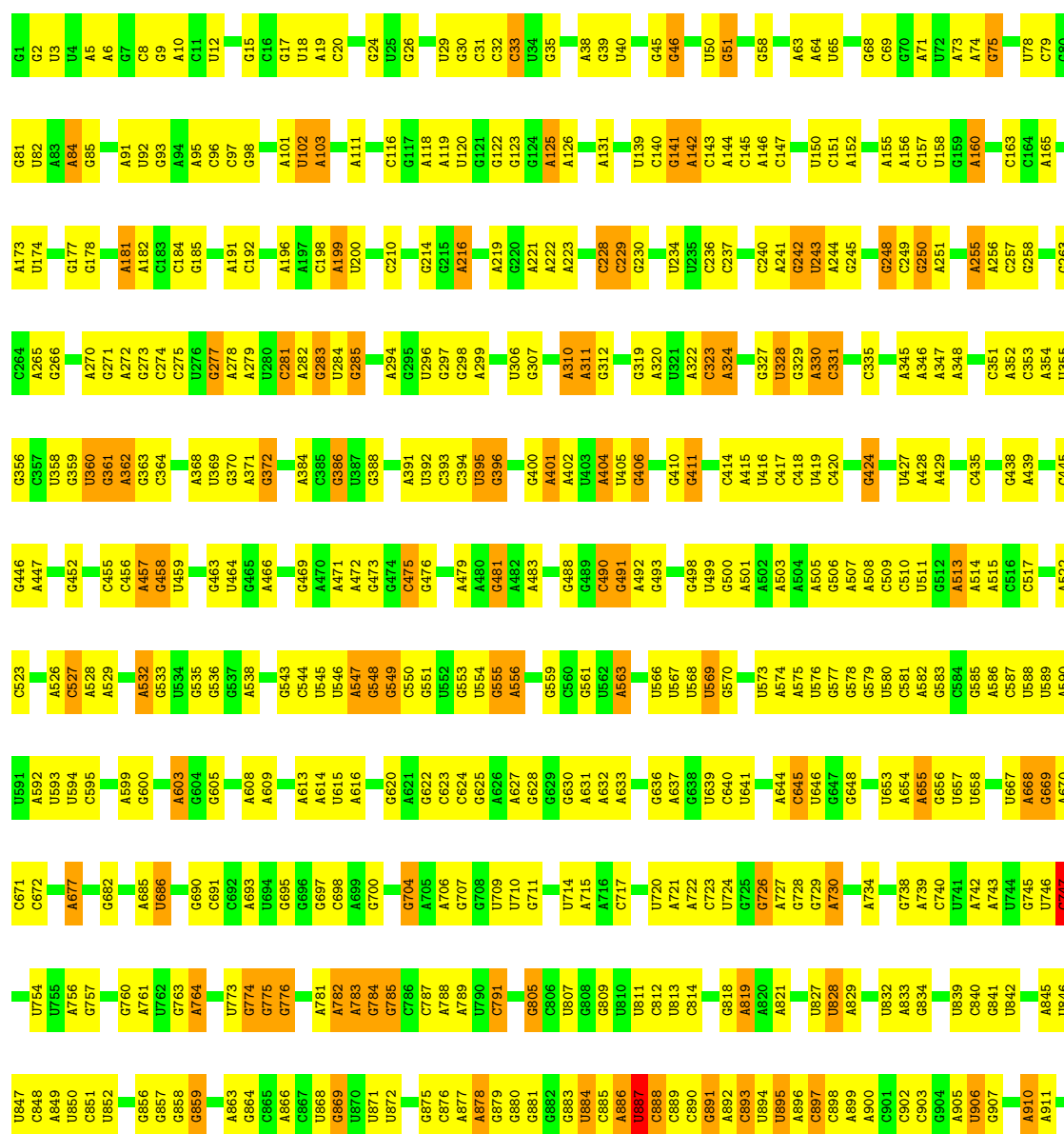
- Molecule 6: 50S ribosomal protein L10



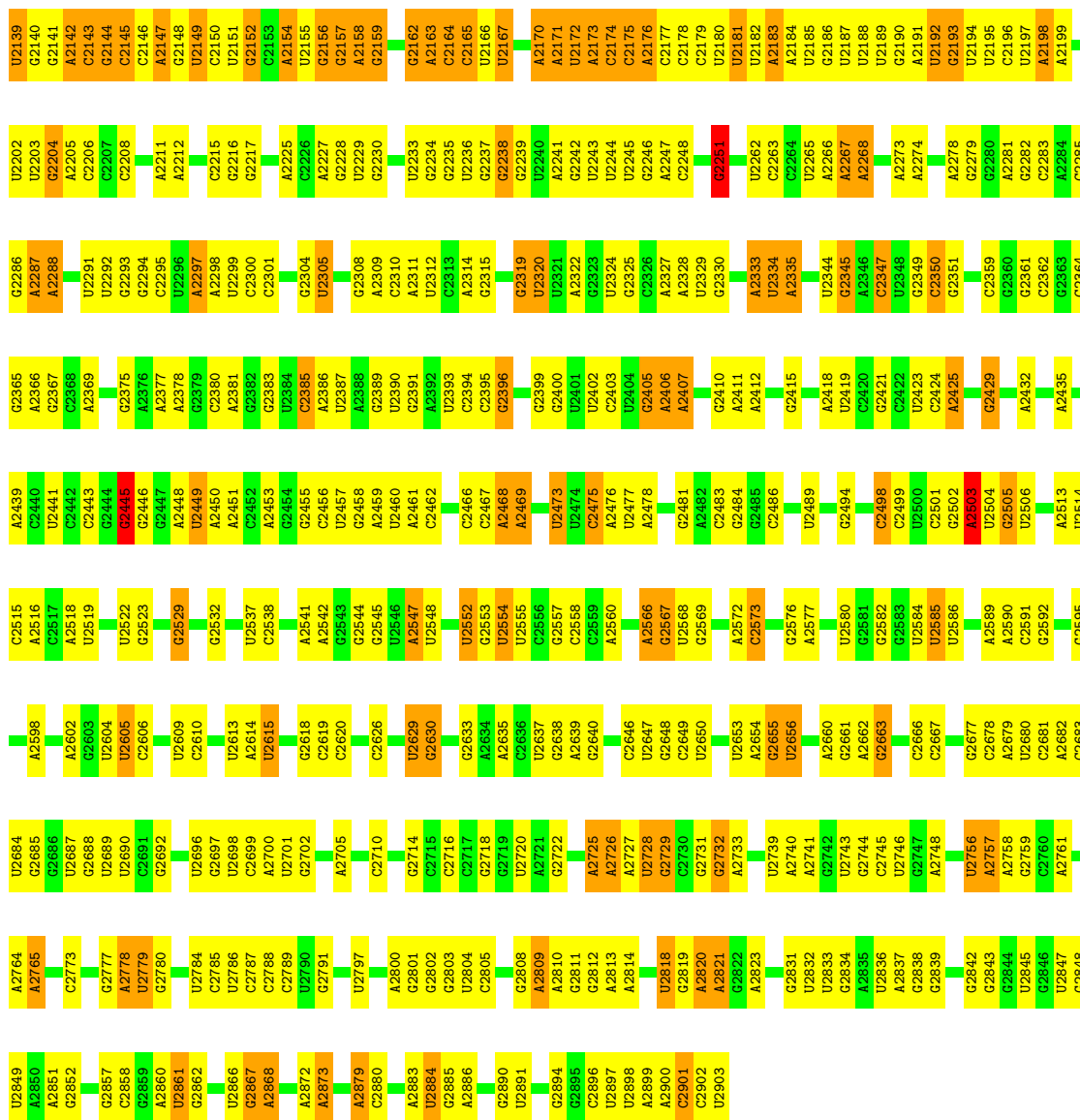
- Molecule 7: 50S ribosomal protein L31



- Molecule 8: 23S ribosomal RNA

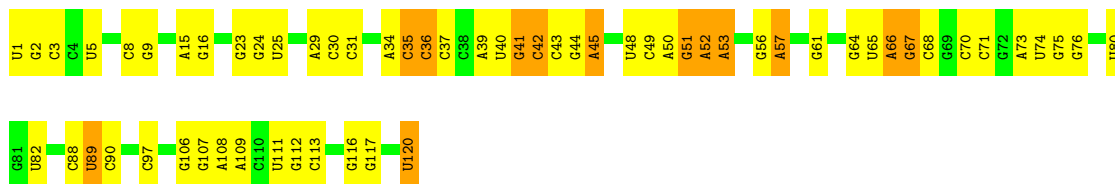


G2069	U1971	G1884	C1795	U1720	A1632	A1548	G1478	U1397	G1317	U1141	C1072	A1000	G916
A2070	G1972	A1885	U1796	G1721	G1633	A1548	G1482	C1398	U1318	A1142	A1073	A1001	A917
A2071	U1982	A1889	G1797	A1722	A1634	A1549	A1482	C1399	G1319	A1143	G1074	U1004	A918
C2073	U1982	A1890	U1798	G1723	A1635	C1550	G1483	U1406	C1320	G1149	C1075	C1005	A925
U2074	U1991	G1890	C1800	G1726	U1636	A1551	U1484	U1405	A1321	C1150	C1076	A1009	G926
U2075	G1992	G1891	A1801	C1727	A1637	U1554	U1485	G1407	A1322	C1153	A1077	A1010	A927
U2076	C1996	A1900	A1802	C1728	G1645	C1558	U1487	G1408	G1324	G1154	C1079	G1011	G930
A2079	C1997	A1901	A1803	U1729	G1646	U1563	A1490	U1409	U1325	A1155	A1080	U1012	U931
U2080	U1997	G1903	A1808	G1730	U1647	U1563	G1491	G1410	U1326	A1156	U1081	C1013	U932
U2081	U2011	G1904	A1809	C1731	G1648	C1565	G1492	U1411	A1327	U1159	U1082	U1019	U933
G2082	G2012	G1905	A1812	G1732	A1650	C1565	C1493	U1412	G1331	G1160	U1083	U1019	U934
G2087	A2013	G1906	U1813	G1733	G1651	A1566	A1494	C1413	G1332	G1169	A1084	A1020	C935
A2088	A2014	U1911	G1813	G1734	A1652	A1566	A1495	C1414	U1333	A1175	A1085	A1021	A936
G2093	A2015	U1912	G1814	U1736	A1653	A1569	A1496	U1415	G1338	C1170	A1086	A1022	C937
U2096	U2016	A1913	A1815	G1737	A1654	A1570	U1498	C1417	U1339	G1171	G1087	U1022	U938
C2097	U2017	A1914	A1816	G1738	A1655	A1571	C1498	G1429	U1340	C1172	A1088	U1023	A941
U2098	A2020	C2019	G1817	G1739	A1656	A1572	A1499	U1420	G1341	U1173	A1089	G1025	G942
U2099	U2021	C2019	U1818	G1740	U1657	C1577	G1500	G1421	C1349	U1174	C1092	G1026	A945
G2100	U2022	U1917	G1824	U1742	G1659	U1578	A1502	A1427	C1350	U1175	G1093	A1028	C946
A2101	C2023	A1918	G1825	G1743	G1667	A1579	A1503	C1428	C1351	U1176	U1094	A1029	A947
G2102	G2024	A1919	U1826	G1744	G1667	A1580	A1504	G1429	U1352	C1178	A1095	A1032	C948
U2105	U2025	U1923	U1827	A1745	A1672	G1581	U1505	G1430	A1353	U1179	A1096	U1033	G953
U2106	U2026	C1924	G1828	A1746	G1673	C1582	U1506	A1431	A1354	U1180	U1097	U1033	G954
G2107	G2029	A1924	A1829	U1747	U1674	A1583	C1507	G1432	G1358	U1181	A1098	G1036	U955
A2108	U2030	A1927	G1830	G1753	C1675	U1584	A1508	A1433	U1359	G1182	A1099	G1037	A959
U2109	A2031	G1928	G1831	U1754	A1678	A1586	A1509	A1434	G1360	U1183	U1101	A1039	A960
G2110	G2032	G1929	U1835	A1755	A1679	G1587	G1510	G1435	G1361	G1186	C1102	A1040	C961
U2111	U2033	G1930	G1836	G1756	U1679	U1588	G1511	C1437	C1362	U1187	A1103	U1043	G966
G2112	U2034	U1931	G1842	G1760	G1682	U1589	G1512	G1441	G1363	U1188	C1104	C1043	U967
A2114	G2038	A1932	C1843	C1763	U1683	A1590	G1514	U1442	A1365	A1189	U1105	C1044	C968
G2115	U2039	G1933	G1847	G1764	G1684	U1594	G1516	U1443	A1366	G1190	G1106	G1047	G969
G2116	G2040	A1936	A1848	C1764	C1685	C1595	G1519	G1444	A1367	A1048	U1109	A1048	U970
A2117	U2041	A1937	A1853	C1771	A1689	U1599	A1522	C1447	G1368	C1196	G1110	G1051	G971
G2118	C2042	U1938	A1854	A1772	A1690	C1600	U1523	G1448	G1369	U1198	G1112	C1052	A972
A2119	A2043	U1939	U1855	A1773	C1691	C1904	U1524	C1451	U1370	U1199	U1113	C1053	A973
G2120	G2046	C1942	U1856	G1774	U1692	C1904	G1524	C1452	G1371	C1291	C1114	C1054	G974
G2121	C2047	U1943	G1857	U1775	U1693	C1607	G1527	A1453	U1372	U1201	G1115	A1054	A975
U2122	G2048	A1943	A1858	G1776	C1694	C1607	G1527	C1454	A1378	G1202	G1116	G1055	G976
G2123	U2049	U1946	U1859	C1776	U1694	A1608	A1528	U1294	U1379	U1205	C1117	G1056	A983
G2124	C2050	C1947	G1860	U1779	G1699	A1609	A1529	C1295	A1383	G1206	C1118	A1057	A984
A2126	A2051	A1952	U1864	A1780	A1700	A1610	C1533	C1296	A1384	U1209	U1119	U1058	C987
G2127	G2052	U1955	U1865	U1781	A1701	C1611	U1534	G1459	A1385	G1210	C1123	U1060	A988
G2128	C2055	U1955	U1866	U1782	G1702	C1612	A1535	C1461	A1386	C1211	G1124	U1061	G989
C2129	G2056	U1955	G1867	A1783	G1703	G1613	C1536	C1461	A1387	G1212	A1126	C1062	A990
U2130	U2060	C1961	C1868	U1785	C1704	A1614	G1537	A1469	G1388	C1305	U1130	C1064	C991
U2131	G2061	C1962	G1869	A1786	G1710	A1618	G1537	A1470	U1389	G1306	U1131	U1066	G993
G2133	A2062	U1963	A1872	A1787	A1711	G1622	G1540	G1471	U1390	U1216	U1132	U1067	C992
A2134	C2063	C1964	G1873	C1788	C1541	C1541	G1540	G1472	U1391	U1219	U1133	G1068	G994
A2135	C2064	A1965	C1874	C1790	U1542	A1826	U1542	U1474	A1392	G1220	A1133	A1069	C995
G2136	U2137	A1967	G1878	A1791	G1716	G1627	G1543	G1475	A1393	U1226	C1135	A1070	A996
G2138	C2066	A1970	G1878	A1794	G1719	G1631	A1545	A1476	U1394	A1226	U1316	G1071	U999



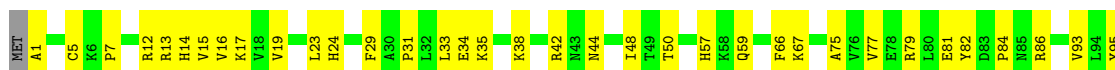
• Molecule 9: 5S ribosomal RNA

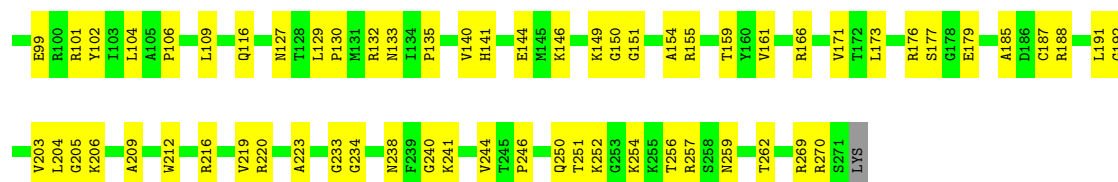
Chain B: 49% 40% 11%



• Molecule 10: 50S ribosomal protein L2

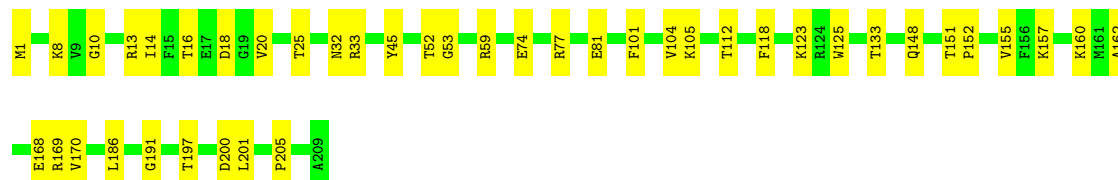
Chain C: 64% 36%





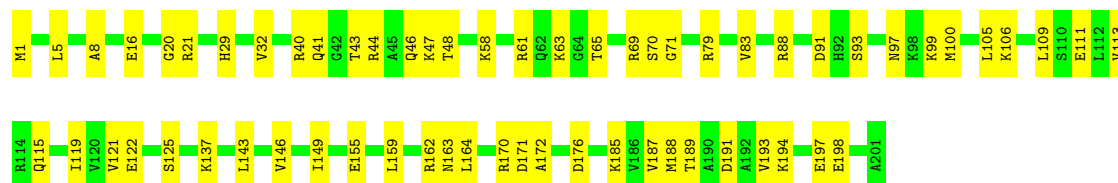
• Molecule 11: 50S ribosomal protein L3

Chain D: 80% 20%



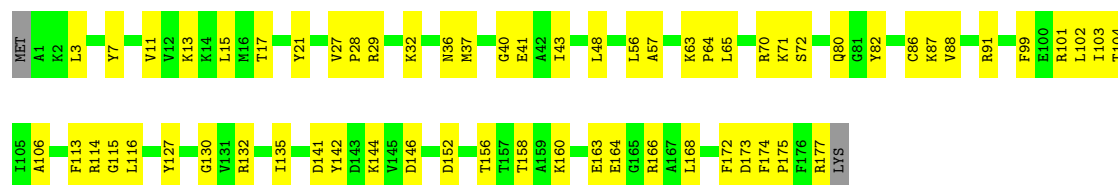
• Molecule 12: 50S ribosomal protein L4

Chain E: 69% 31%



• Molecule 13: 50S ribosomal protein L5

Chain F: 64% 35%



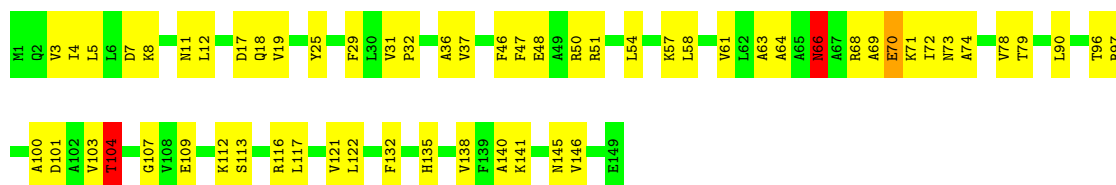
• Molecule 14: 50S ribosomal protein L6

Chain G: 74% 25%

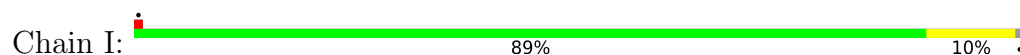


• Molecule 15: 50S ribosomal protein L9

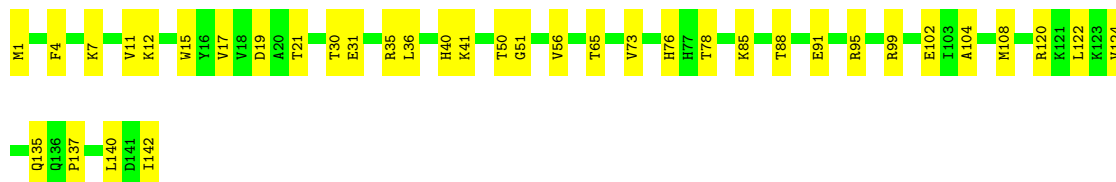
Chain H: 60% 38%



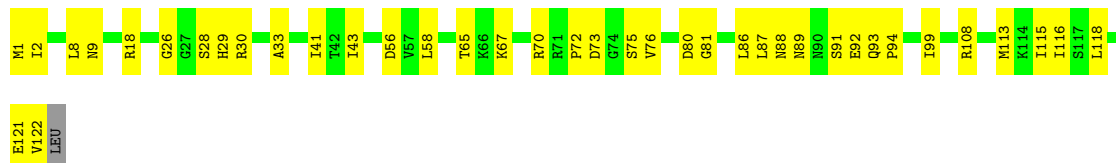
- Molecule 16: 50S ribosomal protein L11



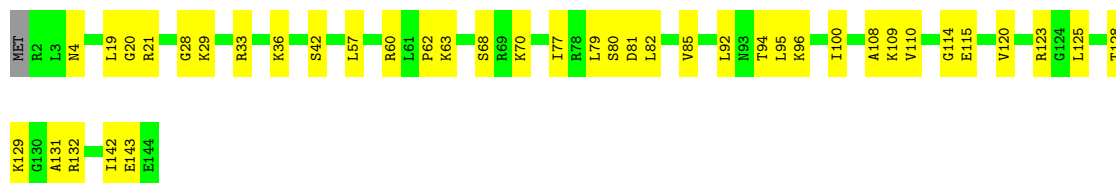
- Molecule 17: 50S ribosomal protein L13



- Molecule 18: 50S ribosomal protein L14



- Molecule 19: 50S ribosomal protein L15



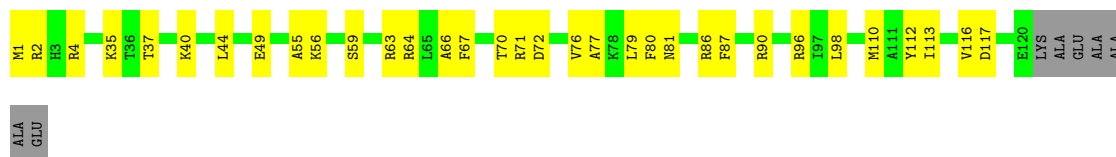
- Molecule 20: 50S ribosomal protein L16





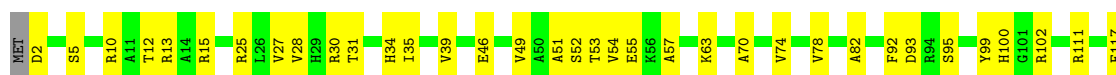
- Molecule 21: 50S ribosomal protein L17

Chain N: 69% 26% 6%



- Molecule 22: 50S ribosomal protein L18

Chain O: 69% 30% 1%



- Molecule 23: 50S ribosomal protein L19

Chain P: 69% 30% 1%



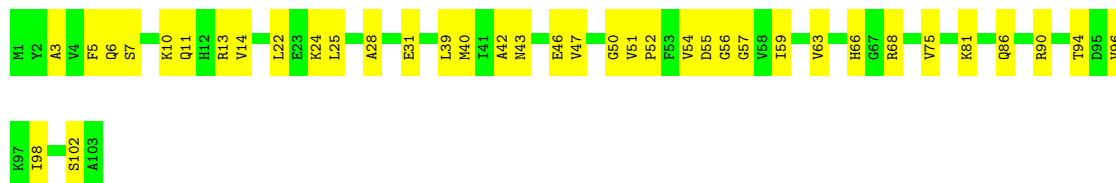
- Molecule 24: 50S ribosomal protein L20

Chain Q: 78% 21% 1%



- Molecule 25: 50S ribosomal protein L21

Chain R: 63% 37%



- Molecule 26: 50S ribosomal protein L22

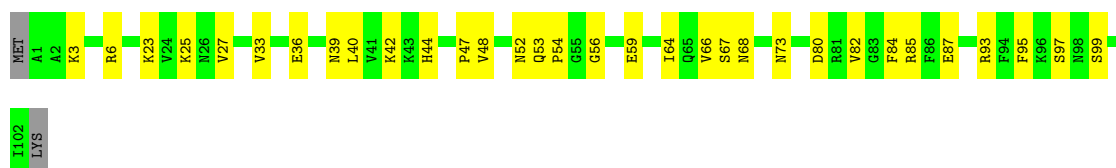
Chain S: 81% 19%



- Molecule 27: 50S ribosomal protein L23



- Molecule 28: 50S ribosomal protein L24



- Molecule 29: 50S ribosomal protein L25



- Molecule 30: 50S ribosomal protein L27



- Molecule 31: 50S ribosomal protein L28

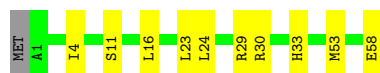


- Molecule 32: 50S ribosomal protein L29



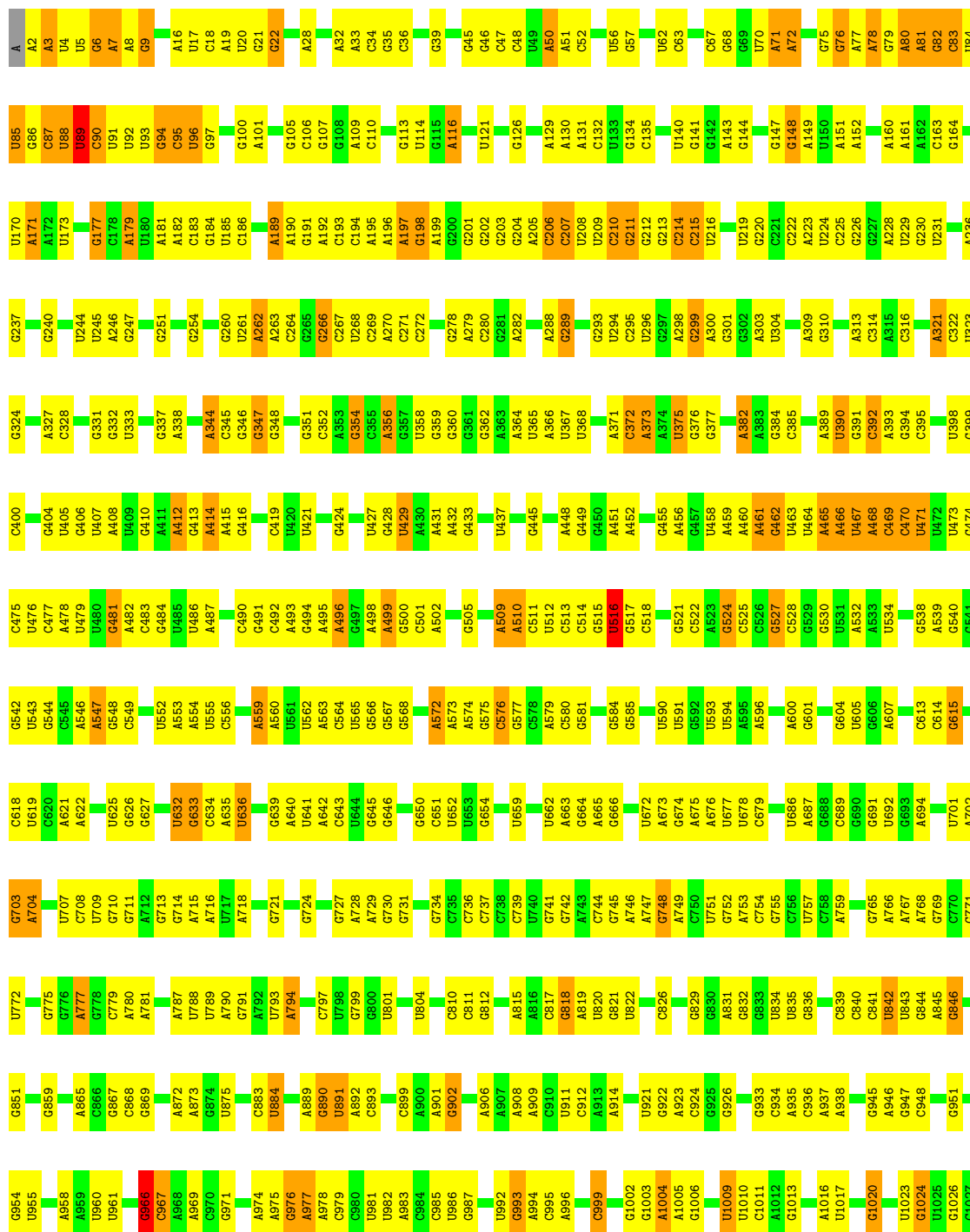
- Molecule 33: 50S ribosomal protein L30

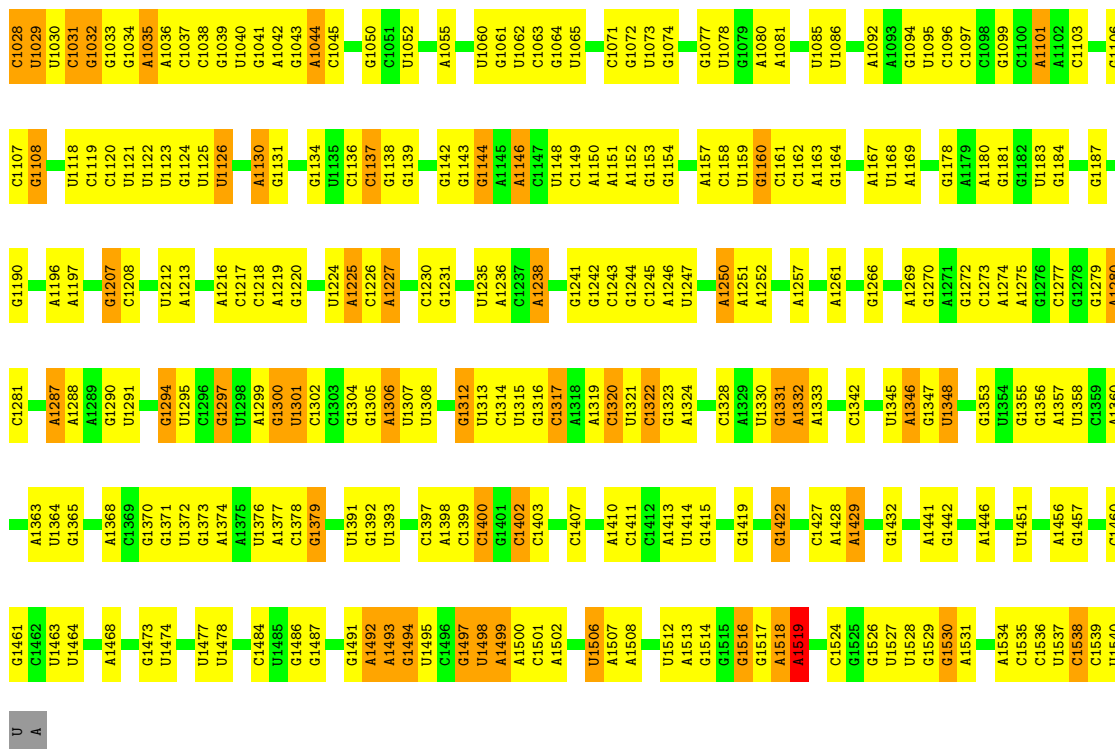
Chain Z:  81% 17%



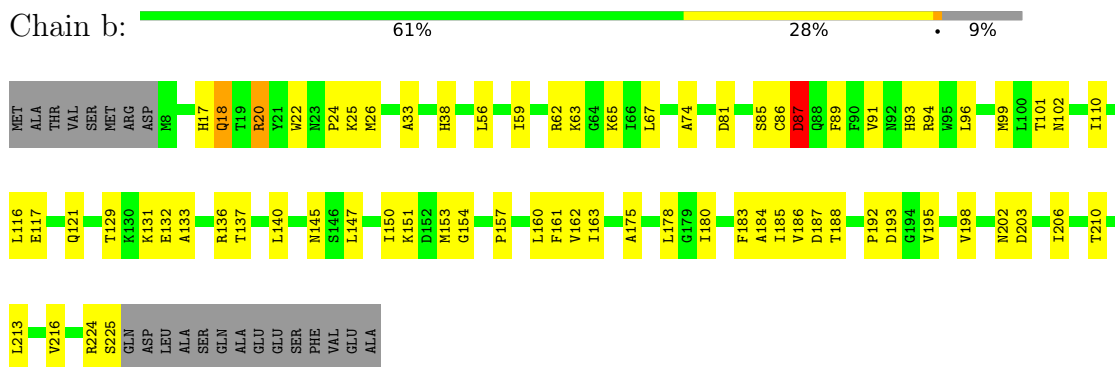
• Molecule 34: 16S ribosomal RNA

Chain a:  45% 45% 10%

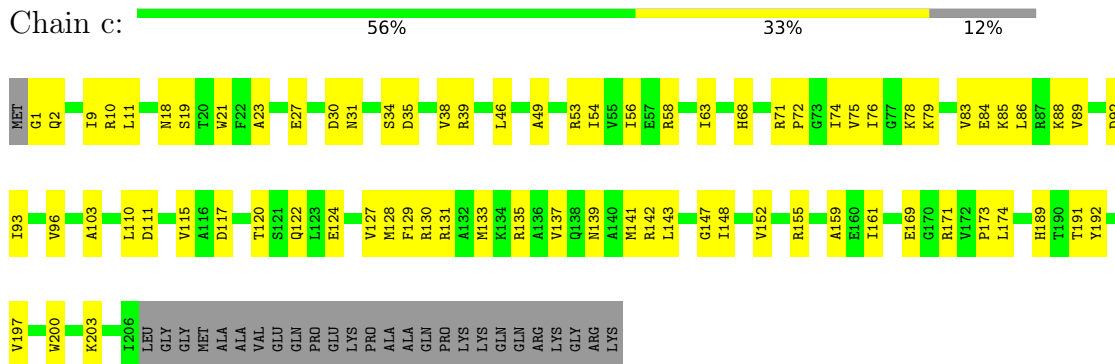




- Molecule 35: 30S ribosomal protein S2



- Molecule 36: 30S ribosomal protein S3



K176	T85	MT
M177	G86	A1
E178	E87	L4
	N88	G5
		P6
F181	L93	K7
P185	E94	L8
E186	G95	
R187	R96	R12
	L97	R13
	D98	R14
A192	N99	G15
D193	V100	T16
I194		D17
N195	R103	
E196	M104	S22
	G105	G23
I199	F106	V24
K205	G107	R25
		A26
		I27
	R110	D28
	A111	T29
	E112	R30
	L116	C31
		K32
	H119	I33
		E34
	M123	Q35
	V124	A36
	N125	P37
		G38
	N130	
		G41
	Y134	
		R46
	P138	L47
	N139	
	D140	R55
	V141	E56
	V142	K57
	S143	Q58
	I144	K59
	R145	V60
	E146	R61
		R62
	K149	
	K150	E68
	Q151	R69
	S152	Q70
	R153	F71
	V154	R72
	K155	N73
		Y74
	E159	
		A78
	P167	A79
	T168	
	W169	N84
	L170	

[illegible]

PRO	M1
MET	R2
VAL	I6
LYS	I6
ALA	M9
ASP	V10
GLU	H11
PHE	P12
ARG	D13
GLY	G14
ARG	S15
ARG	V18
ASP	V18
ASP	M21
PHE	M21
ALA	R38
ASN	R38
GLU	D41
THR	D41
ALA	R45
ASP	Q46
ASP	L47
ALA	A48
GLU	Y49
ALA	P50
GLY	I51
ASP	N52
SER	K53
GLU	L54
GLU	H55
GLU	K56
GLU	A57
GLU	H58
GLU	Y59
	M62
	N63
	I71
	D72
	E73
	T77
	T77
	F80
	N81
	I85
	R86
	R91
	T92
	K93
	T97
	S100

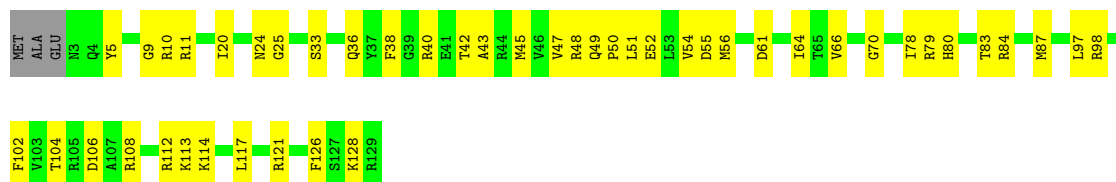
LEU	ASN	G10	G11	D11	K11	S11	R18	L19	E12	L13	S12	D12	E12	N12	K13	V13	K13	E13	D13	V14	H14	R14	M14	A14	E14	A14	M14	K14	A15	H15	TYR	ARG	TRP	LEU	SER	LEU	ARG	SER	PHE	SER	HIS	GLN	ALA	GLY	ALA	SER	SER	LYS	GLN	PRO	ALA	LEU	GLY	TYR	MET	P1	R2	R3	R4	V5	I6	G7	Q8	R9	P13	D14	P15	K24	F25	V26	H27	I28	K35	S36	E39	V42	Y43	L46	E47	T48	L49	A50	E57	A60	F61	E62	V63	A64	L65	E66	T71	V74	R78	T83	Y84	Q85	R91	R95	T103

ME1	S1	S2	I6	I7	A7	D8	M9	L10	T11	R12	I13	R14	I15	K21	P27	S28	S29	K32	V38	L39	K40	E41	I45	E46	D47	L68	E59	L60	T61	Y64	I74	O75	R76	V77	T78	R79	L82	R83	L84	K87	L91	M95	L98	S106
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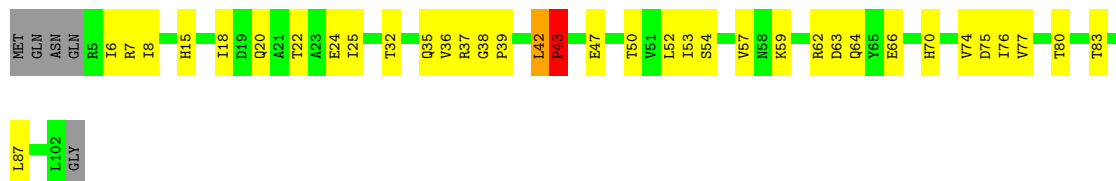
- Molecule 42: 30S ribosomal protein S9

Chain i:  62% 35% .



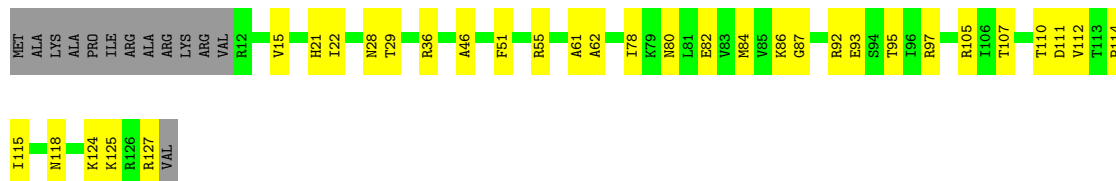
- Molecule 43: 30S ribosomal protein S10

Chain j:  60% 33% .. 5%



- Molecule 44: 30S ribosomal protein S11

Chain k:  65% 25% 10%



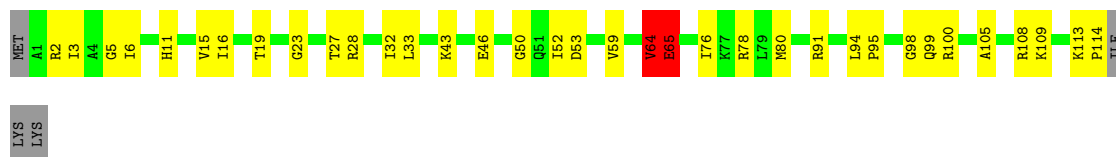
- Molecule 45: 30S ribosomal protein S12

Chain l:  76% 23% .

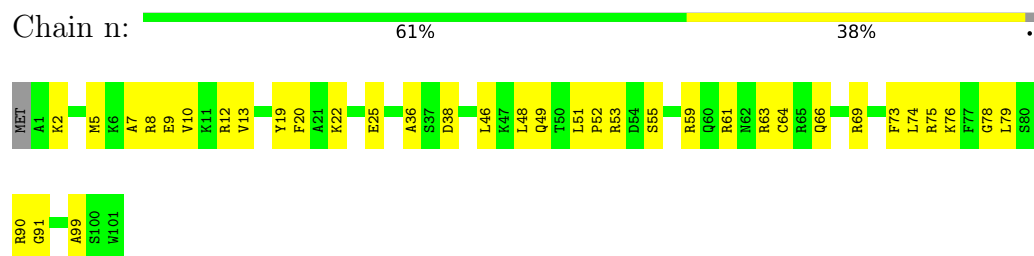


- Molecule 46: 30S ribosomal protein S13

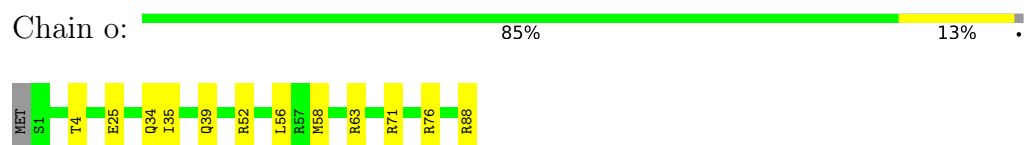
Chain m:  67% 28% . .



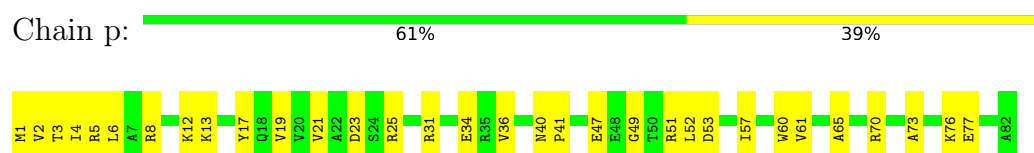
- Molecule 47: 30S ribosomal protein S14



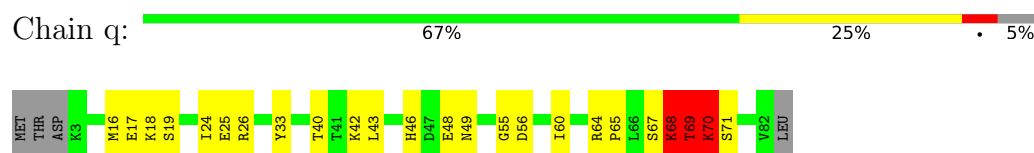
- Molecule 48: 30S ribosomal protein S15



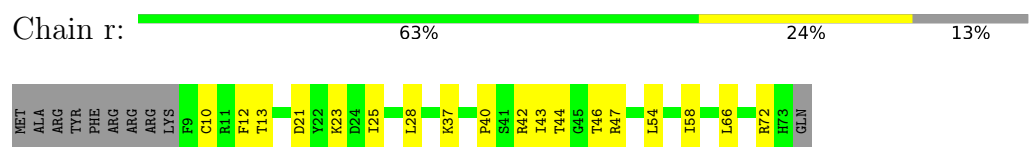
- Molecule 49: 30S ribosomal protein S16



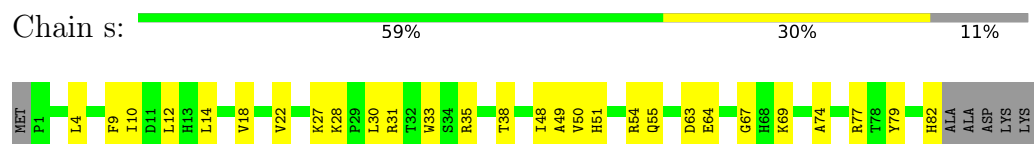
- Molecule 50: 30S ribosomal protein S17



- Molecule 51: 30S ribosomal protein S18



- Molecule 52: 30S ribosomal protein S19



- Molecule 53: 30S ribosomal protein S20





- Molecule 54: 30S ribosomal protein S21

Chain u: 65% 25% 8%



- Molecule 55: P-site fMet-Phe-tRNA(Phe)

Chain v: 50% 50%



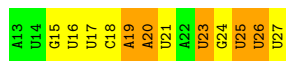
- Molecule 56: P-site fMet-Phe-tRNA(Phe)

Chain w: 42% 46% 8%



- Molecule 57: mRNA

Chain x: 20% 47% 33%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	25347	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	15.609	Depositor
Minimum map value	-7.539	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	0.035	Depositor
Map size (Å)	334.08, 334.08, 334.08	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.6525, 0.6525, 0.6525	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: OMG, 2MG, 5MU, 3TD, 6MZ, MA6, MIA, 1MG, PSU, 4SU, 4OC, ZN, 5MC, CL, NA, OMC, 2MA, UR3, G7M, OMU, MG

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	0	0.29	0/450	0.46	0/599
2	1	0.25	0/416	0.42	0/554
3	2	0.33	0/380	0.43	0/498
4	3	0.39	0/513	0.53	0/676
5	4	0.31	0/303	0.47	0/397
6	5	0.23	0/646	0.55	0/898
7	6	0.21	0/531	0.47	0/709
8	A	0.33	3/69263 (0.0%)	0.34	0/108050
9	B	0.29	1/2873 (0.0%)	0.31	0/4478
10	C	0.34	0/2121	0.47	0/2852
11	D	0.32	0/1586	0.45	0/2134
12	E	0.30	0/1571	0.42	0/2113
13	F	0.27	0/1434	0.52	2/1926 (0.1%)
14	G	0.24	0/1343	0.42	0/1816
15	H	0.30	0/1122	0.58	1/1515 (0.1%)
16	I	0.19	0/692	0.50	0/960
17	J	0.31	0/1152	0.38	0/1551
18	K	0.32	0/947	0.44	0/1268
19	L	0.31	0/1054	0.52	0/1403
20	M	0.30	0/1093	0.42	0/1460
21	N	0.31	0/973	0.50	0/1301
22	O	0.25	0/902	0.47	0/1209
23	P	0.30	0/929	0.43	0/1242
24	Q	0.36	0/960	0.42	0/1278
25	R	0.31	0/829	0.44	0/1107
26	S	0.30	0/864	0.43	0/1156
27	T	0.26	0/744	0.46	0/994
28	U	0.25	0/787	0.44	0/1051
29	V	0.28	0/766	0.42	0/1025
30	W	0.31	0/582	0.40	0/769
31	X	0.32	0/635	0.47	0/848

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Y	0.28	0/510	0.75	5/677 (0.7%)
33	Z	0.29	0/453	0.41	0/605
34	a	0.29	0/36700	0.34	5/57246 (0.0%)
35	b	0.25	0/1735	0.55	3/2338 (0.1%)
36	c	0.27	0/1651	0.43	0/2225
37	d	1.18	11/1665 (0.7%)	0.99	21/2227 (0.9%)
38	e	0.28	0/1154	0.48	0/1554
39	f	0.27	0/835	0.50	0/1128
40	g	0.23	0/1195	0.48	0/1602
41	h	0.27	0/989	0.42	0/1326
42	i	0.25	0/1034	0.52	0/1375
43	j	1.09	4/796 (0.5%)	0.86	9/1077 (0.8%)
44	k	0.25	0/885	0.42	0/1195
45	l	0.28	0/969	0.48	0/1300
46	m	1.07	4/892 (0.4%)	0.73	4/1193 (0.3%)
47	n	0.26	0/811	0.45	0/1081
48	o	0.25	0/722	0.40	0/964
49	p	0.31	0/659	0.49	0/884
50	q	1.10	5/657 (0.8%)	1.14	8/881 (0.9%)
51	r	0.27	0/544	0.49	0/731
52	s	0.24	0/675	0.36	0/908
53	t	1.04	3/671 (0.4%)	0.88	6/888 (0.7%)
54	u	0.45	1/512 (0.2%)	1.17	5/683 (0.7%)
55	v	5.90	4/19 (21.1%)	2.15	2/23 (8.7%)
56	w	0.82	10/1650 (0.6%)	0.52	5/2569 (0.2%)
57	x	0.22	0/349	0.30	0/540
All	All	0.37	46/157193 (0.0%)	0.41	76/235057 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
43	j	0	1
46	m	0	1
50	q	0	2
53	t	0	2
56	w	0	1
All	All	0	7

All (46) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
37	d	35	GLN	C-O	-26.77	0.95	1.23
43	j	42	LEU	C-O	-21.75	0.96	1.24
53	t	7	LYS	C-O	-21.38	0.92	1.24
46	m	64	VAL	C-O	-21.33	0.98	1.24
50	q	70	LYS	C-O	-17.47	1.01	1.24
37	d	36	ALA	C-O	-17.29	1.01	1.24
55	v	101	MET	CG-SD	-16.16	1.40	1.80
43	j	43	PRO	N-CD	-15.90	1.25	1.47
37	d	37	PRO	C-O	-15.68	1.03	1.24
37	d	37	PRO	N-CA	-15.61	1.27	1.47
55	v	102	PHE	C-O	15.42	1.54	1.23
46	m	65	GLU	C-O	-15.29	1.04	1.24
56	w	76	A	P-OP2	-12.93	1.23	1.49
50	q	68	LYS	C-O	-12.65	1.07	1.24
56	w	75	C	O3'-P	-12.59	1.42	1.61
37	d	35	GLN	CA-C	-11.03	1.41	1.53
37	d	37	PRO	N-CD	-10.48	1.33	1.47
37	d	34	GLU	C-O	-9.77	1.11	1.24
46	m	65	GLU	CD-OE2	-9.53	1.07	1.25
50	q	69	THR	C-O	-9.30	1.12	1.24
53	t	7	LYS	CA-C	-9.29	1.41	1.52
56	w	76	A	P-OP1	-8.78	1.31	1.49
56	w	76	A	O4'-C1'	-8.44	1.29	1.42
37	d	37	PRO	CA-CB	-8.38	1.41	1.53
55	v	101	MET	SD-CE	-7.56	1.60	1.79
56	w	16	U	C5-C6	7.53	1.49	1.34
56	w	20	U	C5-C6	7.51	1.49	1.34
8	A	2449	U	C5-C6	7.18	1.48	1.34
55	v	101	MET	N-CA	-6.96	1.33	1.46
37	d	36	ALA	CA-C	-6.64	1.44	1.52
46	m	65	GLU	CD-OE1	-6.58	1.12	1.25
43	j	43	PRO	N-CA	-6.56	1.39	1.47
56	w	76	A	C4'-O4'	-6.26	1.36	1.45
8	A	887	U	C1'-N1	5.98	1.56	1.47
53	t	6	ALA	CA-CB	-5.97	1.45	1.52
54	u	13	VAL	CA-CB	-5.96	1.47	1.54
50	q	67	SER	C-N	-5.91	1.24	1.33
56	w	20	U	C2-N3	5.86	1.49	1.37
56	w	16	U	C2-N3	5.84	1.49	1.37
37	d	35	GLN	C-N	-5.72	1.23	1.33
9	B	120	U	C1'-N1	5.47	1.56	1.48
8	A	2449	U	C2-N3	5.46	1.48	1.37
43	j	43	PRO	CA-CB	-5.43	1.46	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	w	20	U	N1-C2	5.38	1.49	1.38
50	q	68	LYS	C-N	-5.32	1.26	1.33
37	d	34	GLU	C-N	-5.30	1.26	1.34

All (76) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	u	13	VAL	N-CA-C	-17.13	96.74	113.53
53	t	7	LYS	N-CA-C	-15.64	91.03	112.30
37	d	37	PRO	N-CA-CB	-15.21	87.28	103.25
56	w	76	A	C1'-C2'-O2'	13.25	131.67	111.80
50	q	70	LYS	CA-C-N	-12.19	102.71	122.95
50	q	70	LYS	C-N-CA	-12.19	102.71	122.95
54	u	12	ASP	O-C-N	11.69	138.14	122.59
50	q	68	LYS	N-CA-CB	-10.80	94.13	110.33
50	q	70	LYS	N-CA-C	-10.75	87.91	110.80
50	q	67	SER	O-C-N	10.12	130.70	123.11
37	d	34	GLU	CB-CG-CD	-10.11	95.42	112.60
43	j	43	PRO	N-CA-C	9.43	131.88	112.47
54	u	12	ASP	CA-C-N	-9.35	110.49	121.71
54	u	12	ASP	C-N-CA	-9.35	110.49	121.71
46	m	64	VAL	CA-C-N	9.03	138.79	121.54
46	m	64	VAL	C-N-CA	9.03	138.79	121.54
43	j	42	LEU	O-C-N	-8.73	111.29	121.32
34	a	214	C	C2'-C3'-O3'	8.45	126.37	113.70
34	a	90	C	O4'-C1'-C2'	-8.43	99.17	107.60
37	d	146	GLU	CA-C-O	-8.29	112.03	121.15
46	m	64	VAL	CA-CB-CG1	7.67	123.44	110.40
56	w	76	A	C5'-C4'-O4'	-7.55	97.77	109.10
50	q	70	LYS	CA-C-O	-7.55	109.71	120.51
37	d	78	ALA	CA-C-N	7.20	135.29	121.54
37	d	78	ALA	C-N-CA	7.20	135.29	121.54
37	d	79	ALA	CA-C-N	-7.17	108.31	120.58
37	d	79	ALA	C-N-CA	-7.17	108.31	120.58
37	d	149	LYS	CA-C-N	7.15	135.20	121.54
37	d	149	LYS	C-N-CA	7.15	135.20	121.54
35	b	87	ASP	CA-C-N	-7.14	110.05	123.27
35	b	87	ASP	C-N-CA	-7.14	110.05	123.27
53	t	6	ALA	CA-C-O	6.92	132.69	122.38
37	d	37	PRO	N-CA-C	6.85	126.59	112.47
43	j	43	PRO	N-CA-CB	-6.75	96.16	103.25
34	a	90	C	C4'-C3'-O3'	6.68	123.03	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	F	173	ASP	CA-C-O	-6.68	110.96	120.51
37	d	37	PRO	CA-CB-CG	-6.68	91.81	104.50
32	Y	13	GLU	CA-C-N	-6.59	111.44	122.64
32	Y	13	GLU	C-N-CA	-6.59	111.44	122.64
37	d	79	ALA	N-CA-C	-6.57	96.81	110.80
37	d	34	GLU	CB-CA-C	-6.54	97.41	110.42
56	w	75	C	P-O3'-C3'	6.53	130.00	120.20
50	q	69	THR	CB-CA-C	-6.47	97.55	110.42
53	t	7	LYS	CA-C-O	-6.43	112.32	119.78
37	d	150	LYS	N-CA-C	-6.39	97.18	110.80
32	Y	13	GLU	N-CA-CB	6.28	121.11	110.49
56	w	76	A	O5'-P-OP1	6.00	126.00	108.00
43	j	42	LEU	CA-C-O	-5.94	112.02	120.16
43	j	43	PRO	N-CD-CG	-5.93	94.30	103.20
13	F	173	ASP	CB-CA-C	5.82	122.00	110.42
53	t	5	SER	CA-C-N	5.80	130.78	122.08
53	t	5	SER	C-N-CA	5.80	130.78	122.08
50	q	69	THR	N-CA-C	-5.74	98.58	110.80
37	d	146	GLU	O-C-N	5.74	129.97	122.97
37	d	79	ALA	N-CA-CB	5.71	120.14	110.49
34	a	214	C	C3'-C2'-O2'	5.71	119.26	110.70
37	d	145	ARG	CA-C-N	5.67	128.89	120.90
37	d	145	ARG	C-N-CA	5.67	128.89	120.90
43	j	43	PRO	CB-CG-CD	-5.53	88.40	106.10
56	w	76	A	C4'-C3'-O3'	-5.53	101.11	109.40
37	d	37	PRO	N-CD-CG	-5.52	94.92	103.20
32	Y	12	GLU	CA-C-N	5.50	132.04	121.54
32	Y	12	GLU	C-N-CA	5.50	132.04	121.54
43	j	43	PRO	CA-CB-CG	-5.47	94.10	104.50
34	a	89	U	P-O3'-C3'	5.47	128.40	120.20
37	d	37	PRO	O-C-N	5.45	130.00	122.64
55	v	101	MET	CA-C-N	-5.42	111.95	121.70
55	v	101	MET	C-N-CA	-5.42	111.95	121.70
46	m	64	VAL	CG1-CB-CG2	-5.39	98.95	110.80
37	d	150	LYS	N-CA-CB	5.36	119.55	110.49
54	u	13	VAL	O-C-N	5.26	130.57	121.67
15	H	66	ASN	N-CA-C	-5.26	104.55	111.96
53	t	7	LYS	CB-CG-CD	-5.17	99.42	111.30
43	j	43	PRO	CA-C-N	-5.11	113.45	120.71
43	j	43	PRO	C-N-CA	-5.11	113.45	120.71
35	b	87	ASP	CB-CA-C	-5.05	100.37	110.42

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
43	j	42	LEU	Mainchain
46	m	64	VAL	Mainchain
50	q	69	THR	Mainchain
50	q	70	LYS	Mainchain
53	t	5	SER	Mainchain
53	t	7	LYS	Mainchain
56	w	76	A	Sidechain

5.2 Too-close contacts [i](#)

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	0	444	0	461	21	0
2	1	409	0	440	16	0
3	2	377	0	418	9	0
4	3	504	0	574	25	0
5	4	302	0	340	13	0
6	5	647	0	336	10	0
7	6	522	0	521	30	0
8	A	62336	0	31365	1177	0
9	B	2570	0	1301	48	0
10	C	2082	0	2157	80	0
11	D	1565	0	1616	34	0
12	E	1552	0	1619	45	0
13	F	1410	0	1447	48	0
14	G	1323	0	1374	32	0
15	H	1111	0	1147	44	0
16	I	693	0	347	13	0
17	J	1129	0	1162	27	0
18	K	938	0	1012	30	0
19	L	1045	0	1117	36	0
20	M	1074	0	1157	33	0
21	N	960	0	1000	25	0
22	O	892	0	923	30	0
23	P	917	0	965	29	0
24	Q	947	0	1022	24	0
25	R	816	0	839	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	S	857	0	920	16	0
27	T	738	0	807	15	0
28	U	779	0	834	28	0
29	V	753	0	780	19	0
30	W	575	0	592	18	0
31	X	625	0	655	26	0
32	Y	509	0	543	18	0
33	Z	449	0	491	7	0
34	a	33028	0	16640	701	0
35	b	1704	0	1732	51	0
36	c	1624	0	1699	58	0
37	d	1643	0	1710	70	0
38	e	1141	0	1170	32	0
39	f	817	0	808	33	0
40	g	1181	0	1240	49	0
41	h	979	0	1034	30	0
42	i	1022	0	1070	43	0
43	j	786	0	828	25	0
44	k	869	0	878	25	0
45	l	955	0	1019	22	0
46	m	883	0	944	26	0
47	n	799	0	841	32	0
48	o	714	0	737	11	0
49	p	649	0	666	31	0
50	q	648	0	688	22	0
51	r	535	0	552	13	0
52	s	658	0	685	29	0
53	t	665	0	714	21	0
54	u	506	0	502	14	0
55	v	19	0	17	8	0
56	w	1631	0	834	28	0
57	x	314	0	158	11	0
58	0	1	0	0	0	0
58	6	1	0	0	0	0
58	A	236	0	0	0	0
58	B	5	0	0	0	0
58	O	1	0	0	0	0
58	Q	1	0	0	0	0
58	T	1	0	0	0	0
58	a	82	0	0	0	0
58	g	1	0	0	0	0
58	w	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	4	1	0	0	0	0
59	6	1	0	0	0	0
60	A	1	0	0	0	0
61	A	1	0	0	0	0
61	V	1	0	0	0	0
62	A	1	0	0	0	0
62	a	1	0	0	0	0
All	All	145959	0	97448	2988	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 13.

All (2988) 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)
15:H:63:ALA:C	15:H:66:ASN:OD1	1.71	1.32
8:A:2165:C:N4	8:A:2171:A:H62	1.41	1.16
8:A:2165:C:H42	8:A:2171:A:N6	1.41	1.15
34:a:615:G:N2	34:a:626:G:C4	2.21	1.08
15:H:63:ALA:O	15:H:66:ASN:OD1	1.72	1.07
8:A:887:U:H5'	46:m:91:ARG:HD3	1.40	1.03
8:A:1057:A:H62	8:A:1079:C:H42	1.08	0.99
8:A:2061:G:N2	55:v:101:MET:O	1.96	0.98
34:a:207:C:H1'	34:a:213:G:N1	1.77	0.98
8:A:1054:A:C6	8:A:1106:G:O6	2.16	0.97
34:a:765:G:H1	34:a:812:G:HO2'	1.12	0.97
8:A:1057:A:H62	8:A:1079:C:N4	1.62	0.97
15:H:63:ALA:CA	15:H:66:ASN:OD1	2.14	0.95
6:5:31:ARG:HA	8:A:1054:A:O2'	1.66	0.94
8:A:1036:G:H1	8:A:1119:U:H3	1.05	0.92
8:A:2451:A:N3	56:w:76:A:O2'	2.03	0.91
34:a:615:G:N1	34:a:626:G:C5	2.45	0.85
8:A:475:C:O2	8:A:479:A:N6	2.10	0.84
8:A:886:A:H1'	8:A:887:U:H2'	1.56	0.84
8:A:277:G:H1'	8:A:361:G:H1	1.43	0.84
34:a:90:C:H3'	34:a:90:C:H6	1.43	0.84
8:A:481:G:O2'	8:A:506:G:N2	2.11	0.84
56:w:26:A:H61	56:w:44:G:H1	1.23	0.83
8:A:1607:C:N4	8:A:1622:G:OP2	2.11	0.83
34:a:615:G:N1	34:a:626:G:C6	2.48	0.82
8:A:1054:A:N6	8:A:1106:G:O6	2.12	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:563:A:N3	24:Q:36:GLN:NE2	2.28	0.81
8:A:2144:G:H5'	8:A:2145:C:H5'	1.62	0.81
8:A:2157:G:N3	8:A:2158:A:N6	2.27	0.81
8:A:284:U:H3	8:A:356:G:H1	0.81	0.81
34:a:1028:C:O2	34:a:1034:G:N2	2.13	0.81
8:A:1529:G:H1	8:A:1542:U:H3	1.24	0.81
34:a:615:G:C2	34:a:626:G:C4	2.69	0.81
34:a:1006:G:H1	34:a:1023:U:H3	1.25	0.80
27:T:56:GLU:HG2	27:T:88:LYS:HG2	1.62	0.80
41:h:91:LEU:O	41:h:116:ARG:NH2	2.14	0.80
34:a:1038:C:H2'	34:a:1039:G:H8	1.45	0.80
8:A:2279:G:N7	30:W:10:ARG:NH2	2.30	0.79
8:A:1779:U:OP2	8:A:1784:A:N6	2.15	0.79
13:F:114:ARG:HB2	13:F:177:ARG:HH21	1.48	0.79
11:D:14:ILE:HA	23:P:11:GLN:HE22	1.47	0.78
15:H:63:ALA:HA	15:H:66:ASN:OD1	1.83	0.78
8:A:2063:C:H4'	55:v:102:PHE:CZ	2.18	0.78
9:B:51:G:OP1	22:O:63:LYS:NZ	2.17	0.78
6:5:31:ARG:HA	8:A:1054:A:HO2'	1.49	0.78
34:a:205:A:H3'	34:a:207:C:H41	1.48	0.78
34:a:1031:C:O2'	34:a:1032:G:N2	2.18	0.77
50:q:24:ILE:HD11	50:q:60:ILE:HD11	1.64	0.77
34:a:632:U:H5'	34:a:633:G:H8	1.50	0.77
8:A:545:U:O2	8:A:548:G:O6	2.01	0.77
8:A:2165:C:H42	8:A:2171:A:H62	0.77	0.77
37:d:13:ARG:NH1	37:d:36:ALA:HB1	2.00	0.77
15:H:101:ASP:HA	15:H:107:GLY:HA2	1.65	0.77
8:A:1171:G:H22	8:A:1177:G:H1	1.33	0.77
44:k:92:ARG:NH2	44:k:111:ASP:OD2	2.18	0.77
8:A:1817:G:OP1	10:C:86:ARG:NH2	2.18	0.76
9:B:31:C:O2	9:B:53:A:N6	2.18	0.76
12:E:143:LEU:HB3	12:E:146:VAL:HG11	1.68	0.76
7:6:36:VAL:HG11	7:6:41:HIS:HD2	1.51	0.76
8:A:886:A:H61	8:A:891:G:H8	1.31	0.76
18:K:108:ARG:HH12	23:P:33:GLU:HA	1.51	0.76
34:a:89:U:H2'	34:a:90:C:C4	2.21	0.76
32:Y:13:GLU:O	32:Y:16:THR:OG1	2.02	0.76
8:A:1936:A:H2	8:A:1943:U:H3	1.32	0.75
37:d:70:GLN:N	37:d:73:ASN:OD1	2.18	0.75
4:3:28:LEU:HA	4:3:32:LEU:HD21	1.69	0.75
8:A:2445:2MG:P	12:E:69:ARG:HH22	2.08	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:C:106:PRO:HD2	10:C:109:LEU:HD22	1.69	0.75
54:u:38:GLU:HG2	54:u:46:ARG:HH11	1.49	0.75
8:A:2076:U:OP2	8:A:2238:G:N2	2.16	0.75
42:i:83:THR:HG21	42:i:102:PHE:HB3	1.66	0.75
8:A:886:A:N6	8:A:891:G:C8	2.55	0.75
8:A:1486:U:O4	8:A:1502:A:N6	2.20	0.75
34:a:501:C:OP1	45:l:113:ARG:NH2	2.19	0.75
8:A:2638:G:O2'	8:A:2778:A:N6	2.20	0.74
21:N:77:ALA:O	21:N:81:ASN:HB2	1.85	0.74
34:a:544:G:OP1	37:d:55:ARG:NH2	2.20	0.74
47:n:49:GLN:HE21	52:s:12:LEU:HG	1.52	0.74
34:a:207:C:O4'	34:a:213:G:N2	2.20	0.74
34:a:90:C:H3'	34:a:90:C:C6	2.22	0.74
34:a:94:G:H4'	34:a:95:C:H5'	1.69	0.74
8:A:84:A:H62	8:A:101:A:H2	1.34	0.74
8:A:1057:A:N6	8:A:1079:C:H42	1.85	0.74
8:A:2063:C:C4'	55:v:102:PHE:CZ	2.70	0.74
8:A:2683:C:OP1	23:P:50:ARG:NH2	2.19	0.74
10:C:15:VAL:HG22	10:C:205:GLY:HA3	1.70	0.74
34:a:207:C:C1'	34:a:213:G:N1	2.51	0.74
10:C:24:HIS:CG	10:C:79:ARG:HD3	2.23	0.73
8:A:2469:A:N6	8:A:2481:G:O2'	2.21	0.73
8:A:2333:A:H4'	8:A:2334:U:H3'	1.70	0.73
34:a:615:G:C6	34:a:626:G:C6	2.76	0.73
34:a:673:A:H2'	34:a:674:G:C8	2.23	0.73
37:d:71:PHE:HA	37:d:74:TYR:HB2	1.70	0.73
8:A:1212:G:HO2'	8:A:1236:G:N2	1.86	0.73
8:A:1858:A:N6	8:A:1884:G:O2'	2.21	0.73
34:a:202:G:H22	34:a:215:C:H5	1.35	0.73
35:b:56:LEU:HD23	35:b:59:ILE:HD11	1.71	0.73
34:a:427:U:OP1	37:d:12:ARG:NH2	2.21	0.73
34:a:677:U:H3	34:a:713:G:H22	1.37	0.73
8:A:1076:C:H1'	16:I:90:GLY:HA2	1.70	0.72
34:a:1026:G:H1	34:a:1035:A:N6	1.86	0.72
34:a:356:A:N3	34:a:368:U:O2'	2.19	0.72
34:a:615:G:N2	34:a:626:G:N3	2.36	0.72
10:C:154:ALA:HB2	10:C:161:VAL:HG23	1.69	0.72
4:3:7:ARG:NH1	8:A:243:U:OP1	2.21	0.72
9:B:1:U:H2'	9:B:2:G:H8	1.52	0.72
34:a:1144:G:H21	34:a:1146:A:H62	1.37	0.72
8:A:1392:A:N6	27:T:18:GLU:OE1	2.18	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:30:SER:O	8:A:1054:A:H1'	1.89	0.72
8:A:2139:U:O2	8:A:2152:G:O6	2.07	0.72
13:F:141:ASP:H	13:F:144:LYS:HZ2	1.37	0.72
49:p:6:LEU:HB3	49:p:17:TYR:HB3	1.70	0.72
8:A:2666:C:N4	14:G:108:PHE:O	2.22	0.72
34:a:107:G:N7	53:t:9:ARG:NH1	2.38	0.72
34:a:147:G:H2'	34:a:148:G:C8	2.24	0.72
10:C:159:THR:HG23	10:C:176:ARG:HG2	1.71	0.72
34:a:264:C:O2'	50:q:65:PRO:O	2.07	0.72
38:e:152:VAL:HG21	41:h:98:LEU:HD13	1.71	0.72
9:B:37:C:O2	22:O:100:HIS:NE2	2.21	0.72
8:A:2032:G:N2	11:D:151:THR:OG1	2.22	0.71
4:3:7:ARG:NH2	8:A:244:A:OP2	2.20	0.71
8:A:1900:A:H1'	8:A:1970:A:H2'	1.70	0.71
50:q:46:HIS:HA	50:q:70:LYS:HE3	1.71	0.71
20:M:66:ARG:NH1	20:M:104:GLU:OE2	2.23	0.71
34:a:9:G:OP2	38:e:125:LYS:NZ	2.20	0.71
8:A:1565:C:O2'	8:A:1566:A:O5'	2.08	0.71
19:L:20:GLY:HA2	19:L:28:GLY:HA2	1.72	0.71
52:s:27:LYS:HB3	52:s:28:LYS:HD2	1.73	0.71
18:K:76:VAL:HG12	23:P:72:VAL:HB	1.73	0.71
34:a:1530:G:N7	54:u:45:LYS:NZ	2.36	0.71
8:A:500:G:N1	8:A:503:A:OP2	2.23	0.71
8:A:585:G:N7	24:Q:5:ARG:NH1	2.39	0.71
34:a:979:C:O2	47:n:59:ARG:NH1	2.24	0.71
4:3:39:ARG:NH1	8:A:2362:C:OP1	2.22	0.71
8:A:1315:C:O2'	8:A:1392:A:N3	2.21	0.71
34:a:618:C:O2	34:a:622:A:N6	2.23	0.71
8:A:2308:G:O6	8:A:2311:A:N6	2.16	0.71
13:F:163:GLU:OE1	13:F:166:ARG:NH1	2.24	0.71
34:a:1376:U:O4	40:g:9:ARG:NH1	2.24	0.71
8:A:1063:G:N2	16:I:131:THR:O	2.23	0.70
8:A:1071:G:O2'	8:A:1089:A:N7	2.21	0.70
8:A:1825:U:O2	10:C:252:LYS:NZ	2.24	0.70
8:A:2230:G:N3	31:X:31:ASN:ND2	2.40	0.70
43:j:47:GLU:OE1	47:n:76:LYS:NZ	2.23	0.70
8:A:1089:A:N1	8:A:1102:C:N4	2.39	0.70
8:A:1799:G:OP1	10:C:257:ARG:NH1	2.25	0.70
14:G:136:ASP:HB3	14:G:139:VAL:HG22	1.74	0.70
8:A:630:G:N2	8:A:633:A:OP2	2.19	0.70
42:i:51:LEU:HB3	42:i:56:MET:HB3	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:q:25:GLU:HG3	50:q:40:THR:HG22	1.71	0.70
6:5:31:ARG:CA	8:A:1054:A:O2'	2.37	0.70
12:E:119:ILE:HB	12:E:187:VAL:HG12	1.73	0.70
52:s:35:ARG:NH2	52:s:74:ALA:O	2.25	0.70
8:A:1365:A:OP1	31:X:2:ARG:NH1	2.25	0.70
8:A:2439:A:N6	8:A:2585:U:O2'	2.25	0.70
8:A:2473:U:OP1	8:A:2475:C:N4	2.24	0.70
34:a:615:G:C2	34:a:626:G:C2	2.80	0.70
7:6:45:THR:HG22	7:6:46:GLY:H	1.56	0.69
34:a:254:G:OP1	50:q:68:LYS:HB3	1.93	0.69
34:a:458:U:H2'	34:a:459:A:H8	1.56	0.69
34:a:1130:A:H2'	34:a:1131:G:H8	1.56	0.69
35:b:17:HIS:ND1	35:b:187:ASP:OD2	2.26	0.69
56:w:26:A:N6	56:w:44:G:H1	1.91	0.69
1:0:12:ARG:NH2	8:A:517:C:OP1	2.25	0.69
8:A:848:C:H2'	8:A:849:A:H8	1.57	0.69
15:H:79:THR:HG23	15:H:145:ASN:HB3	1.75	0.69
40:g:111:GLY:HA2	40:g:118:ARG:HD3	1.75	0.69
8:A:284:U:O2	8:A:356:G:N2	2.21	0.69
8:A:869:G:H1'	20:M:8:LYS:HE3	1.75	0.69
10:C:259:ASN:ND2	10:C:262:THR:OG1	2.25	0.69
34:a:875:U:O2'	41:h:14:ARG:NH1	2.26	0.69
53:t:34:VAL:HG21	53:t:53:MET:HG2	1.75	0.69
28:U:47:PRO:HB2	28:U:53:GLN:HB3	1.74	0.69
50:q:69:THR:O	50:q:69:THR:OG1	2.03	0.69
8:A:2121:G:OP2	8:A:2171:A:O2'	2.10	0.68
34:a:1123:U:O2'	43:j:39:PRO:O	2.11	0.68
3:2:12:ARG:NH2	8:A:686:U:O4	2.25	0.68
8:A:84:A:N1	8:A:98:G:O2'	2.24	0.68
8:A:1799:G:OP2	10:C:269:ARG:NH2	2.25	0.68
8:A:2467:C:O2	20:M:123:LYS:NZ	2.21	0.68
34:a:9:G:H4'	38:e:108:GLY:H	1.57	0.68
35:b:91:VAL:HG22	35:b:150:ILE:HD11	1.74	0.68
37:d:26:ALA:HB3	37:d:29:THR:HG22	1.75	0.68
8:A:1012:U:OP2	24:Q:69:ARG:NH1	2.26	0.68
30:W:7:ARG:O	30:W:10:ARG:NH1	2.27	0.68
34:a:362:G:N2	34:a:365:U:OP2	2.26	0.68
45:l:39:THR:HB	45:l:89:LEU:HD11	1.76	0.68
20:M:47:GLU:OE2	20:M:50:ARG:NH1	2.24	0.68
34:a:615:G:C2	34:a:626:G:C5	2.82	0.68
34:a:826:C:O2	41:h:15:ASN:ND2	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:993:G:O2'	34:a:994:A:N7	2.26	0.68
8:A:1212:G:O2'	8:A:1236:G:N2	2.27	0.68
8:A:2445:2MG:OP1	12:E:69:ARG:NH2	2.22	0.68
8:A:2484:G:OP1	20:M:44:ARG:NH2	2.25	0.68
8:A:2566:A:N1	18:K:28:SER:OG	2.25	0.68
8:A:2759:G:N2	14:G:138:GLN:OE1	2.27	0.68
34:a:28:A:O2'	34:a:296:U:OP1	2.11	0.68
34:a:477:C:H2'	34:a:478:A:C8	2.28	0.68
34:a:1101:A:H61	35:b:101:THR:HG21	1.59	0.68
46:m:32:ILE:HD13	46:m:59:VAL:HG22	1.76	0.68
8:A:1028:A:H2'	8:A:1029:A:C8	2.29	0.68
1:0:4:GLN:OE1	8:A:2056:G:O2'	2.11	0.68
8:A:2123:G:O2'	8:A:2176:A:N1	2.27	0.68
8:A:1798:U:OP2	10:C:270:ARG:NH2	2.24	0.67
8:A:2136:G:O6	8:A:2154:A:N6	2.27	0.67
32:Y:18:LEU:HD11	32:Y:54:LYS:HG2	1.76	0.67
8:A:270:A:N1	8:A:369:U:O2'	2.25	0.67
15:H:100:ALA:O	15:H:104:THR:HG22	1.93	0.67
8:A:2107:G:N7	8:A:2108:A:N6	2.42	0.67
8:A:2780:G:O6	17:J:99:ARG:NH1	2.27	0.67
20:M:56:ALA:HB2	20:M:119:LEU:HD12	1.77	0.67
40:g:4:ARG:HH12	40:g:6:ILE:HA	1.58	0.67
8:A:2898:U:H2'	8:A:2899:A:H8	1.60	0.67
34:a:664:G:H22	34:a:741:G:H1	1.40	0.67
40:g:26:VAL:HG22	40:g:42:VAL:HG11	1.75	0.67
4:3:11:LYS:NZ	8:A:249:C:O2	2.28	0.67
34:a:859:G:OP2	34:a:869:G:N1	2.22	0.67
36:c:76:ILE:HA	36:c:83:VAL:HG23	1.77	0.67
43:j:50:THR:HG22	43:j:62:ARG:HD3	1.76	0.67
22:O:99:TYR:OH	22:O:111:ARG:NH1	2.28	0.67
34:a:689:C:OP1	44:k:28:ASN:ND2	2.27	0.67
34:a:1077:G:N2	34:a:1080:A:OP2	2.25	0.67
34:a:1266:G:N2	34:a:1269:A:OP2	2.26	0.67
3:2:29:GLN:NE2	8:A:210:C:OP1	2.26	0.66
8:A:805:G:N2	8:A:829:A:OP1	2.28	0.66
34:a:966:2MG:HM22	56:w:34:G:H5'	1.77	0.66
34:a:1040:U:H2'	34:a:1041:G:C8	2.30	0.66
39:f:38:ARG:HH21	39:f:63:ASN:HD21	1.43	0.66
11:D:77:ARG:NH2	11:D:200:ASP:OD1	2.28	0.66
40:g:15:PRO:HB3	42:i:45:MET:HG2	1.77	0.66
8:A:355:U:H2'	8:A:356:G:H8	1.61	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1373:G:H5''	40:g:35:LYS:HD2	1.76	0.66
38:e:104:ILE:O	38:e:111:ARG:NH1	2.25	0.66
8:A:633:A:H5''	19:L:70:LYS:HD2	1.77	0.66
8:A:1070:A:H61	16:I:23:VAL:HA	1.60	0.66
34:a:492:C:H2'	34:a:493:A:C8	2.31	0.66
8:A:1054:A:C6	8:A:1106:G:C6	2.84	0.66
8:A:75:G:H22	8:A:111:A:H2	1.44	0.65
9:B:30:C:H1'	9:B:57:A:H61	1.61	0.65
34:a:462:G:H21	34:a:471:U:H3	1.43	0.65
36:c:84:GLU:OE2	36:c:88:LYS:NZ	2.29	0.65
49:p:47:GLU:O	49:p:49:GLY:N	2.29	0.65
6:5:1:MET:N	8:A:1105:U:OP1	2.25	0.65
9:B:48:U:H4'	22:O:100:HIS:HD2	1.59	0.65
8:A:704:G:O2'	8:A:727:A:N6	2.29	0.65
8:A:1226:A:OP1	24:Q:15:LYS:NZ	2.26	0.65
8:A:2618:G:H21	11:D:155:VAL:HG21	1.61	0.65
8:A:2857:G:N2	8:A:2860:A:OP2	2.27	0.65
36:c:23:ALA:HB1	36:c:27:GLU:HG2	1.78	0.65
8:A:639:U:H2'	8:A:640:C:C6	2.30	0.65
8:A:781:A:OP1	10:C:216:ARG:NH2	2.29	0.65
8:A:2523:G:HO2'	8:A:2764:A:HO2'	1.39	0.65
34:a:458:U:H2'	34:a:459:A:C8	2.31	0.65
34:a:842:U:O2'	34:a:845:A:OP2	2.12	0.65
34:a:1414:U:H2'	34:a:1415:G:H8	1.62	0.65
35:b:163:ILE:HD11	35:b:213:LEU:HD21	1.79	0.65
8:A:764:A:OP1	10:C:206:LYS:NZ	2.28	0.65
12:E:189:THR:HG22	12:E:191:ASP:H	1.61	0.65
23:P:70:GLU:OE2	23:P:100:ARG:NE	2.30	0.65
40:g:4:ARG:HH22	40:g:7:GLY:H	1.44	0.65
18:K:9:ASN:OD1	18:K:18:ARG:NH1	2.29	0.65
34:a:528:C:N4	45:l:45:ASN:OD1	2.28	0.65
34:a:1345:U:OP1	42:i:121:ARG:NH1	2.30	0.65
34:a:1360:A:OP2	47:n:75:ARG:NH2	2.30	0.65
35:b:116:LEU:HB3	35:b:140:LEU:HD12	1.79	0.65
8:A:155:A:H2'	8:A:156:A:C8	2.31	0.65
8:A:1799:G:N7	10:C:177:SER:OG	2.29	0.65
8:A:2728:U:H2'	8:A:2729:G:C8	2.32	0.65
9:B:1:U:H2'	9:B:2:G:C8	2.32	0.65
23:P:105:LYS:O	23:P:108:ARG:NH2	2.29	0.65
4:3:31:ILE:O	4:3:31:ILE:HG13	1.95	0.64
11:D:10:GLY:H	11:D:197:THR:HG23	1.61	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1316:G:N1	34:a:1319:A:OP2	2.30	0.64
8:A:181:A:H2'	8:A:182:A:C8	2.33	0.64
8:A:299:A:N3	8:A:319:G:O2'	2.31	0.64
29:V:10:LYS:HD2	29:V:10:LYS:H	1.61	0.64
8:A:2305:U:H5''	13:F:130:GLY:HA3	1.78	0.64
26:S:82:MET:HB2	26:S:98:LYS:HB2	1.78	0.64
34:a:126:G:OP1	34:a:605:U:O2'	2.11	0.64
8:A:2446:G:N2	8:A:2449:U:O2	2.29	0.64
8:A:813:U:H2'	8:A:814:C:H6	1.62	0.64
8:A:1779:U:H5	8:A:1784:A:N7	1.94	0.64
8:A:2705:A:O2'	8:A:2852:G:OP1	2.15	0.64
34:a:464:U:N3	34:a:467:U:OP2	2.30	0.64
36:c:72:PRO:HA	36:c:75:VAL:HG12	1.78	0.64
37:d:155:LYS:O	37:d:159:GLU:HG2	1.98	0.64
8:A:954:G:OP2	20:M:16:ARG:NH1	2.30	0.64
8:A:1326:U:H2'	8:A:1327:A:H8	1.62	0.64
8:A:1366:A:OP1	31:X:1:SER:OG	2.13	0.64
8:A:1645:G:H5''	8:A:1646:C:H5'	1.79	0.64
34:a:80:A:OP2	34:a:86:G:N2	2.29	0.64
34:a:1270:G:HO2'	34:a:1313:U:HO2'	1.44	0.64
10:C:141:HIS:ND1	10:C:192:GLY:O	2.26	0.64
29:V:42:LEU:HD13	29:V:47:VAL:HG21	1.78	0.64
14:G:40:VAL:O	14:G:54:ARG:NH2	2.30	0.64
28:U:3:LYS:HD3	28:U:82:VAL:HB	1.79	0.64
34:a:1040:U:H2'	34:a:1041:G:H8	1.63	0.64
4:3:15:LYS:HE2	4:3:19:GLY:HA2	1.79	0.64
8:A:690:G:H21	10:C:42:ARG:HH12	1.45	0.64
12:E:41:GLN:NE2	12:E:43:THR:OG1	2.29	0.64
34:a:946:A:H2'	34:a:947:G:C8	2.33	0.64
34:a:1356:G:H2'	34:a:1357:A:C8	2.33	0.64
34:a:1500:A:H5''	34:a:1508:A:H5''	1.80	0.64
8:A:1056:G:OP1	8:A:1085:A:N6	2.30	0.64
8:A:2199:A:OP1	31:X:36:ARG:NH2	2.29	0.64
10:C:250:GLN:NE2	10:C:251:THR:O	2.31	0.64
12:E:58:LYS:HG2	12:E:71:GLY:HA2	1.80	0.64
18:K:121:GLU:HG2	18:K:122:VAL:HG23	1.79	0.64
38:e:45:VAL:HG11	38:e:113:VAL:HG23	1.80	0.64
8:A:310:A:O2'	8:A:311:A:O5'	2.15	0.63
8:A:788:A:OP1	8:A:791:C:N4	2.27	0.63
35:b:96:LEU:H	35:b:99:MET:HE3	1.61	0.63
35:b:186:VAL:HG11	35:b:192:PRO:HB3	1.78	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:6:3:LYS:NZ	9:B:36:C:OP1	2.30	0.63
8:A:284:U:O4	8:A:356:G:O6	2.15	0.63
8:A:1219:U:OP2	24:Q:18:LYS:NZ	2.31	0.63
8:A:2116:G:N1	8:A:2163:A:OP2	2.31	0.63
8:A:2117:A:H5''	8:A:2148:G:H5'	1.80	0.63
34:a:68:G:H1'	34:a:171:A:C2	2.33	0.63
34:a:206:C:H5'	34:a:207:C:H5	1.63	0.63
8:A:639:U:H2'	8:A:640:C:H6	1.63	0.63
34:a:110:C:O2'	49:p:25:ARG:O	2.15	0.63
34:a:246:A:N1	34:a:278:G:O2'	2.31	0.63
8:A:1089:A:O2'	8:A:1090:A:O5'	2.17	0.63
8:A:1385:A:O2'	8:A:1396:U:O2	2.14	0.63
8:A:1432:G:H2'	8:A:1433:A:C8	2.34	0.63
8:A:2187:U:H2'	8:A:2188:U:H6	1.63	0.63
8:A:2584:U:H3'	8:A:2585:U:H5''	1.80	0.63
22:O:53:THR:HG21	22:O:70:ALA:HB1	1.78	0.63
34:a:842:U:H2'	34:a:844:G:H5''	1.80	0.63
34:a:1144:G:N2	34:a:1146:A:H62	1.96	0.63
39:f:9:MET:HE3	39:f:86:ARG:HB2	1.80	0.63
2:1:13:SER:OG	2:1:47:ILE:O	2.12	0.63
7:6:18:CYS:HB2	7:6:40:CYS:HB3	1.80	0.63
8:A:1914:C:H2'	8:A:1915:3TD:O4	1.98	0.63
10:C:132:ARG:O	10:C:166:ARG:NH1	2.28	0.63
17:J:99:ARG:NH1	17:J:102:GLU:OE1	2.32	0.63
35:b:157:PRO:HG2	35:b:180:ILE:HD13	1.79	0.63
8:A:1437:C:HO2'	8:A:1516:G:HO2'	1.42	0.63
34:a:718:A:H5'	44:k:118:ASN:ND2	2.14	0.63
43:j:52:LEU:HD23	43:j:62:ARG:HG2	1.81	0.63
8:A:219:A:N3	8:A:234:U:O2'	2.26	0.63
34:a:85:U:O5'	34:a:87:C:N4	2.31	0.63
49:p:4:ILE:HG12	49:p:21:VAL:HG22	1.80	0.63
8:A:2133:G:O2'	8:A:2158:A:N1	2.30	0.63
18:K:65:THR:HG22	18:K:67:LYS:H	1.64	0.63
25:R:25:LEU:H	25:R:94:THR:HG21	1.62	0.63
28:U:40:LEU:HB3	28:U:59:GLU:OE2	1.99	0.63
30:W:55:LEU:HD12	30:W:76:ILE:HD12	1.79	0.63
34:a:746:A:H2'	34:a:747:A:C8	2.34	0.63
2:1:29:LYS:NZ	8:A:2286:G:OP1	2.31	0.62
8:A:335:C:O2	28:U:67:SER:OG	2.15	0.62
8:A:547:A:O2'	8:A:548:G:O5'	2.17	0.62
8:A:1487:U:N3	8:A:1502:A:N6	2.47	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:C:23:LEU:HD13	10:C:82:TYR:HB2	1.80	0.62
11:D:33:ARG:NH1	11:D:53:GLY:O	2.32	0.62
31:X:3:VAL:HG22	31:X:10:ARG:HB3	1.80	0.62
34:a:407:U:O2'	37:d:112:GLU:OE1	2.16	0.62
34:a:993:G:H2'	34:a:995:C:H41	1.64	0.62
10:C:140:VAL:HG12	10:C:191:LEU:HD23	1.82	0.62
15:H:113:SER:O	15:H:116:ARG:NH1	2.32	0.62
8:A:2589:A:H2	8:A:2605:PSU:O4	1.82	0.62
8:A:2809:A:OP2	8:A:2890:G:N1	2.25	0.62
29:V:31:TYR:HE1	29:V:90:ASP:HB3	1.65	0.62
34:a:90:C:C6	34:a:90:C:C3'	2.81	0.62
34:a:951:G:OP2	46:m:100:ARG:NH2	2.32	0.62
34:a:105:G:OP2	53:t:12:GLN:NE2	2.32	0.62
39:f:11:HIS:ND1	39:f:13:ASP:OD1	2.30	0.62
8:A:1063:G:H2'	16:l:88:GLY:HA3	1.82	0.62
8:A:2898:U:H2'	8:A:2899:A:C8	2.34	0.62
36:c:10:ARG:NH2	36:c:174:LEU:O	2.32	0.62
7:6:38:SER:HB3	13:F:104:THR:HA	1.81	0.62
14:G:120:ILE:HD11	14:G:139:VAL:HG23	1.80	0.62
24:Q:85:ALA:HB2	24:Q:115:ALA:HB2	1.80	0.62
34:a:1125:U:H2'	34:a:1126:U:H2'	1.81	0.62
40:g:13:PRO:HG2	42:i:45:MET:HE1	1.80	0.62
56:w:23:A:H2'	56:w:24:G:C8	2.34	0.62
8:A:818:G:N1	8:A:1188:U:OP2	2.23	0.62
14:G:1:SER:OG	14:G:2:ARG:N	2.33	0.62
9:B:8:C:O3'	22:O:25:ARG:NH1	2.32	0.62
34:a:633:G:OP2	41:h:87:ARG:NH2	2.30	0.62
34:a:714:G:H2'	34:a:715:A:C8	2.35	0.62
34:a:1013:G:N2	34:a:1016:A:OP2	2.26	0.62
8:A:2116:G:N2	8:A:2162:G:OP1	2.29	0.62
8:A:2788:C:H2'	8:A:2789:C:C6	2.34	0.62
34:a:1305:G:O2'	34:a:1306:A:O5'	2.18	0.62
4:3:22:LYS:NZ	8:A:631:A:OP2	2.30	0.61
8:A:2063:C:H5'	55:v:102:PHE:CZ	2.35	0.61
8:A:2128:G:H1'	8:A:2173:A:H1'	1.81	0.61
8:A:2291:U:H2'	8:A:2292:U:C6	2.35	0.61
11:D:1:MET:HG3	11:D:205:PRO:HG2	1.81	0.61
34:a:1261:A:N6	34:a:1274:A:O2'	2.33	0.61
34:a:1356:G:H2'	34:a:1357:A:H8	1.64	0.61
35:b:33:ALA:HB2	35:b:38:HIS:HA	1.82	0.61
43:j:35:GLN:HB3	43:j:77:VAL:HB	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:m:11:HIS:HA	46:m:43:LYS:HD3	1.81	0.61
8:A:2847:U:H2'	8:A:2848:G:O4'	2.00	0.61
34:a:553:A:H5''	45:l:20:VAL:HG21	1.81	0.61
8:A:884:U:O5'	8:A:884:U:H6	1.83	0.61
8:A:2125:G:O2'	8:A:2173:A:N6	2.30	0.61
34:a:202:G:H21	34:a:466:A:H61	1.47	0.61
34:a:254:G:N2	50:q:17:GLU:OE1	2.25	0.61
34:a:1004:A:C5	34:a:1026:G:H1'	2.35	0.61
8:A:1826:G:O2'	8:A:1971:U:OP2	2.17	0.61
10:C:250:GLN:HB3	10:C:254:LYS:HD2	1.83	0.61
34:a:113:G:H1'	34:a:354:G:H5'	1.82	0.61
34:a:1218:C:H2'	34:a:1219:A:C8	2.35	0.61
8:A:351:C:H2'	8:A:352:A:H8	1.65	0.61
40:g:91:ARG:O	40:g:95:ARG:HG3	2.00	0.61
8:A:463:G:N2	8:A:466:A:OP2	2.30	0.61
8:A:2773:C:OP1	11:D:169:ARG:NH2	2.33	0.61
8:A:1036:G:O6	8:A:1119:U:O4	2.18	0.61
8:A:1503:A:OP1	8:A:1503:A:H4'	1.99	0.61
8:A:1734:G:H2'	8:A:1735:A:C8	2.35	0.61
36:c:85:LYS:O	36:c:89:VAL:HG22	2.01	0.61
37:d:169:TRP:CE2	37:d:185:PRO:HB3	2.36	0.61
8:A:538:A:H4'	17:J:7:LYS:HG2	1.83	0.61
8:A:559:G:N2	24:Q:48:ASP:OD1	2.34	0.61
8:A:1682:G:OP2	8:A:1699:G:N2	2.34	0.61
8:A:2757:A:N1	14:G:66:THR:OG1	2.33	0.61
25:R:24:LYS:HA	25:R:94:THR:HG23	1.83	0.61
17:J:31:GLU:HG2	17:J:142:ILE:HB	1.83	0.61
34:a:83:C:O2'	34:a:85:U:OP2	2.19	0.61
40:g:78:ARG:HB3	40:g:83:THR:HA	1.82	0.61
8:A:282:A:H2'	8:A:283:G:C8	2.35	0.60
8:A:1502:A:H3'	8:A:1503:A:H5''	1.83	0.60
51:r:21:ASP:OD1	51:r:23:LYS:NZ	2.29	0.60
8:A:511:U:H4'	8:A:1235:G:H4'	1.83	0.60
8:A:1913:A:H5'	34:a:1493:A:H2	1.65	0.60
8:A:2305:U:O2'	13:F:132:ARG:NH2	2.33	0.60
30:W:30:GLY:N	30:W:57:ALA:O	2.26	0.60
32:Y:10:SER:HB3	32:Y:12:GLU:O	2.01	0.60
34:a:713:G:H2'	34:a:714:G:C8	2.35	0.60
34:a:958:A:N7	52:s:54:ARG:NH1	2.48	0.60
34:a:1151:A:HO2'	34:a:1152:A:H8	1.48	0.60
56:w:68:C:H2'	56:w:69:G:H8	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:G:45:ALA:O	14:G:48:THR:OG1	2.18	0.60
34:a:89:U:H2'	34:a:90:C:C5	2.37	0.60
34:a:1092:A:OP2	40:g:3:ARG:NH2	2.34	0.60
37:d:112:GLU:OE2	37:d:153:ARG:NH2	2.35	0.60
7:6:36:VAL:HG11	7:6:41:HIS:CD2	2.34	0.60
8:A:1099:G:H2'	8:A:1100:C:C6	2.37	0.60
8:A:714:U:OP2	48:o:88:ARG:NE	2.28	0.60
8:A:782:A:O2'	10:C:223:ALA:O	2.20	0.60
34:a:309:A:O2'	34:a:607:A:N1	2.34	0.60
34:a:1033:G:O2'	34:a:1034:G:O4'	2.18	0.60
37:d:125:ASN:N	37:d:141:VAL:O	2.28	0.60
7:6:18:CYS:HB2	7:6:40:CYS:CB	2.30	0.60
8:A:742:A:H2'	8:A:743:A:C8	2.36	0.60
12:E:1:MET:HE3	12:E:20:GLY:HA3	1.84	0.60
37:d:94:GLU:HA	37:d:99:ASN:ND2	2.17	0.60
8:A:2646:C:OP2	8:A:2732:G:O2'	2.18	0.60
15:H:90:LEU:HD23	15:H:122:LEU:HD22	1.83	0.60
44:k:87:GLY:O	44:k:92:ARG:NH1	2.34	0.60
12:E:146:VAL:HG12	12:E:185:LYS:HB2	1.81	0.60
37:d:99:ASN:OD1	37:d:110:ARG:NH2	2.35	0.60
4:3:29:ARG:HH11	19:L:62:PRO:HB2	1.67	0.60
8:A:483:A:O2'	28:U:56:GLY:N	2.35	0.60
8:A:886:A:H8	8:A:886:A:OP2	1.85	0.60
8:A:887:U:C5'	46:m:91:ARG:HD3	2.24	0.60
8:A:1509:A:H2'	8:A:1510:G:C8	2.37	0.60
8:A:1919:A:N1	34:a:1495:U:O2'	2.29	0.60
8:A:2328:A:H2'	8:A:2329:U:C6	2.37	0.60
8:A:2683:C:O2	18:K:70:ARG:NH2	2.35	0.60
10:C:1:ALA:N	10:C:19:VAL:O	2.35	0.60
34:a:509:A:N3	34:a:543:U:O2'	2.30	0.60
34:a:745:G:H2'	34:a:746:A:C8	2.36	0.60
5:4:1:MET:SD	5:4:36:ARG:HB2	2.42	0.60
8:A:930:G:H1'	33:Z:24:LEU:HD21	1.84	0.60
8:A:1490:A:O2'	8:A:1491:G:OP1	2.20	0.60
13:F:141:ASP:H	13:F:144:LYS:NZ	1.99	0.60
14:G:25:ILE:HG22	14:G:78:VAL:HG21	1.84	0.60
34:a:546:A:O2'	34:a:548:G:O2'	2.19	0.60
37:d:116:LEU:HD21	37:d:144:ILE:HD11	1.84	0.60
5:4:2:LYS:NZ	5:4:32:LYS:O	2.35	0.59
8:A:2:G:H2'	8:A:3:U:C6	2.37	0.59
8:A:2299:U:OP1	13:F:71:LYS:NZ	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:B:5:U:OP1	9:B:61:G:O2'	2.15	0.59
10:C:129:LEU:HD12	10:C:133:ASN:HB2	1.83	0.59
17:J:73:VAL:HG22	17:J:88:THR:HG22	1.84	0.59
34:a:264:C:H4'	50:q:64:ARG:HD2	1.84	0.59
8:A:181:A:H2'	8:A:182:A:H8	1.66	0.59
8:A:1212:G:HO2'	8:A:1236:G:H22	1.42	0.59
24:Q:39:ILE:HG22	24:Q:43:GLN:HE21	1.68	0.59
37:d:57:LYS:NZ	37:d:68:GLU:OE2	2.35	0.59
9:B:48:U:H2'	9:B:49:C:C6	2.38	0.59
10:C:132:ARG:HG3	10:C:185:ALA:HB1	1.84	0.59
11:D:33:ARG:NH2	11:D:74:GLU:O	2.35	0.59
17:J:19:ASP:OD1	17:J:21:THR:OG1	2.18	0.59
44:k:93:GLU:OE2	44:k:97:ARG:NH1	2.35	0.59
8:A:1469:A:H2'	8:A:1470:A:C8	2.37	0.59
34:a:460:A:H2'	34:a:461:A:C8	2.37	0.59
34:a:559:A:H4'	34:a:560:A:H3'	1.83	0.59
34:a:789:U:O2'	34:a:791:G:N7	2.26	0.59
34:a:1218:C:H2'	34:a:1219:A:H8	1.66	0.59
40:g:139:ASP:OD1	40:g:142:ARG:NH2	2.31	0.59
8:A:155:A:H2'	8:A:156:A:H8	1.65	0.59
36:c:39:ARG:NH1	36:c:54:ILE:O	2.35	0.59
8:A:1817:G:OP2	10:C:155:ARG:NH2	2.35	0.59
9:B:41:G:H8	13:F:65:LEU:HD11	1.67	0.59
34:a:496:A:N3	34:a:496:A:H2'	2.17	0.59
34:a:727:G:N2	34:a:730:G:OP2	2.32	0.59
34:a:911:U:H2'	34:a:912:C:C6	2.38	0.59
40:g:114:SER:O	40:g:118:ARG:NE	2.35	0.59
40:g:147:ASN:OD1	44:k:55:ARG:NH2	2.34	0.59
2:1:7:LYS:HA	2:1:23:THR:HA	1.84	0.59
34:a:201:G:H1	34:a:216:U:H3	1.50	0.59
8:A:839:U:H2'	8:A:840:C:C6	2.37	0.59
8:A:2698:U:H2'	8:A:2699:C:C6	2.38	0.59
8:A:1338:G:O2'	8:A:1393:A:N1	2.32	0.59
17:J:36:LEU:HD11	17:J:122:LEU:HD13	1.84	0.59
19:L:77:ILE:HD11	19:L:108:ALA:HB1	1.84	0.59
34:a:1374:A:OP1	40:g:35:LYS:NZ	2.36	0.59
8:A:1864:U:OP1	8:A:2410:G:O2'	2.20	0.59
11:D:151:THR:HB	11:D:152:PRO:HD3	1.83	0.59
17:J:4:PHE:O	24:Q:63:ARG:NH2	2.31	0.59
56:w:65:G:H2'	56:w:66:U:C6	2.38	0.59
8:A:2514:U:H2'	8:A:2515:C:C6	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2532:G:N2	8:A:2663:G:O2'	2.36	0.58
13:F:103:ILE:HD11	13:F:174:PHE:H	1.66	0.58
34:a:976:G:OP2	34:a:1358:U:O2'	2.21	0.58
34:a:1086:U:H3	34:a:1099:G:H1	1.51	0.58
5:4:23:ILE:HD13	8:A:1032:A:H1'	1.84	0.58
8:A:910:A:H62	20:M:12:MET:HA	1.68	0.58
8:A:1802:A:H2'	8:A:1803:A:C8	2.38	0.58
8:A:1847:G:HO2'	8:A:1848:A:H8	1.50	0.58
8:A:184:C:H2'	8:A:185:G:H8	1.68	0.58
8:A:813:U:H2'	8:A:814:C:C6	2.38	0.58
8:A:2395:C:OP1	19:L:63:LYS:NZ	2.33	0.58
18:K:99:ILE:HD12	18:K:118:LEU:HB2	1.85	0.58
20:M:50:ARG:HD3	20:M:65:ILE:HD11	1.83	0.58
28:U:6:ARG:NH2	28:U:25:LYS:O	2.35	0.58
34:a:1060:U:H4'	43:j:53:ILE:HG23	1.86	0.58
42:i:49:GLN:OE1	42:i:79:ARG:NH1	2.34	0.58
3:2:12:ARG:NE	3:2:44:VAL:HG21	2.18	0.58
7:6:56:ARG:HH11	52:s:67:GLY:HA3	1.68	0.58
8:A:1242:U:O2	19:L:4:ASN:ND2	2.30	0.58
11:D:25:THR:OG1	11:D:191:GLY:O	2.21	0.58
15:H:4:ILE:HG23	15:H:37:VAL:HG23	1.85	0.58
34:a:474:G:H2'	34:a:475:C:C6	2.38	0.58
34:a:475:C:H2'	34:a:476:U:O2	2.03	0.58
34:a:1026:G:H1	34:a:1035:A:H61	1.48	0.58
8:A:774:G:O2'	8:A:775:G:H5''	2.03	0.58
8:A:2649:C:H2'	8:A:2650:U:H6	1.69	0.58
17:J:17:VAL:HG23	17:J:137:PRO:HB2	1.84	0.58
34:a:373:A:H1'	34:a:481:G:C8	2.38	0.58
34:a:626:G:O3'	49:p:51:ARG:NH2	2.36	0.58
37:d:149:LYS:HG3	37:d:177:MET:SD	2.43	0.58
6:5:31:ARG:CB	8:A:1054:A:O2'	2.52	0.58
8:A:370:G:O2'	8:A:424:G:OP1	2.19	0.58
8:A:414:C:O3'	8:A:1878:G:N2	2.36	0.58
8:A:1022:G:N2	8:A:1023:U:O4	2.34	0.58
8:A:2406:A:H4'	8:A:2407:A:O5'	2.03	0.58
14:G:21:GLN:OE1	14:G:54:ARG:NH2	2.37	0.58
7:6:63:ARG:HH11	52:s:4:LEU:HD11	1.68	0.58
8:A:1053:C:H2'	8:A:1053:C:OP2	2.03	0.58
8:A:1339:G:OP2	27:T:15:HIS:NE2	2.35	0.58
34:a:68:G:H1'	34:a:171:A:N3	2.18	0.58
34:a:1321:U:O3'	52:s:77:ARG:NH2	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:m:113:LYS:HB2	46:m:114:PRO:HD3	1.84	0.58
8:A:1434:A:H2'	8:A:1435:G:H8	1.68	0.58
8:A:1794:A:H2'	8:A:1795:C:C6	2.38	0.58
34:a:1071:C:H2'	34:a:1072:G:H8	1.68	0.58
38:e:54:GLU:HG3	38:e:56:PRO:HD2	1.85	0.58
8:A:2262:U:H5	30:W:12:SER:HG	1.51	0.58
34:a:1153:G:OP1	43:j:15:HIS:NE2	2.37	0.58
42:i:66:VAL:HG11	42:i:78:ILE:HD11	1.85	0.58
42:i:104:THR:HG22	42:i:106:ASP:H	1.69	0.58
8:A:1096:A:C2	16:I:26:ALA:HB2	2.39	0.58
8:A:1964:G:O2'	8:A:1967:C:OP2	2.19	0.58
8:A:2187:U:H2'	8:A:2188:U:C6	2.39	0.58
36:c:124:GLU:OE2	36:c:189:HIS:N	2.37	0.58
38:e:135:VAL:O	38:e:139:THR:HG23	2.04	0.58
1:0:38:LEU:HB2	1:0:41:HIS:HB2	1.84	0.57
8:A:363:G:H2'	8:A:364:C:C6	2.39	0.57
8:A:848:C:H2'	8:A:849:A:C8	2.38	0.57
28:U:73:ASN:ND2	28:U:80:ASP:OD2	2.37	0.57
34:a:331:G:H2'	53:t:4:LYS:HE3	1.86	0.57
34:a:337:G:H2'	34:a:338:A:H8	1.69	0.57
34:a:1305:G:H1'	34:a:1332:A:N6	2.19	0.57
40:g:25:PHE:HZ	40:g:119:LEU:HD11	1.69	0.57
8:A:476:G:N1	8:A:479:A:OP2	2.33	0.57
8:A:871:U:H2'	8:A:872:U:C6	2.39	0.57
8:A:2314:A:OP1	13:F:87:LYS:NZ	2.37	0.57
18:K:81:GLY:N	23:P:67:GLU:OE2	2.37	0.57
37:d:47:LEU:HD21	37:d:55:ARG:HG3	1.87	0.57
8:A:691:C:OP1	10:C:216:ARG:NH1	2.36	0.57
8:A:1057:A:OP2	8:A:1089:A:N6	2.37	0.57
8:A:1341:G:OP2	8:A:1394:U:O2'	2.19	0.57
8:A:1653:G:H3'	21:N:2:ARG:HG2	1.87	0.57
14:G:34:ARG:HE	14:G:70:LEU:HD13	1.68	0.57
34:a:207:C:H1'	34:a:213:G:C6	2.37	0.57
34:a:229:U:O2'	49:p:23:ASP:OD2	2.21	0.57
53:t:14:GLU:OE2	53:t:17:ARG:NH2	2.36	0.57
8:A:587:C:O2	19:L:33:ARG:NH1	2.37	0.57
8:A:859:G:O2'	8:A:916:G:O6	2.18	0.57
14:G:37:ASN:HD22	14:G:63:GLN:HG2	1.68	0.57
15:H:4:ILE:HD13	15:H:18:GLN:HG2	1.86	0.57
27:T:6:ARG:O	27:T:10:VAL:HG23	2.04	0.57
34:a:89:U:H3'	34:a:89:U:H6	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:c:46:LEU:HD21	36:c:86:LEU:HD11	1.86	0.57
41:h:45:ILE:HD11	41:h:60:LEU:HB3	1.86	0.57
8:A:1415:U:H3	8:A:1587:G:H1	1.51	0.57
34:a:203:G:N2	34:a:204:G:O6	2.37	0.57
34:a:1095:U:P	34:a:1108:G:H1	2.28	0.57
34:a:1224:U:O2'	34:a:1322:C:OP1	2.21	0.57
31:X:11:PRO:HB3	31:X:29:LEU:HD23	1.87	0.57
34:a:946:A:O2'	34:a:1333:A:N3	2.32	0.57
34:a:1120:C:H2'	34:a:1121:U:H6	1.70	0.57
38:e:45:VAL:O	38:e:71:ILE:N	2.36	0.57
31:X:39:VAL:O	31:X:43:LYS:N	2.37	0.57
34:a:634:C:H2'	34:a:635:A:C8	2.38	0.57
5:4:34:LYS:NZ	8:A:2743:U:OP1	2.37	0.57
8:A:698:C:O2'	8:A:734:A:N6	2.35	0.57
8:A:1061:U:N3	16:I:12:VAL:HA	2.20	0.57
8:A:2728:U:O2'	8:A:2729:G:O5'	2.22	0.57
34:a:202:G:H1	34:a:215:C:H41	1.51	0.57
8:A:50:U:H3'	8:A:51:G:H5'	1.87	0.57
8:A:2114:A:N6	8:A:2117:A:N7	2.52	0.57
8:A:2375:G:N2	8:A:2378:A:OP2	2.34	0.57
34:a:464:U:O2'	34:a:465:A:OP1	2.23	0.57
34:a:1526:G:OP1	54:u:44:ARG:NH2	2.35	0.57
8:A:1090:A:C2	8:A:1102:C:H1'	2.40	0.57
8:A:1363:C:O2'	8:A:1809:A:N3	2.31	0.57
34:a:635:A:O2'	34:a:636:U:O4'	2.22	0.57
53:t:44:ALA:O	53:t:48:LYS:HG2	2.04	0.57
8:A:214:G:N2	8:A:216:A:N3	2.51	0.56
8:A:1570:A:H2'	8:A:1571:A:C8	2.40	0.56
19:L:115:GLU:N	19:L:115:GLU:OE1	2.38	0.56
30:W:33:ILE:HG21	30:W:76:ILE:HG21	1.87	0.56
34:a:555:U:H2'	34:a:556:C:C6	2.40	0.56
34:a:1323:G:H2'	34:a:1324:A:C8	2.40	0.56
46:m:76:ILE:HG22	46:m:80:MET:HE2	1.87	0.56
8:A:24:G:O2'	26:S:78:GLU:O	2.21	0.56
8:A:490:C:H4'	8:A:491:G:OP2	2.06	0.56
8:A:1056:G:H22	8:A:1102:C:H5'	1.70	0.56
8:A:1080:A:H1'	16:I:130:GLY:HA3	1.87	0.56
8:A:1796:U:H2'	8:A:1797:G:C8	2.40	0.56
34:a:462:G:H2'	34:a:470:C:H41	1.69	0.56
34:a:1355:G:H2'	34:a:1356:G:H8	1.70	0.56
43:j:63:ASP:OD2	47:n:85:ARG:NH1	2.34	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:324:A:OP2	8:A:1205:A:N6	2.37	0.56
8:A:878:A:H3'	8:A:879:G:H8	1.69	0.56
8:A:1416:G:H2'	8:A:1417:C:C6	2.41	0.56
8:A:2453:A:O2'	8:A:2572:A:H1'	2.05	0.56
8:A:2839:G:O2'	21:N:49:GLU:OE1	2.15	0.56
8:A:2901:C:N3	8:A:2902:C:N4	2.53	0.56
12:E:46:GLN:HB3	12:E:83:VAL:HG21	1.86	0.56
34:a:56:U:H2'	34:a:57:G:H8	1.69	0.56
34:a:207:C:H1'	34:a:213:G:C2	2.40	0.56
34:a:515:G:O2'	34:a:516:PSU:O5'	2.23	0.56
34:a:1034:G:H2'	34:a:1035:A:H8	1.69	0.56
34:a:1187:G:H5'	42:i:114:LYS:HE3	1.88	0.56
34:a:1316:G:H2'	34:a:1317:C:H5''	1.86	0.56
42:i:50:PRO:HD3	42:i:79:ARG:HG3	1.86	0.56
47:n:9:GLU:HG3	47:n:63:ARG:HD2	1.86	0.56
8:A:2102:G:H1	8:A:2187:U:H3	1.53	0.56
14:G:94:ARG:HG3	14:G:105:SER:HB3	1.87	0.56
23:P:90:ALA:HB3	23:P:110:LYS:HG3	1.86	0.56
34:a:474:G:H2'	34:a:475:C:H6	1.69	0.56
40:g:50:ALA:HB2	40:g:57:GLU:HG3	1.87	0.56
8:A:851:C:H2'	8:A:852:U:C6	2.41	0.56
8:A:1064:C:OP1	16:I:88:GLY:N	2.39	0.56
8:A:1068:G:N2	16:I:21:PRO:O	2.38	0.56
8:A:1565:C:O2'	8:A:1566:A:H2'	2.06	0.56
8:A:1689:A:H2'	8:A:1690:A:C8	2.41	0.56
18:K:99:ILE:HD13	18:K:115:ILE:HG23	1.87	0.56
36:c:21:TRP:HB3	36:c:58:ARG:H	1.69	0.56
51:r:25:ILE:HA	51:r:28:LEU:HB2	1.87	0.56
8:A:328:U:O2'	28:U:68:ASN:OD1	2.23	0.56
8:A:2173:A:H2'	8:A:2174:C:C6	2.40	0.56
8:A:2848:G:H2'	8:A:2867:G:N2	2.20	0.56
9:B:66:A:O2'	9:B:67:G:O5'	2.23	0.56
12:E:171:ASP:OD1	12:E:172:ALA:N	2.38	0.56
13:F:43:ILE:HA	13:F:82:TYR:CE2	2.41	0.56
13:F:135:ILE:HD11	13:F:142:TYR:HB2	1.87	0.56
43:j:36:VAL:HG22	43:j:38:GLY:H	1.70	0.56
8:A:868:U:O2	20:M:8:LYS:NZ	2.30	0.56
8:A:1548:A:H2'	8:A:1549:A:C8	2.41	0.56
8:A:1796:U:H2'	8:A:1797:G:H8	1.71	0.56
10:C:67:LYS:HG2	10:C:150:GLY:HA2	1.88	0.56
12:E:109:LEU:O	12:E:113:VAL:HG23	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:198:G:H2'	34:a:199:A:H8	1.71	0.56
34:a:299:G:N2	34:a:565:U:O2	2.38	0.56
8:A:1537:G:O2'	8:A:1538:G:O4'	2.24	0.56
12:E:111:GLU:OE2	12:E:115:GLN:NE2	2.35	0.56
31:X:39:VAL:HG12	31:X:42:GLU:H	1.71	0.56
34:a:1103:C:H5''	35:b:96:LEU:HD22	1.88	0.56
34:a:1397:C:H41	57:x:21:U:H5''	1.70	0.56
41:h:27:PRO:O	41:h:32:LYS:NZ	2.27	0.56
19:L:79:LEU:HD11	19:L:131:ALA:HA	1.88	0.56
34:a:505:G:H5'	34:a:534:U:H2'	1.88	0.56
35:b:67:LEU:HG	35:b:153:MET:HE1	1.87	0.56
37:d:74:TYR:OH	37:d:96:ARG:NH1	2.38	0.56
8:A:1799:G:O2'	10:C:179:GLU:OE2	2.13	0.56
9:B:111:U:H2'	9:B:112:G:H8	1.71	0.56
10:C:7:PRO:HA	10:C:13:ARG:HA	1.87	0.56
34:a:769:G:H4'	34:a:1513:A:H4'	1.88	0.56
37:d:97:LEU:HB2	37:d:134:TYR:HB3	1.87	0.56
39:f:6:ILE:HD11	39:f:71:ILE:HD11	1.88	0.56
56:w:50:U:H2'	56:w:51:C:C6	2.41	0.56
8:A:568:U:H1'	8:A:2030:6MZ:H9C1	1.88	0.55
8:A:1011:G:OP2	24:Q:65:ASN:ND2	2.37	0.55
8:A:1502:A:H3'	8:A:1503:A:C5'	2.36	0.55
34:a:16:A:N3	34:a:1080:A:O2'	2.37	0.55
34:a:701:U:OP1	34:a:702:A:O2'	2.12	0.55
34:a:754:C:O5'	48:o:71:ARG:NH2	2.39	0.55
44:k:29:THR:HG21	44:k:62:ALA:HB2	1.88	0.55
8:A:177:G:OP2	8:A:177:G:N2	2.24	0.55
8:A:833:A:H2'	8:A:834:G:C8	2.40	0.55
8:A:1495:A:H2'	8:A:1496:A:C8	2.42	0.55
8:A:2139:U:O2	8:A:2152:G:C6	2.59	0.55
10:C:42:ARG:HH21	10:C:48:ILE:HD11	1.72	0.55
18:K:88:ASN:OD1	18:K:89:ASN:N	2.37	0.55
36:c:21:TRP:NE1	36:c:35:ASP:OD2	2.37	0.55
36:c:135:ARG:O	36:c:139:ASN:ND2	2.39	0.55
38:e:106:ALA:O	38:e:111:ARG:NH2	2.39	0.55
47:n:79:LEU:HB2	47:n:84:VAL:HG23	1.88	0.55
8:A:742:A:H2'	8:A:743:A:H8	1.70	0.55
8:A:1915:3TD:H2'	8:A:1916:A:O4'	2.06	0.55
28:U:3:LYS:O	28:U:93:ARG:NH2	2.38	0.55
32:Y:32:ALA:HB2	32:Y:37:LEU:HD23	1.88	0.55
34:a:604:G:H2'	34:a:605:U:O4'	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:c:110:LEU:O	36:c:203:LYS:NZ	2.33	0.55
8:A:547:A:OP1	8:A:548:G:N2	2.40	0.55
8:A:743:A:O2'	8:A:1659:G:OP1	2.19	0.55
8:A:1198:U:H2'	8:A:1199:U:C6	2.41	0.55
8:A:1734:G:H2'	8:A:1735:A:H8	1.68	0.55
8:A:2243:U:H2'	8:A:2244:U:C6	2.41	0.55
14:G:23:ILE:HD11	14:G:42:VAL:HG11	1.87	0.55
15:H:104:THR:OG1	15:H:109:GLU:HB3	2.06	0.55
34:a:460:A:H2'	34:a:461:A:H8	1.71	0.55
36:c:11:LEU:HD11	47:n:91:GLY:HA2	1.87	0.55
37:d:138:PRO:HA	37:d:181:PHE:HD2	1.72	0.55
8:A:555:G:O2'	8:A:556:A:O5'	2.22	0.55
8:A:1715:G:O2'	8:A:1716:U:H6	1.90	0.55
8:A:2722:G:H4'	21:N:4:ARG:HB2	1.88	0.55
27:T:3:ARG:NH2	27:T:5:GLU:OE2	2.39	0.55
32:Y:2:LYS:NZ	32:Y:6:LEU:HD22	2.20	0.55
34:a:399:G:H2'	34:a:400:C:C6	2.42	0.55
34:a:539:A:OP2	45:l:111:GLN:NE2	2.40	0.55
35:b:202:ASN:OD1	35:b:203:ASP:N	2.39	0.55
46:m:64:VAL:O	46:m:64:VAL:HG23	2.06	0.55
8:A:492:A:H2	26:S:7:HIS:CD2	2.24	0.55
8:A:1141:U:OP2	17:J:65:THR:OG1	2.20	0.55
8:A:1502:A:C8	8:A:1503:A:H5''	2.41	0.55
8:A:2120:G:O2'	8:A:2121:G:O5'	2.22	0.55
34:a:190:A:H8	34:a:190:A:O5'	1.90	0.55
34:a:1287:A:H2'	34:a:1288:A:C8	2.41	0.55
39:f:72:ASP:O	39:f:76:THR:HG23	2.06	0.55
46:m:43:LYS:N	46:m:46:GLU:OE1	2.39	0.55
46:m:94:LEU:C	46:m:108:ARG:HG2	2.32	0.55
57:x:19:A:O2'	57:x:20:A:O4'	2.25	0.55
8:A:1000:A:H2'	8:A:1001:A:C8	2.42	0.55
8:A:1812:U:O2'	10:C:44:ASN:N	2.39	0.55
8:A:1818:U:H2'	10:C:155:ARG:HG2	1.88	0.55
15:H:57:LYS:O	15:H:61:VAL:HG23	2.06	0.55
34:a:376:G:H2'	34:a:377:G:H8	1.71	0.55
34:a:908:A:H2'	34:a:909:A:H8	1.71	0.55
34:a:1120:C:H2'	34:a:1121:U:C6	2.41	0.55
41:h:46:GLU:HB3	41:h:61:THR:HB	1.88	0.55
8:A:1028:A:N6	8:A:1125:G:H2'	2.21	0.55
8:A:1359:A:OP2	8:A:1371:G:N1	2.29	0.55
8:A:1482:G:H2'	8:A:1483:G:H8	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:135:C:N3	49:p:1:MET:N	2.43	0.55
34:a:410:G:OP1	37:d:25:ARG:HD2	2.07	0.55
34:a:867:G:O2'	34:a:873:A:N1	2.34	0.55
1:0:51:ARG:HD2	1:0:53:VAL:HG12	1.87	0.55
4:3:25:HIS:NE2	4:3:47:ALA:HB2	2.22	0.55
8:A:856:G:H2'	8:A:857:G:C8	2.41	0.55
34:a:966:2MG:HM21	42:i:128:LYS:HD2	1.89	0.55
34:a:1477:U:H2'	34:a:1478:U:C6	2.42	0.55
42:i:64:ILE:HG21	42:i:78:ILE:HG12	1.89	0.55
8:A:177:G:H3'	8:A:178:G:H8	1.71	0.55
8:A:391:A:O2'	8:A:410:G:OP1	2.19	0.55
8:A:782:A:N7	10:C:219:VAL:HG21	2.22	0.55
8:A:1394:U:H2'	8:A:1395:A:O4'	2.07	0.55
8:A:2115:G:O2'	8:A:2147:A:O3'	2.24	0.55
40:g:63:VAL:HA	40:g:66:GLU:HG2	1.89	0.55
46:m:23:GLY:O	46:m:28:ARG:NH1	2.37	0.55
1:0:52:LYS:HE2	1:0:55:ALA:HA	1.89	0.54
4:3:28:LEU:HA	4:3:32:LEU:CD2	2.36	0.54
8:A:1496:A:N3	8:A:1577:C:O2'	2.35	0.54
8:A:2629:U:HO2'	8:A:2630:G:P	2.30	0.54
14:G:158:GLY:O	14:G:162:ARG:NH1	2.34	0.54
17:J:91:GLU:HB3	17:J:95:ARG:NH2	2.22	0.54
22:O:34:HIS:HA	22:O:53:THR:OG1	2.07	0.54
23:P:90:ALA:HB2	23:P:112:ARG:HA	1.88	0.54
34:a:1119:C:OP1	42:i:84:ARG:NH2	2.38	0.54
34:a:1320:C:O2	52:s:35:ARG:NH1	2.40	0.54
35:b:22:TRP:CZ3	35:b:24:PRO:HA	2.41	0.54
45:l:98:ARG:HB2	45:l:116:TYR:HA	1.89	0.54
53:t:2:ASN:HB2	53:t:7:LYS:HD2	1.88	0.54
8:A:299:A:N1	8:A:322:A:O2'	2.35	0.54
8:A:568:U:O4	25:R:81:LYS:NZ	2.40	0.54
8:A:887:U:H5'	46:m:91:ARG:CD	2.26	0.54
34:a:1149:C:H2'	34:a:1150:A:H8	1.73	0.54
34:a:1355:G:H2'	34:a:1356:G:C8	2.42	0.54
8:A:240:C:OP2	8:A:241:A:O2'	2.16	0.54
8:A:632:A:H4'	19:L:68:SER:HB2	1.90	0.54
8:A:2192:U:H2'	8:A:2193:G:H8	1.73	0.54
34:a:204:G:H2'	34:a:205:A:C8	2.41	0.54
34:a:501:C:O2	34:a:549:C:O2'	2.23	0.54
39:f:49:TYR:HE1	39:f:86:ARG:HH22	1.56	0.54
8:A:78:U:H2'	8:A:79:C:C6	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:242:G:H4'	8:A:243:U:O5'	2.08	0.54
8:A:2164:C:C4	8:A:2165:C:H1'	2.43	0.54
34:a:210:C:O2'	34:a:211:G:N2	2.40	0.54
34:a:675:A:O2'	44:k:115:ILE:O	2.25	0.54
34:a:1162:C:H2'	34:a:1163:A:H8	1.71	0.54
34:a:1190:G:O2'	36:c:2:GLN:HB2	2.06	0.54
34:a:1312:G:H5'	52:s:4:LEU:HD22	1.89	0.54
40:g:4:ARG:NH1	40:g:6:ILE:HA	2.22	0.54
44:k:15:VAL:HG23	44:k:78:ILE:HD11	1.90	0.54
53:t:75:LYS:O	53:t:79:THR:HG23	2.08	0.54
3:2:19:ARG:NE	8:A:125:A:OP2	2.29	0.54
7:6:38:SER:N	13:F:104:THR:O	2.41	0.54
8:A:277:G:H1'	8:A:361:G:N1	2.20	0.54
8:A:729:G:O2'	8:A:763:G:H4'	2.08	0.54
8:A:1527:G:N1	8:A:1544:A:OP2	2.29	0.54
8:A:2138:G:O2'	8:A:2139:U:OP1	2.25	0.54
13:F:152:ASP:N	13:F:152:ASP:OD1	2.41	0.54
34:a:632:U:H5'	34:a:633:G:C8	2.37	0.54
34:a:1041:G:H2'	34:a:1042:A:C8	2.43	0.54
8:A:1021:A:O2'	8:A:1123:C:OP1	2.22	0.54
8:A:1062:G:H1'	8:A:1088:A:C5	2.43	0.54
18:K:75:SER:HB3	23:P:72:VAL:O	2.08	0.54
34:a:1519:MA6:OP2	34:a:1519:MA6:H8	2.08	0.54
37:d:70:GLN:CA	37:d:73:ASN:OD1	2.56	0.54
41:h:28:SER:HB2	41:h:58:LEU:HB2	1.90	0.54
41:h:95:MET:SD	41:h:129:ALA:HB1	2.48	0.54
48:o:34:GLN:HG2	48:o:58:MET:SD	2.48	0.54
3:2:25:LYS:HE2	8:A:1367:A:O2'	2.08	0.54
8:A:641:U:O2'	8:A:2350:C:OP1	2.25	0.54
8:A:1733:G:H2'	8:A:1734:G:H8	1.72	0.54
8:A:2590:A:H2'	8:A:2591:C:H6	1.72	0.54
13:F:15:LEU:HD13	13:F:28:PRO:HD2	1.89	0.54
34:a:337:G:H2'	34:a:338:A:C8	2.43	0.54
34:a:437:U:O2'	37:d:119:HIS:ND1	2.28	0.54
34:a:651:C:N4	34:a:753:A:OP2	2.37	0.54
34:a:1037:C:H2'	34:a:1038:C:C6	2.43	0.54
37:d:96:ARG:O	37:d:100:VAL:HG23	2.08	0.54
39:f:18:VAL:HG21	39:f:58:HIS:ND1	2.23	0.54
8:A:1110:G:H4'	8:A:1111:A:OP1	2.07	0.54
8:A:1115:G:H2'	8:A:1116:G:H8	1.73	0.54
9:B:42:C:C5	13:F:65:LEU:HD22	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:17:U:H2'	34:a:18:C:C6	2.43	0.54
34:a:465:A:H2'	34:a:466:A:C8	2.43	0.54
34:a:1456:A:H2'	34:a:1457:G:O4'	2.08	0.54
56:w:68:C:H2'	56:w:69:G:C8	2.43	0.54
8:A:690:G:H21	10:C:42:ARG:NH1	2.06	0.54
15:H:71:LYS:NZ	15:H:104:THR:O	2.37	0.54
20:M:69:PRO:HA	20:M:94:ALA:HB2	1.90	0.54
32:Y:2:LYS:HZ3	32:Y:6:LEU:HD22	1.72	0.54
34:a:384:G:H2'	34:a:385:C:C6	2.43	0.54
34:a:615:G:C2	34:a:626:G:C6	2.96	0.54
34:a:674:G:H2'	34:a:675:A:C8	2.43	0.54
40:g:39:GLU:CD	42:i:40:ARG:HH11	2.16	0.54
8:A:228:C:H4'	8:A:229:C:O5'	2.06	0.54
8:A:667:U:H2'	8:A:668:A:O4'	2.08	0.54
8:A:2063:C:H5'	55:v:102:PHE:CE2	2.42	0.54
8:A:2154:A:N3	8:A:2156:G:N2	2.56	0.54
8:A:2182:U:H5''	8:A:2183:A:H5'	1.90	0.54
20:M:135:VAL:HG13	29:V:57:TYR:HD2	1.72	0.54
29:V:4:ILE:HG12	29:V:50:MET:HE1	1.90	0.54
34:a:68:G:H4'	34:a:171:A:H1'	1.89	0.54
34:a:261:U:OP2	53:t:73:ARG:NH2	2.34	0.54
34:a:376:G:H5''	49:p:5:ARG:HB2	1.90	0.54
34:a:539:A:H2'	34:a:540:G:C8	2.43	0.54
34:a:908:A:H2'	34:a:909:A:C8	2.42	0.54
40:g:110:ARG:HD3	40:g:122:GLU:HG2	1.89	0.54
51:r:10:CYS:C	51:r:12:PHE:H	2.16	0.54
1:O:48:TYR:OH	8:A:2883:A:OP1	2.25	0.53
8:A:184:C:H2'	8:A:185:G:C8	2.43	0.53
8:A:566:U:H5''	19:L:29:LYS:HE3	1.89	0.53
8:A:693:A:O2'	8:A:1353:A:N3	2.39	0.53
8:A:2804:U:H2'	8:A:2805:C:C6	2.43	0.53
11:D:13:ARG:HH11	23:P:55:HIS:HA	1.73	0.53
19:L:82:LEU:HD23	19:L:120:VAL:HG11	1.90	0.53
29:V:51:GLN:OE1	29:V:79:ARG:NH2	2.38	0.53
35:b:63:LYS:NZ	35:b:225:SER:O	2.40	0.53
40:g:14:ASP:OD1	40:g:43:TYR:OH	2.19	0.53
2:1:24:LYS:HD2	2:1:26:LYS:HG2	1.88	0.53
2:1:39:ASP:O	2:1:43:ARG:N	2.38	0.53
8:A:1278:C:H2'	8:A:1279:G:H8	1.73	0.53
8:A:1405:U:H2'	8:A:1406:U:C6	2.42	0.53
8:A:1542:U:H2'	8:A:1543:G:O4'	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:1604:C:O2'	8:A:1610:A:N1	2.33	0.53
8:A:2233:U:H2'	8:A:2234:G:C8	2.43	0.53
36:c:46:LEU:HD22	36:c:75:VAL:HG23	1.88	0.53
37:d:151:GLN:HG3	37:d:153:ARG:HG2	1.90	0.53
56:w:63:G:H2'	56:w:64:A:C8	2.43	0.53
3:2:7:PRO:HG3	8:A:1612:C:H5'	1.90	0.53
8:A:605:G:OP1	12:E:99:LYS:NZ	2.41	0.53
8:A:819:A:OP2	8:A:1187:G:N2	2.32	0.53
8:A:1496:A:H2'	8:A:1498:C:C5	2.43	0.53
8:A:2158:A:O2'	8:A:2159:G:H5''	2.09	0.53
8:A:2202:U:O2'	8:A:2204:G:OP1	2.23	0.53
8:A:2547:A:H2'	8:A:2548:U:C6	2.44	0.53
14:G:15:ASP:HB3	14:G:26:LYS:HB3	1.90	0.53
34:a:193:C:H2'	34:a:194:C:C6	2.44	0.53
34:a:674:G:H2'	34:a:675:A:H8	1.74	0.53
43:j:52:LEU:HB2	47:n:81:ARG:HD2	1.90	0.53
53:t:14:GLU:HG3	53:t:18:LYS:HE2	1.90	0.53
8:A:1125:G:OP2	8:A:1126:A:O2'	2.23	0.53
8:A:2393:U:H5''	19:L:62:PRO:HB3	1.90	0.53
8:A:2660:A:H2'	8:A:2661:G:O4'	2.08	0.53
9:B:39:A:H2'	9:B:40:U:C6	2.43	0.53
11:D:123:LYS:HE2	21:N:1:MET:HE1	1.91	0.53
15:H:72:ILE:HG13	15:H:73:ASN:OD1	2.09	0.53
30:W:14:ALA:O	30:W:16:ARG:NH1	2.33	0.53
34:a:1241:G:H2'	34:a:1242:G:H8	1.73	0.53
8:A:141:G:H4'	8:A:142:A:OP1	2.07	0.53
8:A:1283:G:N1	8:A:1286:A:OP2	2.41	0.53
8:A:1416:G:H2'	8:A:1417:C:H6	1.74	0.53
8:A:1434:A:H2'	8:A:1435:G:C8	2.43	0.53
8:A:1563:U:H2'	8:A:1564:C:C6	2.44	0.53
29:V:35:GLU:CD	29:V:35:GLU:H	2.17	0.53
34:a:68:G:H5'	34:a:171:A:O2'	2.08	0.53
36:c:155:ARG:NH2	36:c:159:ALA:O	2.35	0.53
47:n:46:LEU:HB3	52:s:12:LEU:HD21	1.90	0.53
5:4:16:ILE:HD13	5:4:25:VAL:HG22	1.90	0.53
8:A:2063:C:C5'	55:v:102:PHE:CZ	2.91	0.53
8:A:2655:G:O2'	8:A:2656:U:O5'	2.24	0.53
12:E:125:SER:O	12:E:137:LYS:NZ	2.41	0.53
13:F:72:SER:OG	13:F:80:GLN:N	2.41	0.53
14:G:37:ASN:OD1	14:G:38:ASP:N	2.42	0.53
33:Z:4:ILE:HD11	33:Z:58:GLU:HG2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:35:G:H2'	34:a:36:C:C6	2.43	0.53
34:a:405:U:O4	37:d:1:ALA:N	2.42	0.53
37:d:139:ASN:N	37:d:181:PHE:O	2.31	0.53
8:A:833:A:H2'	8:A:834:G:H8	1.73	0.53
8:A:1387:A:H5'	8:A:1469:A:H1'	1.91	0.53
12:E:61:ARG:HH11	12:E:65:THR:HG23	1.73	0.53
8:A:574:A:N6	8:A:2034:U:OP1	2.41	0.53
8:A:893:C:H3'	8:A:893:C:H6	1.74	0.53
8:A:2093:G:O2'	8:A:2198:A:N1	2.40	0.53
8:A:2467:C:H2'	8:A:2468:A:O4'	2.09	0.53
8:A:2514:U:H2'	8:A:2515:C:H6	1.73	0.53
8:A:2537:U:H2'	8:A:2538:C:C6	2.44	0.53
15:H:7:ASP:OD1	15:H:8:LYS:N	2.41	0.53
23:P:77:SER:OG	23:P:79:VAL:HG12	2.09	0.53
31:X:2:ARG:HD2	31:X:29:LEU:HD22	1.89	0.53
34:a:313:A:H2'	34:a:314:C:C6	2.44	0.53
34:a:686:U:O2'	34:a:687:A:O4'	2.27	0.53
36:c:131:ARG:HE	36:c:135:ARG:HH21	1.56	0.53
51:r:44:THR:OG1	51:r:46:THR:OG1	2.15	0.53
8:A:1808:A:H3'	8:A:1809:A:C8	2.44	0.53
8:A:1873:G:H2'	8:A:1874:C:C6	2.44	0.53
8:A:2287:A:O2'	8:A:2288:A:O5'	2.22	0.53
15:H:121:VAL:HG23	15:H:122:LEU:H	1.71	0.53
22:O:28:VAL:O	22:O:95:SER:OG	2.19	0.53
34:a:1498:UR3:H6	34:a:1499:A:H62	1.73	0.53
8:A:306:U:H2'	8:A:307:G:O4'	2.09	0.53
8:A:586:A:N1	8:A:809:G:O2'	2.34	0.53
8:A:910:A:H2'	8:A:911:A:C8	2.44	0.53
8:A:1059:G:H3'	8:A:1060:U:H5'	1.91	0.53
8:A:1070:A:H2'	8:A:1096:A:H4'	1.91	0.53
8:A:1211:C:O2'	8:A:1212:G:OP1	2.27	0.53
8:A:2126:A:C2	8:A:2171:A:H5''	2.44	0.53
8:A:2190:G:H2'	8:A:2191:A:H8	1.73	0.53
8:A:2391:G:H2'	8:A:2424:C:H41	1.74	0.53
8:A:2522:U:O2'	8:A:2647:U:OP1	2.16	0.53
29:V:31:TYR:CE1	29:V:90:ASP:HB3	2.44	0.53
34:a:673:A:O3'	39:f:86:ARG:NH2	2.42	0.53
35:b:129:THR:HG22	35:b:131:LYS:H	1.73	0.53
38:e:88:HIS:CE1	38:e:137:ARG:HD3	2.44	0.53
52:s:33:TRP:HD1	52:s:51:HIS:ND1	2.07	0.53
8:A:173:A:H2'	8:A:174:U:C6	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:1149:G:H2'	8:A:1150:C:C6	2.44	0.52
8:A:1509:A:H2'	8:A:1510:G:H8	1.74	0.52
8:A:1585:C:H3'	8:A:1586:A:H8	1.74	0.52
8:A:2756:U:H1'	8:A:2757:A:H5''	1.91	0.52
14:G:114:HIS:HB2	14:G:150:TYR:HE2	1.74	0.52
15:H:69:ALA:O	15:H:71:LYS:N	2.42	0.52
20:M:10:ARG:HH22	56:w:64:A:H4'	1.74	0.52
34:a:635:A:HO2'	34:a:636:U:H6	1.55	0.52
34:a:1073:U:O2	35:b:102:ASN:ND2	2.41	0.52
34:a:1391:U:H2'	34:a:1392:G:C8	2.44	0.52
42:i:80:HIS:CE1	42:i:84:ARG:HD2	2.44	0.52
8:A:1458:U:H4'	8:A:1459:G:O5'	2.09	0.52
8:A:1847:G:O2'	8:A:1848:A:H8	1.92	0.52
8:A:2649:C:H2'	8:A:2650:U:C6	2.44	0.52
13:F:115:GLY:HA3	13:F:177:ARG:HB2	1.90	0.52
34:a:810:C:H1'	34:a:899:C:H41	1.72	0.52
34:a:985:C:H2'	34:a:986:U:C6	2.44	0.52
40:g:71:THR:HA	40:g:95:ARG:HH12	1.75	0.52
49:p:36:VAL:HG11	49:p:57:ILE:HG13	1.92	0.52
53:t:24:ARG:O	53:t:28:ARG:HG2	2.09	0.52
8:A:1064:C:H2'	8:A:1075:C:N3	2.25	0.52
8:A:1171:G:N2	8:A:1177:G:H22	2.06	0.52
34:a:499:A:H61	34:a:547:A:H5''	1.74	0.52
34:a:1272:G:H2'	34:a:1273:C:C6	2.44	0.52
35:b:74:ALA:HB1	35:b:206:ILE:HG13	1.92	0.52
8:A:897:C:H2'	8:A:898:C:H6	1.74	0.52
10:C:204:LEU:HD22	10:C:209:ALA:HB1	1.91	0.52
12:E:194:LYS:O	12:E:198:GLU:HG2	2.08	0.52
34:a:332:G:O3'	53:t:2:ASN:ND2	2.28	0.52
34:a:544:G:OP2	37:d:62:ARG:NH2	2.42	0.52
34:a:715:A:H2'	34:a:716:A:C8	2.44	0.52
34:a:890:G:O2'	34:a:891:U:O5'	2.26	0.52
34:a:981:U:H4'	47:n:61:ARG:HG2	1.92	0.52
40:g:144:ALA:C	40:g:146:ALA:H	2.18	0.52
8:A:64:A:H2'	8:A:65:U:C6	2.43	0.52
8:A:1827:U:OP2	10:C:220:ARG:HD2	2.10	0.52
8:A:2190:G:H2'	8:A:2191:A:C8	2.45	0.52
26:S:17:VAL:HA	26:S:43:ALA:HB1	1.91	0.52
46:m:16:ILE:O	46:m:19:THR:OG1	2.26	0.52
48:o:52:ARG:O	48:o:56:LEU:HG	2.09	0.52
8:A:488:G:N2	8:A:491:G:H5''	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:925:A:H2'	8:A:926:G:C8	2.44	0.52
8:A:1292:G:H2'	8:A:1293:C:C6	2.44	0.52
8:A:1429:G:H2'	8:A:1430:G:H8	1.74	0.52
8:A:1451:C:O2'	8:A:1452:G:N2	2.42	0.52
8:A:1992:G:N2	8:A:1996:C:O2'	2.43	0.52
8:A:2554:U:H2'	8:A:2555:U:C6	2.44	0.52
9:B:29:A:H2'	9:B:30:C:C6	2.45	0.52
34:a:407:U:H2'	34:a:408:A:H8	1.73	0.52
40:g:43:TYR:O	40:g:47:GLU:HG2	2.09	0.52
49:p:3:THR:HG23	49:p:5:ARG:HG2	1.90	0.52
8:A:372:G:O2'	8:A:400:G:O6	2.16	0.52
8:A:2589:A:C2	8:A:2605:PSU:O4	2.62	0.52
9:B:49:C:H2'	9:B:50:A:C8	2.45	0.52
34:a:90:C:C2	34:a:91:U:C5	2.97	0.52
34:a:131:A:H2'	34:a:132:C:C6	2.45	0.52
46:m:15:VAL:HG22	46:m:33:LEU:HD12	1.92	0.52
8:A:549:G:H2'	8:A:550:C:C6	2.45	0.52
8:A:729:G:H5'	8:A:730:A:H5''	1.92	0.52
8:A:2262:U:OP2	30:W:15:LYS:NZ	2.43	0.52
13:F:43:ILE:HA	13:F:82:TYR:HE2	1.75	0.52
16:I:75:ALA:HB1	16:I:132:ALA:HB2	1.91	0.52
34:a:89:U:H2'	34:a:90:C:C2	2.45	0.52
42:i:9:GLY:HA2	42:i:80:HIS:ND1	2.25	0.52
4:3:35:LYS:HB2	4:3:40:LYS:HE2	1.90	0.52
8:A:2557:G:H2'	8:A:2558:C:C6	2.45	0.52
8:A:2902:C:H2'	8:A:2903:U:O4'	2.10	0.52
27:T:4:GLU:OE1	27:T:49:LYS:NZ	2.43	0.52
34:a:1071:C:H2'	34:a:1072:G:C8	2.45	0.52
34:a:1118:U:H2'	34:a:1119:C:H6	1.75	0.52
34:a:1314:C:H2'	34:a:1315:U:C6	2.45	0.52
38:e:43:GLY:O	38:e:73:VAL:N	2.42	0.52
1:0:39:ARG:NH2	8:A:2885:G:N7	2.57	0.52
8:A:881:G:O6	8:A:897:C:N4	2.43	0.52
8:A:1889:A:H2'	8:A:1890:A:C8	2.45	0.52
8:A:2106:U:H2'	8:A:2107:G:O4'	2.08	0.52
8:A:2728:U:H2'	8:A:2729:G:H8	1.75	0.52
17:J:56:VAL:HB	17:J:124:VAL:HG22	1.92	0.52
28:U:39:ASN:OD1	28:U:64:ILE:HB	2.09	0.52
34:a:160:A:H2'	34:a:161:A:O4'	2.09	0.52
34:a:212:G:H2'	34:a:213:G:H8	1.75	0.52
34:a:745:G:H2'	34:a:746:A:H8	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1492:A:N1	34:a:1493:A:N6	2.58	0.52
8:A:720:U:H2'	8:A:721:A:C8	2.44	0.51
8:A:1614:A:P	8:A:1614:A:H8	2.33	0.51
8:A:1797:G:HO2'	10:C:256:THR:HG1	1.58	0.51
29:V:21:ARG:HE	29:V:87:GLN:HA	1.75	0.51
34:a:131:A:O2'	34:a:262:A:N3	2.43	0.51
34:a:1062:U:H2'	34:a:1063:C:C6	2.44	0.51
35:b:133:ALA:O	35:b:137:THR:HG23	2.10	0.51
40:g:112:ASP:O	40:g:113:LYS:HD2	2.10	0.51
41:h:21:LYS:O	41:h:64:TYR:OH	2.24	0.51
50:q:68:LYS:C	50:q:68:LYS:CD	2.82	0.51
2:1:9:LYS:HE3	2:1:19:PHE:CG	2.45	0.51
7:6:42:PRO:HB2	7:6:47:LYS:HD3	1.92	0.51
8:A:1064:C:N4	8:A:1069:A:OP1	2.43	0.51
8:A:2025:C:H2'	8:A:2026:U:C6	2.45	0.51
8:A:2162:G:N2	8:A:2172:U:OP1	2.26	0.51
8:A:2584:U:H3'	8:A:2585:U:C5'	2.40	0.51
15:H:103:VAL:HG11	15:H:132:PHE:HZ	1.75	0.51
31:X:58:ILE:HG12	31:X:66:VAL:HG21	1.92	0.51
34:a:524:G:H2'	34:a:525:C:C6	2.45	0.51
34:a:1180:A:OP2	42:i:98:ARG:NH2	2.43	0.51
36:c:128:MET:HE1	36:c:130:ARG:HB2	1.92	0.51
38:e:79:THR:HG22	38:e:121:ASN:HB2	1.90	0.51
39:f:92:THR:O	39:f:93:LYS:HG2	2.11	0.51
8:A:576:U:H2'	8:A:577:G:C8	2.45	0.51
8:A:2086:U:H2'	8:A:2087:G:C8	2.46	0.51
8:A:2298:A:OP1	13:F:70:ARG:NH2	2.39	0.51
29:V:26:PHE:HE2	29:V:89:ILE:HG13	1.74	0.51
34:a:207:C:O2'	34:a:212:G:N1	2.41	0.51
38:e:93:VAL:HG22	38:e:110:MET:HE2	1.92	0.51
8:A:45:G:H5'	8:A:46:G:OP1	2.10	0.51
8:A:1361:G:H2'	8:A:1362:C:C6	2.45	0.51
13:F:64:PRO:HA	13:F:88:VAL:HG22	1.93	0.51
26:S:24:ILE:HG13	26:S:24:ILE:O	2.11	0.51
31:X:36:ARG:HG2	31:X:45:PHE:HB3	1.92	0.51
34:a:662:U:H2'	34:a:663:A:C8	2.45	0.51
34:a:739:C:OP1	39:f:2:ARG:NH1	2.43	0.51
34:a:1026:G:N2	34:a:1035:A:N1	2.58	0.51
34:a:1273:C:H2'	34:a:1274:A:O4'	2.11	0.51
41:h:79:ARG:HH12	41:h:82:LEU:HD23	1.74	0.51
57:x:15:G:N3	57:x:15:G:H2'	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:26:G:H1'	8:A:514:A:N6	2.25	0.51
8:A:1055:G:H1	8:A:1104:C:H42	1.58	0.51
8:A:2014:A:H2'	8:A:2015:A:C8	2.46	0.51
10:C:144:GLU:HG2	10:C:151:GLY:N	2.26	0.51
19:L:95:LEU:HD11	19:L:125:LEU:HD21	1.92	0.51
34:a:207:C:C1'	34:a:213:G:H1	2.23	0.51
34:a:639:G:O6	34:a:640:A:N6	2.43	0.51
35:b:150:ILE:HG23	35:b:153:MET:SD	2.50	0.51
42:i:113:LYS:NZ	42:i:117:LEU:O	2.40	0.51
49:p:2:VAL:HG23	49:p:65:ALA:HA	1.91	0.51
49:p:34:GLU:OE2	49:p:60:TRP:NE1	2.43	0.51
8:A:1891:G:HO2'	8:A:2235:G:HO2'	1.55	0.51
8:A:1923:U:H2'	8:A:1924:C:C6	2.45	0.51
13:F:29:ARG:N	13:F:158:THR:OG1	2.37	0.51
17:J:35:ARG:HH12	17:J:140:LEU:HD11	1.76	0.51
18:K:80:ASP:OD1	23:P:61:ARG:NH2	2.39	0.51
21:N:86:ARG:CZ	21:N:117:ASP:HB3	2.41	0.51
27:T:33:LYS:HG2	27:T:80:TRP:CZ3	2.46	0.51
27:T:43:ILE:O	27:T:47:VAL:HG23	2.11	0.51
34:a:82:G:H2'	34:a:83:C:H4'	1.93	0.51
34:a:494:G:H2'	34:a:496:A:H8	1.75	0.51
34:a:672:U:H3	34:a:734:G:H1	1.57	0.51
34:a:1009:U:O4	34:a:1020:G:O6	2.29	0.51
34:a:1160:G:C2	34:a:1161:C:C6	2.99	0.51
8:A:273:G:H2'	8:A:274:C:C6	2.45	0.51
8:A:672:C:OP2	19:L:42:SER:OG	2.21	0.51
8:A:871:U:H2'	8:A:872:U:H6	1.75	0.51
8:A:1156:A:C8	24:Q:50:ARG:HG2	2.45	0.51
34:a:515:G:O2'	34:a:516:PSU:H6	1.94	0.51
34:a:575:G:H4'	34:a:576:C:H5''	1.92	0.51
36:c:130:ARG:HH22	57:x:25:U:H1'	1.75	0.51
43:j:50:THR:HG23	43:j:64:GLN:HG2	1.92	0.51
7:6:48:GLN:OE1	7:6:48:GLN:N	2.42	0.51
8:A:310:A:O2'	8:A:311:A:H2'	2.11	0.51
8:A:360:U:H3'	8:A:361:G:C8	2.46	0.51
25:R:68:ARG:HB3	25:R:90:ARG:HB3	1.93	0.51
27:T:54:GLU:HB3	27:T:88:LYS:HE3	1.91	0.51
34:a:56:U:H2'	34:a:57:G:C8	2.45	0.51
34:a:468:A:H2'	34:a:469:C:C6	2.46	0.51
50:q:71:SER:O	50:q:71:SER:OG	2.23	0.51
8:A:419:U:H2'	8:A:420:C:C6	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:622:G:H2'	8:A:623:C:C6	2.45	0.51
8:A:655:A:H4'	8:A:656:G:H5'	1.93	0.51
8:A:1565:C:O2'	8:A:1566:A:H8	1.94	0.51
8:A:2108:A:H2'	8:A:2109:U:C6	2.46	0.51
8:A:2123:G:H1'	8:A:2176:A:H61	1.74	0.51
8:A:2192:U:H2'	8:A:2193:G:C8	2.46	0.51
31:X:4:CYS:SG	31:X:7:THR:OG1	2.66	0.51
34:a:90:C:C6	34:a:91:U:H5	2.28	0.51
34:a:1119:C:P	42:i:84:ARG:HH22	2.33	0.51
34:a:1328:C:OP1	46:m:27:THR:OG1	2.25	0.51
37:d:8:LEU:HD23	37:d:31:CYS:HB3	1.92	0.51
37:d:167:PRO:HB2	37:d:170:LEU:HD13	1.90	0.51
40:g:134:VAL:O	40:g:138:GLU:HG2	2.11	0.51
6:5:30:SER:O	8:A:1054:A:O2'	2.28	0.51
8:A:310:A:HO2'	8:A:311:A:P	2.34	0.51
8:A:555:G:O2'	8:A:556:A:H8	1.93	0.51
8:A:2725:A:O2'	8:A:2726:A:P	2.69	0.51
8:A:2899:A:H2'	8:A:2900:A:H8	1.76	0.51
13:F:56:LEU:HD13	13:F:88:VAL:HG23	1.92	0.51
25:R:6:GLN:HG2	25:R:11:GLN:HG2	1.93	0.51
34:a:219:U:C2	34:a:220:G:C8	2.99	0.51
37:d:104:MET:HE1	37:d:142:VAL:HG11	1.92	0.51
40:g:128:GLU:HG3	40:g:130:LYS:HG2	1.93	0.51
47:n:2:LYS:O	47:n:5:MET:N	2.44	0.51
2:1:5:ARG:NH1	8:A:2285:C:OP2	2.42	0.50
4:3:22:LYS:HA	4:3:47:ALA:O	2.11	0.50
8:A:1019:U:H3	8:A:1142:A:H62	1.60	0.50
8:A:1065:U:O4'	8:A:1074:G:N2	2.43	0.50
8:A:1386:C:H2'	8:A:1387:A:C8	2.46	0.50
8:A:2171:A:O2'	8:A:2172:U:H4'	2.11	0.50
8:A:2335:A:OP1	22:O:13:ARG:NH1	2.44	0.50
23:P:30:TRP:CD2	23:P:37:LYS:HE3	2.47	0.50
28:U:85:ARG:NH1	28:U:99:SER:OG	2.44	0.50
34:a:148:G:H2'	34:a:149:A:O4'	2.11	0.50
34:a:1043:G:H2'	34:a:1044:A:C8	2.46	0.50
34:a:1137:C:O2'	34:a:1138:G:N2	2.44	0.50
46:m:11:HIS:ND1	46:m:11:HIS:O	2.44	0.50
57:x:19:A:O2'	57:x:20:A:O5'	2.30	0.50
8:A:577:G:O2'	8:A:1254:A:OP1	2.28	0.50
8:A:1051:G:H2'	8:A:1052:C:C6	2.46	0.50
15:H:135:HIS:H	15:H:138:VAL:HG21	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:K:108:ARG:HG2	18:K:116:ILE:HG12	1.93	0.50
34:a:1010:U:H2'	34:a:1011:C:C6	2.47	0.50
34:a:1096:C:H2'	34:a:1097:C:C6	2.47	0.50
34:a:1230:C:H5'	56:w:30:G:H5''	1.92	0.50
35:b:153:MET:HE1	35:b:157:PRO:HB3	1.93	0.50
36:c:46:LEU:HB3	36:c:49:ALA:HB3	1.92	0.50
37:d:70:GLN:HA	37:d:73:ASN:OD1	2.12	0.50
37:d:104:MET:HE1	37:d:142:VAL:HG21	1.92	0.50
41:h:112:ASP:N	41:h:112:ASP:OD1	2.44	0.50
8:A:415:A:H2'	8:A:416:U:C6	2.46	0.50
8:A:871:U:OP1	20:M:5:LYS:NZ	2.37	0.50
8:A:947:A:H2'	8:A:948:C:C6	2.46	0.50
8:A:1080:A:N3	8:A:1081:U:H5''	2.27	0.50
8:A:1212:G:HO2'	8:A:1236:G:H1	1.60	0.50
27:T:22:THR:O	27:T:26:LYS:HG3	2.11	0.50
34:a:237:G:H5''	50:q:26:ARG:NH2	2.26	0.50
39:f:51:ILE:HD13	39:f:86:ARG:HG3	1.93	0.50
47:n:64:CYS:HB3	47:n:69:ARG:H	1.76	0.50
8:A:353:C:H2'	8:A:354:A:H8	1.75	0.50
8:A:452:G:N2	8:A:457:A:O2'	2.45	0.50
8:A:1028:A:OP2	8:A:1126:A:N6	2.42	0.50
8:A:2680:U:O2'	8:A:2681:C:H5'	2.11	0.50
9:B:41:G:C8	13:F:65:LEU:HD11	2.45	0.50
18:K:88:ASN:HB3	18:K:91:SER:O	2.11	0.50
20:M:17:ASN:O	20:M:38:ARG:HD3	2.12	0.50
34:a:9:G:H5'	38:e:107:GLY:HA3	1.93	0.50
34:a:212:G:H2'	34:a:213:G:C8	2.46	0.50
34:a:254:G:O2'	50:q:16:MET:O	2.29	0.50
34:a:455:G:H2'	34:a:456:A:C8	2.46	0.50
34:a:459:A:H2'	34:a:460:A:C8	2.47	0.50
34:a:1125:U:OP1	43:j:37:ARG:NH1	2.44	0.50
34:a:1227:A:OP1	52:s:79:TYR:OH	2.23	0.50
45:l:35:ARG:HB2	45:l:53:ARG:HB3	1.93	0.50
51:r:10:CYS:HB3	51:r:13:THR:HG22	1.93	0.50
4:3:29:ARG:NH1	19:L:63:LYS:O	2.44	0.50
8:A:1631:G:N1	8:A:1634:A:OP2	2.41	0.50
8:A:2030:6MZ:C2	8:A:2499:C:H5''	2.41	0.50
10:C:146:LYS:HB2	10:C:149:LYS:HB2	1.92	0.50
25:R:66:HIS:ND1	25:R:94:THR:HG22	2.26	0.50
34:a:6:G:O2'	34:a:7:A:H5'	2.11	0.50
34:a:812:G:OP1	34:a:902:G:N2	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:e:93:VAL:HG11	38:e:139:THR:HG22	1.94	0.50
52:s:35:ARG:HH21	52:s:74:ALA:HB3	1.75	0.50
8:A:1730:C:O2'	8:A:1731:G:O4'	2.28	0.50
8:A:2107:G:H21	8:A:2183:A:N6	2.09	0.50
8:A:2115:G:H1'	8:A:2147:A:H4'	1.92	0.50
8:A:2455:G:H2'	8:A:2456:C:C6	2.46	0.50
8:A:2468:A:O2'	8:A:2469:A:O5'	2.28	0.50
8:A:2591:C:H2'	8:A:2592:G:H8	1.77	0.50
12:E:58:LYS:NZ	12:E:70:SER:O	2.33	0.50
12:E:91:ASP:OD2	12:E:93:SER:OG	2.30	0.50
15:H:25:TYR:HE1	15:H:29:PHE:HD2	1.60	0.50
26:S:2:GLU:HA	26:S:108:SER:HB3	1.94	0.50
28:U:23:LYS:HG2	28:U:36:GLU:OE1	2.11	0.50
28:U:33:VAL:HG13	28:U:66:VAL:HG12	1.91	0.50
34:a:2:A:O2'	34:a:3:A:O4'	2.29	0.50
38:e:35:LEU:HD11	38:e:136:VAL:HG11	1.94	0.50
46:m:78:ARG:HD2	52:s:64:GLU:OE1	2.12	0.50
8:A:191:A:H2'	8:A:192:C:C6	2.47	0.50
8:A:700:G:O2'	8:A:1632:A:N3	2.42	0.50
8:A:1172:C:H2'	8:A:1173:U:H4'	1.92	0.50
8:A:1541:C:H2'	8:A:1542:U:C6	2.46	0.50
8:A:2450:A:N6	8:A:2501:C:O2	2.45	0.50
8:A:2803:G:H2'	8:A:2804:U:H6	1.77	0.50
9:B:29:A:H2'	9:B:30:C:H6	1.76	0.50
10:C:81:GLU:OE1	10:C:102:TYR:OH	2.20	0.50
15:H:97:ARG:NH1	15:H:112:LYS:HB2	2.27	0.50
34:a:90:C:C6	34:a:90:C:O5'	2.65	0.50
34:a:207:C:C1'	34:a:213:G:C2	2.95	0.50
34:a:263:A:OP1	53:t:73:ARG:NH1	2.45	0.50
34:a:707:U:H4'	44:k:21:HIS:CD2	2.47	0.50
38:e:15:ILE:HD11	38:e:37:VAL:HG13	1.94	0.50
48:o:25:GLU:OE2	48:o:76:ARG:NH1	2.45	0.50
2:1:10:LEU:HB3	2:1:48:TYR:HB3	1.94	0.50
6:5:67:THR:O	6:5:69:PHE:N	2.44	0.50
8:A:624:C:O2'	8:A:657:U:OP1	2.27	0.50
8:A:1052:C:H2'	8:A:1053:C:H5'	1.92	0.50
8:A:1538:G:H2'	8:A:1539:U:H6	1.77	0.50
8:A:1856:U:H2'	8:A:1857:G:O4'	2.11	0.50
8:A:2591:C:H2'	8:A:2592:G:C8	2.47	0.50
8:A:2725:A:H2'	8:A:2726:A:H2'	1.93	0.50
26:S:17:VAL:HG11	26:S:103:ILE:HG12	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:223:A:H2'	34:a:224:U:C6	2.47	0.50
34:a:600:A:H2'	34:a:601:G:C8	2.47	0.50
34:a:1219:A:H2'	34:a:1220:G:C8	2.47	0.50
34:a:1491:G:O2'	34:a:1492:A:OP1	2.28	0.50
49:p:36:VAL:HG13	49:p:53:ASP:HB3	1.94	0.50
52:s:30:LEU:HB2	52:s:48:ILE:HG12	1.94	0.50
54:u:12:ASP:H	54:u:15:LEU:H	1.59	0.50
1:0:53:VAL:HG23	1:0:54:ILE:HG12	1.93	0.50
8:A:811:U:H2'	19:L:21:ARG:HA	1.93	0.50
8:A:2605:PSU:H2'	8:A:2606:C:C6	2.47	0.50
25:R:6:GLN:HG3	25:R:39:LEU:HD11	1.94	0.50
34:a:177:G:OP2	53:t:63:LYS:NZ	2.44	0.50
34:a:197:A:N1	34:a:220:G:O2'	2.31	0.50
34:a:202:G:N2	34:a:466:A:H61	2.09	0.50
34:a:309:A:H2'	34:a:310:G:H8	1.77	0.50
34:a:481:G:O2'	34:a:483:C:N4	2.44	0.50
37:d:187:ARG:HH22	37:d:192:ALA:HA	1.77	0.50
41:h:10:LEU:HD12	41:h:76:ARG:HB2	1.94	0.50
44:k:22:ILE:HG21	44:k:95:THR:HG21	1.93	0.50
1:0:3:GLN:HA	8:A:2615:U:C2	2.47	0.49
8:A:85:G:OP1	28:U:6:ARG:N	2.45	0.49
8:A:514:A:N3	8:A:581:C:O2'	2.44	0.49
8:A:1370:C:O3'	10:C:44:ASN:ND2	2.34	0.49
8:A:2515:C:H2'	8:A:2516:A:H8	1.77	0.49
8:A:2900:A:C6	8:A:2901:C:N4	2.80	0.49
21:N:56:LYS:HE2	21:N:87:PHE:O	2.12	0.49
36:c:111:ASP:O	36:c:115:VAL:HG23	2.12	0.49
49:p:17:TYR:HE2	49:p:41:PRO:HG3	1.77	0.49
8:A:886:A:N6	8:A:891:G:H8	2.04	0.49
8:A:925:A:H2'	8:A:926:G:H8	1.76	0.49
8:A:1589:U:H2'	8:A:1590:A:H8	1.77	0.49
22:O:39:VAL:HB	22:O:49:VAL:HB	1.93	0.49
34:a:62:U:H2'	34:a:63:C:C6	2.47	0.49
34:a:135:C:O2	49:p:1:MET:HB2	2.13	0.49
34:a:615:G:C2	34:a:626:G:N3	2.76	0.49
34:a:718:A:C2	51:r:37:LYS:HG2	2.47	0.49
34:a:1346:A:H61	34:a:1374:A:H5''	1.77	0.49
51:r:25:ILE:HG21	51:r:66:LEU:HB3	1.92	0.49
56:w:18:G:O2'	56:w:57:G:N1	2.42	0.49
56:w:50:U:H2'	56:w:51:C:H6	1.75	0.49
8:A:550:C:H2'	8:A:551:G:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:657:U:H2'	8:A:658:U:C6	2.47	0.49
8:A:832:U:H2'	8:A:833:A:C8	2.48	0.49
8:A:878:A:C8	8:A:899:A:H2	2.30	0.49
8:A:897:C:H2'	8:A:898:C:C6	2.47	0.49
8:A:2204:G:H4'	10:C:149:LYS:HD3	1.95	0.49
8:A:2572:A:O2'	8:A:2573:C:OP2	2.29	0.49
8:A:2698:U:H2'	8:A:2699:C:H6	1.78	0.49
10:C:29:PHE:O	10:C:33:LEU:HD13	2.12	0.49
23:P:89:GLY:O	23:P:112:ARG:NH1	2.44	0.49
26:S:20:VAL:HG11	26:S:44:ALA:HA	1.93	0.49
31:X:31:ASN:OD1	31:X:33:HIS:NE2	2.46	0.49
36:c:21:TRP:CD1	36:c:58:ARG:HG3	2.47	0.49
40:g:15:PRO:HB3	42:i:42:THR:HA	1.94	0.49
42:i:87:MET:HE3	42:i:97:LEU:HD23	1.94	0.49
43:j:8:ILE:HB	43:j:74:VAL:HB	1.95	0.49
2:1:8:ILE:HD13	2:1:24:LYS:HE3	1.94	0.49
5:4:2:LYS:HB2	5:4:35:GLN:HB3	1.93	0.49
8:A:177:G:H3'	8:A:178:G:C8	2.45	0.49
8:A:532:A:H4'	8:A:533:G:C8	2.46	0.49
8:A:966:G:O4'	8:A:2267:A:N6	2.45	0.49
8:A:1433:A:H2'	8:A:1434:A:C8	2.48	0.49
8:A:2637:U:H2'	8:A:2638:G:O4'	2.12	0.49
8:A:2836:U:H2'	8:A:2837:A:C8	2.47	0.49
19:L:109:LYS:HE2	19:L:128:THR:HG22	1.95	0.49
21:N:59:SER:O	21:N:63:ARG:HG2	2.13	0.49
31:X:65:THR:O	31:X:69:GLU:HG3	2.12	0.49
34:a:89:U:H2'	34:a:90:C:N3	2.28	0.49
34:a:270:A:H2'	34:a:271:C:C6	2.47	0.49
34:a:1225:A:H2'	34:a:1225:A:N3	2.27	0.49
37:d:144:ILE:HD13	37:d:154:VAL:HG11	1.94	0.49
39:f:38:ARG:HG3	39:f:97:THR:HA	1.94	0.49
8:A:471:A:OP1	12:E:79:ARG:NH2	2.37	0.49
8:A:677:A:O2'	8:A:2071:A:H5'	2.12	0.49
8:A:1060:U:O2'	8:A:1071:G:OP1	2.23	0.49
8:A:1469:A:H2'	8:A:1470:A:H8	1.78	0.49
8:A:1499:C:C2	8:A:1500:G:C8	3.00	0.49
8:A:1682:G:H2'	8:A:1683:U:C6	2.46	0.49
8:A:1703:G:H2'	8:A:1704:C:C6	2.47	0.49
8:A:1788:C:OP1	10:C:220:ARG:NH2	2.44	0.49
10:C:77:VAL:HA	10:C:93:VAL:HG12	1.94	0.49
27:T:53:VAL:HG11	27:T:92:ASN:HB2	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:X:37:PHE:HZ	31:X:50:VAL:HG21	1.77	0.49
34:a:1081:A:H5'	38:e:22:LYS:HG3	1.94	0.49
34:a:1300:G:H1'	34:a:1301:U:H5	1.77	0.49
43:j:7:ARG:HD3	43:j:75:ASP:HB2	1.94	0.49
44:k:36:ARG:NH1	44:k:82:GLU:OE2	2.45	0.49
8:A:1494:A:H2'	8:A:1495:A:C8	2.48	0.49
8:A:1932:A:H2'	8:A:1933:G:O4'	2.12	0.49
17:J:76:HIS:CE1	17:J:85:LYS:HB2	2.47	0.49
18:K:87:LEU:HA	18:K:94:PRO:HA	1.95	0.49
34:a:310:G:H5''	49:p:31:ARG:HB2	1.95	0.49
34:a:621:A:H2'	34:a:622:A:C8	2.47	0.49
34:a:1428:A:H2'	34:a:1429:A:O4'	2.13	0.49
8:A:322:A:OP2	12:E:163:ASN:HB2	2.12	0.49
8:A:499:U:H2'	8:A:500:G:O4'	2.13	0.49
8:A:545:U:O2	8:A:548:G:C6	2.66	0.49
8:A:1288:G:OP2	8:A:1288:G:N2	2.42	0.49
8:A:1571:A:H2'	8:A:1572:A:C8	2.47	0.49
8:A:2304:G:H22	8:A:2312:U:H3	1.60	0.49
10:C:104:LEU:HD11	10:C:155:ARG:HB2	1.95	0.49
13:F:146:ASP:OD1	13:F:146:ASP:N	2.46	0.49
15:H:78:VAL:HG21	15:H:103:VAL:HA	1.95	0.49
34:a:95:C:H2'	34:a:96:U:C6	2.48	0.49
34:a:1106:G:H5''	36:c:171:ARG:HG2	1.94	0.49
34:a:1317:C:H4'	47:n:48:LEU:HG	1.95	0.49
36:c:141:MET:HG3	36:c:169:GLU:HG2	1.94	0.49
7:6:63:ARG:O	7:6:66:ILE:HG13	2.12	0.49
8:A:471:A:H2'	8:A:472:A:O4'	2.13	0.49
8:A:1816:C:N4	10:C:34:GLU:OE2	2.32	0.49
8:A:2262:U:H5	30:W:12:SER:OG	1.94	0.49
28:U:97:SER:O	28:U:97:SER:OG	2.30	0.49
34:a:982:U:H4'	34:a:983:A:O4'	2.12	0.49
34:a:1036:A:H2'	34:a:1037:C:C6	2.48	0.49
34:a:1148:U:H2'	34:a:1149:C:O4'	2.12	0.49
34:a:1400:C:H5'	57:x:18:C:N4	2.27	0.49
39:f:21:MET:HE2	39:f:81:ASN:HD21	1.77	0.49
43:j:32:THR:O	43:j:80:THR:OG1	2.30	0.49
56:w:16:U:N3	56:w:59:U:O2	2.46	0.49
8:A:447:A:OP1	24:Q:4:LYS:NZ	2.46	0.49
8:A:971:G:OP2	8:A:974:G:N2	2.46	0.49
8:A:1004:U:H1'	8:A:1010:A:H2'	1.94	0.49
8:A:1174:U:OP1	8:A:1176:U:N3	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2184:A:H2'	8:A:2185:U:O4'	2.13	0.49
8:A:2845:U:H5''	23:P:51:ASN:O	2.12	0.49
34:a:407:U:H2'	34:a:408:A:C8	2.48	0.49
34:a:938:A:H1'	34:a:1376:U:O2'	2.12	0.49
35:b:93:HIS:ND1	35:b:145:ASN:O	2.45	0.49
41:h:46:GLU:HG3	41:h:47:ASP:H	1.78	0.49
42:i:5:TYR:HB2	42:i:20:ILE:HG12	1.95	0.49
43:j:54:SER:O	47:n:81:ARG:NH1	2.40	0.49
46:m:6:ILE:HG12	46:m:65:GLU:OE2	2.13	0.49
8:A:1170:C:H42	8:A:1178:C:H41	1.61	0.49
8:A:2129:C:O2'	8:A:2130:U:O4'	2.14	0.49
8:A:2677:G:H2'	8:A:2678:C:C6	2.48	0.49
20:M:11:LYS:HD3	20:M:86:LYS:HG2	1.95	0.49
21:N:96:ARG:HD3	21:N:98:LEU:HD21	1.95	0.49
23:P:64:SER:O	23:P:66:GLY:N	2.46	0.49
23:P:81:ASP:OD2	23:P:82:SER:OG	2.25	0.49
34:a:1297:G:N2	40:g:113:LYS:O	2.45	0.49
34:a:1513:A:H2'	34:a:1514:G:C8	2.48	0.49
35:b:65:LYS:HB3	35:b:157:PRO:HA	1.95	0.49
8:A:1292:G:H2'	8:A:1293:C:H6	1.78	0.48
8:A:2127:G:H21	8:A:2173:A:H5'	1.78	0.48
8:A:2157:G:H1'	8:A:2158:A:C6	2.48	0.48
8:A:2246:G:H2'	8:A:2247:A:C8	2.48	0.48
34:a:1052:U:O2'	34:a:1055:A:OP2	2.19	0.48
34:a:1060:U:C5	36:c:1:GLY:HA3	2.48	0.48
34:a:1314:C:H2'	34:a:1315:U:H6	1.78	0.48
37:d:106:PHE:HA	37:d:154:VAL:HG13	1.95	0.48
41:h:77:VAL:HG12	41:h:84:ILE:HD12	1.95	0.48
44:k:107:THR:HB	54:u:6:ARG:HH22	1.78	0.48
47:n:46:LEU:O	47:n:49:GLN:HG2	2.13	0.48
1:O:15:ARG:HA	8:A:2046:G:H5'	1.95	0.48
8:A:507:A:H5''	8:A:508:A:H3'	1.95	0.48
8:A:1097:U:H2'	8:A:1098:A:H5'	1.95	0.48
8:A:1246:A:H2'	8:A:1247:A:O4'	2.13	0.48
11:D:186:LEU:HD21	23:P:3:ILE:HG21	1.95	0.48
17:J:122:LEU:HG	17:J:124:VAL:HG23	1.95	0.48
34:a:140:U:O2'	34:a:183:C:N4	2.44	0.48
44:k:86:LYS:NZ	44:k:112:VAL:O	2.40	0.48
1:O:9:ARG:HG3	1:O:12:ARG:NH2	2.28	0.48
4:3:21:PHE:O	4:3:49:VAL:HG23	2.14	0.48
8:A:75:G:N3	8:A:75:G:H2'	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:1684:G:H2'	8:A:1685:C:C6	2.48	0.48
8:A:1710:G:H2'	8:A:1711:A:C8	2.48	0.48
8:A:2297:A:N6	8:A:2319:G:H1'	2.28	0.48
8:A:2503:2MA:O2'	8:A:2505:G:OP2	2.24	0.48
14:G:104:LEU:HB2	14:G:112:VAL:HB	1.94	0.48
15:H:64:ALA:C	15:H:66:ASN:H	2.21	0.48
30:W:33:ILE:HD11	30:W:78:ILE:HD11	1.95	0.48
34:a:392:C:C2	34:a:393:A:C8	3.02	0.48
39:f:38:ARG:HG3	39:f:97:THR:HG22	1.93	0.48
43:j:20:GLN:O	43:j:24:GLU:HG3	2.13	0.48
45:l:86:VAL:HG11	45:l:89:LEU:HB3	1.94	0.48
8:A:401:A:H2'	8:A:402:A:C8	2.48	0.48
8:A:2849:U:O2'	8:A:2866:U:O2	2.23	0.48
18:K:41:ILE:HD11	18:K:86:LEU:HD22	1.94	0.48
22:O:49:VAL:HG21	22:O:82:ALA:HA	1.95	0.48
34:a:90:C:H2'	34:a:91:U:H6	1.77	0.48
34:a:198:G:H2'	34:a:199:A:C8	2.48	0.48
34:a:613:C:H2'	34:a:614:C:C6	2.49	0.48
35:b:25:LYS:NZ	35:b:193:ASP:OD2	2.28	0.48
35:b:162:VAL:O	35:b:184:ALA:HA	2.13	0.48
37:d:16:THR:OG1	37:d:17:ASP:N	2.46	0.48
44:k:51:PHE:HD1	44:k:55:ARG:HB3	1.77	0.48
51:r:10:CYS:SG	51:r:47:ARG:HG2	2.53	0.48
8:A:832:U:H2'	8:A:833:A:H8	1.78	0.48
8:A:1349:C:C2	8:A:1350:C:C5	3.01	0.48
8:A:1565:C:HO2'	8:A:1566:A:P	2.35	0.48
8:A:1720:U:H2'	8:A:1721:G:O4'	2.14	0.48
8:A:2537:U:H2'	8:A:2538:C:H6	1.79	0.48
11:D:20:VAL:HG22	18:K:72:PRO:HB2	1.96	0.48
20:M:40:ARG:HG2	20:M:95:LEU:HD23	1.93	0.48
24:Q:39:ILE:O	24:Q:43:GLN:HG3	2.14	0.48
25:R:50:GLY:HA3	25:R:54:VAL:HG22	1.96	0.48
34:a:195:A:H1'	34:a:222:C:O2'	2.13	0.48
34:a:469:C:C4	34:a:470:C:H1'	2.47	0.48
34:a:538:G:H5''	45:l:110:LYS:HB2	1.95	0.48
34:a:745:G:OP1	34:a:851:G:O2'	2.24	0.48
34:a:1347:G:H4'	34:a:1348:U:O5'	2.13	0.48
47:n:73:PHE:CZ	47:n:78:GLY:HA2	2.49	0.48
1:O:4:GLN:O	8:A:2017:U:H4'	2.14	0.48
8:A:880:G:C2	8:A:881:G:C8	3.02	0.48
25:R:63:VAL:HA	25:R:96:VAL:HG12	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:W:49:CYS:SG	30:W:53:HIS:HA	2.54	0.48
32:Y:15:ASN:O	32:Y:19:LEU:HD23	2.13	0.48
34:a:86:G:O2'	34:a:88:U:N3	2.46	0.48
34:a:501:C:H2'	34:a:502:A:C8	2.48	0.48
34:a:1096:C:H2'	34:a:1097:C:H6	1.79	0.48
35:b:195:VAL:HB	35:b:198:VAL:HG12	1.96	0.48
39:f:45:ARG:O	39:f:56:LYS:HA	2.13	0.48
45:l:2:THR:O	45:l:5:GLN:N	2.29	0.48
49:p:40:ASN:HB3	49:p:49:GLY:HA2	1.95	0.48
7:6:14:ALA:HB3	7:6:22:MET:HG2	1.95	0.48
8:A:458:G:O2'	8:A:459:U:OP2	2.32	0.48
8:A:1872:A:H8	8:A:1872:A:O5'	1.96	0.48
8:A:2389:G:H5''	8:A:2390:U:O4'	2.14	0.48
8:A:2547:A:H4'	18:K:29:HIS:NE2	2.29	0.48
8:A:2831:G:OP2	11:D:59:ARG:NH1	2.47	0.48
12:E:48:THR:HG21	12:E:88:ARG:HH12	1.79	0.48
12:E:149:ILE:HB	12:E:188:MET:HG2	1.95	0.48
15:H:66:ASN:C	15:H:68:ARG:N	2.70	0.48
25:R:10:LYS:HB3	25:R:10:LYS:HE3	1.69	0.48
34:a:45:G:H2'	34:a:46:G:C8	2.49	0.48
34:a:131:A:N3	34:a:262:A:H2	2.11	0.48
34:a:452:A:H1'	49:p:70:ARG:HD3	1.95	0.48
34:a:1526:G:OP2	54:u:41:THR:HG23	2.14	0.48
36:c:148:ILE:HG13	36:c:200:TRP:O	2.14	0.48
41:h:38:VAL:HG21	41:h:109:VAL:HG12	1.95	0.48
6:5:55:VAL:HA	8:A:1084:A:H5''	1.95	0.48
8:A:12:U:O2	8:A:2626:C:H4'	2.14	0.48
8:A:887:U:H1'	8:A:888:C:H5	1.78	0.48
8:A:1009:A:N3	8:A:1153:C:O2'	2.43	0.48
8:A:1842:G:H2'	8:A:1843:C:C6	2.49	0.48
8:A:2105:U:H3'	8:A:2106:U:H6	1.79	0.48
8:A:2364:C:OP1	30:W:51:ARG:NH1	2.43	0.48
8:A:2803:G:H2'	8:A:2804:U:C6	2.49	0.48
10:C:38:LYS:NZ	10:C:57:HIS:O	2.35	0.48
30:W:42:HIS:HB2	30:W:75:PHE:CD1	2.48	0.48
34:a:81:A:H8	34:a:82:G:N7	2.12	0.48
34:a:502:A:O3'	45:l:115:LYS:NZ	2.47	0.48
34:a:539:A:H2'	34:a:540:G:H8	1.79	0.48
34:a:625:U:H2'	34:a:626:G:H8	1.79	0.48
36:c:92:ASP:OD1	36:c:93:ILE:N	2.47	0.48
8:A:498:G:H1'	28:U:44:HIS:HE1	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:644:A:H2'	8:A:645:C:O4'	2.14	0.48
8:A:895:U:O2	8:A:895:U:H3'	2.13	0.48
8:A:1057:A:C6	8:A:1086:A:H2'	2.48	0.48
8:A:1231:U:H2'	8:A:1232:G:H8	1.79	0.48
8:A:1715:G:HO2'	8:A:1716:U:H6	1.62	0.48
8:A:1918:A:O2'	8:A:1919:A:N7	2.38	0.48
17:J:11:VAL:HG11	17:J:50:THR:HA	1.95	0.48
19:L:85:VAL:HG22	19:L:94:THR:HG22	1.95	0.48
21:N:90:ARG:HH12	21:N:116:VAL:HB	1.79	0.48
34:a:901:A:O2'	34:a:1513:A:OP1	2.25	0.48
56:w:19:G:OP1	56:w:60:U:N3	2.45	0.48
7:6:43:PHE:HZ	13:F:177:ARG:HA	1.78	0.48
8:A:361:G:H8	8:A:361:G:OP2	1.97	0.48
8:A:417:C:H2'	8:A:418:C:C6	2.48	0.48
8:A:510:C:OP1	8:A:511:U:OP2	2.31	0.48
8:A:1853:A:H2'	8:A:1854:A:C8	2.49	0.48
8:A:2598:A:H5'	10:C:233:GLY:HA3	1.96	0.48
15:H:25:TYR:HE1	15:H:29:PHE:CD2	2.32	0.48
34:a:113:G:H2'	34:a:114:U:C6	2.49	0.48
34:a:500:G:H2'	34:a:501:C:C6	2.49	0.48
34:a:542:G:H5'	37:d:38:GLY:CA	2.43	0.48
34:a:842:U:H4'	34:a:846:G:C6	2.49	0.48
34:a:890:G:H2'	34:a:906:A:N6	2.28	0.48
8:A:600:G:H1'	12:E:100:MET:HG2	1.96	0.47
8:A:1564:C:H2'	8:A:1565:C:C6	2.49	0.47
10:C:16:VAL:HB	10:C:203:VAL:HG22	1.96	0.47
12:E:121:VAL:HG23	12:E:122:GLU:O	2.14	0.47
13:F:28:PRO:HB2	13:F:168:LEU:HD22	1.95	0.47
28:U:27:VAL:HG22	28:U:33:VAL:HG12	1.95	0.47
28:U:99:SER:OG	28:U:99:SER:O	2.32	0.47
29:V:21:ARG:HA	29:V:25:LYS:O	2.14	0.47
34:a:634:C:H2'	34:a:635:A:H8	1.78	0.47
34:a:642:A:N7	41:h:106:SER:HA	2.29	0.47
37:d:27:ILE:HG23	37:d:33:ILE:HG21	1.96	0.47
40:g:65:LEU:HD23	40:g:103:ILE:HD12	1.95	0.47
43:j:6:ILE:HG13	43:j:76:ILE:HB	1.95	0.47
4:3:53:ASP:HB3	19:L:57:LEU:HD22	1.96	0.47
8:A:26:G:H1'	8:A:514:A:H61	1.79	0.47
8:A:1070:A:OP1	8:A:1075:C:N4	2.47	0.47
8:A:2246:G:H2'	8:A:2247:A:H8	1.78	0.47
34:a:181:A:H61	34:a:194:C:H3'	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:222:C:H2'	34:a:223:A:H8	1.79	0.47
34:a:344:A:H5''	34:a:345:C:H5	1.79	0.47
34:a:412:A:H62	34:a:431:A:H61	1.62	0.47
34:a:490:C:H2'	34:a:491:G:H8	1.78	0.47
34:a:966:2MG:CM2	56:w:34:G:H5'	2.43	0.47
37:d:146:GLU:HA	37:d:149:LYS:HB3	1.95	0.47
40:g:111:GLY:HA2	40:g:118:ARG:CD	2.43	0.47
47:n:8:ARG:HB3	47:n:12:ARG:NH1	2.29	0.47
3:2:7:PRO:HB2	8:A:1309:G:H4'	1.96	0.47
6:5:31:ARG:CA	8:A:1054:A:HO2'	2.19	0.47
8:A:355:U:H2'	8:A:356:G:C8	2.45	0.47
8:A:2158:A:H4'	8:A:2159:G:O5'	2.15	0.47
8:A:2720:U:OP1	23:P:52:ARG:NH2	2.47	0.47
8:A:2834:G:H2'	8:A:2879:A:H61	1.79	0.47
18:K:2:ILE:HB	18:K:33:ALA:HB3	1.97	0.47
22:O:53:THR:HG23	22:O:74:VAL:CG2	2.43	0.47
34:a:82:G:H1	34:a:86:G:H1'	1.79	0.47
34:a:254:G:OP1	50:q:68:LYS:CB	2.60	0.47
34:a:1002:G:H2'	34:a:1003:G:C8	2.49	0.47
36:c:9:ILE:HG23	36:c:10:ARG:HG3	1.96	0.47
37:d:105:GLY:C	37:d:107:GLY:H	2.22	0.47
41:h:10:LEU:HD22	41:h:74:ILE:HD11	1.95	0.47
8:A:1114:C:H2'	8:A:1115:G:C8	2.50	0.47
8:A:1548:A:H2'	8:A:1549:A:H8	1.78	0.47
8:A:1913:A:H2'	34:a:1493:A:N1	2.29	0.47
8:A:2385:C:H2'	8:A:2386:A:C8	2.50	0.47
8:A:2458:G:O2'	8:A:2460:U:O4	2.26	0.47
13:F:21:TYR:OH	13:F:164:GLU:OE2	2.23	0.47
14:G:23:ILE:HG21	14:G:71:LEU:HD21	1.95	0.47
20:M:19:GLY:O	20:M:38:ARG:NH1	2.45	0.47
34:a:90:C:C5	34:a:91:U:H5	2.32	0.47
34:a:691:G:H2'	34:a:692:U:C6	2.50	0.47
34:a:691:G:O2'	34:a:797:C:H4'	2.14	0.47
34:a:933:G:O6	40:g:2:ARG:NH2	2.46	0.47
35:b:150:ILE:HD12	35:b:150:ILE:H	1.79	0.47
41:h:38:VAL:O	41:h:41:GLU:HG2	2.14	0.47
5:4:4:ARG:HH22	8:A:2477:U:H2'	1.79	0.47
8:A:145:C:H2'	8:A:146:A:C8	2.49	0.47
8:A:160:A:N3	8:A:2208:C:O2'	2.40	0.47
8:A:828:U:H2'	8:A:829:A:C8	2.50	0.47
8:A:1443:U:H2'	8:A:1444:G:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:C:209:ALA:HA	10:C:212:TRP:CE2	2.49	0.47
13:F:13:LYS:O	13:F:17:THR:HG23	2.14	0.47
19:L:123:ARG:NE	19:L:143:GLU:OE2	2.47	0.47
27:T:13:ALA:O	27:T:33:LYS:N	2.41	0.47
34:a:20:U:H2'	34:a:21:G:O4'	2.14	0.47
34:a:45:G:H2'	34:a:46:G:H8	1.79	0.47
34:a:747:A:H2'	34:a:748:G:O4'	2.15	0.47
45:l:54:VAL:HG21	45:l:79:ILE:HD11	1.97	0.47
47:n:19:TYR:CE1	47:n:51:LEU:HD22	2.50	0.47
49:p:12:LYS:HG2	49:p:13:LYS:HG2	1.96	0.47
2:1:35:LEU:HD11	8:A:2286:G:N7	2.29	0.47
8:A:64:A:H2'	8:A:65:U:H6	1.80	0.47
8:A:706:A:H2'	8:A:707:G:O4'	2.15	0.47
8:A:974:G:H8	8:A:990:A:H62	1.61	0.47
8:A:1000:A:OP2	8:A:1154:G:N1	2.33	0.47
8:A:1053:C:H1'	8:A:1054:A:C8	2.49	0.47
8:A:1079:C:O2'	8:A:1080:A:O4'	2.24	0.47
8:A:1105:U:H2'	8:A:1106:G:H8	1.80	0.47
8:A:1219:U:H2'	8:A:1220:G:C8	2.50	0.47
8:A:1710:G:H4'	8:A:2858:C:O2	2.15	0.47
8:A:2692:G:H1'	8:A:2847:U:H1'	1.95	0.47
17:J:78:THR:HG21	17:J:85:LYS:HE2	1.96	0.47
23:P:105:LYS:HB3	23:P:108:ARG:NH2	2.30	0.47
34:a:116:A:H61	34:a:313:A:H1'	1.79	0.47
34:a:210:C:HO2'	34:a:211:G:N2	2.11	0.47
34:a:971:G:OP2	34:a:1231:G:N2	2.41	0.47
34:a:1216:A:H2'	34:a:1217:C:H6	1.78	0.47
36:c:34:SER:O	36:c:38:VAL:HG13	2.13	0.47
40:g:74:VAL:HB	40:g:85:GLN:HB3	1.97	0.47
1:0:28:SER:O	1:0:36:LYS:HA	2.14	0.47
2:1:20:TYR:OH	8:A:2347:C:O2'	2.19	0.47
5:4:4:ARG:NH2	8:A:2477:U:O2	2.47	0.47
8:A:323:C:H3'	12:E:163:ASN:OD1	2.14	0.47
8:A:323:C:O2'	8:A:324:A:OP2	2.32	0.47
8:A:569:U:H5''	8:A:821:A:C2	2.50	0.47
8:A:784:G:H5'	8:A:785:G:OP1	2.15	0.47
8:A:905:A:H2'	8:A:906:U:H5'	1.96	0.47
8:A:1324:G:O2'	8:A:1326:U:OP2	2.31	0.47
8:A:1902:C:H4'	10:C:241:LYS:O	2.15	0.47
8:A:2031:A:N3	8:A:2455:G:O2'	2.37	0.47
8:A:2098:U:H2'	8:A:2099:U:O4'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2127:G:N2	8:A:2173:A:H5'	2.29	0.47
8:A:2136:G:H2'	8:A:2136:G:N3	2.30	0.47
8:A:2327:A:H2'	8:A:2328:A:C8	2.50	0.47
8:A:2461:A:H2'	8:A:2462:C:C6	2.50	0.47
9:B:52:A:O2'	9:B:53:A:O5'	2.32	0.47
15:H:68:ARG:HD2	15:H:70:GLU:HB3	1.96	0.47
23:P:87:ARG:NH2	23:P:109:ILE:O	2.47	0.47
26:S:14:ALA:O	26:S:18:ARG:HB2	2.15	0.47
29:V:3:THR:HA	29:V:62:THR:O	2.15	0.47
31:X:67:LEU:HD23	31:X:70:LEU:HD12	1.95	0.47
34:a:179:A:H61	34:a:196:A:H62	1.62	0.47
34:a:780:A:N6	34:a:801:U:OP2	2.35	0.47
34:a:981:U:H2'	34:a:982:U:C5	2.49	0.47
35:b:160:LEU:HD22	35:b:175:ALA:HB2	1.96	0.47
36:c:30:ASP:OD1	36:c:31:ASN:N	2.46	0.47
36:c:78:LYS:HD3	36:c:79:LYS:HE3	1.95	0.47
36:c:137:VAL:HG13	36:c:148:ILE:HG23	1.96	0.47
36:c:155:ARG:NH1	36:c:192:TYR:O	2.48	0.47
41:h:95:MET:O	41:h:98:LEU:HG	2.15	0.47
42:i:25:GLY:N	42:i:61:ASP:OD1	2.37	0.47
42:i:51:LEU:O	42:i:56:MET:HB3	2.15	0.47
8:A:198:C:O2'	8:A:199:A:H5'	2.14	0.47
8:A:353:C:H2'	8:A:354:A:C8	2.49	0.47
8:A:905:A:C2'	8:A:906:U:H5'	2.44	0.47
8:A:1159:U:N3	8:A:1160:G:N7	2.63	0.47
8:A:1872:A:H2'	8:A:1873:G:O4'	2.15	0.47
8:A:2123:G:H21	8:A:2175:C:N4	2.12	0.47
8:A:2804:U:H2'	8:A:2805:C:H6	1.78	0.47
13:F:102:LEU:HD12	13:F:106:ALA:HB3	1.95	0.47
22:O:70:ALA:O	22:O:74:VAL:HG23	2.15	0.47
24:Q:97:ILE:HG22	24:Q:105:PHE:HB2	1.97	0.47
26:S:7:HIS:CE1	26:S:10:ALA:HA	2.50	0.47
33:Z:23:LEU:HD11	33:Z:53:MET:SD	2.54	0.47
34:a:96:U:H2'	34:a:97:G:H8	1.79	0.47
34:a:676:A:H5''	44:k:114:PRO:HB3	1.95	0.47
34:a:1005:A:H3'	34:a:1006:G:H8	1.79	0.47
35:b:63:LYS:HD3	35:b:63:LYS:HA	1.76	0.47
39:f:15:SER:HA	39:f:18:VAL:HG23	1.96	0.47
39:f:38:ARG:HH21	39:f:63:ASN:ND2	2.11	0.47
41:h:95:MET:HE2	41:h:98:LEU:HD11	1.95	0.47
49:p:73:ALA:O	49:p:77:GLU:HG2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:32:LEU:HA	4:3:35:LYS:HZ3	1.80	0.47
8:A:593:U:H2'	8:A:594:U:C6	2.50	0.47
8:A:987:C:O2'	8:A:1000:A:N3	2.43	0.47
8:A:2233:U:H2'	8:A:2234:G:H8	1.80	0.47
8:A:2820:A:HO2'	8:A:2821:A:P	2.38	0.47
11:D:16:THR:OG1	11:D:18:ASP:OD1	2.21	0.47
18:K:58:LEU:HA	18:K:89:ASN:ND2	2.30	0.47
34:a:509:A:O2'	34:a:510:A:OP1	2.31	0.47
34:a:1463:U:H2'	34:a:1464:U:C6	2.50	0.47
47:n:36:ALA:O	47:n:38:ASP:N	2.48	0.47
47:n:74:LEU:HD12	47:n:84:VAL:HG21	1.97	0.47
52:s:50:VAL:HG13	52:s:74:ALA:HB2	1.97	0.47
3:2:5:PHE:O	3:2:6:GLN:NE2	2.47	0.47
8:A:739:A:H1'	8:A:740:C:H5	1.80	0.47
8:A:891:G:H2'	8:A:891:G:N3	2.30	0.47
8:A:1473:G:C6	8:A:1519:G:C6	3.03	0.47
8:A:2105:U:H3'	8:A:2106:U:C6	2.50	0.47
8:A:2265:U:OP2	8:A:2266:A:O2'	2.18	0.47
9:B:66:A:O5'	9:B:108:A:N6	2.48	0.47
29:V:10:LYS:HD2	29:V:10:LYS:N	2.30	0.47
34:a:19:A:O2'	34:a:572:A:N1	2.44	0.47
34:a:322:C:H2'	34:a:323:U:C6	2.50	0.47
34:a:563:A:H2'	34:a:567:G:C8	2.50	0.47
34:a:687:A:N6	34:a:703:G:H1'	2.30	0.47
34:a:974:A:OP1	47:n:69:ARG:NH2	2.47	0.47
57:x:19:A:C4	57:x:20:A:H8	2.33	0.47
8:A:296:U:H2'	8:A:297:G:C8	2.50	0.46
8:A:1753:G:H5''	23:P:92:ARG:HD3	1.97	0.46
8:A:2204:G:H2'	8:A:2205:A:H8	1.80	0.46
8:A:2731:G:O2'	8:A:2732:G:H5'	2.14	0.46
9:B:42:C:OP1	13:F:63:LYS:NZ	2.45	0.46
14:G:39:ALA:HA	14:G:57:TYR:CD2	2.50	0.46
19:L:79:LEU:HA	19:L:82:LEU:HD13	1.95	0.46
20:M:78:LEU:HD12	20:M:79:ALA:H	1.80	0.46
34:a:615:G:C6	34:a:626:G:O6	2.68	0.46
34:a:1305:G:O2'	34:a:1306:A:O4'	2.33	0.46
34:a:1530:G:H2'	34:a:1531:A:H8	1.79	0.46
36:c:171:ARG:NH2	36:c:173:PRO:HG3	2.30	0.46
54:u:14:ALA:HA	54:u:17:ARG:HG2	1.98	0.46
56:w:20:U:H2'	56:w:21:A:H5''	1.97	0.46
4:3:44:ARG:NH2	8:A:2349:G:OP1	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:250:G:H2'	8:A:251:A:C8	2.50	0.46
8:A:351:C:H2'	8:A:352:A:C8	2.48	0.46
8:A:563:A:H2'	24:Q:36:GLN:HE21	1.79	0.46
8:A:1275:A:N1	8:A:1295:C:O2'	2.44	0.46
8:A:1353:A:H5''	10:C:35:LYS:NZ	2.31	0.46
8:A:1675:C:O2	11:D:133:THR:OG1	2.28	0.46
8:A:1829:A:N3	10:C:14:HIS:NE2	2.52	0.46
8:A:2121:G:C8	8:A:2122:U:H5	2.33	0.46
8:A:2194:U:H2'	8:A:2195:U:H6	1.81	0.46
8:A:2629:U:O2'	8:A:2630:G:O5'	2.31	0.46
8:A:2818:U:H2'	8:A:2819:G:C8	2.50	0.46
17:J:12:LYS:O	17:J:41:LYS:NZ	2.48	0.46
34:a:8:A:H1'	38:e:107:GLY:HA2	1.96	0.46
34:a:50:A:O2'	34:a:360:G:N2	2.41	0.46
34:a:779:C:H2'	34:a:780:A:O4'	2.14	0.46
35:b:89:PHE:CD2	35:b:153:MET:HG3	2.50	0.46
54:u:30:GLU:OE2	54:u:33:ARG:NH2	2.48	0.46
7:6:56:ARG:HD2	7:6:56:ARG:HA	1.68	0.46
8:A:396:G:H1'	31:X:28:PHE:HB3	1.98	0.46
8:A:404:A:H1'	8:A:406:G:C4	2.49	0.46
8:A:685:A:N1	8:A:787:C:H1'	2.30	0.46
8:A:1332:G:N7	8:A:1609:A:O2'	2.40	0.46
8:A:1586:A:H2'	8:A:1587:G:O4'	2.16	0.46
8:A:2635:A:O2'	11:D:81:GLU:OE1	2.28	0.46
20:M:41:LEU:HD11	20:M:102:LEU:HD13	1.97	0.46
25:R:55:ASP:OD1	25:R:56:GLY:N	2.48	0.46
34:a:90:C:C5	34:a:90:C:OP2	2.69	0.46
34:a:501:C:H2'	34:a:502:A:H8	1.81	0.46
34:a:1506:U:O2	44:k:127:ARG:HD2	2.15	0.46
37:d:46:ARG:NH2	57:x:26:U:O4	2.48	0.46
37:d:71:PHE:HE2	37:d:93:LEU:HD11	1.80	0.46
39:f:2:ARG:HD3	39:f:91:ARG:NH1	2.31	0.46
8:A:150:U:H2'	8:A:151:C:C6	2.50	0.46
8:A:347:A:H2'	8:A:348:A:C8	2.51	0.46
8:A:839:U:H2'	8:A:840:C:H6	1.81	0.46
8:A:1433:A:H2'	8:A:1434:A:H8	1.79	0.46
8:A:2700:A:H2'	8:A:2701:U:C6	2.50	0.46
9:B:106:G:H2'	9:B:107:G:O4'	2.16	0.46
15:H:50:ARG:HE	15:H:51:ARG:HD2	1.80	0.46
19:L:77:ILE:N	19:L:109:LYS:O	2.35	0.46
34:a:77:A:H2'	34:a:78:A:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:839:C:H2'	34:a:840:C:C6	2.50	0.46
34:a:868:C:H2'	34:a:869:G:O4'	2.16	0.46
38:e:151:MET:HE2	38:e:151:MET:HA	1.97	0.46
8:A:285:G:C6	8:A:356:G:C6	3.03	0.46
8:A:863:A:H2'	8:A:864:G:H8	1.80	0.46
8:A:942:G:O2'	8:A:1189:A:N3	2.46	0.46
8:A:1064:C:H41	8:A:1069:A:P	2.38	0.46
8:A:2050:C:H2'	8:A:2051:A:O4'	2.15	0.46
14:G:101:VAL:HG22	14:G:115:GLN:HA	1.97	0.46
19:L:128:THR:OG1	19:L:129:LYS:N	2.46	0.46
25:R:14:VAL:HG21	25:R:98:ILE:HG13	1.97	0.46
30:W:37:ARG:O	30:W:53:HIS:ND1	2.48	0.46
34:a:46:G:H2'	34:a:366:A:N7	2.31	0.46
34:a:106:C:H2'	34:a:107:G:O4'	2.15	0.46
34:a:707:U:H2'	34:a:708:C:H6	1.80	0.46
34:a:766:A:OP2	34:a:812:G:N2	2.45	0.46
37:d:22:SER:HB3	37:d:24:VAL:HG13	1.98	0.46
46:m:95:PRO:HB3	46:m:99:GLN:HB2	1.97	0.46
1:O:3:GLN:NE2	8:A:2016:U:O2	2.43	0.46
8:A:878:A:H3'	8:A:879:G:C8	2.48	0.46
8:A:1339:G:P	27:T:15:HIS:HE2	2.38	0.46
8:A:1923:U:H2'	8:A:1924:C:H6	1.81	0.46
8:A:2812:G:H2'	8:A:2813:A:C8	2.51	0.46
8:A:2818:U:H2'	8:A:2819:G:H8	1.79	0.46
10:C:66:PHE:HB3	10:C:150:GLY:O	2.15	0.46
10:C:75:ALA:HB2	10:C:95:TYR:CD1	2.51	0.46
10:C:79:ARG:HD2	10:C:81:GLU:OE2	2.15	0.46
33:Z:30:ARG:HG2	33:Z:33:HIS:HB2	1.97	0.46
34:a:303:A:H2'	34:a:304:U:O4'	2.16	0.46
34:a:427:U:OP2	34:a:428:G:O2'	2.20	0.46
34:a:1064:G:O2'	34:a:1190:G:N2	2.48	0.46
35:b:132:GLU:O	35:b:136:ARG:HG3	2.16	0.46
37:d:143:SER:O	37:d:145:ARG:N	2.49	0.46
39:f:47:LEU:HD21	39:f:57:ALA:HB3	1.97	0.46
40:g:25:PHE:CZ	40:g:119:LEU:HD11	2.50	0.46
2:1:4:ILE:O	2:1:27:ARG:NH2	2.45	0.46
4:3:60:CYS:O	4:3:62:PRO:HD3	2.16	0.46
8:A:145:C:H2'	8:A:146:A:H8	1.81	0.46
8:A:240:C:H3'	8:A:241:A:H2'	1.98	0.46
8:A:1159:U:C2	8:A:1160:G:C8	3.04	0.46
8:A:1182:G:H2'	8:A:1183:U:O4'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:1295:C:C2	8:A:1296:G:C8	3.04	0.46
8:A:1490:A:HO2'	8:A:1491:G:P	2.39	0.46
8:A:1746:A:H2'	8:A:1747:U:C6	2.50	0.46
8:A:2047:C:H2'	8:A:2048:G:H8	1.81	0.46
8:A:2483:C:N3	20:M:123:LYS:NZ	2.60	0.46
8:A:2801:G:H2'	8:A:2802:G:C8	2.50	0.46
15:H:103:VAL:HG11	15:H:132:PHE:CZ	2.51	0.46
26:S:43:ALA:O	26:S:47:VAL:HG12	2.16	0.46
32:Y:42:LEU:HA	32:Y:45:GLN:HG2	1.98	0.46
34:a:89:U:C6	34:a:89:U:C3'	2.99	0.46
34:a:405:U:C5	37:d:4:LEU:HD11	2.50	0.46
34:a:694:A:N1	34:a:787:A:O2'	2.47	0.46
35:b:161:PHE:HA	35:b:183:PHE:O	2.15	0.46
49:p:17:TYR:CE2	49:p:41:PRO:HG3	2.50	0.46
54:u:38:GLU:HG3	54:u:42:THR:OG1	2.15	0.46
8:A:879:G:H2'	8:A:880:G:C8	2.51	0.46
8:A:918:A:H5''	9:B:97:C:O2'	2.16	0.46
8:A:1744:A:H3'	8:A:1745:A:H8	1.80	0.46
8:A:2063:C:H4'	55:v:102:PHE:CE1	2.50	0.46
8:A:2291:U:H2'	8:A:2292:U:H6	1.79	0.46
8:A:2319:G:O2'	8:A:2320:U:O5'	2.33	0.46
8:A:2567:G:H2'	8:A:2568:U:C6	2.51	0.46
12:E:188:MET:HE2	12:E:193:VAL:HG22	1.98	0.46
22:O:15:ARG:HH21	22:O:95:SER:HB2	1.80	0.46
34:a:236:A:H2'	34:a:237:G:C8	2.50	0.46
40:g:145:GLU:HA	40:g:148:LYS:HG3	1.97	0.46
8:A:265:A:N1	8:A:427:U:O2'	2.44	0.46
8:A:580:U:O3'	24:Q:30:VAL:HG13	2.16	0.46
8:A:760:G:H2'	8:A:761:A:O4'	2.16	0.46
8:A:1316:U:H2'	8:A:1317:G:H8	1.81	0.46
8:A:1718:G:H1	8:A:1742:U:H3	1.63	0.46
9:B:43:C:O2'	13:F:91:ARG:HG2	2.16	0.46
12:E:97:ASN:ND2	12:E:100:MET:SD	2.89	0.46
22:O:92:PHE:HB2	22:O:117:PHE:CD2	2.50	0.46
34:a:191:G:H2'	34:a:192:A:C8	2.51	0.46
34:a:193:C:H2'	34:a:194:C:H6	1.81	0.46
34:a:1118:U:OP1	42:i:10:ARG:HD2	2.16	0.46
34:a:1216:A:H2'	34:a:1217:C:C6	2.51	0.46
34:a:1300:G:HO2'	34:a:1301:U:P	2.39	0.46
34:a:1422:G:H1	34:a:1478:U:H3	1.62	0.46
35:b:187:ASP:OD1	35:b:188:THR:N	2.41	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:k:115:ILE:HD11	54:u:27:VAL:HG23	1.98	0.46
47:n:52:PRO:O	47:n:55:SER:OG	2.33	0.46
52:s:9:PHE:O	52:s:38:THR:HG22	2.16	0.46
8:A:352:A:H2'	8:A:353:C:C6	2.50	0.46
8:A:458:G:O2'	8:A:469:G:N1	2.47	0.46
8:A:1794:A:H2'	8:A:1795:C:H6	1.78	0.46
8:A:2589:A:H2'	8:A:2590:A:C8	2.51	0.46
9:B:49:C:H2'	9:B:50:A:H8	1.80	0.46
11:D:8:LYS:HB2	11:D:201:LEU:HD11	1.97	0.46
14:G:43:LYS:HB2	14:G:43:LYS:HE3	1.70	0.46
31:X:53:LYS:O	31:X:57:VAL:HG23	2.15	0.46
34:a:62:U:OP1	34:a:385:C:O2'	2.34	0.46
34:a:1107:C:C4	34:a:1108:G:C8	3.04	0.46
2:1:8:ILE:HD13	2:1:24:LYS:HB2	1.98	0.45
8:A:245:G:O2'	8:A:384:A:N1	2.44	0.45
8:A:312:G:H4'	8:A:331:C:C2	2.51	0.45
8:A:368:A:H2'	8:A:369:U:O4'	2.15	0.45
8:A:704:G:H2'	8:A:726:G:N2	2.31	0.45
8:A:1753:G:N1	8:A:1756:G:OP2	2.47	0.45
8:A:2291:U:OP1	8:A:2380:C:O2'	2.33	0.45
15:H:46:PHE:O	15:H:50:ARG:HB3	2.16	0.45
22:O:27:VAL:HA	22:O:93:ASP:HB3	1.97	0.45
34:a:67:C:H2'	34:a:68:G:C8	2.51	0.45
34:a:554:A:H2'	34:a:555:U:C6	2.51	0.45
34:a:1241:G:H2'	34:a:1242:G:C8	2.51	0.45
34:a:1427:C:H2'	34:a:1428:A:H8	1.81	0.45
56:w:63:G:H2'	56:w:64:A:H8	1.79	0.45
8:A:91:A:H4'	8:A:92:U:H5'	1.96	0.45
8:A:549:G:H2'	8:A:550:C:H6	1.81	0.45
8:A:1048:A:OP2	8:A:1110:G:N2	2.48	0.45
8:A:1197:G:H2'	8:A:1198:U:H6	1.81	0.45
8:A:1201:U:H2'	8:A:1202:G:H8	1.80	0.45
8:A:1814:G:H4'	10:C:50:THR:HG21	1.97	0.45
8:A:2861:U:H2'	8:A:2862:G:H8	1.81	0.45
14:G:74:MET:O	14:G:78:VAL:HG22	2.16	0.45
15:H:31:VAL:N	15:H:32:PRO:HD2	2.31	0.45
21:N:96:ARG:HH12	21:N:116:VAL:HG13	1.81	0.45
31:X:6:VAL:HG23	31:X:50:VAL:HG12	1.98	0.45
34:a:552:U:C2	34:a:553:A:C8	3.04	0.45
34:a:883:C:O2'	34:a:884:U:H5'	2.16	0.45
34:a:1157:A:H4'	34:a:1158:C:O4'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:c:191:THR:HG23	36:c:192:TYR:CD2	2.51	0.45
8:A:322:A:OP1	12:E:162:ARG:NE	2.45	0.45
8:A:1038:G:H2'	8:A:1039:A:C8	2.51	0.45
8:A:1201:U:H2'	8:A:1202:G:C8	2.51	0.45
8:A:1411:U:H2'	8:A:1412:U:C6	2.51	0.45
8:A:1473:G:H2'	8:A:1474:U:C6	2.51	0.45
8:A:2126:A:N3	8:A:2171:A:H5''	2.31	0.45
9:B:75:G:O4'	29:V:29:ILE:HD12	2.16	0.45
19:L:132:ARG:HG3	19:L:142:ILE:HD12	1.98	0.45
21:N:66:ALA:O	21:N:70:THR:OG1	2.29	0.45
34:a:109:A:H5'	34:a:110:C:C5	2.52	0.45
34:a:269:C:H2'	34:a:270:A:C8	2.51	0.45
34:a:642:A:H2'	34:a:643:C:H6	1.81	0.45
34:a:865:A:H5'	34:a:1078:U:C5	2.52	0.45
34:a:1460:C:H2'	34:a:1461:G:O4'	2.17	0.45
42:i:38:PHE:C	42:i:40:ARG:H	2.25	0.45
44:k:112:VAL:HA	51:r:72:ARG:NH1	2.31	0.45
46:m:2:ARG:HH12	46:m:5:GLY:HA2	1.82	0.45
47:n:22:LYS:O	47:n:25:GLU:HG2	2.17	0.45
1:0:47:TYR:HA	1:0:51:ARG:O	2.16	0.45
8:A:361:G:O2'	8:A:362:A:H5'	2.16	0.45
8:A:492:A:H2'	8:A:493:G:O4'	2.17	0.45
8:A:685:A:O2'	8:A:773:U:O4	2.27	0.45
8:A:1266:G:O2'	8:A:2012:G:O6	2.23	0.45
8:A:1495:A:N3	8:A:1578:U:O2'	2.35	0.45
8:A:2294:G:OP1	22:O:10:ARG:HD3	2.16	0.45
8:A:2460:U:C2	8:A:2461:A:C8	3.05	0.45
14:G:26:LYS:HB2	14:G:31:GLU:OE2	2.17	0.45
21:N:37:THR:HG22	21:N:110:MET:HE1	1.98	0.45
34:a:85:U:H4'	34:a:87:C:H41	1.82	0.45
34:a:945:G:C2	34:a:946:A:C8	3.05	0.45
34:a:1244:G:H2'	34:a:1245:C:C6	2.51	0.45
34:a:1507:A:H2'	34:a:1508:A:C8	2.52	0.45
8:A:671:C:H2'	8:A:672:C:C6	2.52	0.45
8:A:863:A:H2'	8:A:864:G:C8	2.50	0.45
8:A:967:U:H2'	8:A:968:C:C6	2.52	0.45
8:A:1171:G:H22	8:A:1177:G:H22	1.63	0.45
8:A:1538:G:H2'	8:A:1539:U:C6	2.50	0.45
8:A:1727:C:H2'	8:A:1728:C:H6	1.82	0.45
8:A:2377:A:H2'	8:A:2378:A:C8	2.50	0.45
21:N:44:LEU:HD23	21:N:113:ILE:HD13	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:323:U:H2'	34:a:324:G:O4'	2.17	0.45
34:a:517:G:H8	34:a:517:G:OP2	2.00	0.45
34:a:593:U:H2'	34:a:594:U:H6	1.81	0.45
34:a:687:A:H61	34:a:703:G:H1'	1.81	0.45
34:a:744:C:H2'	34:a:745:G:H8	1.82	0.45
34:a:1371:G:O3'	42:i:70:GLY:HA3	2.17	0.45
34:a:1486:G:H2'	34:a:1487:G:O4'	2.17	0.45
42:i:24:ASN:N	42:i:61:ASP:OD1	2.50	0.45
8:A:30:G:H2'	8:A:31:C:C6	2.52	0.45
8:A:265:A:O2'	8:A:428:A:N6	2.50	0.45
8:A:2292:U:H2'	8:A:2293:G:H8	1.82	0.45
8:A:2848:G:H1'	8:A:2868:A:H61	1.82	0.45
13:F:99:PHE:O	13:F:103:ILE:HG22	2.16	0.45
18:K:2:ILE:HG13	18:K:8:LEU:HD21	1.99	0.45
25:R:7:SER:OG	25:R:22:LEU:HD13	2.17	0.45
34:a:266:G:H1'	34:a:268:U:OP2	2.16	0.45
34:a:269:C:H2'	34:a:270:A:H8	1.82	0.45
34:a:922:G:H2'	34:a:923:A:C8	2.51	0.45
40:g:71:THR:HA	40:g:95:ARG:NH1	2.32	0.45
42:i:33:SER:OG	42:i:36:GLN:HG2	2.16	0.45
43:j:15:HIS:HB3	43:j:70:HIS:CE1	2.52	0.45
44:k:84:MET:SD	44:k:110:THR:HB	2.56	0.45
49:p:57:ILE:O	49:p:61:VAL:HG13	2.16	0.45
7:6:45:THR:HG22	7:6:46:GLY:N	2.28	0.45
8:A:709:U:H2'	8:A:710:U:C6	2.52	0.45
8:A:959:A:H2'	8:A:960:A:C8	2.51	0.45
8:A:1021:A:N6	8:A:1142:A:H61	2.15	0.45
8:A:1068:G:N3	16:I:22:PRO:HA	2.31	0.45
8:A:1408:G:H2'	8:A:1409:U:C6	2.52	0.45
8:A:2577:A:H2'	8:A:2614:A:N6	2.32	0.45
8:A:2726:A:H1'	18:K:1:MET:HE1	1.98	0.45
34:a:211:G:C5	34:a:212:G:H1'	2.52	0.45
34:a:224:U:H2'	34:a:225:C:C6	2.52	0.45
34:a:565:U:H3'	34:a:566:G:H2'	1.98	0.45
34:a:739:C:P	39:f:2:ARG:HH12	2.40	0.45
34:a:1060:U:H2'	34:a:1061:G:H8	1.82	0.45
34:a:1347:G:O6	42:i:11:ARG:NH2	2.50	0.45
36:c:122:GLN:HB3	36:c:127:VAL:HB	1.99	0.45
41:h:6:ILE:O	41:h:10:LEU:HG	2.17	0.45
5:4:36:ARG:HH11	5:4:37:GLN:HB3	1.82	0.45
8:A:569:U:H5''	8:A:821:A:N1	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:644:A:C2	8:A:2369:A:H1'	2.51	0.45
8:A:1109:C:H3'	8:A:1110:G:C8	2.52	0.45
8:A:1179:G:OP2	8:A:1180:U:H5''	2.16	0.45
8:A:1824:G:O3'	10:C:246:PRO:HD3	2.17	0.45
8:A:2063:C:O4'	55:v:102:PHE:CE2	2.69	0.45
8:A:2121:G:H8	8:A:2123:G:N7	2.15	0.45
8:A:2216:G:H2'	8:A:2217:G:H8	1.82	0.45
8:A:2273:A:H2'	8:A:2274:A:C8	2.52	0.45
8:A:2329:U:H2'	8:A:2330:G:C8	2.52	0.45
8:A:2505:G:N2	8:A:2506:U:O4	2.47	0.45
8:A:2647:U:H2'	8:A:2648:G:H8	1.81	0.45
8:A:2667:C:O2	14:G:108:PHE:HB3	2.17	0.45
8:A:2682:A:H61	8:A:2728:U:H1'	1.81	0.45
8:A:2780:G:OP2	17:J:120:ARG:NE	2.50	0.45
11:D:74:GLU:OE1	11:D:74:GLU:N	2.39	0.45
25:R:3:ALA:HA	25:R:40:MET:O	2.17	0.45
35:b:87:ASP:OD2	35:b:224:ARG:NH2	2.50	0.45
37:d:143:SER:HA	37:d:178:GLU:HB3	1.99	0.45
41:h:8:ASP:HA	41:h:11:THR:HG22	1.99	0.45
8:A:102:U:O2'	8:A:103:A:OP1	2.28	0.45
8:A:1441:G:H2'	8:A:1442:U:C6	2.52	0.45
8:A:1775:U:O4	8:A:1789:A:H2	2.00	0.45
8:A:2590:A:H2'	8:A:2591:C:C6	2.52	0.45
9:B:75:G:H2'	9:B:76:G:O4'	2.17	0.45
9:B:82:U:H5''	33:Z:16:LEU:HD11	1.99	0.45
12:E:97:ASN:HB2	12:E:100:MET:HG3	1.98	0.45
14:G:51:PHE:CE1	14:G:71:LEU:HD22	2.52	0.45
21:N:55:ALA:HB2	21:N:79:LEU:HB3	1.99	0.45
34:a:1246:A:H2'	34:a:1247:U:C6	2.51	0.45
34:a:1347:G:H5''	42:i:108:ARG:HB2	1.98	0.45
42:i:43:ALA:O	42:i:47:VAL:HG23	2.16	0.45
45:l:73:LEU:HD11	45:l:103:CYS:SG	2.57	0.45
8:A:1172:C:N3	8:A:1176:U:O4	2.50	0.45
8:A:2266:A:H4'	8:A:2267:A:N3	2.32	0.45
8:A:2328:A:H2'	8:A:2329:U:H6	1.81	0.45
8:A:2901:C:H2'	8:A:2902:C:C5	2.52	0.45
17:J:40:HIS:CE1	17:J:41:LYS:HG3	2.52	0.45
19:L:77:ILE:CD1	19:L:108:ALA:HB1	2.46	0.45
34:a:19:A:OP1	38:e:134:ASN:ND2	2.44	0.45
34:a:82:G:C5	34:a:83:C:H1'	2.52	0.45
34:a:170:U:C5	34:a:170:U:OP2	2.70	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:207:C:O4'	34:a:213:G:C2	2.70	0.45
34:a:270:A:H2'	34:a:271:C:H6	1.82	0.45
34:a:382:A:H8	34:a:382:A:OP2	2.00	0.45
34:a:615:G:N3	34:a:626:G:C2	2.85	0.45
34:a:793:U:H5'	34:a:794:A:H5''	1.99	0.45
34:a:1414:U:H2'	34:a:1415:G:C8	2.47	0.45
35:b:17:HIS:CE1	35:b:18:GLN:HE21	2.35	0.45
8:A:282:A:N6	8:A:359:G:O6	2.50	0.44
8:A:608:A:H2'	8:A:609:A:C8	2.53	0.44
8:A:2262:U:H2'	8:A:2263:C:H6	1.82	0.44
15:H:100:ALA:HA	15:H:103:VAL:HG12	1.99	0.44
22:O:2:ASP:OD1	22:O:2:ASP:N	2.50	0.44
34:a:246:A:C2	34:a:282:A:C5	3.05	0.44
34:a:568:G:O2'	34:a:574:A:N1	2.47	0.44
34:a:1002:G:H2'	34:a:1003:G:H8	1.81	0.44
34:a:1220:G:OP1	47:n:53:ARG:NH2	2.34	0.44
53:t:29:THR:HA	53:t:32:LYS:HG2	1.98	0.44
8:A:2:G:H2'	8:A:3:U:H6	1.81	0.44
8:A:116:C:O2'	8:A:126:A:N3	2.40	0.44
8:A:1171:G:N2	8:A:1177:G:H1	2.10	0.44
8:A:1487:U:N3	8:A:1502:A:C6	2.85	0.44
8:A:1754:A:C8	23:P:93:LYS:HE3	2.52	0.44
8:A:2282:G:H4'	8:A:2389:G:O2'	2.18	0.44
8:A:2595:G:N2	8:A:2598:A:OP2	2.39	0.44
8:A:2679:A:H4'	11:D:170:VAL:HG21	2.00	0.44
34:a:89:U:H2'	34:a:90:C:C6	2.52	0.44
34:a:207:C:O2'	34:a:212:G:N2	2.48	0.44
34:a:375:U:H5''	49:p:70:ARG:HG3	1.99	0.44
34:a:1149:C:H2'	34:a:1150:A:C8	2.52	0.44
34:a:1244:G:H2'	34:a:1245:C:H6	1.82	0.44
37:d:69:ARG:O	37:d:70:GLN:HB3	2.18	0.44
37:d:100:VAL:O	37:d:104:MET:HE2	2.17	0.44
38:e:32:PHE:CD2	38:e:55:VAL:HG22	2.52	0.44
42:i:54:VAL:HG12	42:i:55:ASP:H	1.81	0.44
43:j:25:ILE:HG21	43:j:74:VAL:HG21	1.99	0.44
44:k:93:GLU:HG3	54:u:19:LYS:HD3	1.99	0.44
8:A:330:A:H8	8:A:1210:G:C5	2.35	0.44
8:A:362:A:N6	8:A:363:G:N3	2.65	0.44
8:A:445:C:H2'	8:A:446:G:O4'	2.18	0.44
8:A:550:C:H2'	8:A:551:G:C8	2.52	0.44
8:A:754:U:O2'	8:A:1272:A:N1	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:1528:A:OP2	8:A:1543:G:N2	2.45	0.44
8:A:2096:C:H2'	8:A:2097:A:C8	2.52	0.44
8:A:2118:U:C5	8:A:2148:G:H1'	2.52	0.44
8:A:2215:C:H2'	8:A:2216:G:C8	2.52	0.44
8:A:2687:U:H2'	8:A:2688:G:O4'	2.17	0.44
13:F:40:GLY:O	13:F:43:ILE:HG23	2.18	0.44
17:J:104:ALA:O	17:J:108:MET:HG3	2.16	0.44
22:O:31:THR:C	22:O:102:ARG:HH12	2.25	0.44
34:a:211:G:C4	34:a:212:G:H1'	2.52	0.44
34:a:414:A:H2'	34:a:415:A:H8	1.82	0.44
34:a:971:G:H1'	34:a:1365:G:O2'	2.18	0.44
34:a:1322:C:H5''	46:m:98:GLY:HA3	1.99	0.44
36:c:139:ASN:OD1	36:c:142:ARG:NH2	2.47	0.44
38:e:113:VAL:HG11	38:e:139:THR:OG1	2.17	0.44
2:1:22:THR:OG1	2:1:23:THR:N	2.48	0.44
7:6:20:ASN:HB2	7:6:39:LYS:HE2	1.99	0.44
8:A:394:C:H2'	8:A:395:U:O4'	2.17	0.44
8:A:458:G:HO2'	8:A:469:G:H1	1.64	0.44
8:A:536:G:H4'	24:Q:56:PHE:CZ	2.53	0.44
8:A:555:G:HO2'	8:A:556:A:P	2.41	0.44
8:A:722:A:H2'	8:A:723:C:C6	2.52	0.44
8:A:1199:U:H2'	8:A:1200:C:C6	2.52	0.44
8:A:2096:C:H2'	8:A:2097:A:H8	1.82	0.44
8:A:2405:G:HO2'	8:A:2406:A:P	2.41	0.44
9:B:52:A:O2'	9:B:53:A:P	2.75	0.44
18:K:113:MET:HA	18:K:116:ILE:HG22	2.00	0.44
30:W:64:LYS:HD2	30:W:65:PHE:H	1.82	0.44
34:a:224:U:H2'	34:a:225:C:H6	1.83	0.44
34:a:711:G:OP1	39:f:53:LYS:NZ	2.50	0.44
34:a:728:A:H2'	34:a:729:A:C8	2.52	0.44
34:a:921:U:H2'	34:a:922:G:O4'	2.18	0.44
34:a:924:C:O2'	34:a:1502:A:N1	2.49	0.44
34:a:954:G:H2'	34:a:955:U:C6	2.52	0.44
34:a:1041:G:H2'	34:a:1042:A:H8	1.83	0.44
34:a:1161:C:H2'	34:a:1162:C:H6	1.83	0.44
34:a:1251:A:H2'	34:a:1252:A:C8	2.52	0.44
34:a:1427:C:H2'	34:a:1428:A:C8	2.52	0.44
39:f:46:GLN:HA	39:f:56:LYS:HA	1.99	0.44
50:q:48:GLU:O	50:q:49:ASN:C	2.59	0.44
56:w:8:4SU:O2'	56:w:21:A:N1	2.42	0.44
8:A:191:A:H2'	8:A:192:C:H6	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:279:A:P	8:A:279:A:H8	2.40	0.44
8:A:528:A:C2	8:A:2042:A:H2'	2.52	0.44
8:A:580:U:H2'	8:A:581:C:C6	2.53	0.44
8:A:1186:G:H2'	8:A:1187:G:O4'	2.17	0.44
8:A:1637:A:H5'	8:A:1760:C:O2'	2.17	0.44
8:A:2149:U:H3'	8:A:2150:C:C6	2.53	0.44
8:A:2364:C:H2'	8:A:2365:G:O4'	2.18	0.44
8:A:2395:C:H2'	8:A:2396:G:O4'	2.17	0.44
8:A:2443:C:OP1	12:E:63:LYS:HD3	2.18	0.44
8:A:2589:A:H2'	8:A:2590:A:H8	1.83	0.44
8:A:2861:U:H2'	8:A:2862:G:C8	2.52	0.44
11:D:112:THR:HA	11:D:168:GLU:O	2.17	0.44
20:M:12:MET:SD	20:M:72:PRO:HD2	2.58	0.44
34:a:33:A:H2'	34:a:34:C:C6	2.53	0.44
34:a:1250:A:H2'	34:a:1251:A:C8	2.52	0.44
34:a:1300:G:O2'	34:a:1301:U:P	2.75	0.44
34:a:1328:C:H5''	46:m:27:THR:HG21	1.98	0.44
34:a:1377:A:C8	40:g:6:ILE:HD13	2.52	0.44
34:a:1516:2MG:H2'	34:a:1518:MA6:OP2	2.16	0.44
36:c:128:MET:SD	36:c:130:ARG:HB2	2.58	0.44
38:e:24:VAL:N	38:e:27:GLY:O	2.50	0.44
40:g:61:PHE:CZ	40:g:65:LEU:HD11	2.53	0.44
44:k:80:ASN:HA	44:k:105:ARG:O	2.17	0.44
4:3:31:ILE:HG22	8:A:2421:G:OP2	2.18	0.44
8:A:69:C:O2	8:A:73:A:O2'	2.31	0.44
8:A:173:A:H2'	8:A:174:U:H6	1.80	0.44
8:A:513:A:H5''	8:A:1216:G:O2'	2.18	0.44
8:A:528:A:C2	8:A:2043:C:H4'	2.53	0.44
8:A:774:G:O2'	8:A:775:G:H8	2.00	0.44
8:A:849:A:H2'	8:A:850:U:H6	1.82	0.44
8:A:1389:G:H2'	8:A:1390:U:O4'	2.17	0.44
8:A:1511:G:H2'	8:A:1512:C:C6	2.53	0.44
8:A:1571:A:H2'	8:A:1572:A:H8	1.83	0.44
8:A:1727:C:H2'	8:A:1728:C:C6	2.52	0.44
8:A:2314:A:H2'	8:A:2315:G:C8	2.53	0.44
8:A:2391:G:O2'	8:A:2429:G:N2	2.51	0.44
11:D:32:ASN:ND2	11:D:52:THR:HB	2.32	0.44
13:F:15:LEU:HD12	13:F:27:VAL:HG13	1.98	0.44
21:N:79:LEU:O	21:N:80:PHE:HB2	2.17	0.44
34:a:68:G:C1'	34:a:171:A:N3	2.80	0.44
34:a:627:G:H5'	49:p:51:ARG:HH22	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:771:G:H2'	34:a:772:U:C6	2.53	0.44
34:a:958:A:C2	52:s:54:ARG:HB3	2.53	0.44
34:a:958:A:H1'	34:a:985:C:O2'	2.18	0.44
34:a:958:A:C5	52:s:54:ARG:HD3	2.52	0.44
34:a:977:A:H2'	34:a:978:A:H5''	1.98	0.44
34:a:1010:U:H2'	34:a:1011:C:H6	1.81	0.44
46:m:105:ALA:O	46:m:109:LYS:HB2	2.17	0.44
52:s:31:ARG:HA	52:s:49:ALA:HB3	2.00	0.44
8:A:841:G:H2'	8:A:842:U:C6	2.53	0.44
8:A:902:C:C2	8:A:903:C:C5	3.06	0.44
8:A:1614:A:C6	26:S:87:PRO:HB3	2.52	0.44
8:A:2418:A:H2'	8:A:2419:U:O4'	2.18	0.44
9:B:34:A:HO2'	9:B:35:C:H5	1.63	0.44
14:G:153:PRO:HA	14:G:159:LYS:O	2.18	0.44
34:a:999:C:N3	34:a:1042:A:N6	2.64	0.44
34:a:1029:U:O2'	34:a:1033:G:N2	2.40	0.44
34:a:1346:A:OP1	34:a:1346:A:H4'	2.18	0.44
34:a:1432:G:O2'	34:a:1468:A:N6	2.51	0.44
36:c:174:LEU:HD21	36:c:200:TRP:CD1	2.53	0.44
45:l:86:VAL:HG13	45:l:89:LEU:H	1.83	0.44
50:q:17:GLU:O	50:q:18:LYS:HB2	2.17	0.44
8:A:686:U:H2'	8:A:788:A:N1	2.33	0.44
8:A:995:C:OP2	24:Q:53:LYS:NZ	2.47	0.44
8:A:1790:C:H2'	8:A:1791:A:C5	2.53	0.44
8:A:2065:C:H2'	8:A:2066:C:H6	1.83	0.44
8:A:2142:A:H2'	8:A:2143:C:H5''	2.00	0.44
8:A:2823:A:OP1	11:D:118:PHE:HB2	2.18	0.44
9:B:2:G:H2'	9:B:3:C:H6	1.83	0.44
10:C:116:GLN:N	10:C:127:ASN:OD1	2.51	0.44
10:C:135:PRO:HG2	39:f:80:PHE:HD1	1.82	0.44
12:E:47:LYS:HE2	12:E:47:LYS:HB3	1.83	0.44
21:N:72:ASP:O	21:N:76:VAL:HG23	2.17	0.44
28:U:52:ASN:C	28:U:54:PRO:HD3	2.43	0.44
34:a:892:A:H2'	34:a:893:C:C6	2.52	0.44
42:i:87:MET:HE2	42:i:87:MET:HA	2.00	0.44
8:A:697:G:H2'	8:A:698:C:C6	2.53	0.44
8:A:1656:C:H2'	8:A:1657:U:H6	1.83	0.44
8:A:1857:G:O2'	8:A:1885:A:N6	2.51	0.44
8:A:2267:A:H5''	8:A:2268:A:H5'	1.99	0.44
8:A:2405:G:O2'	8:A:2406:A:OP2	2.35	0.44
8:A:2620:C:O2'	11:D:162:ALA:O	2.25	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:80:SER:N	19:L:114:GLY:O	2.50	0.44
25:R:5:PHE:HB3	25:R:59:ILE:HD12	2.00	0.44
34:a:412:A:N1	34:a:414:A:H1'	2.32	0.44
34:a:1121:U:H2'	34:a:1122:U:C6	2.53	0.44
34:a:1477:U:H2'	34:a:1478:U:H6	1.79	0.44
35:b:213:LEU:HA	35:b:216:VAL:HG12	2.00	0.44
41:h:40:LYS:HE2	41:h:47:ASP:HA	1.99	0.44
1:O:5:ASN:ND2	8:A:2020:A:H62	2.15	0.43
7:6:11:GLU:OE2	7:6:23:LYS:HE3	2.18	0.43
8:A:297:G:H5''	28:U:84:PHE:HB2	2.00	0.43
8:A:911:A:H2'	20:M:9:PHE:CZ	2.53	0.43
8:A:1353:A:H2'	8:A:1354:A:C8	2.53	0.43
8:A:1412:U:H2'	8:A:1413:A:H8	1.83	0.43
8:A:2136:G:C4	8:A:2137:U:C5	3.06	0.43
8:A:2300:C:H2'	8:A:2301:C:C6	2.53	0.43
28:U:85:ARG:HD2	28:U:87:GLU:OE2	2.18	0.43
34:a:21:G:H2'	34:a:22:G:C8	2.53	0.43
34:a:321:A:H2'	34:a:322:C:C6	2.53	0.43
34:a:469:C:C5	34:a:470:C:H1'	2.53	0.43
34:a:514:C:N4	34:a:515:G:O6	2.51	0.43
34:a:1492:A:H2'	34:a:1493:A:C8	2.53	0.43
35:b:86:CYS:SG	35:b:87:ASP:N	2.83	0.43
42:i:54:VAL:HG12	42:i:55:ASP:OD1	2.18	0.43
42:i:112:ARG:O	42:i:114:LYS:NZ	2.51	0.43
43:j:59:LYS:HE2	43:j:62:ARG:HH22	1.82	0.43
48:o:35:ILE:O	48:o:39:GLN:HG2	2.18	0.43
48:o:63:ARG:NH1	48:o:88:ARG:HH22	2.16	0.43
8:A:19:A:H2'	8:A:20:C:C6	2.54	0.43
8:A:39:G:H2'	8:A:40:U:C6	2.53	0.43
8:A:157:C:H2'	8:A:158:U:O4'	2.18	0.43
8:A:1198:U:H2'	8:A:1199:U:H6	1.82	0.43
8:A:2245:U:H5''	8:A:2246:G:H5'	2.00	0.43
8:A:2884:U:H2'	8:A:2885:G:C8	2.54	0.43
9:B:48:U:H4'	22:O:100:HIS:CD2	2.47	0.43
10:C:234:GLY:HA3	10:C:238:ASN:HB2	1.99	0.43
12:E:189:THR:O	12:E:193:VAL:HG23	2.18	0.43
31:X:66:VAL:HA	31:X:69:GLU:OE2	2.18	0.43
34:a:299:G:OP2	34:a:299:G:H8	2.01	0.43
34:a:513:C:H2'	34:a:514:C:C6	2.53	0.43
37:d:104:MET:HE3	37:d:104:MET:HB2	1.76	0.43
37:d:105:GLY:O	37:d:107:GLY:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:f:41:ASP:OD1	39:f:58:HIS:NE2	2.45	0.43
40:g:125:ASP:HA	40:g:128:GLU:HG2	2.00	0.43
56:w:11:C:H2'	56:w:12:U:C6	2.53	0.43
2:1:32:LYS:HB3	2:1:32:LYS:HE2	1.75	0.43
8:A:32:C:H2'	8:A:33:C:C6	2.52	0.43
8:A:281:C:H2'	8:A:282:A:H8	1.83	0.43
8:A:589:U:H2'	8:A:590:A:C8	2.53	0.43
8:A:723:C:H2'	8:A:724:U:O4'	2.17	0.43
8:A:756:A:H2'	8:A:757:G:O4'	2.17	0.43
8:A:1077:A:O2'	8:A:1078:U:O4'	2.33	0.43
8:A:2394:C:H5''	19:L:63:LYS:HE2	2.01	0.43
8:A:2544:G:H2'	8:A:2545:G:O4'	2.19	0.43
21:N:96:ARG:NH1	21:N:116:VAL:HG13	2.33	0.43
31:X:37:PHE:CZ	31:X:50:VAL:HG21	2.53	0.43
34:a:7:A:H5''	34:a:298:A:H5'	2.00	0.43
34:a:709:U:H2'	34:a:710:G:H8	1.83	0.43
34:a:1151:A:O2'	34:a:1152:A:H8	2.00	0.43
34:a:1158:C:C4	34:a:1160:G:C8	3.06	0.43
56:w:18:G:O2'	56:w:57:G:N2	2.50	0.43
7:6:7:PRO:HG3	13:F:57:ALA:O	2.18	0.43
8:A:721:A:H2'	8:A:722:A:C8	2.54	0.43
8:A:1454:C:H5'	21:N:63:ARG:CZ	2.48	0.43
8:A:1594:U:H2'	8:A:1595:C:C6	2.54	0.43
8:A:1942:C:H2'	8:A:1943:U:C5	2.54	0.43
8:A:2247:A:H2'	8:A:2248:C:H6	1.81	0.43
8:A:2498:OMC:HM22	8:A:2499:C:H5'	2.00	0.43
8:A:2692:G:N3	8:A:2847:U:O2'	2.50	0.43
8:A:2784:U:H2'	8:A:2785:C:C6	2.53	0.43
34:a:34:C:H2'	34:a:35:G:H8	1.84	0.43
34:a:35:G:O2'	45:l:114:SER:O	2.25	0.43
34:a:134:G:H2'	34:a:135:C:O4'	2.18	0.43
34:a:324:G:N1	34:a:327:A:OP2	2.50	0.43
34:a:459:A:H2'	34:a:460:A:H8	1.84	0.43
34:a:584:G:H2'	34:a:585:G:C8	2.53	0.43
34:a:600:A:H2'	34:a:601:G:H8	1.83	0.43
34:a:642:A:H2'	34:a:643:C:C6	2.54	0.43
34:a:677:U:O2	34:a:777:A:O2'	2.33	0.43
34:a:767:A:O2'	34:a:1524:C:O2	2.36	0.43
34:a:1402:4OC:H2'	34:a:1403:C:O4'	2.19	0.43
36:c:84:GLU:O	36:c:88:LYS:HG2	2.18	0.43
5:4:8:LYS:HE2	5:4:8:LYS:HB2	1.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:391:A:H1'	8:A:411:G:O4'	2.19	0.43
8:A:415:A:H2'	8:A:416:U:H6	1.83	0.43
8:A:671:C:H2'	8:A:672:C:H6	1.84	0.43
8:A:690:G:N2	10:C:42:ARG:HH12	2.14	0.43
8:A:1290:C:H2'	8:A:1291:C:H6	1.83	0.43
8:A:2170:A:O2'	8:A:2171:A:O4'	2.36	0.43
8:A:2405:G:H2'	8:A:2411:A:H62	1.84	0.43
8:A:2848:G:H1'	8:A:2868:A:N6	2.33	0.43
15:H:11:ASN:O	15:H:12:LEU:HD23	2.18	0.43
19:L:81:ASP:HB3	19:L:100:ILE:HD13	1.99	0.43
20:M:36:VAL:HG21	20:M:129:THR:HG23	2.00	0.43
23:P:17:PRO:HG3	23:P:83:ILE:O	2.18	0.43
34:a:206:C:N4	34:a:214:C:O2'	2.51	0.43
34:a:581:G:N1	34:a:759:A:OP2	2.34	0.43
34:a:754:C:P	48:o:71:ARG:HH22	2.41	0.43
34:a:1004:A:C6	34:a:1026:G:H1'	2.53	0.43
36:c:68:HIS:HA	36:c:103:ALA:HB3	2.01	0.43
38:e:47:PHE:CZ	38:e:137:ARG:HG2	2.53	0.43
49:p:47:GLU:OE1	49:p:51:ARG:NH1	2.52	0.43
8:A:5:A:H2'	8:A:6:A:C8	2.54	0.43
8:A:146:A:H2'	8:A:147:C:C6	2.54	0.43
8:A:582:A:H2'	8:A:583:G:H8	1.84	0.43
8:A:829:A:N7	8:A:2247:A:O2'	2.50	0.43
8:A:902:C:H2'	8:A:903:C:H6	1.83	0.43
8:A:926:G:H2'	8:A:927:A:C8	2.54	0.43
8:A:1429:G:H2'	8:A:1430:G:C8	2.53	0.43
8:A:1599:U:H2'	8:A:1600:C:H6	1.83	0.43
8:A:1654:A:O2'	11:D:118:PHE:O	2.25	0.43
8:A:1701:A:OP1	8:A:1763:G:N1	2.46	0.43
8:A:2314:A:H2'	8:A:2315:G:H8	1.83	0.43
8:A:2519:U:O4'	8:A:2542:A:N6	2.52	0.43
8:A:2557:G:H2'	8:A:2558:C:H6	1.82	0.43
8:A:2812:G:H2'	8:A:2813:A:O4'	2.18	0.43
28:U:48:VAL:O	28:U:53:GLN:HG3	2.17	0.43
34:a:228:A:H2'	34:a:229:U:O4'	2.19	0.43
34:a:448:A:H3'	34:a:449:G:H8	1.84	0.43
34:a:947:G:H2'	34:a:948:C:C6	2.53	0.43
34:a:1006:G:N2	34:a:1023:U:O2	2.39	0.43
34:a:1319:A:C8	34:a:1323:G:C6	3.06	0.43
36:c:53:ARG:HB2	36:c:68:HIS:HB2	2.00	0.43
38:e:133:ILE:O	38:e:137:ARG:HG3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:g:46:LEU:HB3	40:g:57:GLU:HB3	2.01	0.43
41:h:2:MET:HE1	41:h:8:ASP:OD2	2.18	0.43
1:0:45:ASP:OD1	1:0:46:GLY:N	2.52	0.43
8:A:976:G:O2'	8:A:1155:A:O2'	2.34	0.43
8:A:1319:C:O2'	8:A:1320:C:H5'	2.19	0.43
8:A:2102:G:N2	8:A:2187:U:O2	2.42	0.43
8:A:2725:A:C2'	8:A:2726:A:H2'	2.49	0.43
8:A:2740:A:H2'	8:A:2741:A:C8	2.54	0.43
34:a:958:A:C4	52:s:54:ARG:HD3	2.52	0.43
34:a:1163:A:H2'	34:a:1164:G:C8	2.53	0.43
34:a:1330:U:C2'	34:a:1331:G:H5'	2.48	0.43
37:d:84:ASN:ND2	37:d:87:GLU:HG2	2.34	0.43
41:h:28:SER:OG	41:h:29:SER:N	2.52	0.43
47:n:7:ALA:HA	47:n:10:VAL:HG12	1.99	0.43
56:w:27:G:H2'	56:w:28:G:H8	1.84	0.43
7:6:15:SER:OG	7:6:21:VAL:HG12	2.18	0.43
8:A:273:G:C6	8:A:274:C:N4	2.87	0.43
8:A:593:U:H2'	8:A:594:U:H6	1.83	0.43
8:A:1061:U:H5'	8:A:1062:G:H5''	2.01	0.43
8:A:1087:G:C4	8:A:1089:A:C6	3.06	0.43
8:A:1248:G:OP1	12:E:44:ARG:NH1	2.52	0.43
8:A:1297:C:OP1	8:A:2710:C:H4'	2.18	0.43
8:A:2065:C:H2'	8:A:2066:C:C6	2.54	0.43
8:A:2262:U:OP1	8:A:2387:U:O2'	2.33	0.43
8:A:2281:A:O2'	8:A:2282:G:H5'	2.19	0.43
8:A:2700:A:H2'	8:A:2701:U:H6	1.84	0.43
14:G:49:LEU:HD23	14:G:49:LEU:HA	1.82	0.43
14:G:165:ASP:OD1	14:G:165:ASP:N	2.47	0.43
17:J:15:TRP:CE2	17:J:135:GLN:HG2	2.54	0.43
34:a:5:U:H5''	34:a:6:G:OP1	2.19	0.43
34:a:390:U:H2'	34:a:391:G:H8	1.84	0.43
34:a:575:G:O2'	34:a:821:G:H5'	2.18	0.43
34:a:1162:C:H2'	34:a:1163:A:C8	2.50	0.43
34:a:1163:A:H2'	34:a:1164:G:H8	1.84	0.43
34:a:1300:G:O2'	34:a:1301:U:O5'	2.28	0.43
34:a:1321:U:O2'	52:s:77:ARG:NH2	2.52	0.43
36:c:117:ASP:O	36:c:120:THR:HG22	2.19	0.43
37:d:94:GLU:OE2	37:d:103:ARG:NH1	2.51	0.43
38:e:75:LEU:HD13	38:e:78:GLY:H	1.83	0.43
47:n:20:PHE:C	47:n:22:LYS:H	2.25	0.43
8:A:122:G:H2'	8:A:123:G:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:362:A:H8	8:A:362:A:OP2	2.01	0.43
8:A:553:G:H2'	8:A:554:U:C6	2.53	0.43
8:A:620:G:N3	8:A:620:G:H5'	2.34	0.43
8:A:902:C:H2'	8:A:903:C:C6	2.54	0.43
8:A:941:A:O2'	8:A:1190:G:O3'	2.35	0.43
8:A:1028:A:N3	8:A:2486:C:O2'	2.52	0.43
8:A:1360:G:N7	8:A:1361:G:C8	2.87	0.43
8:A:2265:U:H3'	8:A:2266:A:H2'	1.99	0.43
8:A:2300:C:H2'	8:A:2301:C:H6	1.82	0.43
9:B:70:C:H2'	9:B:71:C:H6	1.84	0.43
13:F:41:GLU:HG3	13:F:48:LEU:HD23	2.01	0.43
14:G:66:THR:O	14:G:70:LEU:HG	2.18	0.43
15:H:69:ALA:C	15:H:71:LYS:H	2.27	0.43
34:a:202:G:N2	34:a:215:C:H5	2.08	0.43
34:a:223:A:H2'	34:a:224:U:H6	1.83	0.43
34:a:590:U:H2'	34:a:591:U:C6	2.53	0.43
34:a:651:C:H2'	34:a:652:U:C6	2.54	0.43
34:a:1157:A:N3	34:a:1181:G:C2	2.87	0.43
34:a:1243:C:H2'	34:a:1244:G:H8	1.82	0.43
34:a:1305:G:O2'	34:a:1306:A:H8	2.02	0.43
34:a:1319:A:O2'	34:a:1323:G:N7	2.47	0.43
35:b:151:LYS:HE2	35:b:151:LYS:HB3	1.77	0.43
36:c:18:ASN:ND2	47:n:90:ARG:O	2.52	0.43
43:j:18:ILE:O	43:j:22:THR:HG22	2.19	0.43
48:o:63:ARG:HH12	48:o:88:ARG:HH22	1.67	0.43
53:t:19:HIS:O	53:t:22:SER:OG	2.35	0.43
8:A:17:G:H2'	8:A:18:U:C6	2.54	0.43
8:A:632:A:H2'	8:A:633:A:C8	2.54	0.43
8:A:639:U:C2	8:A:640:C:C5	3.07	0.43
8:A:936:A:H2'	8:A:937:C:C6	2.54	0.43
8:A:1028:A:H2'	8:A:1029:A:H8	1.80	0.43
8:A:1196:C:C2	8:A:1197:G:C8	3.07	0.43
8:A:1735:A:H2'	8:A:1736:U:C6	2.53	0.43
8:A:1847:G:O2'	8:A:1848:A:O5'	2.37	0.43
8:A:2229:U:O2	31:X:33:HIS:HE1	2.01	0.43
8:A:2896:C:H2'	8:A:2897:U:C6	2.53	0.43
13:F:36:ASN:OD1	13:F:37:MET:N	2.52	0.43
15:H:54:LEU:O	15:H:58:LEU:HG	2.18	0.43
17:J:99:ARG:HA	17:J:99:ARG:HD2	1.65	0.43
27:T:8:LEU:HA	27:T:50:LEU:HD21	2.01	0.43
34:a:501:C:H1'	34:a:549:C:H1'	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:516:PSU:H2'	34:a:517:G:C8	2.53	0.43
34:a:678:U:H2'	34:a:679:C:H6	1.84	0.43
39:f:18:VAL:HG21	39:f:58:HIS:CE1	2.53	0.43
39:f:45:ARG:HB2	39:f:59:TYR:CE1	2.54	0.43
52:s:38:THR:HA	52:s:69:LYS:HA	1.99	0.43
7:6:36:VAL:HG12	7:6:37:CYS:H	1.83	0.42
8:A:248:G:O2'	8:A:2432:A:OP1	2.27	0.42
8:A:1055:G:N2	8:A:1104:C:C2	2.83	0.42
8:A:1587:G:C4	8:A:1588:G:C8	3.07	0.42
10:C:130:PRO:HA	10:C:188:ARG:HA	2.01	0.42
18:K:26:GLY:O	18:K:30:ARG:HD2	2.19	0.42
19:L:19:LEU:O	19:L:21:ARG:NH2	2.52	0.42
32:Y:21:LEU:HB3	32:Y:50:VAL:HG22	2.00	0.42
34:a:645:G:C2	34:a:646:G:C8	3.06	0.42
34:a:767:A:H2'	34:a:768:A:O4'	2.19	0.42
34:a:834:U:H2'	34:a:835:U:C6	2.54	0.42
34:a:1122:U:H2'	34:a:1123:U:C6	2.54	0.42
34:a:1342:C:H4'	42:i:126:PHE:O	2.19	0.42
38:e:51:LYS:HB2	38:e:51:LYS:HE3	1.68	0.42
39:f:10:VAL:HG13	39:f:58:HIS:HB3	2.01	0.42
39:f:12:PRO:HD2	39:f:54:LEU:HD11	2.01	0.42
40:g:24:LYS:O	40:g:28:ILE:HG13	2.19	0.42
40:g:135:LYS:HA	40:g:135:LYS:HD3	1.84	0.42
47:n:66:GLN:HG3	47:n:79:LEU:HD22	1.99	0.42
52:s:18:VAL:O	52:s:22:VAL:HG23	2.18	0.42
8:A:498:G:H1'	28:U:44:HIS:CE1	2.53	0.42
8:A:599:A:H2'	8:A:600:G:H8	1.84	0.42
8:A:851:C:H2'	8:A:852:U:H6	1.83	0.42
8:A:878:A:C5	8:A:879:G:H1'	2.54	0.42
8:A:1504:A:H2'	8:A:1505:A:C8	2.54	0.42
8:A:1952:A:N3	8:A:2560:A:O2'	2.42	0.42
8:A:2087:G:H2'	8:A:2088:A:H8	1.83	0.42
8:A:2745:C:H2'	8:A:2746:U:C6	2.54	0.42
8:A:2801:G:H2'	8:A:2802:G:H8	1.83	0.42
9:B:116:G:H2'	9:B:117:G:C8	2.53	0.42
13:F:116:LEU:HB3	13:F:127:TYR:OH	2.19	0.42
19:L:108:ALA:HB3	19:L:125:LEU:HG	2.01	0.42
21:N:77:ALA:O	21:N:81:ASN:CB	2.64	0.42
22:O:51:ALA:HB3	22:O:78:VAL:HB	2.02	0.42
24:Q:49:ARG:HG2	24:Q:52:ARG:NH2	2.34	0.42
34:a:419:C:OP1	34:a:513:C:O2'	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:678:U:H2'	34:a:679:C:C6	2.55	0.42
34:a:1157:A:N6	34:a:1178:G:H1'	2.34	0.42
34:a:1300:G:H1'	34:a:1301:U:C5	2.54	0.42
35:b:81:ASP:O	35:b:85:SER:HB3	2.20	0.42
8:A:51:G:H8	8:A:51:G:OP2	2.03	0.42
8:A:58:G:O2'	8:A:73:A:N1	2.47	0.42
8:A:879:G:H2'	8:A:880:G:H8	1.82	0.42
8:A:954:G:O2'	8:A:2274:A:N1	2.42	0.42
8:A:1447:C:H2'	8:A:1448:G:H8	1.84	0.42
8:A:1569:A:H2'	8:A:1570:A:C8	2.54	0.42
8:A:1889:A:H2'	8:A:1890:A:H8	1.84	0.42
8:A:1904:G:O2'	8:A:1928:A:N1	2.49	0.42
8:A:2074:U:H2'	8:A:2075:U:C6	2.54	0.42
8:A:2848:G:O2'	8:A:2868:A:N6	2.52	0.42
9:B:66:A:H4'	9:B:67:G:OP1	2.18	0.42
12:E:21:ARG:HD3	12:E:106:LYS:HB3	2.00	0.42
15:H:140:ALA:O	15:H:141:LYS:HD2	2.18	0.42
16:I:63:ASP:C	16:I:65:SER:H	2.27	0.42
22:O:52:SER:OG	22:O:54:VAL:HG12	2.19	0.42
31:X:40:GLU:O	31:X:43:LYS:HG3	2.20	0.42
34:a:210:C:O2'	34:a:211:G:H5''	2.19	0.42
34:a:709:U:H2'	34:a:710:G:C8	2.55	0.42
34:a:839:C:H2'	34:a:840:C:H6	1.83	0.42
34:a:1307:U:H2'	34:a:1308:U:O4'	2.20	0.42
34:a:1410:A:H2'	34:a:1411:C:C6	2.54	0.42
34:a:1413:A:H2	34:a:1487:G:H22	1.67	0.42
34:a:1512:U:H2'	34:a:1513:A:C8	2.54	0.42
36:c:27:GLU:OE1	36:c:27:GLU:N	2.52	0.42
49:p:52:LEU:HD12	49:p:57:ILE:HD11	2.01	0.42
7:6:44:PHE:CE1	13:F:175:PRO:HG3	2.54	0.42
8:A:68:G:H2'	8:A:69:C:O4'	2.20	0.42
8:A:481:G:H4'	8:A:481:G:OP1	2.20	0.42
8:A:567:U:O3'	19:L:36:LYS:NZ	2.52	0.42
8:A:781:A:O2'	8:A:1788:C:O2	2.34	0.42
8:A:886:A:H2'	8:A:886:A:O5'	2.19	0.42
8:A:918:A:N3	9:B:80:U:O2'	2.50	0.42
8:A:1188:U:H4'	25:R:81:LYS:O	2.19	0.42
8:A:1830:C:H2'	8:A:1831:G:H8	1.84	0.42
8:A:1873:G:H2'	8:A:1874:C:H6	1.84	0.42
8:A:2071:A:H2'	8:A:2072:C:C6	2.54	0.42
8:A:2087:G:H2'	8:A:2088:A:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2655:G:HO2'	8:A:2656:U:P	2.42	0.42
8:A:2684:U:O4'	18:K:70:ARG:NH1	2.52	0.42
9:B:23:G:H2'	9:B:24:G:C8	2.55	0.42
13:F:32:LYS:HG2	13:F:156:THR:HB	2.01	0.42
15:H:47:PHE:CD2	15:H:48:GLU:HG2	2.55	0.42
20:M:53:MET:HE1	20:M:103:TYR:CG	2.54	0.42
34:a:147:G:H4'	34:a:148:G:OP1	2.19	0.42
34:a:757:U:OP1	34:a:822:U:O2'	2.36	0.42
34:a:890:G:O2'	34:a:891:U:P	2.78	0.42
34:a:1074:G:O2'	34:a:1101:A:N1	2.42	0.42
35:b:206:ILE:O	35:b:210:THR:HG23	2.19	0.42
36:c:129:PHE:O	36:c:133:MET:HG3	2.19	0.42
36:c:143:LEU:O	36:c:143:LEU:HD23	2.19	0.42
45:l:24:GLU:CD	45:l:58:ASN:HD22	2.27	0.42
52:s:10:ILE:HD11	52:s:14:LEU:HD23	2.00	0.42
56:w:70:G:H2'	56:w:71:G:H8	1.84	0.42
1:0:47:TYR:CE1	1:0:52:LYS:HD3	2.54	0.42
7:6:41:HIS:CE1	13:F:113:PHE:HD2	2.37	0.42
8:A:143:C:H2'	8:A:144:A:C8	2.54	0.42
8:A:648:G:O2'	8:A:2351:G:OP1	2.33	0.42
8:A:893:C:C3'	8:A:893:C:C6	3.03	0.42
8:A:1072:C:O2'	8:A:1090:A:H5''	2.19	0.42
8:A:1130:U:C2	8:A:2025:C:H5''	2.53	0.42
8:A:1197:G:H2'	8:A:1198:U:C6	2.55	0.42
8:A:1246:A:H4'	12:E:40:ARG:HH22	1.83	0.42
8:A:1278:C:H2'	8:A:1279:G:C8	2.53	0.42
8:A:1614:A:C2	26:S:93:ALA:HB2	2.55	0.42
9:B:76:G:N3	29:V:78:GLN:NE2	2.56	0.42
15:H:32:PRO:HA	31:X:38:TRP:CD1	2.54	0.42
29:V:6:ALA:HB1	29:V:40:ILE:CG2	2.49	0.42
34:a:244:U:O4	34:a:906:A:H1'	2.20	0.42
34:a:936:C:C4	34:a:937:A:N7	2.88	0.42
34:a:1142:G:C2	34:a:1143:G:H1'	2.53	0.42
37:d:14:GLU:HG2	37:d:59:LYS:HB2	2.00	0.42
45:l:3:VAL:CG2	50:q:33:TYR:HB3	2.50	0.42
49:p:8:ARG:HD3	49:p:17:TYR:CE1	2.55	0.42
52:s:51:HIS:HD2	52:s:55:GLN:O	2.01	0.42
56:w:65:G:H2'	56:w:66:U:H6	1.83	0.42
2:1:4:ILE:C	2:1:27:ARG:HH22	2.27	0.42
5:4:4:ARG:HB3	8:A:2466:C:OP1	2.20	0.42
7:6:14:ALA:HB1	7:6:34:LEU:HD12	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:5:A:H2'	8:A:6:A:H8	1.85	0.42
8:A:475:C:N3	8:A:479:A:N7	2.68	0.42
8:A:1043:C:H2'	8:A:1044:C:H5''	2.00	0.42
8:A:1118:C:H2'	8:A:1119:U:O4'	2.19	0.42
8:A:1305:C:H2'	8:A:1306:C:O4'	2.20	0.42
8:A:1478:G:H1	8:A:1513:U:H3	1.66	0.42
8:A:1722:A:H2'	8:A:1723:G:O4'	2.20	0.42
8:A:2118:U:H5	8:A:2148:G:H1'	1.84	0.42
8:A:2236:U:H2'	8:A:2237:G:O4'	2.20	0.42
10:C:106:PRO:HB3	10:C:141:HIS:CE1	2.54	0.42
10:C:204:LEU:O	10:C:206:LYS:N	2.46	0.42
11:D:105:LYS:HE2	11:D:105:LYS:HB3	1.82	0.42
18:K:73:ASP:OD2	23:P:79:VAL:HG11	2.20	0.42
20:M:74:THR:HG22	20:M:89:VAL:HG22	2.00	0.42
34:a:96:U:H2'	34:a:97:G:C8	2.54	0.42
34:a:100:G:C4	34:a:101:A:C8	3.07	0.42
34:a:185:U:H2'	34:a:186:C:C6	2.54	0.42
34:a:268:U:H2'	34:a:269:C:C6	2.54	0.42
34:a:486:U:H2'	34:a:487:A:H8	1.83	0.42
34:a:687:A:C2	34:a:704:A:C5	3.08	0.42
35:b:94:ARG:NH1	35:b:96:LEU:HD23	2.34	0.42
36:c:152:VAL:HG22	36:c:197:VAL:HG22	2.02	0.42
40:g:49:LEU:HD22	40:g:123:LEU:HB3	2.00	0.42
44:k:46:ALA:HB1	44:k:61:ALA:HB1	2.02	0.42
49:p:36:VAL:HG13	49:p:53:ASP:CB	2.50	0.42
53:t:68:LYS:HB3	53:t:68:LYS:HE2	1.82	0.42
8:A:8:C:H2'	8:A:9:G:O4'	2.20	0.42
8:A:297:G:H2'	8:A:298:G:O4'	2.20	0.42
8:A:547:A:H1'	8:A:548:G:C5	2.54	0.42
8:A:721:A:H2'	8:A:722:A:H8	1.85	0.42
8:A:886:A:OP2	8:A:886:A:C8	2.70	0.42
8:A:1039:A:H2'	8:A:1040:A:O4'	2.19	0.42
8:A:1063:G:H1	16:I:134:SER:CB	2.31	0.42
8:A:1351:C:H2'	8:A:1352:U:O4'	2.18	0.42
8:A:2251:OMG:H1'	8:A:2251:OMG:HM23	1.65	0.42
8:A:2359:C:O2	19:L:60:ARG:NH1	2.51	0.42
8:A:2541:A:O2'	8:A:2765:A:N1	2.48	0.42
8:A:2552:OMU:C5	8:A:2554:U:H5'	2.49	0.42
10:C:24:HIS:HB2	10:C:79:ARG:HD3	2.02	0.42
10:C:59:GLN:OE1	10:C:84:PRO:HB2	2.20	0.42
15:H:122:LEU:HD11	15:H:146:VAL:HG21	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:92:LEU:O	19:L:96:LYS:HG3	2.19	0.42
34:a:143:A:H2	34:a:220:G:H1	1.68	0.42
34:a:580:C:H2'	34:a:581:G:O4'	2.18	0.42
34:a:664:G:H2'	34:a:666:G:OP1	2.19	0.42
35:b:117:GLU:O	35:b:121:GLN:HG2	2.19	0.42
35:b:153:MET:O	35:b:154:GLY:C	2.63	0.42
36:c:92:ASP:OD1	36:c:93:ILE:HG23	2.19	0.42
37:d:12:ARG:HG2	37:d:33:ILE:HA	2.01	0.42
37:d:60:VAL:HG22	37:d:194:ILE:HD13	2.02	0.42
39:f:21:MET:HE2	39:f:81:ASN:ND2	2.35	0.42
43:j:83:THR:O	43:j:87:LEU:HD23	2.20	0.42
52:s:35:ARG:NH2	52:s:74:ALA:HB3	2.35	0.42
4:3:7:ARG:HE	4:3:7:ARG:HB3	1.53	0.42
8:A:96:C:H2'	8:A:97:C:H6	1.84	0.42
8:A:150:U:H2'	8:A:151:C:H6	1.85	0.42
8:A:2038:G:H2'	8:A:2039:U:O4'	2.19	0.42
8:A:2039:U:H2'	8:A:2040:G:C8	2.54	0.42
8:A:2196:C:H2'	8:A:2197:U:C6	2.54	0.42
8:A:2619:C:OP1	11:D:157:LYS:HE2	2.19	0.42
22:O:30:ARG:HH11	22:O:102:ARG:HH11	1.68	0.42
25:R:42:ALA:HA	25:R:47:VAL:HG23	2.01	0.42
34:a:299:G:H2'	34:a:300:A:C8	2.55	0.42
34:a:473:U:C2	34:a:474:G:C8	3.08	0.42
34:a:615:G:C2	34:a:626:G:N1	2.88	0.42
34:a:1236:A:H4'	34:a:1304:G:H4'	2.01	0.42
34:a:1379:G:O6	40:g:1:PRO:HB3	2.20	0.42
34:a:1526:G:H3'	54:u:41:THR:HG22	2.01	0.42
35:b:110:ILE:HG13	35:b:147:LEU:HD13	2.02	0.42
42:i:51:LEU:HB3	42:i:56:MET:CB	2.45	0.42
54:u:20:ARG:O	54:u:24:LYS:HG2	2.20	0.42
8:A:522:A:H2'	8:A:523:C:C6	2.55	0.42
8:A:774:G:N2	8:A:787:C:O2'	2.52	0.42
8:A:1196:C:H2'	8:A:1197:G:O4'	2.19	0.42
8:A:1260:A:H2'	8:A:1261:C:O4'	2.20	0.42
8:A:1300:G:H4'	8:A:1301:A:H5''	2.01	0.42
8:A:2553:G:H2'	8:A:2554:U:O4'	2.20	0.42
13:F:37:MET:HB2	13:F:86:CYS:SG	2.59	0.42
15:H:5:LEU:HD11	15:H:19:VAL:HG12	2.02	0.42
18:K:43:ILE:HD12	18:K:56:ASP:HB2	2.02	0.42
34:a:202:G:O2'	34:a:468:A:H1'	2.19	0.42
34:a:371:A:H2'	34:a:372:C:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:567:G:H2'	34:a:568:G:O4'	2.20	0.42
34:a:1038:C:H2'	34:a:1039:G:C8	2.37	0.42
34:a:1290:G:H2'	34:a:1291:U:O4'	2.20	0.42
34:a:1323:G:H2'	34:a:1324:A:H8	1.84	0.42
34:a:1498:UR3:H3U2	57:x:17:U:H4'	2.01	0.42
47:n:9:GLU:O	47:n:13:VAL:HG13	2.20	0.42
49:p:19:VAL:HB	49:p:36:VAL:O	2.20	0.42
56:w:70:G:H2'	56:w:71:G:C8	2.55	0.42
8:A:631:A:N3	8:A:2415:G:O2'	2.51	0.42
8:A:669:G:H3'	8:A:670:A:C8	2.55	0.42
8:A:1550:C:H2'	8:A:1551:A:C8	2.55	0.42
8:A:1678:A:H2'	8:A:1679:A:O4'	2.19	0.42
8:A:1771:C:H2'	8:A:1772:A:C8	2.54	0.42
8:A:2187:U:C2	8:A:2188:U:C5	3.07	0.42
8:A:2227:A:H2'	8:A:2228:G:O4'	2.20	0.42
8:A:2262:U:P	30:W:15:LYS:HZ3	2.43	0.42
8:A:2266:A:H4'	8:A:2267:A:O5'	2.19	0.42
8:A:2366:A:H2'	8:A:2367:G:O4'	2.20	0.42
11:D:125:TRP:CE3	11:D:160:LYS:HD3	2.55	0.42
32:Y:19:LEU:O	32:Y:23:ARG:HD3	2.20	0.42
32:Y:56:LEU:O	32:Y:60:LYS:HG2	2.19	0.42
34:a:394:G:H2'	34:a:395:C:C6	2.54	0.42
34:a:966:2MG:H5''	34:a:966:2MG:C8	2.55	0.42
34:a:978:A:O2'	34:a:1322:C:N3	2.42	0.42
34:a:1118:U:H2'	34:a:1119:C:C6	2.54	0.42
34:a:1277:C:H2'	34:a:1279:G:H21	1.84	0.42
34:a:1280:A:O2'	34:a:1281:C:H5'	2.20	0.42
34:a:1497:G:H1'	34:a:1518:MA6:H2	2.02	0.42
34:a:1538:C:C5	34:a:1539:C:H1'	2.55	0.42
36:c:63:ILE:HG22	36:c:96:VAL:HG23	2.01	0.42
37:d:85:THR:HA	37:d:88:ASN:HB2	2.02	0.42
40:g:60:ALA:O	40:g:63:VAL:HG12	2.20	0.42
1:0:46:GLY:O	1:0:53:VAL:HG22	2.20	0.41
8:A:200:U:O2	8:A:386:G:N2	2.53	0.41
8:A:592:A:H2'	8:A:593:U:C6	2.55	0.41
8:A:783:A:H2'	8:A:784:G:H4'	2.02	0.41
8:A:989:G:OP2	33:Z:11:SER:OG	2.25	0.41
8:A:1209:U:O2	8:A:1210:G:N2	2.52	0.41
8:A:1667:G:O2'	8:A:1991:U:O4	2.30	0.41
8:A:1842:G:H2'	8:A:1843:C:H6	1.84	0.41
8:A:2851:A:O3'	21:N:64:ARG:NH2	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:J:36:LEU:O	17:J:51:GLY:HA3	2.20	0.41
17:J:91:GLU:O	17:J:95:ARG:HD3	2.20	0.41
22:O:30:ARG:HA	22:O:35:ILE:HG13	2.02	0.41
24:Q:88:GLU:O	25:R:11:GLN:NE2	2.38	0.41
29:V:50:MET:HE2	29:V:56:PHE:HE1	1.85	0.41
34:a:260:G:H2'	34:a:261:U:C6	2.55	0.41
34:a:1207:2MG:H2'	34:a:1208:C:H6	1.85	0.41
34:a:1371:G:H2'	34:a:1372:U:C6	2.55	0.41
37:d:146:GLU:HB3	37:d:149:LYS:HE2	2.02	0.41
39:f:73:GLU:O	39:f:77:THR:HG23	2.20	0.41
40:g:36:SER:OG	42:i:40:ARG:NH2	2.53	0.41
47:n:51:LEU:HD23	47:n:51:LEU:HA	1.93	0.41
3:2:3:ARG:HD3	3:2:3:ARG:HA	1.74	0.41
4:3:13:PHE:O	4:3:14:LYS:HD3	2.20	0.41
8:A:38:A:H2'	8:A:39:G:O4'	2.20	0.41
8:A:271:G:C2	8:A:272:A:C5	3.08	0.41
8:A:329:G:OP1	28:U:68:ASN:ND2	2.36	0.41
8:A:527:C:C2	8:A:2779:U:H2'	2.55	0.41
8:A:1728:C:H2'	8:A:1729:U:H5''	2.02	0.41
8:A:2170:A:H2'	8:A:2171:A:C8	2.55	0.41
8:A:2179:C:C5'	8:A:2181:U:H3	2.31	0.41
8:A:2445:2MG:P	12:E:69:ARG:NH2	2.86	0.41
8:A:2653:U:OP2	8:A:2654:A:O2'	2.26	0.41
8:A:2786:U:H2'	8:A:2787:C:H6	1.84	0.41
10:C:5:CYS:SG	10:C:17:LYS:HD3	2.60	0.41
10:C:99:GLU:OE2	10:C:101:ARG:NE	2.53	0.41
34:a:8:A:N6	37:d:205:LYS:HB2	2.35	0.41
34:a:90:C:H6	34:a:90:C:O5'	2.03	0.41
34:a:986:U:H2'	34:a:987:G:O4'	2.20	0.41
35:b:59:ILE:HG22	35:b:62:ARG:HH22	1.85	0.41
35:b:101:THR:HA	35:b:178:LEU:HD11	2.00	0.41
36:c:152:VAL:HG13	36:c:197:VAL:HG22	2.01	0.41
37:d:123:MET:HE2	37:d:123:MET:HB3	1.90	0.41
39:f:10:VAL:HG11	39:f:18:VAL:HG22	2.02	0.41
56:w:18:G:C5	56:w:58:A:C6	3.07	0.41
57:x:20:A:H3'	57:x:20:A:N3	2.36	0.41
4:3:44:ARG:NH1	8:A:2350:C:OP2	2.53	0.41
5:4:11:CYS:HB3	5:4:33:HIS:CE1	2.55	0.41
8:A:78:U:P	32:Y:2:LYS:HE2	2.60	0.41
8:A:570:G:H2'	8:A:2030:6MZ:N7	2.36	0.41
8:A:728:G:H5''	10:C:12:ARG:HH21	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:747:5MC:O2	8:A:2014:A:H1'	2.20	0.41
8:A:992:C:OP1	24:Q:46:TYR:OH	2.17	0.41
8:A:1321:A:C4	8:A:1322:A:C8	3.08	0.41
8:A:2297:A:H61	8:A:2319:G:H1'	1.86	0.41
8:A:2333:A:OP1	30:W:73:ARG:NH1	2.51	0.41
9:B:74:U:O2	29:V:29:ILE:HD13	2.20	0.41
10:C:171:VAL:HG23	10:C:185:ALA:HB2	2.02	0.41
12:E:5:LEU:HD23	12:E:8:ALA:HB3	2.02	0.41
22:O:55:GLU:OE2	22:O:57:ALA:HB3	2.20	0.41
34:a:364:A:H2'	34:a:365:U:C6	2.55	0.41
34:a:398:U:H2'	34:a:399:G:H8	1.85	0.41
34:a:707:U:H2'	34:a:708:C:C6	2.55	0.41
34:a:1120:C:C2	34:a:1121:U:C5	3.08	0.41
34:a:1243:C:H2'	34:a:1244:G:C8	2.54	0.41
35:b:26:MET:HE3	35:b:26:MET:HB3	1.98	0.41
37:d:187:ARG:HE	37:d:196:GLU:CD	2.27	0.41
39:f:9:MET:HB2	39:f:85:ILE:O	2.21	0.41
43:j:59:LYS:HE2	43:j:62:ARG:NH2	2.35	0.41
46:m:3:ILE:HD11	46:m:52:ILE:HG23	2.02	0.41
49:p:76:LYS:HE3	49:p:76:LYS:HB3	1.83	0.41
1:0:12:ARG:HD2	1:0:16:ARG:NH2	2.35	0.41
1:0:21:LEU:HB2	26:S:23:LEU:HD21	2.03	0.41
5:4:2:LYS:NZ	8:A:2478:A:OP2	2.49	0.41
8:A:438:G:H2'	8:A:439:A:C8	2.56	0.41
8:A:1102:C:C2	8:A:1103:A:C8	3.09	0.41
8:A:1287:A:O2'	8:A:1288:G:H5'	2.20	0.41
8:A:1544:A:H2'	8:A:1545:A:C8	2.55	0.41
8:A:2030:6MZ:N3	8:A:2499:C:H5''	2.36	0.41
8:A:2345:G:N3	8:A:2381:A:H2'	2.36	0.41
8:A:2872:A:O2'	8:A:2873:A:H5'	2.21	0.41
34:a:303:A:O2'	34:a:555:U:H4'	2.19	0.41
34:a:333:U:P	53:t:2:ASN:HD21	2.40	0.41
36:c:21:TRP:CG	36:c:58:ARG:HG3	2.56	0.41
37:d:27:ILE:HD12	37:d:27:ILE:HA	1.84	0.41
39:f:38:ARG:O	39:f:62:MET:HA	2.21	0.41
42:i:48:ARG:O	42:i:52:GLU:HG2	2.20	0.41
7:6:25:ARG:O	13:F:101:ARG:NH2	2.53	0.41
8:A:257:C:H2'	8:A:258:G:O4'	2.20	0.41
8:A:582:A:H2'	8:A:583:G:C8	2.55	0.41
8:A:640:C:H2'	8:A:641:U:H6	1.86	0.41
8:A:969:G:H2'	8:A:970:U:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:1361:G:H2'	8:A:1362:C:H6	1.85	0.41
8:A:1386:C:H1'	8:A:1470:A:H1'	2.03	0.41
8:A:1443:U:H2'	8:A:1444:G:C8	2.56	0.41
8:A:1580:A:H2'	8:A:1581:G:O4'	2.20	0.41
8:A:2241:A:H2'	8:A:2242:G:C8	2.56	0.41
8:A:2655:G:O2'	8:A:2656:U:P	2.79	0.41
8:A:2758:A:C2	14:G:70:LEU:HD11	2.56	0.41
8:A:2810:A:H2'	8:A:2811:G:O4'	2.19	0.41
9:B:64:G:H2'	9:B:65:U:C6	2.55	0.41
10:C:29:PHE:CE2	10:C:31:PRO:HD2	2.56	0.41
11:D:45:TYR:OH	11:D:81:GLU:OE2	2.38	0.41
11:D:157:LYS:HE3	11:D:157:LYS:HB2	1.81	0.41
27:T:8:LEU:O	32:Y:29:ARG:NH1	2.54	0.41
30:W:37:ARG:HA	30:W:37:ARG:HE	1.86	0.41
32:Y:9:LYS:HD2	32:Y:9:LYS:O	2.19	0.41
34:a:8:A:C4	37:d:205:LYS:HD3	2.55	0.41
34:a:236:A:H5''	50:q:43:LEU:HD21	2.03	0.41
34:a:288:A:H2'	34:a:289:G:H4'	2.02	0.41
34:a:659:U:H5''	48:o:4:THR:HG23	2.03	0.41
34:a:1473:G:H2'	34:a:1474:U:O4'	2.21	0.41
34:a:1527:U:H2'	34:a:1528:U:C6	2.55	0.41
41:h:79:ARG:NH1	41:h:82:LEU:HB3	2.35	0.41
44:k:111:ASP:O	51:r:72:ARG:NH1	2.54	0.41
45:l:81:ILE:HD13	45:l:81:ILE:HA	1.81	0.41
45:l:89:LEU:HD23	45:l:92:VAL:HG21	2.02	0.41
50:q:68:LYS:O	50:q:68:LYS:HD3	2.20	0.41
8:A:95:A:O2'	32:Y:41:HIS:ND1	2.36	0.41
8:A:263:G:O2'	8:A:429:A:N3	2.41	0.41
8:A:579:G:H2'	8:A:580:U:C6	2.54	0.41
8:A:628:G:C6	8:A:636:G:C2	3.08	0.41
8:A:819:A:H5'	8:A:973:A:N1	2.36	0.41
8:A:899:A:H2'	8:A:900:A:H8	1.86	0.41
8:A:1358:G:N1	8:A:1372:U:OP2	2.28	0.41
8:A:1635:A:H2'	8:A:1636:U:O4'	2.21	0.41
8:A:2243:U:H2'	8:A:2244:U:H6	1.85	0.41
8:A:2505:G:H2'	8:A:2576:G:N1	2.35	0.41
8:A:2838:G:C4	8:A:2839:G:C8	3.08	0.41
8:A:2848:G:O2'	8:A:2849:U:O5'	2.28	0.41
9:B:15:A:H3'	9:B:16:G:H8	1.86	0.41
9:B:40:U:H1'	9:B:45:A:H61	1.86	0.41
15:H:96:THR:HG22	15:H:117:LEU:HD11	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:J:1:MET:HE3	17:J:1:MET:HB3	1.93	0.41
24:Q:96:ASP:OD2	25:R:13:ARG:NE	2.53	0.41
26:S:29:VAL:HB	26:S:55:ILE:HD11	2.03	0.41
34:a:71:A:H2'	34:a:72:A:O4'	2.21	0.41
34:a:151:A:H3'	34:a:152:A:H8	1.84	0.41
34:a:189:A:OP2	34:a:189:A:H8	2.04	0.41
34:a:619:U:N3	37:d:130:ASN:OD1	2.52	0.41
34:a:1024:G:H2'	34:a:1024:G:N3	2.34	0.41
34:a:1034:G:H2'	34:a:1035:A:C8	2.54	0.41
36:c:19:SER:HA	36:c:56:ILE:O	2.21	0.41
38:e:59:ILE:O	38:e:63:MET:HG2	2.20	0.41
38:e:110:MET:HE3	38:e:126:ALA:HB2	2.02	0.41
49:p:51:ARG:C	49:p:52:LEU:HD22	2.46	0.41
8:A:29:U:C2	8:A:30:G:C8	3.09	0.41
8:A:244:A:H2'	8:A:245:G:O4'	2.20	0.41
8:A:931:U:OP1	33:Z:29:ARG:NH1	2.52	0.41
8:A:994:C:OP1	24:Q:52:ARG:NH2	2.53	0.41
8:A:1084:A:O2'	8:A:1105:U:O2'	2.25	0.41
8:A:2023:C:H2'	8:A:2024:G:H8	1.86	0.41
8:A:2165:C:C2	8:A:2167:U:H1'	2.56	0.41
10:C:161:VAL:CG1	10:C:173:LEU:HB3	2.50	0.41
10:C:244:VAL:HG12	10:C:250:GLN:HA	2.03	0.41
11:D:148:GLN:HB2	11:D:152:PRO:HG2	2.02	0.41
25:R:57:GLY:HA2	25:R:102:SER:O	2.21	0.41
31:X:14:GLY:HA3	31:X:28:PHE:HE1	1.84	0.41
34:a:522:C:OP2	45:l:65:TYR:OH	2.22	0.41
34:a:741:G:H2'	34:a:742:G:O4'	2.21	0.41
37:d:60:VAL:HG21	37:d:199:ILE:HD11	2.01	0.41
43:j:66:GLU:HB3	47:n:99:ALA:HB2	2.03	0.41
56:w:66:U:H2'	56:w:67:C:C6	2.56	0.41
7:6:12:ILE:HG13	7:6:24:ILE:HG13	2.01	0.41
8:A:236:C:H2'	8:A:237:C:H6	1.86	0.41
8:A:526:A:O2'	8:A:2043:C:O2	2.36	0.41
8:A:941:A:H2'	8:A:942:G:O4'	2.20	0.41
8:A:971:G:H2'	8:A:972:A:O4'	2.20	0.41
8:A:1086:A:H3'	8:A:1086:A:N3	2.36	0.41
8:A:1411:U:H2'	8:A:1412:U:H6	1.85	0.41
8:A:1497:U:H5''	8:A:1498:C:H5	1.84	0.41
8:A:1683:U:H2'	8:A:1684:G:H8	1.86	0.41
8:A:2029:G:H2'	8:A:2031:A:OP1	2.20	0.41
8:A:2295:C:OP1	22:O:10:ARG:NH1	2.30	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:B:41:G:P	9:B:43:C:H41	2.44	0.41
12:E:193:VAL:O	12:E:197:GLU:HG2	2.21	0.41
18:K:92:GLU:O	18:K:93:GLN:C	2.64	0.41
21:N:35:LYS:HB2	21:N:112:TYR:CE1	2.56	0.41
25:R:51:VAL:O	25:R:52:PRO:C	2.63	0.41
32:Y:44:LYS:O	32:Y:48:ARG:HG2	2.20	0.41
32:Y:46:VAL:O	32:Y:50:VAL:HG23	2.21	0.41
34:a:415:A:C4	34:a:416:G:C8	3.09	0.41
34:a:451:A:N6	34:a:481:G:OP2	2.40	0.41
34:a:736:C:H2'	34:a:737:C:C6	2.56	0.41
34:a:831:A:H5''	35:b:20:ARG:NH1	2.35	0.41
34:a:845:A:C2	34:a:846:G:H5'	2.55	0.41
34:a:1086:U:H3	34:a:1099:G:H22	1.69	0.41
34:a:1288:A:N1	34:a:1371:G:H1'	2.36	0.41
34:a:1305:G:HO2'	34:a:1306:A:P	2.42	0.41
34:a:1313:U:H2'	34:a:1314:C:C6	2.56	0.41
36:c:71:ARG:HB3	36:c:74:ILE:HG22	2.03	0.41
41:h:45:ILE:HG23	41:h:46:GLU:O	2.19	0.41
45:l:109:ARG:HD2	45:l:109:ARG:HA	1.84	0.41
8:A:151:C:H2'	8:A:152:A:H8	1.86	0.41
8:A:320:A:H4'	8:A:322:A:C8	2.56	0.41
8:A:515:A:H1'	8:A:581:C:H1'	2.03	0.41
8:A:543:G:H2'	8:A:544:C:C6	2.56	0.41
8:A:567:U:H2'	8:A:568:U:O4'	2.20	0.41
8:A:603:A:N1	8:A:625:G:O2'	2.52	0.41
8:A:776:G:N2	8:A:2241:A:OP1	2.53	0.41
8:A:1322:A:H5''	26:S:82:MET:HE1	2.03	0.41
8:A:1341:G:OP1	8:A:1397:U:N3	2.41	0.41
8:A:1537:G:O2'	8:A:1538:G:O5'	2.39	0.41
8:A:1549:A:H2'	8:A:1550:C:C6	2.54	0.41
8:A:2126:A:H1'	8:A:2162:G:N2	2.36	0.41
8:A:2334:U:H5'	22:O:12:THR:HB	2.02	0.41
9:B:113:C:H1'	22:O:46:GLU:HA	2.03	0.41
10:C:144:GLU:HB2	10:C:187:CYS:HB3	2.03	0.41
20:M:30:SER:OG	20:M:106:ASP:OD1	2.28	0.41
21:N:67:PHE:O	21:N:71:ARG:HD2	2.21	0.41
22:O:49:VAL:HG12	22:O:78:VAL:HG23	2.03	0.41
31:X:55:MET:HE2	31:X:55:MET:HB3	1.82	0.41
34:a:161:A:N1	34:a:347:G:O2'	2.48	0.41
34:a:271:C:H2'	34:a:272:C:H6	1.86	0.41
34:a:639:G:C6	34:a:640:A:N6	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:810:C:C4	34:a:811:C:C5	3.08	0.41
34:a:821:G:H2'	34:a:822:U:C6	2.56	0.41
34:a:955:U:O2'	52:s:82:HIS:HD2	2.03	0.41
34:a:1032:G:N2	34:a:1033:G:C2	2.89	0.41
34:a:1305:G:N2	34:a:1332:A:OP2	2.53	0.41
36:c:147:GLY:HA3	36:c:171:ARG:O	2.21	0.41
37:d:35:GLN:HG2	37:d:41:GLY:O	2.21	0.41
40:g:71:THR:HG23	40:g:141:HIS:HE1	1.85	0.41
46:m:50:GLY:HA2	46:m:53:ASP:OD2	2.21	0.41
46:m:80:MET:O	46:m:91:ARG:NH2	2.48	0.41
48:o:25:GLU:OE2	48:o:76:ARG:HD2	2.21	0.41
50:q:16:MET:HG3	50:q:19:SER:OG	2.21	0.41
50:q:68:LYS:C	50:q:68:LYS:HD3	2.41	0.41
53:t:7:LYS:O	53:t:7:LYS:CG	2.66	0.41
7:6:61:ASN:HA	7:6:64:PHE:HB2	2.03	0.41
8:A:594:U:H2'	8:A:595:C:C6	2.56	0.41
8:A:710:U:C2	8:A:711:G:C8	3.09	0.41
8:A:875:G:H2'	8:A:876:C:C6	2.56	0.41
8:A:1689:A:H2'	8:A:1690:A:H8	1.85	0.41
8:A:1859:U:H2'	8:A:1860:G:C8	2.56	0.41
8:A:2131:U:H1'	8:A:2158:A:C6	2.56	0.41
8:A:2842:G:H2'	8:A:2843:G:O4'	2.21	0.41
12:E:170:ARG:NH1	12:E:176:ASP:OD2	2.44	0.41
15:H:101:ASP:CA	15:H:107:GLY:HA2	2.43	0.41
20:M:15:GLY:O	20:M:16:ARG:HD3	2.20	0.41
23:P:21:PRO:HD3	23:P:49:ILE:HD12	2.03	0.41
28:U:84:PHE:CE1	28:U:93:ARG:HG2	2.56	0.41
32:Y:14:LEU:HD11	32:Y:57:LEU:HD13	2.03	0.41
34:a:263:A:H2'	34:a:264:C:C6	2.56	0.41
34:a:428:G:OP2	37:d:6:PRO:HG2	2.21	0.41
44:k:124:LYS:HG3	44:k:125:LYS:H	1.85	0.41
51:r:40:PRO:HB2	51:r:42:ARG:HG2	2.03	0.41
7:6:64:PHE:O	7:6:64:PHE:CG	2.74	0.40
8:A:555:G:O2'	8:A:556:A:P	2.79	0.40
8:A:561:G:O2'	24:Q:44:TYR:OH	2.17	0.40
8:A:954:G:H5''	20:M:13:HIS:CG	2.56	0.40
8:A:1370:C:H2'	8:A:1371:G:O4'	2.21	0.40
8:A:1589:U:H2'	8:A:1590:A:C8	2.55	0.40
8:A:1626:A:H8	8:A:1626:A:OP2	2.05	0.40
8:A:1693:U:H1'	10:C:13:ARG:NH1	2.36	0.40
8:A:2205:A:H2'	8:A:2206:C:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2391:G:O6	8:A:2425:A:H8	2.04	0.40
8:A:2399:G:H2'	8:A:2400:G:O4'	2.21	0.40
8:A:2639:A:H2'	8:A:2640:G:O4'	2.21	0.40
8:A:2900:A:H2'	8:A:2901:C:C6	2.55	0.40
10:C:24:HIS:CB	10:C:79:ARG:HD3	2.51	0.40
12:E:29:HIS:HA	12:E:32:VAL:HG12	2.03	0.40
13:F:160:LYS:HE3	13:F:160:LYS:HB3	1.86	0.40
15:H:3:VAL:HG22	15:H:36:ALA:HB1	2.03	0.40
22:O:2:ASP:OD1	22:O:5:SER:OG	2.26	0.40
34:a:358:U:H2'	34:a:359:G:C8	2.56	0.40
34:a:404:G:O2'	34:a:498:A:N1	2.45	0.40
34:a:1235:U:O2'	34:a:1305:G:H5'	2.21	0.40
34:a:1393:U:O2'	34:a:1501:C:O2'	2.39	0.40
34:a:1432:G:H1'	34:a:1468:A:H62	1.86	0.40
34:a:1494:G:N3	34:a:1494:G:H2'	2.35	0.40
50:q:42:LYS:HE2	50:q:42:LYS:HB3	1.93	0.40
54:u:4:LYS:HB3	54:u:4:LYS:HE2	1.88	0.40
4:3:63:TYR:CD2	8:A:242:G:H3'	2.55	0.40
7:6:63:ARG:O	7:6:65:ASN:N	2.54	0.40
8:A:146:A:H2'	8:A:147:C:H6	1.86	0.40
8:A:270:A:H5''	8:A:271:G:H5''	2.02	0.40
8:A:392:U:H2'	8:A:393:C:H6	1.85	0.40
8:A:535:G:C6	8:A:559:G:C6	3.09	0.40
8:A:878:A:C6	8:A:900:A:H1'	2.56	0.40
8:A:948:C:H1'	8:A:984:A:C8	2.56	0.40
8:A:1115:G:H2'	8:A:1116:G:C8	2.54	0.40
8:A:1470:A:H2'	8:A:1471:G:O4'	2.20	0.40
8:A:2011:U:H2'	8:A:2012:G:O4'	2.21	0.40
8:A:2079:U:H2'	8:A:2080:A:O4'	2.20	0.40
8:A:2411:A:H2'	8:A:2412:A:C8	2.56	0.40
8:A:2696:U:H2'	8:A:2697:G:H8	1.86	0.40
12:E:105:LEU:HD23	12:E:105:LEU:HA	1.87	0.40
12:E:155:GLU:O	12:E:159:LEU:HG	2.21	0.40
21:N:55:ALA:HA	21:N:80:PHE:CE1	2.56	0.40
25:R:75:VAL:HG22	25:R:86:GLN:HG2	2.03	0.40
28:U:40:LEU:HD22	28:U:59:GLU:HG3	2.03	0.40
34:a:35:G:H2'	34:a:36:C:H6	1.84	0.40
34:a:185:U:H2'	34:a:186:C:H6	1.86	0.40
34:a:294:U:H2'	34:a:295:C:C6	2.57	0.40
34:a:390:U:H2'	34:a:391:G:C8	2.55	0.40
34:a:546:A:P	37:d:68:GLU:HB3	2.61	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:736:C:H2'	34:a:737:C:H6	1.86	0.40
34:a:775:G:N2	34:a:804:U:O4	2.52	0.40
34:a:818:G:C6	34:a:820:U:O2'	2.74	0.40
34:a:1026:G:H2'	34:a:1026:G:N3	2.37	0.40
34:a:1294:G:C5	34:a:1295:U:C4	3.09	0.40
37:d:176:LYS:HE3	37:d:176:LYS:HB3	1.94	0.40
41:h:9:MET:O	41:h:13:ILE:HG13	2.22	0.40
53:t:27:MET:HG3	53:t:57:VAL:HG12	2.04	0.40
53:t:28:ARG:O	53:t:32:LYS:HE3	2.22	0.40
8:A:271:G:C4	8:A:272:A:N7	2.90	0.40
8:A:499:U:H5''	28:U:42:LYS:HE2	2.03	0.40
8:A:1005:C:O2'	17:J:30:THR:HG21	2.21	0.40
8:A:1048:A:C8	8:A:1111:A:N1	2.90	0.40
8:A:1060:U:H4'	8:A:1062:G:H5'	2.03	0.40
8:A:1412:U:C2	8:A:1413:A:C8	3.09	0.40
8:A:1475:G:O2'	8:A:1476:U:H6	2.04	0.40
8:A:1651:G:OP1	21:N:40:LYS:HE3	2.21	0.40
8:A:1961:C:H5'	34:a:1484:C:O2'	2.22	0.40
8:A:2506:U:OP2	8:A:2576:G:N1	2.44	0.40
9:B:111:U:H2'	9:B:112:G:C8	2.54	0.40
10:C:106:PRO:HB3	10:C:141:HIS:HE1	1.85	0.40
13:F:3:LEU:HD12	13:F:172:PHE:CD1	2.56	0.40
15:H:4:ILE:HD12	15:H:17:ASP:O	2.20	0.40
20:M:41:LEU:HD22	20:M:124:LEU:HD22	2.03	0.40
25:R:22:LEU:HD12	25:R:25:LEU:HD11	2.03	0.40
34:a:75:G:C6	34:a:76:G:N7	2.89	0.40
34:a:230:G:H2'	34:a:231:U:O4'	2.20	0.40
34:a:414:A:C4	34:a:415:A:C8	3.09	0.40
34:a:432:A:H2'	34:a:433:G:O4'	2.21	0.40
34:a:633:G:H2'	34:a:634:C:H6	1.86	0.40
34:a:788:U:H2'	34:a:789:U:O4'	2.21	0.40
34:a:1225:A:H5''	34:a:1226:C:OP2	2.21	0.40
34:a:1238:A:H2	34:a:1241:G:N3	2.18	0.40
34:a:1305:G:H1'	34:a:1332:A:H61	1.85	0.40
35:b:183:PHE:N	35:b:183:PHE:CD1	2.87	0.40
36:c:161:ILE:HD12	57:x:23:U:H4'	2.02	0.40
38:e:71:ILE:HD13	38:e:71:ILE:HA	1.91	0.40
38:e:151:MET:O	38:e:155:LYS:HG3	2.21	0.40
40:g:110:ARG:HH11	40:g:122:GLU:HG2	1.87	0.40
42:i:55:ASP:OD1	42:i:55:ASP:N	2.54	0.40
8:A:81:G:H2'	8:A:82:U:O4'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:255:A:H2'	8:A:256:A:O4'	2.22	0.40
8:A:933:A:H5'	8:A:934:U:OP2	2.21	0.40
8:A:1386:C:H2'	8:A:1387:A:H8	1.84	0.40
8:A:2478:A:C8	8:A:2529:G:N7	2.90	0.40
12:E:1:MET:HB2	12:E:16:GLU:HA	2.02	0.40
18:K:108:ARG:NH1	23:P:33:GLU:HA	2.28	0.40
19:L:110:VAL:O	19:L:128:THR:HG23	2.22	0.40
20:M:4:PRO:CG	20:M:70:ASP:HA	2.51	0.40
20:M:47:GLU:OE2	20:M:51:ARG:NE	2.53	0.40
23:P:38:ARG:NH2	34:a:346:G:OP1	2.49	0.40
25:R:43:ASN:ND2	25:R:46:GLU:OE2	2.54	0.40
34:a:2:A:H1'	34:a:613:C:O2'	2.21	0.40
34:a:216:U:H4'	34:a:465:A:OP1	2.22	0.40
34:a:410:G:H2'	34:a:429:U:C5	2.57	0.40
34:a:751:U:H2'	34:a:752:G:O4'	2.21	0.40
34:a:1149:C:OP2	42:i:10:ARG:NH2	2.30	0.40
34:a:1161:C:C2	34:a:1162:C:C5	3.09	0.40
35:b:17:HIS:CG	35:b:18:GLN:H	2.39	0.40
35:b:163:ILE:O	35:b:185:ILE:HB	2.21	0.40
37:d:151:GLN:CG	37:d:153:ARG:HG2	2.51	0.40
42:i:40:ARG:HG3	42:i:42:THR:HG22	2.02	0.40
51:r:54:LEU:O	51:r:58:ILE:HG12	2.21	0.40
52:s:63:ASP:OD1	52:s:63:ASP:N	2.55	0.40
4:3:24:LYS:HG2	19:L:62:PRO:HG2	2.04	0.40
8:A:488:G:H1'	8:A:492:A:N6	2.36	0.40
8:A:709:U:H2'	8:A:710:U:H6	1.85	0.40
8:A:1302:A:H5'	8:A:1608:A:P	2.62	0.40
8:A:1692:U:H2'	8:A:1694:C:C5	2.56	0.40
8:A:1739:A:H2'	8:A:1740:G:O4'	2.22	0.40
8:A:1946:U:H2'	8:A:1947:C:C6	2.57	0.40
8:A:2064:C:O2'	8:A:2251:OMG:N2	2.51	0.40
8:A:2661:G:H2'	8:A:2662:A:C8	2.56	0.40
8:A:2696:U:H2'	8:A:2697:G:C8	2.57	0.40
8:A:2785:C:H2'	8:A:2786:U:H6	1.87	0.40
8:A:2813:A:C4	8:A:2814:A:C8	3.09	0.40
9:B:89:U:H5''	9:B:90:C:C6	2.56	0.40
11:D:101:PHE:HA	11:D:104:VAL:HG22	2.03	0.40
12:E:164:LEU:HD23	12:E:164:LEU:HA	1.91	0.40
13:F:7:TYR:HA	13:F:11:VAL:HB	2.04	0.40
20:M:127:LYS:HA	20:M:127:LYS:HD2	1.83	0.40
25:R:28:ALA:HB3	25:R:31:GLU:HG2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:U:95:PHE:O	28:U:99:SER:HA	2.22	0.40
29:V:6:ALA:HB1	29:V:40:ILE:HG23	2.03	0.40
34:a:82:G:H21	34:a:87:C:N4	2.19	0.40
34:a:384:G:H2'	34:a:385:C:H6	1.86	0.40
34:a:584:G:H2'	34:a:585:G:H8	1.86	0.40
34:a:1399:C:H4'	34:a:1400:C:O5'	2.21	0.40
36:c:18:ASN:C	36:c:39:ARG:HH22	2.28	0.40
45:l:52:CYS:HB3	45:l:66:ILE:HD11	2.04	0.40
50:q:68:LYS:CD	50:q:68:LYS:O	2.70	0.40
51:r:40:PRO:HG2	51:r:43:ILE:HG12	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
2	1	48/55 (87%)	46 (96%)	2 (4%)	0	100	100
3	2	44/46 (96%)	44 (100%)	0	0	100	100
4	3	62/65 (95%)	55 (89%)	7 (11%)	0	100	100
5	4	36/38 (95%)	32 (89%)	4 (11%)	0	100	100
6	5	129/165 (78%)	108 (84%)	21 (16%)	0	100	100
7	6	64/70 (91%)	50 (78%)	14 (22%)	0	100	100
10	C	269/273 (98%)	248 (92%)	20 (7%)	1 (0%)	30	61
11	D	207/209 (99%)	191 (92%)	16 (8%)	0	100	100
12	E	199/201 (99%)	187 (94%)	12 (6%)	0	100	100
13	F	175/179 (98%)	153 (87%)	22 (13%)	0	100	100
14	G	174/177 (98%)	154 (88%)	19 (11%)	1 (1%)	21	52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	H	147/149 (99%)	111 (76%)	33 (22%)	3 (2%)	6	25
16	I	139/142 (98%)	109 (78%)	30 (22%)	0	100	100
17	J	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
18	K	120/123 (98%)	113 (94%)	7 (6%)	0	100	100
19	L	141/144 (98%)	124 (88%)	17 (12%)	0	100	100
20	M	134/136 (98%)	125 (93%)	9 (7%)	0	100	100
21	N	118/127 (93%)	112 (95%)	6 (5%)	0	100	100
22	O	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
23	P	112/115 (97%)	102 (91%)	10 (9%)	0	100	100
24	Q	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
25	R	101/103 (98%)	89 (88%)	12 (12%)	0	100	100
26	S	108/110 (98%)	100 (93%)	8 (7%)	0	100	100
27	T	91/100 (91%)	81 (89%)	10 (11%)	0	100	100
28	U	100/104 (96%)	90 (90%)	10 (10%)	0	100	100
29	V	92/94 (98%)	86 (94%)	6 (6%)	0	100	100
30	W	73/85 (86%)	66 (90%)	7 (10%)	0	100	100
31	X	75/78 (96%)	71 (95%)	4 (5%)	0	100	100
32	Y	61/63 (97%)	57 (93%)	3 (5%)	1 (2%)	7	30
33	Z	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
35	b	216/240 (90%)	188 (87%)	25 (12%)	3 (1%)	9	34
36	c	204/233 (88%)	195 (96%)	9 (4%)	0	100	100
37	d	203/206 (98%)	167 (82%)	29 (14%)	7 (3%)	3	16
38	e	155/167 (93%)	138 (89%)	17 (11%)	0	100	100
39	f	98/135 (73%)	88 (90%)	10 (10%)	0	100	100
40	g	149/179 (83%)	142 (95%)	7 (5%)	0	100	100
41	h	127/130 (98%)	116 (91%)	11 (9%)	0	100	100
42	i	125/130 (96%)	105 (84%)	20 (16%)	0	100	100
43	j	96/103 (93%)	78 (81%)	16 (17%)	2 (2%)	5	25
44	k	114/129 (88%)	107 (94%)	7 (6%)	0	100	100
45	l	121/124 (98%)	105 (87%)	16 (13%)	0	100	100
46	m	112/118 (95%)	101 (90%)	10 (9%)	1 (1%)	14	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
47	n	99/102 (97%)	86 (87%)	13 (13%)	0	100	100
48	o	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
49	p	80/82 (98%)	68 (85%)	12 (15%)	0	100	100
50	q	78/84 (93%)	63 (81%)	13 (17%)	2 (3%)	4	21
51	r	63/75 (84%)	53 (84%)	10 (16%)	0	100	100
52	s	80/92 (87%)	73 (91%)	7 (9%)	0	100	100
53	t	83/87 (95%)	82 (99%)	1 (1%)	0	100	100
54	u	63/71 (89%)	51 (81%)	11 (18%)	1 (2%)	7	30
All	All	5850/6220 (94%)	5250 (90%)	578 (10%)	22 (0%)	31	61

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
35	b	87	ASP
37	d	34	GLU
37	d	37	PRO
37	d	150	LYS
43	j	43	PRO
32	Y	13	GLU
37	d	79	ALA
50	q	70	LYS
14	G	108	PHE
15	H	104	THR
35	b	20	ARG
43	j	57	VAL
46	m	65	GLU
54	u	12	ASP
35	b	18	GLN
37	d	71	PHE
10	C	240	GLY
15	H	70	GLU
15	H	74	ALA
37	d	144	ILE
37	d	38	GLY
50	q	55	GLY

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	0	47/48 (98%)	47 (100%)	0	100	100
2	1	45/49 (92%)	45 (100%)	0	100	100
3	2	38/38 (100%)	38 (100%)	0	100	100
4	3	51/52 (98%)	50 (98%)	1 (2%)	48	72
5	4	34/34 (100%)	34 (100%)	0	100	100
7	6	59/62 (95%)	59 (100%)	0	100	100
10	C	216/218 (99%)	216 (100%)	0	100	100
11	D	164/164 (100%)	164 (100%)	0	100	100
12	E	165/165 (100%)	165 (100%)	0	100	100
13	F	148/150 (99%)	148 (100%)	0	100	100
14	G	137/138 (99%)	137 (100%)	0	100	100
15	H	114/114 (100%)	112 (98%)	2 (2%)	51	73
17	J	116/116 (100%)	116 (100%)	0	100	100
18	K	103/104 (99%)	103 (100%)	0	100	100
19	L	102/103 (99%)	102 (100%)	0	100	100
20	M	109/109 (100%)	109 (100%)	0	100	100
21	N	100/103 (97%)	100 (100%)	0	100	100
22	O	86/87 (99%)	86 (100%)	0	100	100
23	P	99/100 (99%)	99 (100%)	0	100	100
24	Q	89/90 (99%)	89 (100%)	0	100	100
25	R	84/84 (100%)	84 (100%)	0	100	100
26	S	93/93 (100%)	93 (100%)	0	100	100
27	T	80/84 (95%)	79 (99%)	1 (1%)	61	77
28	U	83/85 (98%)	83 (100%)	0	100	100
29	V	78/78 (100%)	78 (100%)	0	100	100
30	W	57/63 (90%)	57 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	X	67/68 (98%)	67 (100%)	0	100	100
32	Y	55/55 (100%)	55 (100%)	0	100	100
33	Z	48/49 (98%)	48 (100%)	0	100	100
35	b	180/198 (91%)	180 (100%)	0	100	100
36	c	170/190 (90%)	170 (100%)	0	100	100
37	d	172/173 (99%)	168 (98%)	4 (2%)	44	70
38	e	114/126 (90%)	114 (100%)	0	100	100
39	f	87/116 (75%)	87 (100%)	0	100	100
40	g	124/147 (84%)	124 (100%)	0	100	100
41	h	104/105 (99%)	104 (100%)	0	100	100
42	i	105/107 (98%)	105 (100%)	0	100	100
43	j	86/90 (96%)	85 (99%)	1 (1%)	63	78
44	k	89/99 (90%)	89 (100%)	0	100	100
45	l	103/104 (99%)	103 (100%)	0	100	100
46	m	92/96 (96%)	92 (100%)	0	100	100
47	n	79/84 (94%)	79 (100%)	0	100	100
48	o	76/77 (99%)	76 (100%)	0	100	100
49	p	65/65 (100%)	65 (100%)	0	100	100
50	q	74/78 (95%)	71 (96%)	3 (4%)	27	59
51	r	56/65 (86%)	56 (100%)	0	100	100
52	s	72/79 (91%)	72 (100%)	0	100	100
53	t	65/66 (98%)	65 (100%)	0	100	100
54	u	46/61 (75%)	46 (100%)	0	100	100
55	v	2/2 (100%)	1 (50%)	1 (50%)	0	0
All	All	4628/4831 (96%)	4615 (100%)	13 (0%)	84	87

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	3	32	LEU
15	H	66	ASN
15	H	104	THR
27	T	37	ASP
37	d	34	GLU

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Mol	Chain	Res	Type
37	d	37	PRO
37	d	73	ASN
37	d	150	LYS
43	j	43	PRO
50	q	56	ASP
50	q	68	LYS
50	q	70	LYS
55	v	101	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (54) such sidechains are listed below:

Mol	Chain	Res	Type
1	0	5	ASN
2	1	25	ASN
3	2	6	GLN
4	3	42	HIS
7	6	41	HIS
7	6	65	ASN
10	C	52	HIS
10	C	152	GLN
10	C	259	ASN
11	D	173	GLN
11	D	185	ASN
12	E	136	GLN
12	E	165	HIS
14	G	29	ASN
14	G	44	HIS
14	G	47	ASN
14	G	63	GLN
14	G	103	ASN
15	H	128	HIS
18	K	5	GLN
18	K	93	GLN
19	L	54	GLN
20	M	13	HIS
21	N	62	ASN
23	P	11	GLN
24	Q	43	GLN
27	T	28	ASN
27	T	70	HIS
28	U	52	ASN
28	U	53	GLN

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Mol	Chain	Res	Type
28	U	73	ASN
30	W	8	ASN
35	b	18	GLN
35	b	169	HIS
36	c	18	ASN
37	d	88	ASN
37	d	197	HIS
38	e	88	HIS
40	g	67	ASN
41	h	66	GLN
43	j	56	HIS
44	k	21	HIS
44	k	39	ASN
46	m	51	GLN
47	n	49	GLN
48	o	34	GLN
48	o	79	GLN
49	p	26	ASN
49	p	29	ASN
49	p	59	HIS
50	q	50	ASN
52	s	82	HIS
53	t	54	GLN
53	t	83	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	a	1538/1542 (99%)	285 (18%)	0
56	w	75/76 (98%)	13 (17%)	0
57	x	14/15 (93%)	8 (57%)	0
8	A	2902/2903 (99%)	579 (19%)	56 (1%)
9	B	119/120 (99%)	18 (15%)	3 (2%)
All	All	4648/4656 (99%)	903 (19%)	59 (1%)

All (903) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	A	10	A
8	A	15	G
8	A	33	C

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Mol	Chain	Res	Type
8	A	35	G
8	A	46	G
8	A	51	G
8	A	63	A
8	A	71	A
8	A	74	A
8	A	75	G
8	A	84	A
8	A	93	G
8	A	102	U
8	A	103	A
8	A	118	A
8	A	119	A
8	A	120	U
8	A	125	A
8	A	131	A
8	A	139	U
8	A	140	C
8	A	141	G
8	A	142	A
8	A	160	A
8	A	163	C
8	A	165	A
8	A	181	A
8	A	196	A
8	A	199	A
8	A	216	A
8	A	221	A
8	A	222	A
8	A	223	A
8	A	228	C
8	A	229	C
8	A	230	G
8	A	242	G
8	A	243	U
8	A	248	G
8	A	250	G
8	A	255	A
8	A	266	G
8	A	275	C
8	A	277	G
8	A	278	A

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Mol	Chain	Res	Type
8	A	281	C
8	A	283	G
8	A	285	G
8	A	294	A
8	A	311	A
8	A	323	C
8	A	324	A
8	A	327	G
8	A	328	U
8	A	330	A
8	A	331	C
8	A	345	A
8	A	346	A
8	A	358	U
8	A	360	U
8	A	361	G
8	A	362	A
8	A	371	A
8	A	372	G
8	A	386	G
8	A	388	G
8	A	395	U
8	A	396	G
8	A	401	A
8	A	404	A
8	A	405	U
8	A	406	G
8	A	411	G
8	A	424	G
8	A	435	C
8	A	455	C
8	A	457	A
8	A	458	G
8	A	473	G
8	A	475	C
8	A	481	G
8	A	491	G
8	A	501	A
8	A	505	A
8	A	509	C
8	A	513	A
8	A	527	C

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Mol	Chain	Res	Type
8	A	529	A
8	A	532	A
8	A	546	U
8	A	548	G
8	A	549	G
8	A	556	A
8	A	563	A
8	A	569	U
8	A	573	U
8	A	575	A
8	A	578	G
8	A	588	U
8	A	603	A
8	A	613	A
8	A	614	A
8	A	615	U
8	A	616	A
8	A	627	A
8	A	637	A
8	A	645	C
8	A	646	U
8	A	653	U
8	A	654	A
8	A	655	A
8	A	668	A
8	A	669	G
8	A	677	A
8	A	682	G
8	A	686	U
8	A	695	G
8	A	704	G
8	A	715	A
8	A	717	C
8	A	726	G
8	A	730	A
8	A	738	G
8	A	747	5MC
8	A	764	A
8	A	774	G
8	A	775	G
8	A	776	G
8	A	782	A

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Mol	Chain	Res	Type
8	A	783	A
8	A	784	G
8	A	785	G
8	A	789	A
8	A	791	C
8	A	805	G
8	A	807	U
8	A	812	C
8	A	819	A
8	A	827	U
8	A	828	U
8	A	845	A
8	A	846	U
8	A	847	U
8	A	858	G
8	A	859	G
8	A	866	A
8	A	869	G
8	A	877	A
8	A	878	A
8	A	883	G
8	A	884	U
8	A	885	C
8	A	886	A
8	A	887	U
8	A	888	C
8	A	889	C
8	A	890	C
8	A	891	G
8	A	892	A
8	A	893	C
8	A	895	U
8	A	896	A
8	A	897	C
8	A	906	U
8	A	907	G
8	A	910	A
8	A	927	A
8	A	931	U
8	A	934	U
8	A	941	A
8	A	945	A

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Mol	Chain	Res	Type
8	A	946	C
8	A	953	G
8	A	961	C
8	A	973	A
8	A	974	G
8	A	975	A
8	A	983	A
8	A	990	A
8	A	995	C
8	A	996	A
8	A	999	U
8	A	1005	C
8	A	1012	U
8	A	1013	C
8	A	1021	A
8	A	1023	U
8	A	1025	G
8	A	1026	G
8	A	1028	A
8	A	1033	U
8	A	1044	C
8	A	1047	G
8	A	1053	C
8	A	1054	A
8	A	1056	G
8	A	1057	A
8	A	1058	U
8	A	1060	U
8	A	1061	U
8	A	1062	G
8	A	1063	G
8	A	1064	C
8	A	1065	U
8	A	1066	U
8	A	1067	A
8	A	1069	A
8	A	1070	A
8	A	1071	G
8	A	1073	A
8	A	1074	G
8	A	1075	C
8	A	1079	C

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Mol	Chain	Res	Type
8	A	1081	U
8	A	1082	U
8	A	1083	U
8	A	1084	A
8	A	1086	A
8	A	1087	G
8	A	1088	A
8	A	1089	A
8	A	1090	A
8	A	1091	G
8	A	1093	G
8	A	1094	U
8	A	1098	A
8	A	1102	C
8	A	1103	A
8	A	1105	U
8	A	1109	C
8	A	1111	A
8	A	1112	G
8	A	1115	G
8	A	1119	U
8	A	1130	U
8	A	1131	G
8	A	1132	U
8	A	1133	A
8	A	1135	C
8	A	1142	A
8	A	1169	A
8	A	1171	G
8	A	1173	U
8	A	1174	U
8	A	1175	A
8	A	1176	U
8	A	1178	C
8	A	1180	U
8	A	1181	U
8	A	1186	G
8	A	1195	G
8	A	1206	G
8	A	1211	C
8	A	1212	G
8	A	1227	G

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Mol	Chain	Res	Type
8	A	1236	G
8	A	1242	U
8	A	1247	A
8	A	1248	G
8	A	1250	G
8	A	1253	A
8	A	1255	U
8	A	1256	G
8	A	1271	G
8	A	1272	A
8	A	1273	U
8	A	1290	C
8	A	1300	G
8	A	1301	A
8	A	1302	A
8	A	1306	C
8	A	1321	A
8	A	1352	U
8	A	1365	A
8	A	1368	G
8	A	1378	A
8	A	1379	U
8	A	1383	A
8	A	1392	A
8	A	1395	A
8	A	1416	G
8	A	1420	A
8	A	1421	G
8	A	1427	A
8	A	1428	C
8	A	1452	G
8	A	1454	C
8	A	1459	G
8	A	1461	C
8	A	1482	G
8	A	1485	U
8	A	1486	U
8	A	1490	A
8	A	1491	G
8	A	1493	C
8	A	1497	U
8	A	1498	C

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Mol	Chain	Res	Type
8	A	1502	A
8	A	1503	A
8	A	1504	A
8	A	1507	C
8	A	1508	A
8	A	1509	A
8	A	1515	A
8	A	1522	A
8	A	1523	U
8	A	1524	G
8	A	1533	C
8	A	1534	U
8	A	1535	A
8	A	1536	C
8	A	1537	G
8	A	1538	G
8	A	1554	U
8	A	1558	C
8	A	1566	A
8	A	1569	A
8	A	1578	U
8	A	1583	A
8	A	1584	U
8	A	1608	A
8	A	1610	A
8	A	1626	A
8	A	1627	G
8	A	1634	A
8	A	1647	U
8	A	1648	U
8	A	1649	G
8	A	1672	A
8	A	1674	G
8	A	1675	C
8	A	1715	G
8	A	1716	U
8	A	1726	C
8	A	1729	U
8	A	1730	C
8	A	1731	G
8	A	1736	U
8	A	1738	G

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Mol	Chain	Res	Type
8	A	1744	A
8	A	1764	C
8	A	1773	A
8	A	1776	G
8	A	1781	U
8	A	1782	U
8	A	1784	A
8	A	1786	A
8	A	1787	A
8	A	1800	C
8	A	1801	A
8	A	1808	A
8	A	1816	C
8	A	1848	A
8	A	1866	A
8	A	1867	G
8	A	1869	G
8	A	1884	G
8	A	1900	A
8	A	1906	G
8	A	1913	A
8	A	1914	C
8	A	1915	3TD
8	A	1919	A
8	A	1927	A
8	A	1929	G
8	A	1930	G
8	A	1937	A
8	A	1938	A
8	A	1955	U
8	A	1965	C
8	A	1967	C
8	A	1970	A
8	A	1971	U
8	A	1972	G
8	A	1982	U
8	A	1991	U
8	A	1996	C
8	A	1997	C
8	A	2020	A
8	A	2022	U
8	A	2023	C

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Mol	Chain	Res	Type
8	A	2030	6MZ
8	A	2031	A
8	A	2032	G
8	A	2033	A
8	A	2043	C
8	A	2046	G
8	A	2052	A
8	A	2055	C
8	A	2056	G
8	A	2060	A
8	A	2061	G
8	A	2062	A
8	A	2069	G7M
8	A	2072	C
8	A	2093	G
8	A	2100	G
8	A	2101	A
8	A	2105	U
8	A	2106	U
8	A	2108	A
8	A	2111	U
8	A	2112	G
8	A	2113	U
8	A	2114	A
8	A	2115	G
8	A	2116	G
8	A	2118	U
8	A	2119	A
8	A	2120	G
8	A	2121	G
8	A	2124	G
8	A	2125	G
8	A	2126	A
8	A	2127	G
8	A	2128	G
8	A	2129	C
8	A	2131	U
8	A	2134	A
8	A	2135	A
8	A	2136	G
8	A	2137	U
8	A	2138	G

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Mol	Chain	Res	Type
8	A	2139	U
8	A	2140	G
8	A	2141	G
8	A	2142	A
8	A	2143	C
8	A	2144	G
8	A	2145	C
8	A	2146	C
8	A	2147	A
8	A	2149	U
8	A	2151	U
8	A	2152	G
8	A	2154	A
8	A	2155	U
8	A	2156	G
8	A	2157	G
8	A	2158	A
8	A	2159	G
8	A	2162	G
8	A	2163	A
8	A	2164	C
8	A	2165	C
8	A	2166	U
8	A	2167	U
8	A	2170	A
8	A	2171	A
8	A	2172	U
8	A	2173	A
8	A	2174	C
8	A	2175	C
8	A	2176	A
8	A	2177	C
8	A	2178	C
8	A	2180	U
8	A	2181	U
8	A	2183	A
8	A	2186	G
8	A	2189	U
8	A	2193	G
8	A	2198	A
8	A	2203	U
8	A	2204	G

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Mol	Chain	Res	Type
8	A	2211	A
8	A	2212	A
8	A	2225	A
8	A	2238	G
8	A	2239	G
8	A	2251	OMG
8	A	2267	A
8	A	2268	A
8	A	2278	A
8	A	2283	C
8	A	2287	A
8	A	2288	A
8	A	2297	A
8	A	2305	U
8	A	2309	A
8	A	2310	C
8	A	2320	U
8	A	2322	A
8	A	2325	G
8	A	2333	A
8	A	2335	A
8	A	2344	U
8	A	2345	G
8	A	2347	C
8	A	2350	C
8	A	2361	G
8	A	2383	G
8	A	2385	C
8	A	2396	G
8	A	2402	U
8	A	2403	C
8	A	2406	A
8	A	2407	A
8	A	2423	U
8	A	2425	A
8	A	2429	G
8	A	2435	A
8	A	2441	U
8	A	2445	2MG
8	A	2448	A
8	A	2459	A
8	A	2469	A

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Mol	Chain	Res	Type
8	A	2473	U
8	A	2475	C
8	A	2476	A
8	A	2489	U
8	A	2494	G
8	A	2502	G
8	A	2503	2MA
8	A	2505	G
8	A	2513	A
8	A	2518	A
8	A	2529	G
8	A	2547	A
8	A	2554	U
8	A	2566	A
8	A	2567	G
8	A	2569	G
8	A	2573	C
8	A	2582	G
8	A	2585	U
8	A	2586	U
8	A	2602	A
8	A	2609	U
8	A	2610	C
8	A	2613	U
8	A	2615	U
8	A	2629	U
8	A	2630	G
8	A	2633	G
8	A	2655	G
8	A	2656	U
8	A	2663	G
8	A	2685	G
8	A	2689	U
8	A	2690	U
8	A	2702	G
8	A	2714	G
8	A	2716	C
8	A	2718	G
8	A	2726	A
8	A	2727	A
8	A	2729	G
8	A	2732	G

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Mol	Chain	Res	Type
8	A	2733	A
8	A	2739	U
8	A	2744	G
8	A	2748	A
8	A	2757	A
8	A	2761	A
8	A	2765	A
8	A	2777	G
8	A	2778	A
8	A	2779	U
8	A	2791	G
8	A	2797	U
8	A	2800	A
8	A	2808	G
8	A	2809	A
8	A	2818	U
8	A	2820	A
8	A	2821	A
8	A	2833	U
8	A	2861	U
8	A	2867	G
8	A	2868	A
8	A	2873	A
8	A	2879	A
8	A	2880	C
8	A	2884	U
8	A	2886	A
8	A	2891	U
8	A	2894	G
8	A	2901	C
9	B	9	G
9	B	25	U
9	B	35	C
9	B	36	C
9	B	41	G
9	B	42	C
9	B	45	A
9	B	51	G
9	B	53	A
9	B	56	G
9	B	57	A
9	B	67	G

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Mol	Chain	Res	Type
9	B	68	C
9	B	73	A
9	B	88	C
9	B	89	U
9	B	109	A
9	B	120	U
34	a	3	A
34	a	4	U
34	a	6	G
34	a	7	A
34	a	9	G
34	a	22	G
34	a	32	A
34	a	39	G
34	a	47	C
34	a	48	C
34	a	50	A
34	a	51	A
34	a	52	C
34	a	70	U
34	a	71	A
34	a	72	A
34	a	76	G
34	a	78	A
34	a	79	G
34	a	80	A
34	a	81	A
34	a	82	G
34	a	83	C
34	a	84	U
34	a	85	U
34	a	87	C
34	a	88	U
34	a	89	U
34	a	92	U
34	a	93	U
34	a	94	G
34	a	95	C
34	a	96	U
34	a	116	A
34	a	121	U
34	a	129	A

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Mol	Chain	Res	Type
34	a	130	A
34	a	141	G
34	a	144	G
34	a	148	G
34	a	163	C
34	a	164	G
34	a	171	A
34	a	173	U
34	a	177	G
34	a	179	A
34	a	182	A
34	a	184	G
34	a	189	A
34	a	197	A
34	a	198	G
34	a	206	C
34	a	207	C
34	a	208	U
34	a	209	U
34	a	210	C
34	a	211	G
34	a	215	C
34	a	226	G
34	a	240	G
34	a	245	U
34	a	247	G
34	a	251	G
34	a	262	A
34	a	266	G
34	a	267	C
34	a	279	A
34	a	280	C
34	a	289	G
34	a	293	G
34	a	299	G
34	a	301	G
34	a	316	C
34	a	321	A
34	a	328	C
34	a	344	A
34	a	347	G
34	a	348	G

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Mol	Chain	Res	Type
34	a	351	G
34	a	352	C
34	a	354	G
34	a	356	A
34	a	367	U
34	a	372	C
34	a	373	A
34	a	375	U
34	a	382	A
34	a	389	A
34	a	390	U
34	a	392	C
34	a	406	G
34	a	412	A
34	a	413	G
34	a	414	A
34	a	421	U
34	a	424	G
34	a	429	U
34	a	445	G
34	a	461	A
34	a	462	G
34	a	463	U
34	a	465	A
34	a	466	A
34	a	467	U
34	a	468	A
34	a	469	C
34	a	470	C
34	a	471	U
34	a	479	U
34	a	481	G
34	a	482	A
34	a	484	G
34	a	495	A
34	a	496	A
34	a	499	A
34	a	509	A
34	a	510	A
34	a	511	C
34	a	512	U
34	a	516	PSU

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Mol	Chain	Res	Type
34	a	518	C
34	a	521	G
34	a	524	G
34	a	527	G7M
34	a	530	G
34	a	532	A
34	a	547	A
34	a	559	A
34	a	562	U
34	a	564	C
34	a	572	A
34	a	573	A
34	a	576	C
34	a	577	G
34	a	579	A
34	a	596	A
34	a	615	G
34	a	632	U
34	a	633	G
34	a	636	U
34	a	641	U
34	a	650	G
34	a	654	G
34	a	665	A
34	a	703	G
34	a	704	A
34	a	721	G
34	a	724	G
34	a	731	G
34	a	748	G
34	a	749	A
34	a	755	G
34	a	777	A
34	a	781	A
34	a	790	A
34	a	794	A
34	a	799	G
34	a	815	A
34	a	817	C
34	a	818	G
34	a	819	A
34	a	829	G

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Mol	Chain	Res	Type
34	a	832	G
34	a	836	G
34	a	841	C
34	a	842	U
34	a	843	U
34	a	846	G
34	a	872	A
34	a	884	U
34	a	889	A
34	a	890	G
34	a	891	U
34	a	902	G
34	a	914	A
34	a	926	G
34	a	934	C
34	a	935	A
34	a	960	U
34	a	961	U
34	a	966	2MG
34	a	967	5MC
34	a	969	A
34	a	975	A
34	a	976	G
34	a	977	A
34	a	992	U
34	a	993	G
34	a	996	A
34	a	999	C
34	a	1004	A
34	a	1009	U
34	a	1017	U
34	a	1020	G
34	a	1024	G
34	a	1028	C
34	a	1029	U
34	a	1030	U
34	a	1031	C
34	a	1032	G
34	a	1035	A
34	a	1044	A
34	a	1045	C
34	a	1050	G

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Mol	Chain	Res	Type
34	a	1065	U
34	a	1085	U
34	a	1094	G
34	a	1101	A
34	a	1108	G
34	a	1124	G
34	a	1126	U
34	a	1130	A
34	a	1134	G
34	a	1136	C
34	a	1137	C
34	a	1139	G
34	a	1144	G
34	a	1146	A
34	a	1154	G
34	a	1159	U
34	a	1160	G
34	a	1167	A
34	a	1168	U
34	a	1169	A
34	a	1183	U
34	a	1184	G
34	a	1196	A
34	a	1197	A
34	a	1212	U
34	a	1213	A
34	a	1225	A
34	a	1227	A
34	a	1238	A
34	a	1250	A
34	a	1257	A
34	a	1275	A
34	a	1280	A
34	a	1287	A
34	a	1294	G
34	a	1297	G
34	a	1299	A
34	a	1300	G
34	a	1301	U
34	a	1302	C
34	a	1306	A
34	a	1312	G

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Mol	Chain	Res	Type
34	a	1317	C
34	a	1320	C
34	a	1322	C
34	a	1331	G
34	a	1332	A
34	a	1346	A
34	a	1348	U
34	a	1353	G
34	a	1363	A
34	a	1364	U
34	a	1368	A
34	a	1370	G
34	a	1378	C
34	a	1379	G
34	a	1398	A
34	a	1400	C
34	a	1419	G
34	a	1422	G
34	a	1429	A
34	a	1441	A
34	a	1442	G
34	a	1446	A
34	a	1451	U
34	a	1492	A
34	a	1493	A
34	a	1494	G
34	a	1497	G
34	a	1499	A
34	a	1506	U
34	a	1517	G
34	a	1519	MA6
34	a	1529	G
34	a	1530	G
34	a	1534	A
34	a	1535	C
34	a	1536	C
34	a	1537	U
34	a	1538	C
34	a	1540	U
56	w	9	A
56	w	13	C
56	w	16	U

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Mol	Chain	Res	Type
56	w	17	C
56	w	18	G
56	w	20	U
56	w	21	A
56	w	22	G
56	w	46	G7M
56	w	47	U
56	w	58	A
56	w	75	C
56	w	76	A
57	x	16	U
57	x	19	A
57	x	20	A
57	x	23	U
57	x	24	G
57	x	25	U
57	x	26	U
57	x	27	U

All (59) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	A	102	U
8	A	141	G
8	A	228	C
8	A	242	G
8	A	310	A
8	A	323	C
8	A	456	C
8	A	464	U
8	A	490	C
8	A	547	A
8	A	555	G
8	A	614	A
8	A	784	G
8	A	883	G
8	A	886	A
8	A	887	U
8	A	890	C
8	A	894	U
8	A	1020	A
8	A	1074	G

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Mol	Chain	Res	Type
8	A	1110	G
8	A	1173	U
8	A	1182	G
8	A	1211	C
8	A	1300	G
8	A	1320	C
8	A	1331	G
8	A	1399	C
8	A	1458	U
8	A	1490	A
8	A	1491	G
8	A	1537	G
8	A	1565	C
8	A	1715	G
8	A	1730	C
8	A	1847	G
8	A	2107	G
8	A	2120	G
8	A	2138	G
8	A	2158	A
8	A	2192	U
8	A	2287	A
8	A	2319	G
8	A	2324	U
8	A	2334	U
8	A	2405	G
8	A	2406	A
8	A	2468	A
8	A	2629	U
8	A	2655	G
8	A	2725	A
8	A	2728	U
8	A	2756	U
8	A	2808	G
8	A	2820	A
8	A	2832	U
9	B	44	G
9	B	52	A
9	B	66	A

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
8	G7M	A	2069	8	23,26,27	3.45	10 (43%)	35,39,42	1.63	8 (22%)
8	PSU	A	955	58,8	18,21,22	1.09	1 (5%)	22,30,33	1.85	5 (22%)
34	MA6	a	1519	34	23,26,27	1.46	5 (21%)	34,38,41	2.87	12 (35%)
8	2MG	A	2445	8	23,26,27	2.87	8 (34%)	32,38,41	2.29	12 (37%)
56	5MU	w	54	56	19,22,23	4.80	7 (36%)	28,32,35	3.65	9 (32%)
8	PSU	A	1917	8	18,21,22	1.03	1 (5%)	22,30,33	1.78	4 (18%)
8	PSU	A	2580	8	18,21,22	1.08	2 (11%)	22,30,33	1.92	5 (22%)
8	6MZ	A	1618	8	22,25,26	2.96	5 (22%)	30,36,39	4.33	14 (46%)
8	3TD	A	1915	58,8	18,22,23	4.33	5 (27%)	22,32,35	1.65	3 (13%)
34	2MG	a	1516	34	23,26,27	2.91	9 (39%)	32,38,41	2.27	12 (37%)
8	OMU	A	2552	8	19,22,23	2.92	8 (42%)	26,31,34	1.79	5 (19%)
34	PSU	a	516	34,58	18,21,22	0.93	2 (11%)	22,30,33	1.76	5 (22%)
8	5MC	A	747	8	18,22,23	3.62	7 (38%)	26,32,35	1.13	2 (7%)
56	PSU	w	32	56	18,21,22	1.00	1 (5%)	22,30,33	1.64	5 (22%)
34	G7M	a	527	34	23,26,27	3.57	10 (43%)	35,39,42	1.65	7 (20%)
34	2MG	a	1207	34	23,26,27	2.89	8 (34%)	32,38,41	2.22	11 (34%)
8	PSU	A	2457	8	18,21,22	1.01	2 (11%)	22,30,33	1.95	6 (27%)
8	5MU	A	1939	8	19,22,23	4.67	7 (36%)	28,32,35	3.75	10 (35%)
8	1MG	A	745	8	22,26,27	2.64	5 (22%)	33,39,42	2.01	8 (24%)
34	MA6	a	1518	34	23,26,27	1.47	5 (21%)	34,38,41	2.77	12 (35%)
8	PSU	A	2605	8	18,21,22	1.33	2 (11%)	22,30,33	1.89	4 (18%)
34	UR3	a	1498	34	19,22,23	2.63	6 (31%)	26,32,35	1.49	3 (11%)
8	PSU	A	746	58,8	18,21,22	1.09	2 (11%)	22,30,33	1.78	4 (18%)
56	4SU	w	8	56	18,21,22	3.61	7 (38%)	26,30,33	2.22	4 (15%)
8	5MC	A	1962	8	18,22,23	3.63	7 (38%)	26,32,35	1.03	2 (7%)
56	PSU	w	39	56	18,21,22	1.01	1 (5%)	22,30,33	1.75	3 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
34	5MC	a	1407	34	18,22,23	3.65	7 (38%)	26,32,35	0.99	1 (3%)
8	PSU	A	2604	8	18,21,22	1.33	2 (11%)	22,30,33	1.98	5 (22%)
8	OMG	A	2251	56,8	23,26,27	2.35	9 (39%)	33,38,41	1.76	7 (21%)
8	2MA	A	2503	58,8	22,25,26	3.71	8 (36%)	33,37,40	2.25	8 (24%)
8	PSU	A	1911	8	18,21,22	1.08	2 (11%)	22,30,33	1.77	4 (18%)
8	2MG	A	1835	8	23,26,27	2.88	8 (34%)	32,38,41	2.30	11 (34%)
34	2MG	a	966	34	23,26,27	2.90	8 (34%)	32,38,41	2.29	12 (37%)
34	5MC	a	967	34	18,22,23	3.69	7 (38%)	26,32,35	1.00	2 (7%)
8	OMC	A	2498	58,8	19,22,23	2.86	7 (36%)	26,31,34	0.82	0
8	PSU	A	2504	8	18,21,22	1.02	1 (5%)	22,30,33	1.90	5 (22%)
34	4OC	a	1402	34	20,23,24	2.97	8 (40%)	26,32,35	0.92	2 (7%)
56	PSU	w	55	56	18,21,22	1.04	1 (5%)	22,30,33	1.84	5 (22%)
8	6MZ	A	2030	8	22,25,26	2.94	5 (22%)	30,36,39	4.38	14 (46%)
56	G7M	w	46	56	23,26,27	2.62	8 (34%)	35,39,42	2.20	10 (28%)
56	MIA	w	37	56	28,31,32	2.51	6 (21%)	40,44,47	2.91	17 (42%)

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
8	G7M	A	2069	8	-	1/7/25/26	0/3/3/3
8	PSU	A	955	58,8	-	0/7/25/26	0/2/2/2
34	MA6	a	1519	34	-	1/11/29/30	0/3/3/3
8	2MG	A	2445	8	-	2/9/27/28	0/3/3/3
56	5MU	w	54	56	-	2/7/25/26	0/2/2/2
8	PSU	A	1917	8	-	0/7/25/26	0/2/2/2
8	PSU	A	2580	8	-	0/7/25/26	0/2/2/2
8	6MZ	A	1618	8	-	1/9/27/28	0/3/3/3
8	3TD	A	1915	58,8	-	3/7/25/26	0/2/2/2
34	2MG	a	1516	34	-	0/9/27/28	0/3/3/3
8	OMU	A	2552	8	-	2/9/27/28	0/2/2/2
34	PSU	a	516	34,58	-	3/7/25/26	0/2/2/2
8	5MC	A	747	8	-	4/7/25/26	0/2/2/2
56	PSU	w	32	56	-	2/7/25/26	0/2/2/2
34	G7M	a	527	34	-	3/7/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	2MG	a	1207	34	-	0/9/27/28	0/3/3/3
8	PSU	A	2457	8	-	0/7/25/26	0/2/2/2
8	5MU	A	1939	8	-	0/7/25/26	0/2/2/2
8	1MG	A	745	8	-	0/7/25/26	0/3/3/3
34	MA6	a	1518	34	-	0/11/29/30	0/3/3/3
8	PSU	A	2605	8	-	1/7/25/26	0/2/2/2
34	UR3	a	1498	34	-	2/7/25/26	0/2/2/2
8	PSU	A	746	58,8	-	1/7/25/26	0/2/2/2
56	4SU	w	8	56	-	0/7/25/26	0/2/2/2
8	5MC	A	1962	8	-	0/7/25/26	0/2/2/2
56	PSU	w	39	56	-	3/7/25/26	0/2/2/2
34	5MC	a	1407	34	-	0/7/25/26	0/2/2/2
8	PSU	A	2604	8	-	1/7/25/26	0/2/2/2
8	OMG	A	2251	56,8	-	3/9/27/28	0/3/3/3
8	2MA	A	2503	58,8	-	2/7/25/26	0/3/3/3
8	PSU	A	1911	8	-	0/7/25/26	0/2/2/2
8	2MG	A	1835	8	-	2/9/27/28	0/3/3/3
34	2MG	a	966	34	-	0/9/27/28	0/3/3/3
34	5MC	a	967	34	-	0/7/25/26	0/2/2/2
8	OMC	A	2498	58,8	-	0/9/27/28	0/2/2/2
8	PSU	A	2504	8	-	0/7/25/26	0/2/2/2
34	4OC	a	1402	34	-	2/9/29/30	0/2/2/2
56	PSU	w	55	56	-	1/7/25/26	0/2/2/2
8	6MZ	A	2030	8	-	2/9/27/28	0/3/3/3
56	G7M	w	46	56	-	3/7/25/26	0/3/3/3
56	MIA	w	37	56	-	3/15/33/34	0/3/3/3

All (220) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1915	3TD	C6-C5	13.20	1.50	1.35
8	A	1618	6MZ	C6-N6	12.23	1.47	1.34
8	A	2030	6MZ	C6-N6	11.94	1.47	1.34
8	A	2503	2MA	C4-N3	11.66	1.49	1.34
56	w	54	5MU	C2-N1	10.85	1.55	1.38
56	w	54	5MU	C6-N1	10.39	1.55	1.38
8	A	1939	5MU	C2-N1	10.23	1.54	1.38
8	A	1939	5MU	C6-N1	10.22	1.55	1.38
34	a	527	G7M	C8-N7	10.18	1.51	1.33
8	A	2069	G7M	C8-N7	10.15	1.51	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	w	54	5MU	C4-C5	10.04	1.61	1.44
8	A	1915	3TD	C2-N1	9.53	1.49	1.37
8	A	1939	5MU	C4-C5	9.49	1.60	1.44
34	a	1407	5MC	C6-C5	9.35	1.50	1.34
34	a	967	5MC	C6-C5	9.19	1.49	1.34
8	A	747	5MC	C6-C5	9.00	1.49	1.34
8	A	1962	5MC	C6-C5	8.95	1.49	1.34
56	w	8	4SU	C4-N3	8.27	1.46	1.37
8	A	1939	5MU	C4-N3	-8.05	1.23	1.38
56	w	54	5MU	C4-N3	-7.82	1.24	1.38
34	a	966	2MG	C2-N3	7.36	1.46	1.31
8	A	745	1MG	C2-N2	7.25	1.47	1.34
34	a	1207	2MG	C2-N3	7.25	1.45	1.31
56	w	8	4SU	C2-N1	7.19	1.50	1.38
34	a	1516	2MG	C2-N3	7.17	1.45	1.31
8	A	1835	2MG	C2-N3	7.17	1.45	1.31
56	w	37	MIA	C13-C14	7.15	1.52	1.32
8	A	2445	2MG	C2-N3	6.99	1.45	1.31
8	A	1962	5MC	C4-N3	6.88	1.45	1.34
34	a	967	5MC	C4-N3	6.88	1.45	1.34
8	A	2552	OMU	C2-N1	6.81	1.49	1.38
8	A	747	5MC	C4-N3	6.76	1.45	1.34
8	A	2503	2MA	C2-N3	6.73	1.46	1.34
34	a	1498	UR3	C2-N1	6.64	1.48	1.38
34	a	1402	4OC	C4-N3	6.60	1.44	1.32
56	w	37	MIA	C2-S10	6.56	1.81	1.75
56	w	37	MIA	C6-N6	6.55	1.44	1.34
34	a	1407	5MC	C4-N3	6.50	1.45	1.34
8	A	2552	OMU	C2-N3	6.39	1.49	1.38
34	a	966	2MG	C4-N3	6.37	1.49	1.34
56	w	46	G7M	C4-N3	6.35	1.49	1.34
34	a	1516	2MG	C4-N3	6.33	1.49	1.34
34	a	1207	2MG	C4-N3	6.29	1.49	1.34
8	A	745	1MG	C4-N3	6.21	1.49	1.34
8	A	1835	2MG	C4-N3	6.21	1.49	1.34
8	A	1962	5MC	C2-N3	6.20	1.48	1.36
8	A	2251	OMG	C4-N3	6.18	1.49	1.34
8	A	2445	2MG	C4-N3	6.15	1.48	1.34
8	A	2498	OMC	C2-N3	6.13	1.48	1.36
34	a	967	5MC	C2-N3	6.13	1.48	1.36
34	a	1207	2MG	C2-N2	6.13	1.47	1.33
8	A	747	5MC	C2-N3	6.12	1.48	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	a	1516	2MG	C2-N2	6.11	1.47	1.33
8	A	2498	OMC	C6-C5	6.11	1.49	1.35
34	a	966	2MG	C2-N2	6.08	1.46	1.33
34	a	1402	4OC	C6-C5	6.07	1.49	1.35
34	a	1407	5MC	C2-N3	6.03	1.48	1.36
8	A	1835	2MG	C2-N2	6.01	1.46	1.33
34	a	1498	UR3	C6-C5	5.97	1.48	1.35
8	A	1915	3TD	C6-N1	5.91	1.46	1.36
8	A	2445	2MG	C2-N2	5.88	1.46	1.33
56	w	8	4SU	C6-C5	5.85	1.48	1.35
56	w	54	5MU	C6-C5	5.83	1.44	1.34
56	w	46	G7M	C2-N3	5.80	1.47	1.33
34	a	527	G7M	C2-N3	5.79	1.47	1.33
8	A	1939	5MU	C6-C5	5.75	1.44	1.34
56	w	8	4SU	C2-N3	5.67	1.48	1.38
8	A	2503	2MA	C6-N1	5.67	1.43	1.35
8	A	2498	OMC	C4-N3	5.63	1.45	1.34
8	A	2503	2MA	C2-N1	5.60	1.44	1.34
34	a	1402	4OC	C2-N3	5.57	1.47	1.36
8	A	745	1MG	C2-N3	5.55	1.44	1.34
34	a	527	G7M	C4-N3	5.53	1.47	1.34
34	a	527	G7M	C8-N9	5.43	1.50	1.35
8	A	2069	G7M	C8-N9	5.43	1.50	1.35
8	A	2552	OMU	C6-C5	5.42	1.47	1.35
8	A	2069	G7M	C2-N3	5.38	1.46	1.33
8	A	2069	G7M	C4-N3	5.28	1.46	1.34
56	w	8	4SU	C4-S4	-5.12	1.58	1.68
8	A	2251	OMG	C2-N3	5.05	1.45	1.33
34	a	967	5MC	C4-N4	4.93	1.46	1.34
56	w	46	G7M	C5-N7	-4.86	1.33	1.39
34	a	1407	5MC	C4-N4	4.85	1.46	1.34
8	A	1962	5MC	C4-N4	4.77	1.46	1.34
8	A	747	5MC	C4-N4	4.77	1.46	1.34
8	A	1915	3TD	C2-N3	4.73	1.49	1.38
34	a	527	G7M	C2-N2	4.71	1.45	1.34
34	a	1498	UR3	C2-N3	4.63	1.48	1.39
34	a	527	G7M	C5-N7	4.61	1.44	1.39
34	a	1407	5MC	C6-N1	4.55	1.45	1.38
34	a	1516	2MG	C2-N1	4.54	1.44	1.36
8	A	2069	G7M	C2-N2	4.50	1.44	1.34
34	a	967	5MC	C6-N1	4.43	1.45	1.38
34	a	1207	2MG	C2-N1	4.42	1.43	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	2251	OMG	C2-N2	4.41	1.44	1.34
8	A	1962	5MC	C6-N1	4.40	1.45	1.38
8	A	1835	2MG	C2-N1	4.37	1.43	1.36
56	w	46	G7M	C2-N2	4.36	1.44	1.34
8	A	2445	2MG	C2-N1	4.34	1.43	1.36
34	a	966	2MG	C2-N1	4.34	1.43	1.36
34	a	967	5MC	C2-N1	4.20	1.49	1.40
8	A	747	5MC	C6-N1	4.19	1.45	1.38
8	A	2503	2MA	C5-C6	4.15	1.52	1.41
8	A	747	5MC	C2-N1	4.10	1.48	1.40
8	A	1962	5MC	C2-N1	4.07	1.48	1.40
34	a	1402	4OC	C4-N4	4.06	1.44	1.35
34	a	1407	5MC	C2-N1	4.01	1.48	1.40
8	A	2069	G7M	C5-N7	3.95	1.43	1.39
34	a	1402	4OC	C5-C4	3.88	1.49	1.40
8	A	2498	OMC	C4-N4	3.83	1.42	1.33
56	w	46	G7M	C5-C6	3.81	1.54	1.43
8	A	2552	OMU	C4-N3	3.74	1.45	1.38
34	a	527	G7M	C2-N1	3.72	1.46	1.37
8	A	2503	2MA	C6-N6	-3.67	1.24	1.34
8	A	2445	2MG	C5-N7	-3.60	1.32	1.39
34	a	1402	4OC	C2-N1	3.59	1.47	1.40
8	A	1835	2MG	C5-N7	-3.56	1.32	1.39
8	A	2445	2MG	O6-C6	-3.54	1.16	1.23
8	A	2069	G7M	C2-N1	3.51	1.46	1.37
8	A	1835	2MG	O6-C6	-3.44	1.17	1.23
34	a	1207	2MG	C5-N7	-3.39	1.32	1.39
8	A	2498	OMC	C2-N1	3.38	1.47	1.40
34	a	966	2MG	C5-N7	-3.37	1.32	1.39
8	A	2030	6MZ	C5-C4	-3.37	1.32	1.39
34	a	527	G7M	C6-N1	3.34	1.45	1.38
8	A	747	5MC	O2-C2	-3.33	1.17	1.23
34	a	1516	2MG	O6-C6	-3.33	1.17	1.23
34	a	1516	2MG	C5-N7	-3.32	1.32	1.39
8	A	2498	OMC	C6-N1	3.29	1.45	1.38
34	a	967	5MC	O2-C2	-3.28	1.17	1.23
34	a	966	2MG	O6-C6	-3.27	1.17	1.23
34	a	1207	2MG	O6-C6	-3.24	1.17	1.23
56	w	55	PSU	C6-C5	3.23	1.39	1.35
8	A	745	1MG	C5-N7	-3.23	1.32	1.39
34	a	1518	MA6	C6-N6	3.22	1.46	1.36
8	A	2251	OMG	C5-N7	-3.22	1.32	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1962	5MC	O2-C2	-3.20	1.17	1.23
34	a	527	G7M	C5-C6	3.20	1.52	1.43
34	a	1518	MA6	C8-N9	-3.19	1.31	1.37
8	A	2605	PSU	C6-C5	3.18	1.39	1.35
8	A	1618	6MZ	C5-C4	-3.17	1.33	1.39
8	A	2604	PSU	C6-C5	3.16	1.39	1.35
56	w	8	4SU	C5-C4	3.15	1.46	1.42
34	a	1407	5MC	O2-C2	-3.13	1.17	1.23
8	A	2069	G7M	C6-N1	3.13	1.44	1.38
8	A	2552	OMU	O4-C4	-3.11	1.18	1.24
8	A	1911	PSU	C6-C5	3.11	1.38	1.35
56	w	37	MIA	C5-C4	-3.09	1.33	1.39
8	A	2030	6MZ	C8-N9	-3.08	1.32	1.37
34	a	1402	4OC	O2-C2	-3.06	1.18	1.23
34	a	1519	MA6	C6-N6	3.05	1.45	1.36
8	A	2503	2MA	C5-N7	-3.04	1.33	1.39
8	A	955	PSU	C6-C5	3.04	1.38	1.35
8	A	1917	PSU	C6-C5	3.03	1.38	1.35
34	a	1519	MA6	C8-N9	-3.02	1.32	1.37
8	A	2069	G7M	C5-C6	3.00	1.51	1.43
34	a	1402	4OC	C6-N1	2.96	1.45	1.38
8	A	2504	PSU	C6-C5	2.94	1.38	1.35
8	A	1618	6MZ	C8-N9	-2.94	1.32	1.37
8	A	2498	OMC	O2-C2	-2.92	1.18	1.23
34	a	1519	MA6	C5-C4	-2.92	1.33	1.39
34	a	1519	MA6	C5-N7	-2.92	1.33	1.39
34	a	1518	MA6	C5-N7	-2.90	1.33	1.39
56	w	32	PSU	C6-C5	2.89	1.38	1.35
8	A	2580	PSU	C6-C5	2.85	1.38	1.35
56	w	37	MIA	C5-N7	-2.84	1.33	1.39
34	a	1498	UR3	C6-N1	2.82	1.44	1.38
8	A	1915	3TD	C4-N3	2.82	1.46	1.40
8	A	746	PSU	C6-C5	2.79	1.38	1.35
8	A	1939	5MU	O2-C2	-2.79	1.17	1.23
34	a	1518	MA6	C5-C4	-2.78	1.33	1.39
56	w	46	G7M	C2-N1	2.75	1.44	1.37
8	A	1939	5MU	O4-C4	-2.74	1.18	1.23
8	A	2030	6MZ	C4-N9	-2.73	1.31	1.37
56	w	54	5MU	O4-C4	-2.72	1.18	1.23
8	A	2069	G7M	O6-C6	-2.69	1.18	1.23
56	w	39	PSU	C6-C5	2.67	1.38	1.35
8	A	2604	PSU	C4-N3	-2.67	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	2552	OMU	C6-N1	2.66	1.44	1.38
8	A	2552	OMU	O2-C2	-2.64	1.18	1.23
34	a	527	G7M	O6-C6	-2.63	1.18	1.23
8	A	2605	PSU	C4-N3	-2.60	1.34	1.38
8	A	745	1MG	C5-C6	2.59	1.52	1.45
8	A	1618	6MZ	C4-N9	-2.57	1.32	1.37
56	w	8	4SU	O2-C2	-2.57	1.18	1.23
56	w	54	5MU	O2-C2	-2.54	1.18	1.23
8	A	2251	OMG	O6-C6	-2.50	1.18	1.23
56	w	46	G7M	O6-C6	-2.49	1.18	1.23
56	w	46	G7M	C6-N1	2.48	1.43	1.38
34	a	966	2MG	C5-C6	2.44	1.53	1.44
8	A	2251	OMG	C5-C6	2.44	1.53	1.44
34	a	1498	UR3	O2-C2	-2.39	1.18	1.22
34	a	1207	2MG	C5-C6	2.38	1.53	1.44
8	A	2251	OMG	C2-N1	2.35	1.43	1.37
56	w	37	MIA	C8-N9	-2.35	1.33	1.37
34	a	1516	2MG	C5-C6	2.35	1.53	1.44
8	A	1835	2MG	C5-C6	2.34	1.53	1.44
34	a	1516	2MG	C6-N1	2.33	1.43	1.38
34	a	516	PSU	C6-C5	2.33	1.38	1.35
34	a	1498	UR3	O4-C4	-2.33	1.18	1.23
8	A	2030	6MZ	C6-N1	-2.32	1.31	1.35
8	A	2457	PSU	C6-C5	2.32	1.38	1.35
8	A	2503	2MA	C4-N9	-2.31	1.32	1.37
8	A	2445	2MG	C4-N9	-2.25	1.32	1.38
8	A	2251	OMG	C6-N1	2.24	1.43	1.38
34	a	1207	2MG	C6-N1	2.23	1.43	1.38
8	A	746	PSU	C4-C5	-2.23	1.37	1.44
8	A	2445	2MG	C5-C6	2.22	1.52	1.44
8	A	2580	PSU	O4'-C1'	-2.20	1.40	1.43
8	A	2552	OMU	C5-C4	2.17	1.48	1.43
8	A	2251	OMG	C4-N9	-2.16	1.32	1.38
34	a	966	2MG	C6-N1	2.15	1.42	1.38
8	A	1835	2MG	C6-N1	2.13	1.42	1.38
8	A	1618	6MZ	C6-N1	-2.12	1.31	1.35
34	a	1518	MA6	C8-N7	2.08	1.35	1.31
8	A	1911	PSU	C4-C5	-2.07	1.38	1.44
8	A	2457	PSU	O4'-C1'	-2.07	1.41	1.43
34	a	1519	MA6	C8-N7	2.06	1.35	1.31
34	a	1516	2MG	C4-N9	-2.03	1.32	1.38
34	a	516	PSU	C4-C5	-2.01	1.38	1.44

All (278) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	2030	6MZ	C4-N9-C8	13.40	120.25	105.73
8	A	1618	6MZ	C4-N9-C8	13.24	120.08	105.73
8	A	1939	5MU	C5-C4-N3	12.36	125.86	115.31
56	w	54	5MU	C5-C4-N3	12.15	125.69	115.31
8	A	2030	6MZ	N9-C8-N7	-10.77	99.18	113.91
8	A	1939	5MU	C5-C6-N1	-10.72	112.31	123.34
8	A	1618	6MZ	N9-C8-N7	-10.48	99.58	113.91
56	w	54	5MU	C5-C6-N1	-10.32	112.72	123.34
34	a	1519	MA6	N1-C6-N6	-9.96	106.19	117.08
56	w	37	MIA	C12-C13-C14	-9.95	107.78	127.14
34	a	1518	MA6	N1-C6-N6	-9.46	106.74	117.08
8	A	1618	6MZ	C5-C6-N1	8.59	127.35	118.20
8	A	2030	6MZ	C5-C6-N1	8.50	127.25	118.20
56	w	8	4SU	C4-N3-C2	-7.69	119.87	127.34
8	A	1835	2MG	C2-N3-C4	6.71	120.36	112.04
8	A	1618	6MZ	N3-C4-N9	6.66	138.06	127.08
56	w	37	MIA	C5-C4-N3	-6.63	119.73	127.19
34	a	1207	2MG	C2-N3-C4	6.49	120.09	112.04
34	a	1516	2MG	C2-N3-C4	6.48	120.07	112.04
34	a	966	2MG	C2-N3-C4	6.38	119.95	112.04
8	A	2445	2MG	C2-N3-C4	6.12	119.62	112.04
8	A	2503	2MA	N9-C8-N7	-6.04	105.66	113.91
8	A	2604	PSU	N1-C2-N3	6.03	121.96	115.13
8	A	2030	6MZ	N3-C4-N9	6.02	137.00	127.08
8	A	2605	PSU	N1-C2-N3	5.98	121.91	115.13
8	A	2030	6MZ	C9-N6-C6	-5.90	117.79	122.87
8	A	2503	2MA	C5-C4-N3	-5.71	120.77	127.19
34	a	1519	MA6	N1-C2-N3	-5.68	119.71	128.60
8	A	1939	5MU	O4-C4-C5	-5.54	118.47	124.90
34	a	1518	MA6	N1-C2-N3	-5.51	119.98	128.60
8	A	1835	2MG	C5-C4-N3	-5.45	119.62	128.46
56	w	8	4SU	C5-C4-N3	5.43	119.72	114.69
8	A	2030	6MZ	N1-C2-N3	-5.38	120.18	128.60
56	w	46	G7M	CN7-N7-C5	5.35	133.41	126.77
56	w	37	MIA	C11-S10-C2	5.28	106.21	102.27
8	A	1618	6MZ	N1-C2-N3	-5.27	120.36	128.60
34	a	966	2MG	C5-C4-N3	-5.23	119.98	128.46
8	A	1939	5MU	C4-N3-C2	-5.19	120.64	127.35
34	a	1519	MA6	C5-C4-N3	-5.18	119.99	126.75
34	a	1207	2MG	C5-C4-N3	-5.17	120.08	128.46
8	A	2552	OMU	C4-N3-C2	-5.16	119.77	126.58
8	A	1915	3TD	N1-C2-N3	5.08	120.15	116.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	745	1MG	C5-C4-N3	-5.06	120.25	128.46
8	A	745	1MG	C1'-N9-C4	-5.05	111.52	126.50
34	a	1516	2MG	C5-C4-N3	-5.03	120.29	128.46
8	A	1618	6MZ	C9-N6-C6	-5.03	118.54	122.87
8	A	2504	PSU	N1-C2-N3	5.02	120.82	115.13
34	a	1518	MA6	C5-C4-N3	-5.01	120.21	126.75
8	A	2445	2MG	C5-C4-N3	-5.00	120.35	128.46
56	w	54	5MU	O4-C4-C5	-4.98	119.13	124.90
8	A	2445	2MG	C2-N1-C6	-4.95	118.78	124.48
8	A	2251	OMG	C5-C4-N3	-4.91	120.50	128.46
8	A	2457	PSU	N1-C2-N3	4.90	120.68	115.13
8	A	2457	PSU	C4-N3-C2	-4.89	119.29	126.34
8	A	2580	PSU	N1-C2-N3	4.85	120.63	115.13
8	A	746	PSU	C4-N3-C2	-4.84	119.36	126.34
8	A	1618	6MZ	C5-C4-N9	-4.84	100.16	105.78
8	A	1835	2MG	C2-N1-C6	-4.80	118.95	124.48
56	w	54	5MU	C4-N3-C2	-4.78	121.17	127.35
8	A	955	PSU	C4-N3-C2	-4.77	119.47	126.34
8	A	955	PSU	N1-C2-N3	4.71	120.46	115.13
34	a	1519	MA6	C5-C6-N6	4.70	133.49	125.30
56	w	39	PSU	C4-N3-C2	-4.68	119.59	126.34
8	A	2503	2MA	C4-N9-C8	4.68	110.80	105.73
56	w	55	PSU	N1-C2-N3	4.67	120.42	115.13
8	A	1939	5MU	N3-C2-N1	4.63	121.04	114.89
8	A	2030	6MZ	C5-N7-C8	4.62	110.07	103.51
8	A	1911	PSU	C4-N3-C2	-4.61	119.69	126.34
8	A	2030	6MZ	C5-C4-N9	-4.60	100.43	105.78
8	A	1917	PSU	C4-N3-C2	-4.58	119.74	126.34
34	a	1518	MA6	C5-C6-N6	4.57	133.27	125.30
34	a	1519	MA6	N9-C8-N7	-4.57	107.66	113.91
8	A	2504	PSU	C4-N3-C2	-4.55	119.79	126.34
8	A	2580	PSU	C4-N3-C2	-4.55	119.79	126.34
56	w	37	MIA	C16-C14-C13	-4.52	109.59	122.65
34	a	966	2MG	C2-N1-C6	-4.50	119.30	124.48
34	a	516	PSU	C4-N3-C2	-4.48	119.88	126.34
56	w	37	MIA	C15-C14-C13	-4.48	109.71	122.65
56	w	39	PSU	N1-C2-N3	4.48	120.20	115.13
34	a	1518	MA6	N9-C8-N7	-4.47	107.80	113.91
34	a	1498	UR3	C4-N3-C2	-4.45	120.38	124.56
8	A	1618	6MZ	C5-N7-C8	4.42	109.78	103.51
8	A	745	1MG	C1'-N9-C8	4.40	139.22	126.70
8	A	1917	PSU	N1-C2-N3	4.40	120.11	115.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	746	PSU	N1-C2-N3	4.40	120.11	115.13
34	a	1516	2MG	C2-N1-C6	-4.39	119.43	124.48
56	w	46	G7M	C2-N3-C4	4.37	120.08	112.30
34	a	527	G7M	C2-N3-C4	4.36	120.06	112.30
8	A	1911	PSU	N1-C2-N3	4.35	120.06	115.13
34	a	1207	2MG	C2-N1-C6	-4.35	119.48	124.48
56	w	32	PSU	C4-N3-C2	-4.35	120.08	126.34
56	w	46	G7M	C5-C4-N3	-4.33	119.84	128.15
8	A	2503	2MA	N3-C4-N9	4.31	132.97	126.99
56	w	55	PSU	C4-N3-C2	-4.30	120.14	126.34
8	A	2251	OMG	C2-N3-C4	4.28	119.92	112.30
56	w	37	MIA	N9-C8-N7	-4.27	108.07	113.91
56	w	54	5MU	N3-C2-N1	4.20	120.46	114.89
34	a	516	PSU	N1-C2-N3	4.19	119.88	115.13
56	w	46	G7M	C1'-N9-C4	-4.13	114.23	126.50
56	w	32	PSU	N1-C2-N3	4.10	119.78	115.13
8	A	2069	G7M	C2-N3-C4	4.08	119.56	112.30
56	w	46	G7M	CN7-N7-C8	-4.07	118.55	124.84
8	A	1915	3TD	C4-N3-C2	-4.04	120.23	124.61
56	w	54	5MU	C5M-C5-C6	-3.96	117.56	122.85
8	A	1618	6MZ	C1'-N9-C8	-3.94	118.24	127.14
8	A	2605	PSU	C4-N3-C2	-3.94	120.67	126.34
8	A	2604	PSU	C4-N3-C2	-3.88	120.75	126.34
34	a	527	G7M	C5-C6-N1	3.87	119.87	111.79
56	w	46	G7M	C5-C6-N1	3.85	119.83	111.79
56	w	54	5MU	C5M-C5-C4	3.84	122.99	118.77
56	w	37	MIA	C4-C5-C6	3.82	119.77	116.81
8	A	2552	OMU	N3-C2-N1	3.81	119.95	114.89
8	A	1618	6MZ	C5-C4-N3	-3.81	121.78	126.75
34	a	527	G7M	C5-C4-N3	-3.78	120.91	128.15
8	A	2503	2MA	C5-N7-C8	3.76	108.85	103.51
56	w	8	4SU	C5-C4-S4	-3.72	119.67	124.47
56	w	37	MIA	N3-C4-N9	3.71	132.14	126.99
34	a	1519	MA6	C2-N3-C4	3.68	120.44	111.75
8	A	2069	G7M	C5-C6-N1	3.66	119.43	111.79
8	A	1939	5MU	C5M-C5-C6	-3.65	117.97	122.85
8	A	1618	6MZ	C2-N3-C4	3.63	120.32	111.75
56	w	8	4SU	N3-C2-N1	3.61	119.69	114.89
8	A	2069	G7M	C5-C4-N3	-3.56	121.32	128.15
8	A	745	1MG	C2-N3-C4	3.55	119.96	111.98
34	a	1518	MA6	C2-N1-C6	3.54	120.10	111.75
34	a	1498	UR3	C1'-N1-C2	3.52	122.93	116.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	a	1518	MA6	C2-N3-C4	3.49	119.99	111.75
8	A	2605	PSU	O2-C2-N1	-3.48	118.96	122.79
8	A	1835	2MG	N9-C4-N3	3.47	132.91	125.94
56	w	46	G7M	O6-C6-C5	-3.47	120.23	128.06
8	A	2604	PSU	O2-C2-N1	-3.47	118.97	122.79
34	a	1519	MA6	C2-N1-C6	3.45	119.91	111.75
8	A	2030	6MZ	C2-N3-C4	3.44	119.88	111.75
34	a	1518	MA6	C4-C5-C6	3.43	119.72	115.88
34	a	527	G7M	O6-C6-C5	-3.42	120.33	128.06
56	w	37	MIA	N3-C2-N1	-3.41	120.69	126.95
8	A	2503	2MA	N3-C2-N1	-3.40	119.47	125.72
8	A	2030	6MZ	C4-C5-C6	-3.37	114.19	116.81
34	a	1519	MA6	C4-C5-C6	3.35	119.63	115.88
8	A	2552	OMU	C5-C4-N3	3.33	119.83	114.84
8	A	745	1MG	N9-C8-N7	-3.30	107.17	113.39
56	w	46	G7M	C1'-N9-C8	3.28	137.81	126.74
8	A	2445	2MG	N9-C8-N7	-3.27	107.24	113.39
8	A	2445	2MG	CM2-N2-C2	-3.26	116.67	123.86
8	A	2069	G7M	O6-C6-C5	-3.24	120.74	128.06
34	a	967	5MC	C5-C6-N1	-3.24	120.01	123.34
34	a	1516	2MG	C1'-N9-C4	-3.23	116.90	126.50
8	A	1939	5MU	C5M-C5-C4	3.22	122.31	118.77
8	A	2445	2MG	C1'-N9-C4	-3.21	116.95	126.50
8	A	747	5MC	C5-C6-N1	-3.21	120.04	123.34
8	A	2030	6MZ	C5-C4-N3	-3.20	122.57	126.75
34	a	1519	MA6	C5-N7-C8	3.19	108.04	103.51
56	w	37	MIA	C12-N6-C6	-3.18	117.83	122.55
34	a	966	2MG	N9-C4-N3	3.18	132.33	125.94
8	A	2580	PSU	O2-C2-N1	-3.18	119.29	122.79
34	a	1207	2MG	N9-C4-N3	3.16	132.29	125.94
8	A	745	1MG	N9-C4-N3	3.16	132.28	125.94
34	a	1518	MA6	C5-N7-C8	3.14	107.97	103.51
8	A	2030	6MZ	C6-C5-N7	3.09	135.74	132.39
56	w	37	MIA	C5-N7-C8	3.08	107.89	103.51
56	w	46	G7M	N9-C4-N3	3.08	132.12	125.94
34	a	1519	MA6	N3-C4-N9	3.07	132.15	127.08
34	a	1518	MA6	N3-C4-N9	3.07	132.14	127.08
34	a	1516	2MG	N9-C8-N7	-3.06	107.63	113.39
56	w	55	PSU	O2-C2-N1	-3.06	119.42	122.79
8	A	2251	OMG	C2-N1-C6	-3.06	119.52	125.10
56	w	46	G7M	C2-N1-C6	-3.05	119.54	125.10
34	a	1407	5MC	C5-C6-N1	-3.04	120.21	123.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	2445	2MG	N9-C4-N3	3.03	132.02	125.94
8	A	2030	6MZ	C1'-N9-C8	-3.02	120.31	127.14
34	a	966	2MG	C1'-N9-C4	-3.01	117.57	126.50
8	A	2030	6MZ	C4-N9-C1'	-3.01	119.43	126.59
8	A	1939	5MU	O2-C2-N1	-3.00	118.79	122.79
34	a	966	2MG	N9-C8-N7	-3.00	107.74	113.39
34	a	1516	2MG	N9-C4-N3	2.98	131.93	125.94
34	a	1207	2MG	C1'-N9-C4	-2.96	117.70	126.50
8	A	1835	2MG	CM2-N2-C2	-2.95	117.34	123.86
8	A	2552	OMU	C1'-N1-C2	2.94	122.90	117.57
8	A	1835	2MG	N9-C8-N7	-2.92	107.89	113.39
8	A	2457	PSU	O2-C2-N1	-2.92	119.58	122.79
56	w	37	MIA	C2-N3-C4	2.92	120.03	112.35
56	w	37	MIA	S10-C2-N1	2.89	126.03	116.01
8	A	2251	OMG	N9-C8-N7	-2.89	107.95	113.39
34	a	516	PSU	O2-C2-N1	-2.82	119.68	122.79
8	A	2251	OMG	N9-C4-N3	2.82	131.61	125.94
8	A	2445	2MG	C5-C6-N1	2.82	120.35	113.19
8	A	2580	PSU	C6-N1-C2	-2.81	119.81	122.68
34	a	1207	2MG	N9-C8-N7	-2.81	108.10	113.39
8	A	1835	2MG	C5-C6-N1	2.78	120.25	113.19
8	A	1917	PSU	O2-C2-N1	-2.78	119.73	122.79
34	a	966	2MG	CM2-N2-C2	-2.77	117.74	123.86
34	a	1516	2MG	C1'-N9-C8	2.77	134.58	126.70
8	A	1618	6MZ	C4-C5-C6	-2.76	114.66	116.81
8	A	2504	PSU	C6-N1-C2	-2.75	119.87	122.68
8	A	2552	OMU	O4-C4-C5	-2.73	120.36	125.16
56	w	55	PSU	C6-C5-C4	2.70	120.09	118.20
34	a	966	2MG	C5-C6-N1	2.70	120.05	113.19
34	a	527	G7M	C2-N1-C6	-2.70	120.18	125.10
34	a	1516	2MG	C5-C6-N1	2.70	120.03	113.19
8	A	2251	OMG	C5-C6-N1	2.68	119.99	113.19
34	a	1207	2MG	C5-C6-N1	2.67	119.97	113.19
8	A	2604	PSU	C3'-C2'-C1'	2.67	104.74	101.64
34	a	1518	MA6	C4-N9-C8	2.64	108.59	105.73
8	A	1962	5MC	C5-C6-N1	-2.63	120.63	123.34
8	A	2069	G7M	C2-N1-C6	-2.63	120.30	125.10
8	A	2445	2MG	C1'-N9-C8	2.61	134.12	126.70
56	w	55	PSU	C6-N1-C2	-2.61	120.02	122.68
34	a	1207	2MG	C1'-N9-C8	2.60	134.11	126.70
8	A	1835	2MG	O6-C6-C5	-2.58	119.75	126.60
8	A	2445	2MG	O6-C6-C5	-2.58	119.76	126.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	w	54	5MU	O4-C4-N3	-2.57	115.19	120.12
8	A	2457	PSU	C6-C5-C4	2.57	120.00	118.20
8	A	745	1MG	C5-C6-N1	2.57	119.88	114.91
34	a	966	2MG	C1'-N9-C8	2.55	133.97	126.70
34	a	1519	MA6	C4-N9-C8	2.55	108.49	105.73
34	a	1516	2MG	O6-C6-C5	-2.54	119.86	126.60
8	A	2504	PSU	O2-C2-N1	-2.53	120.01	122.79
34	a	1516	2MG	N1-C2-N3	-2.50	120.09	123.95
8	A	2457	PSU	C6-N1-C2	-2.48	120.14	122.68
34	a	1207	2MG	O6-C6-C5	-2.47	120.05	126.60
34	a	516	PSU	C6-N1-C2	-2.46	120.17	122.68
8	A	2251	OMG	O6-C6-C5	-2.44	120.12	126.60
34	a	1498	UR3	C6-N1-C2	-2.44	119.61	121.79
8	A	2069	G7M	N9-C8-N7	-2.44	106.19	112.21
8	A	1835	2MG	C1'-N9-C4	-2.43	119.27	126.50
34	a	1207	2MG	N1-C2-N3	-2.43	120.19	123.95
56	w	37	MIA	N6-C6-N1	-2.43	115.40	118.50
8	A	1911	PSU	O2-C2-N1	-2.40	120.15	122.79
8	A	747	5MC	CM5-C5-C6	-2.40	119.64	122.85
34	a	966	2MG	O6-C6-C5	-2.39	120.27	126.60
34	a	1516	2MG	CM2-N2-C2	-2.38	118.60	123.86
8	A	2580	PSU	O4'-C1'-C2'	2.37	108.48	105.14
8	A	1618	6MZ	C6-C5-N7	2.36	134.95	132.39
8	A	746	PSU	C6-C5-C4	2.36	119.85	118.20
8	A	2504	PSU	C6-C5-C4	2.35	119.84	118.20
8	A	1835	2MG	N1-C2-N3	-2.33	120.35	123.95
8	A	1939	5MU	O4-C4-N3	-2.32	115.67	120.12
8	A	955	PSU	C6-N1-C2	-2.32	120.31	122.68
8	A	955	PSU	O2-C2-N1	-2.32	120.24	122.79
34	a	527	G7M	N9-C8-N7	-2.30	106.51	112.21
8	A	1911	PSU	C6-N1-C2	-2.30	120.34	122.68
8	A	1917	PSU	C6-N1-C2	-2.29	120.34	122.68
34	a	966	2MG	N1-C2-N3	-2.28	120.43	123.95
56	w	32	PSU	O2-C2-N1	-2.27	120.29	122.79
8	A	745	1MG	C8-N7-C5	2.25	108.32	104.24
56	w	39	PSU	C6-N1-C2	-2.24	120.39	122.68
34	a	1207	2MG	CM2-N2-C2	-2.21	118.99	123.86
8	A	2457	PSU	O4'-C1'-C2'	2.20	108.25	105.14
34	a	1519	MA6	C4-C5-N7	-2.20	107.94	110.62
8	A	2069	G7M	C5-C4-N9	2.19	110.68	105.89
56	w	54	5MU	O2-C2-N1	-2.18	119.89	122.79
56	w	37	MIA	C16-C14-C15	-2.18	109.80	114.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	a	1402	4OC	C6-C5-C4	2.16	119.60	116.96
34	a	1518	MA6	C4-C5-N7	-2.15	108.00	110.62
34	a	966	2MG	C8-N7-C5	2.15	108.13	104.24
56	w	32	PSU	C6-N1-C2	-2.14	120.49	122.68
56	w	37	MIA	C4-C5-N7	-2.14	108.01	110.62
8	A	2445	2MG	C8-N7-C5	2.12	108.08	104.24
8	A	2503	2MA	N6-C6-N1	2.12	120.03	117.03
8	A	746	PSU	O2-C2-N1	-2.10	120.48	122.79
34	a	1516	2MG	C8-N7-C5	2.09	108.03	104.24
8	A	1618	6MZ	C4-N9-C1'	-2.09	121.62	126.59
34	a	516	PSU	O4'-C1'-C2'	2.08	108.08	105.14
8	A	2445	2MG	N1-C2-N3	-2.07	120.75	123.95
8	A	955	PSU	C6-C5-C4	2.07	119.64	118.20
8	A	1962	5MC	CM5-C5-C6	-2.06	120.10	122.85
8	A	1915	3TD	O4'-C1'-C2'	2.05	108.04	105.14
34	a	1402	4OC	CM4-N4-C4	-2.05	118.45	122.45
8	A	2503	2MA	CM2-C2-N1	2.03	120.32	117.15
8	A	2069	G7M	N2-C2-N1	2.03	121.03	116.71
56	w	32	PSU	O4'-C1'-C2'	2.02	108.00	105.14
34	a	967	5MC	CM5-C5-C6	-2.02	120.15	122.85
56	w	37	MIA	C5-C4-N9	2.01	108.12	105.78
34	a	527	G7M	C5-C4-N9	2.01	110.30	105.89
8	A	2605	PSU	C5-C6-N1	-2.01	119.09	122.11
8	A	1939	5MU	C6-C5-C4	2.01	119.71	118.03
8	A	1835	2MG	C8-N7-C5	2.01	107.87	104.24
8	A	2604	PSU	C5-C6-N1	-2.00	119.11	122.11

There are no chirality outliers.

All (50) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	1618	6MZ	N1-C6-N6-C9
8	A	1915	3TD	C2'-C1'-C5-C4
8	A	1915	3TD	O4'-C1'-C5-C4
8	A	1915	3TD	O4'-C1'-C5-C6
8	A	2030	6MZ	O4'-C4'-C5'-O5'
8	A	2251	OMG	O4'-C4'-C5'-O5'
8	A	2251	OMG	C3'-C4'-C5'-O5'
8	A	2251	OMG	C1'-C2'-O2'-CM2
8	A	2445	2MG	C3'-C4'-C5'-O5'
8	A	2552	OMU	O4'-C1'-N1-C2
8	A	2552	OMU	O4'-C1'-N1-C6

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Mol	Chain	Res	Type	Atoms
34	a	1498	UR3	O4'-C1'-N1-C6
34	a	1498	UR3	O4'-C1'-N1-C2
56	w	32	PSU	O4'-C1'-C5-C4
56	w	32	PSU	O4'-C1'-C5-C6
56	w	37	MIA	C12-C13-C14-C15
56	w	37	MIA	C12-C13-C14-C16
56	w	39	PSU	O4'-C1'-C5-C4
56	w	39	PSU	C2'-C1'-C5-C6
56	w	39	PSU	O4'-C1'-C5-C6
56	w	46	G7M	O4'-C4'-C5'-O5'
8	A	2069	G7M	O4'-C4'-C5'-O5'
8	A	2503	2MA	O4'-C4'-C5'-O5'
34	a	1402	4OC	O4'-C4'-C5'-O5'
56	w	46	G7M	C3'-C4'-C5'-O5'
8	A	2030	6MZ	C3'-C4'-C5'-O5'
8	A	2445	2MG	O4'-C4'-C5'-O5'
34	a	527	G7M	C3'-C4'-C5'-O5'
34	a	1402	4OC	C3'-C4'-C5'-O5'
8	A	747	5MC	C3'-C4'-C5'-O5'
8	A	1835	2MG	O4'-C4'-C5'-O5'
8	A	1835	2MG	C3'-C4'-C5'-O5'
8	A	2503	2MA	C3'-C4'-C5'-O5'
34	a	527	G7M	O4'-C4'-C5'-O5'
34	a	516	PSU	O4'-C4'-C5'-O5'
8	A	747	5MC	C4'-C5'-O5'-P
34	a	1519	MA6	C4'-C5'-O5'-P
8	A	747	5MC	O4'-C4'-C5'-O5'
34	a	516	PSU	C3'-C4'-C5'-O5'
56	w	37	MIA	C3'-C4'-C5'-O5'
8	A	2604	PSU	C3'-C4'-C5'-O5'
34	a	527	G7M	C4'-C5'-O5'-P
8	A	2605	PSU	O4'-C1'-C5-C4
34	a	516	PSU	O4'-C1'-C5-C4
56	w	55	PSU	O4'-C1'-C5-C4
56	w	54	5MU	C3'-C4'-C5'-O5'
8	A	747	5MC	C2'-C1'-N1-C2
8	A	746	PSU	O4'-C1'-C5-C6
56	w	46	G7M	C4'-C5'-O5'-P
56	w	54	5MU	O4'-C4'-C5'-O5'

There are no ring outliers.

18 monomers are involved in 33 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
34	a	1519	MA6	1	0
8	A	2445	2MG	3	0
8	A	1915	3TD	2	0
34	a	1516	2MG	1	0
8	A	2552	OMU	1	0
34	a	516	PSU	3	0
8	A	747	5MC	1	0
34	a	1207	2MG	1	0
34	a	1518	MA6	2	0
8	A	2605	PSU	3	0
34	a	1498	UR3	2	0
56	w	8	4SU	1	0
8	A	2251	OMG	2	0
8	A	2503	2MA	1	0
34	a	966	2MG	4	0
8	A	2498	OMC	1	0
34	a	1402	4OC	1	0
8	A	2030	6MZ	4	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 337 ligands modelled in this entry, 337 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

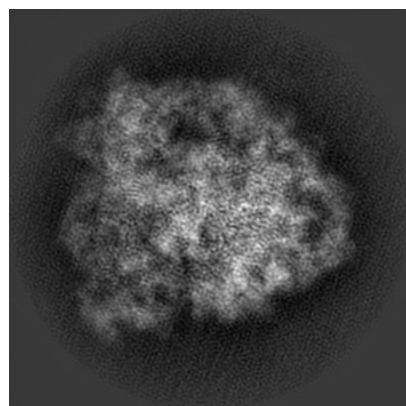
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10905. These allow visual inspection of the internal detail of the map and identification of artifacts.

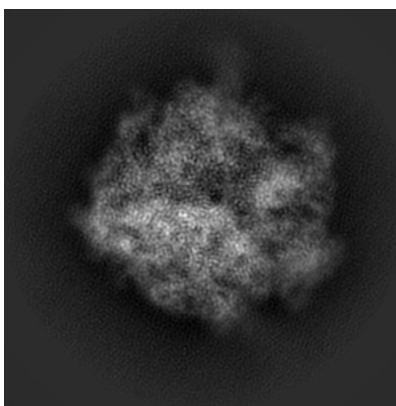
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

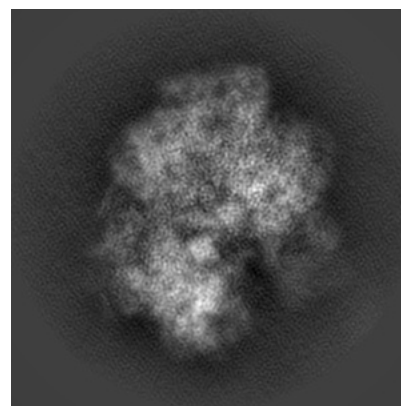
6.1.1 Primary map



X

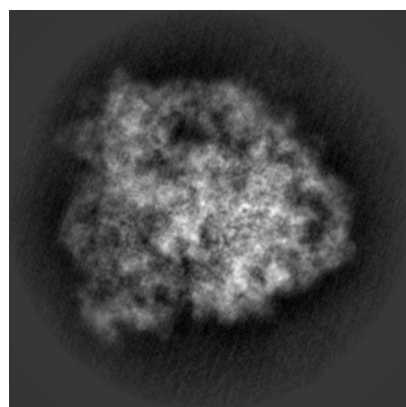


Y

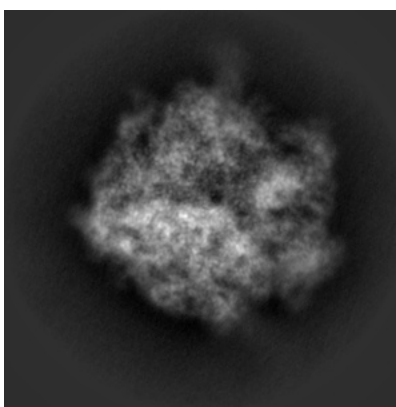


Z

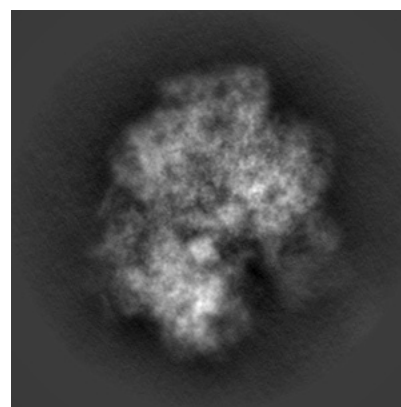
6.1.2 Raw map



X



Y

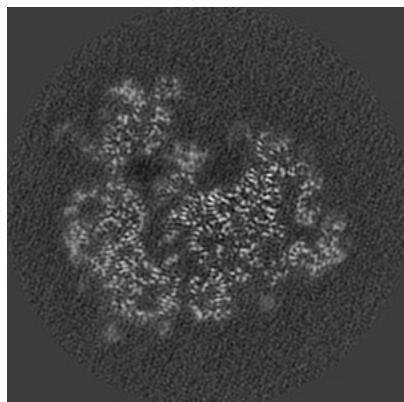


Z

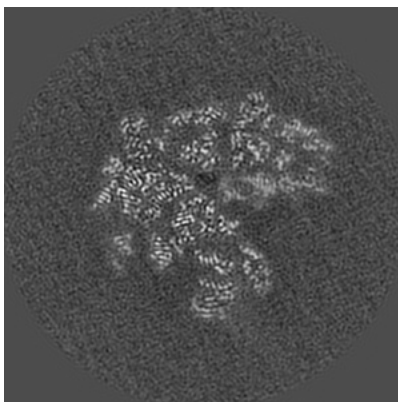
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

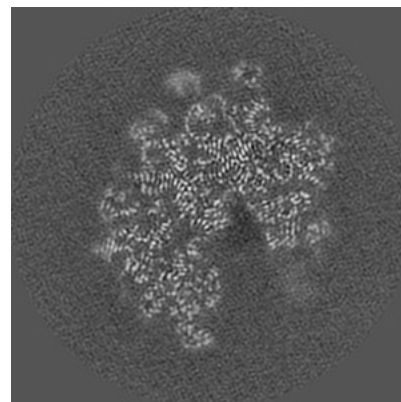
6.2.1 Primary map



X Index: 256

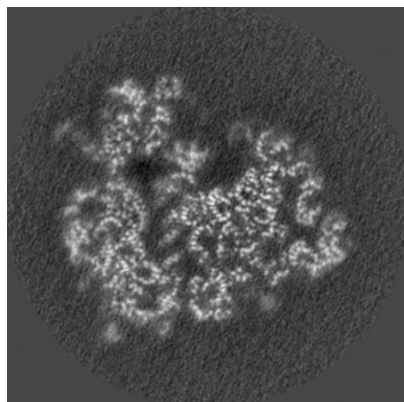


Y Index: 256

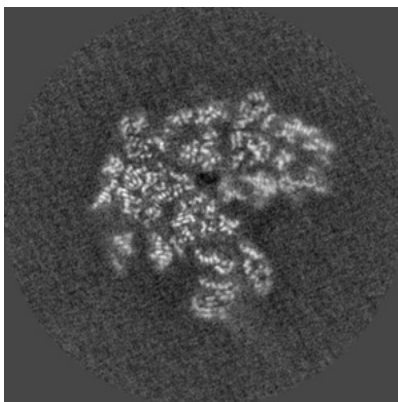


Z Index: 256

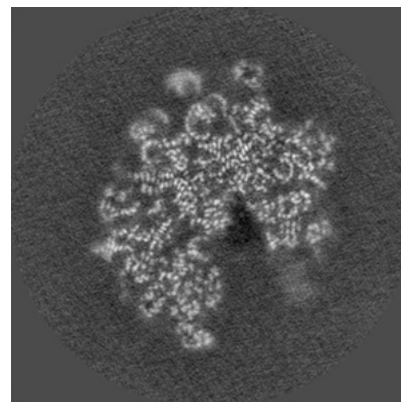
6.2.2 Raw map



X Index: 144



Y Index: 144

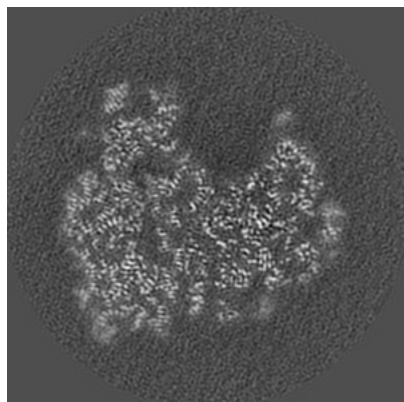


Z Index: 144

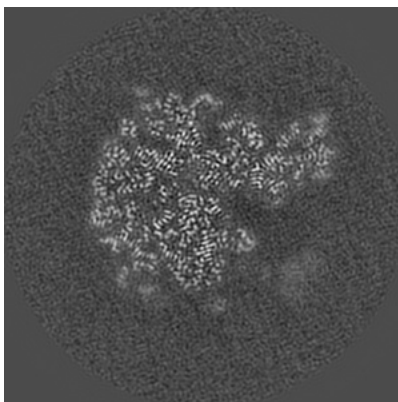
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

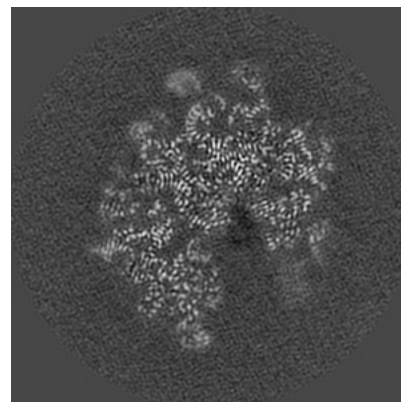
6.3.1 Primary map



X Index: 241

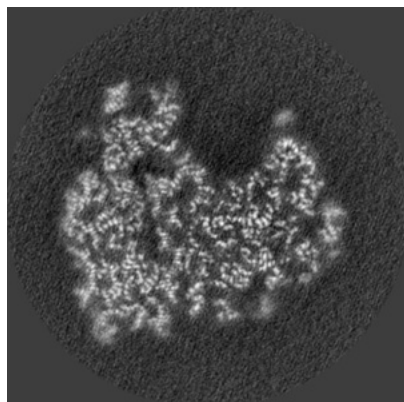


Y Index: 285

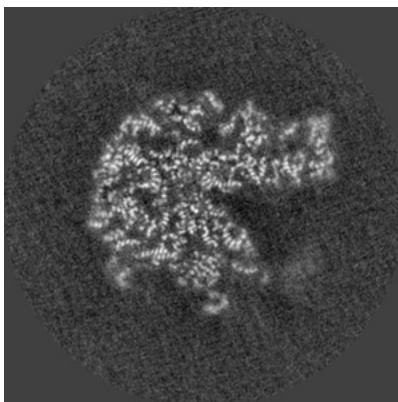


Z Index: 258

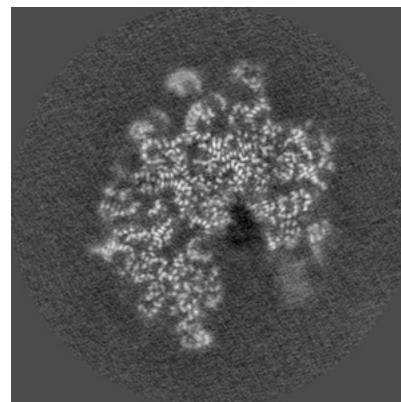
6.3.2 Raw map



X Index: 136



Y Index: 157

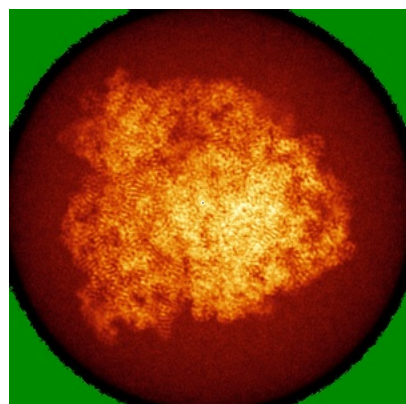


Z Index: 145

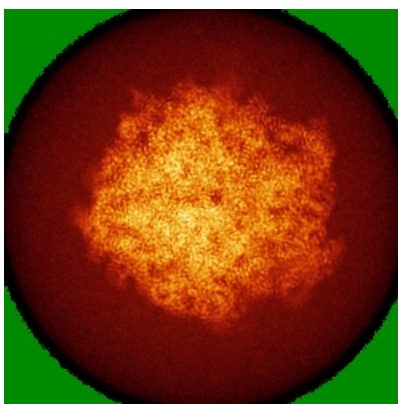
The images above show the largest variance slices of the map in three orthogonal directions.

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

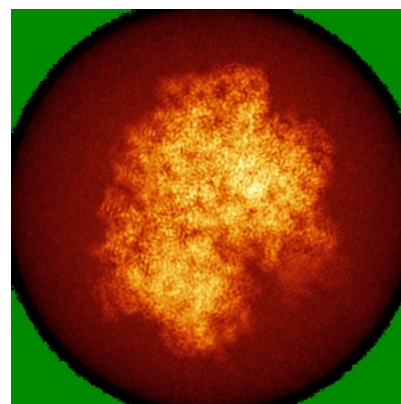
6.4.1 Primary map



X

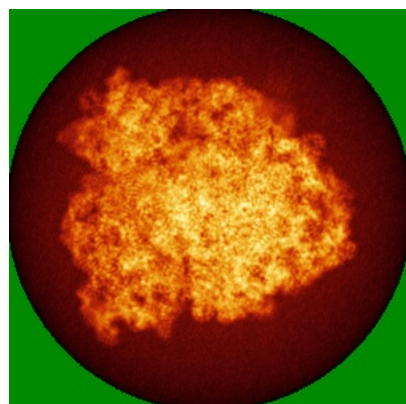


Y

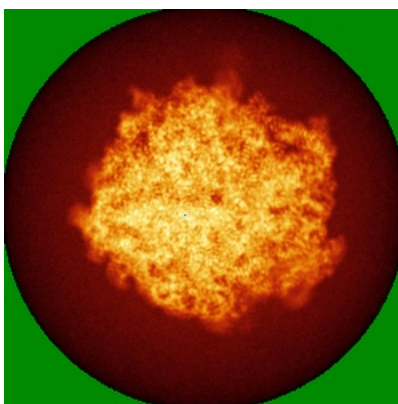


Z

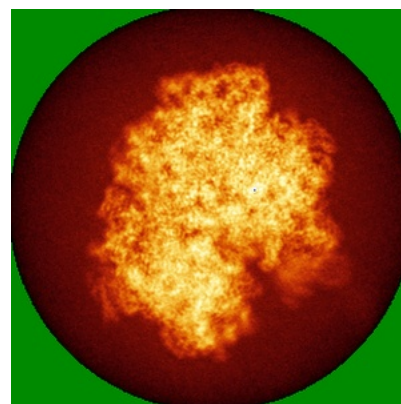
6.4.2 Raw map



X



Y

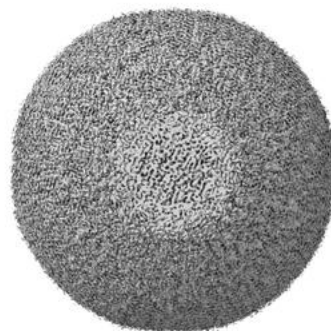


Z

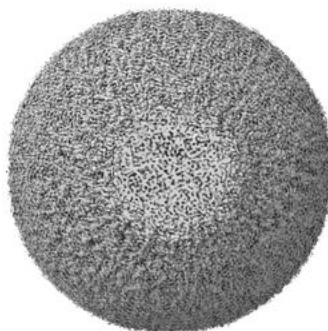
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

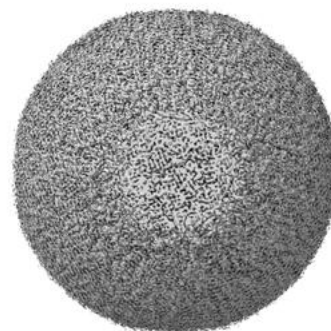
6.5.1 Primary map



X



Y



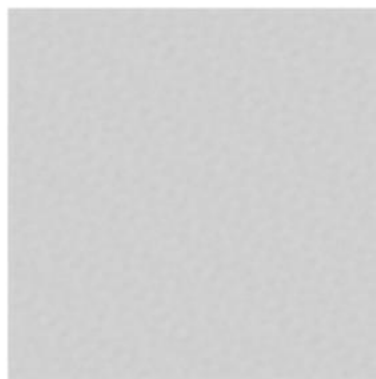
Z

The images above show the 3D surface view of the map at the recommended contour level 0.035. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

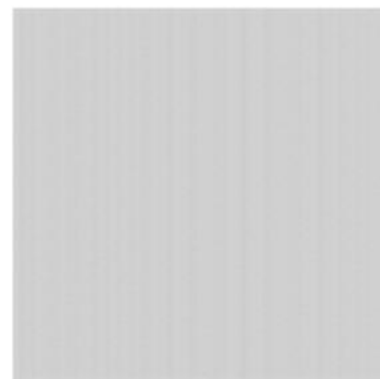
6.5.2 Raw map



X



Y



Z

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.

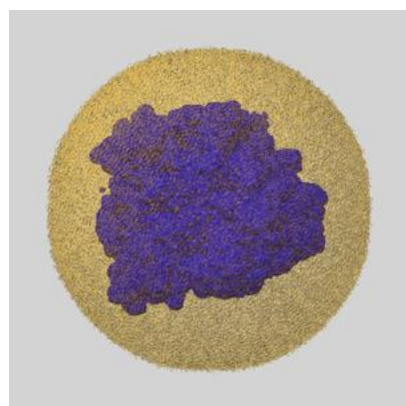
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

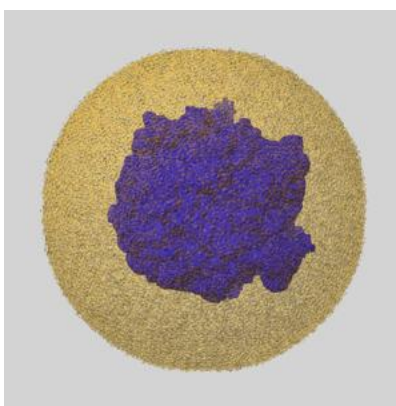
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

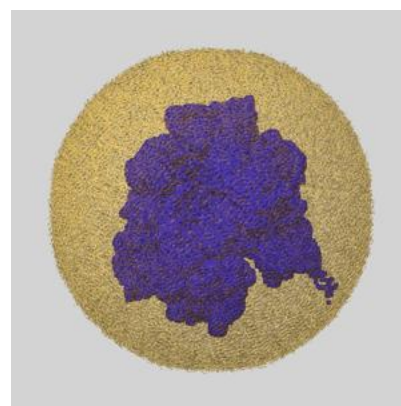
6.6.1 emd_10905_msk_1.map [i](#)



X



Y

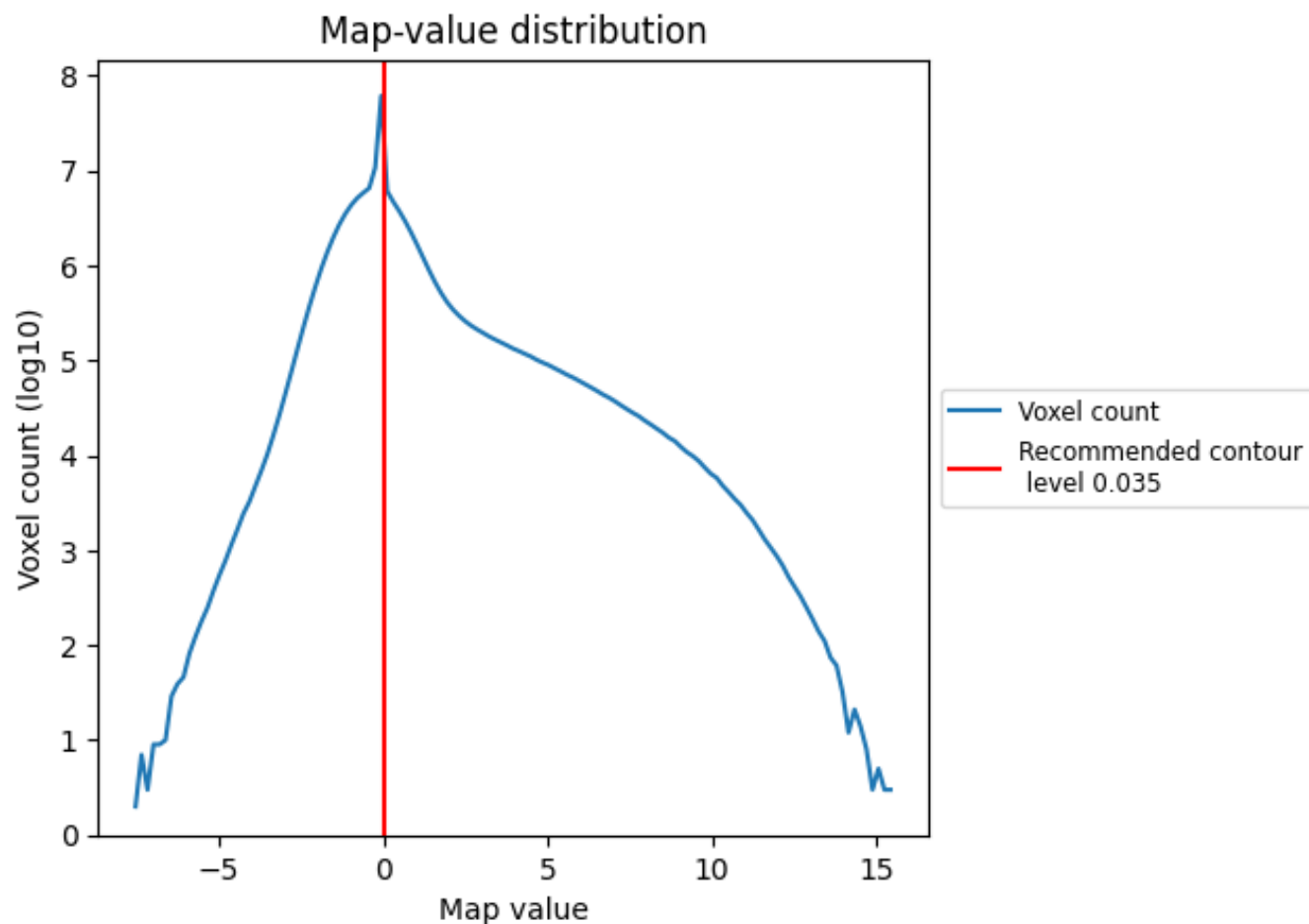


Z

7 Map analysis [i](#)

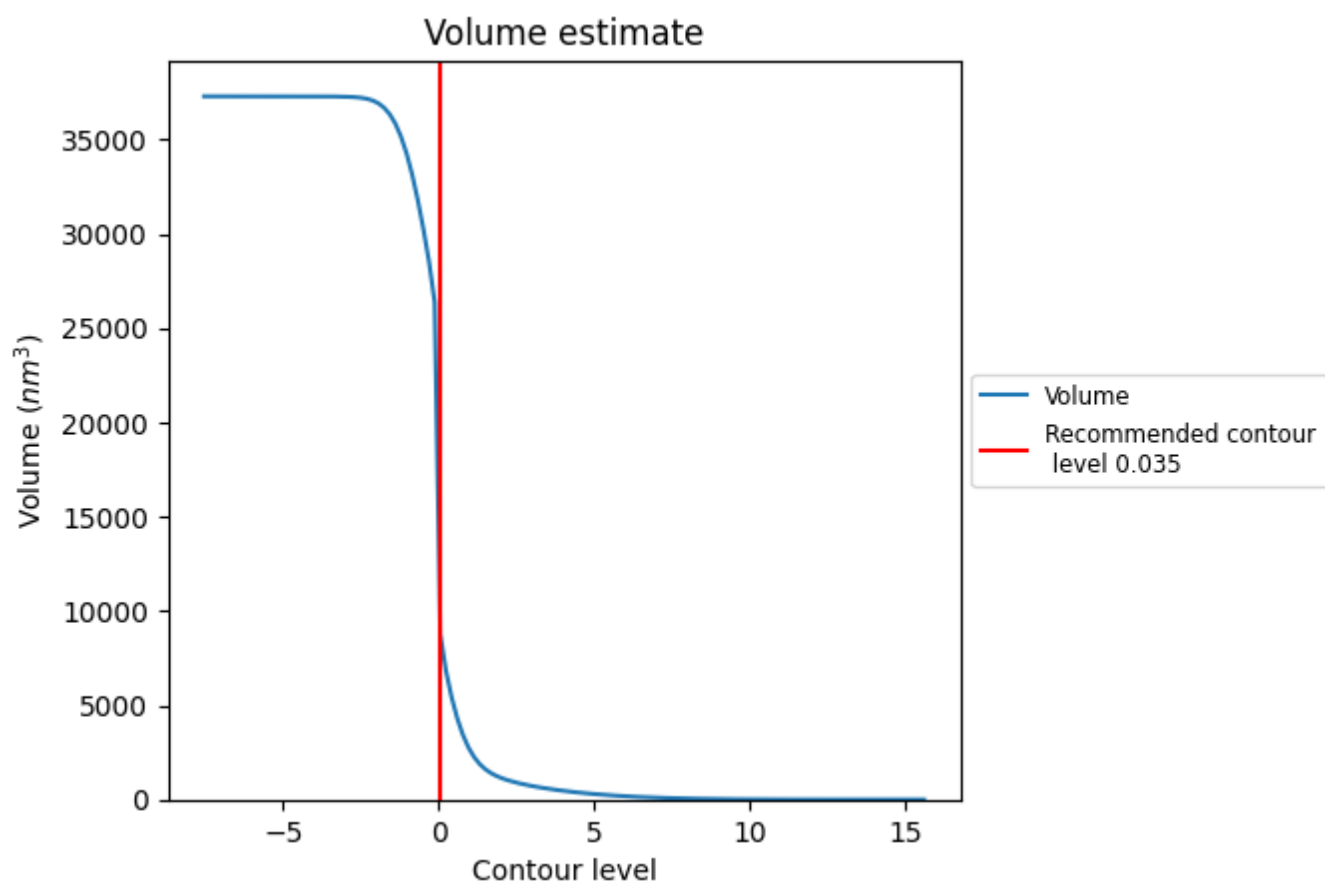
This section contains the results of statistical analysis of the map.

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.

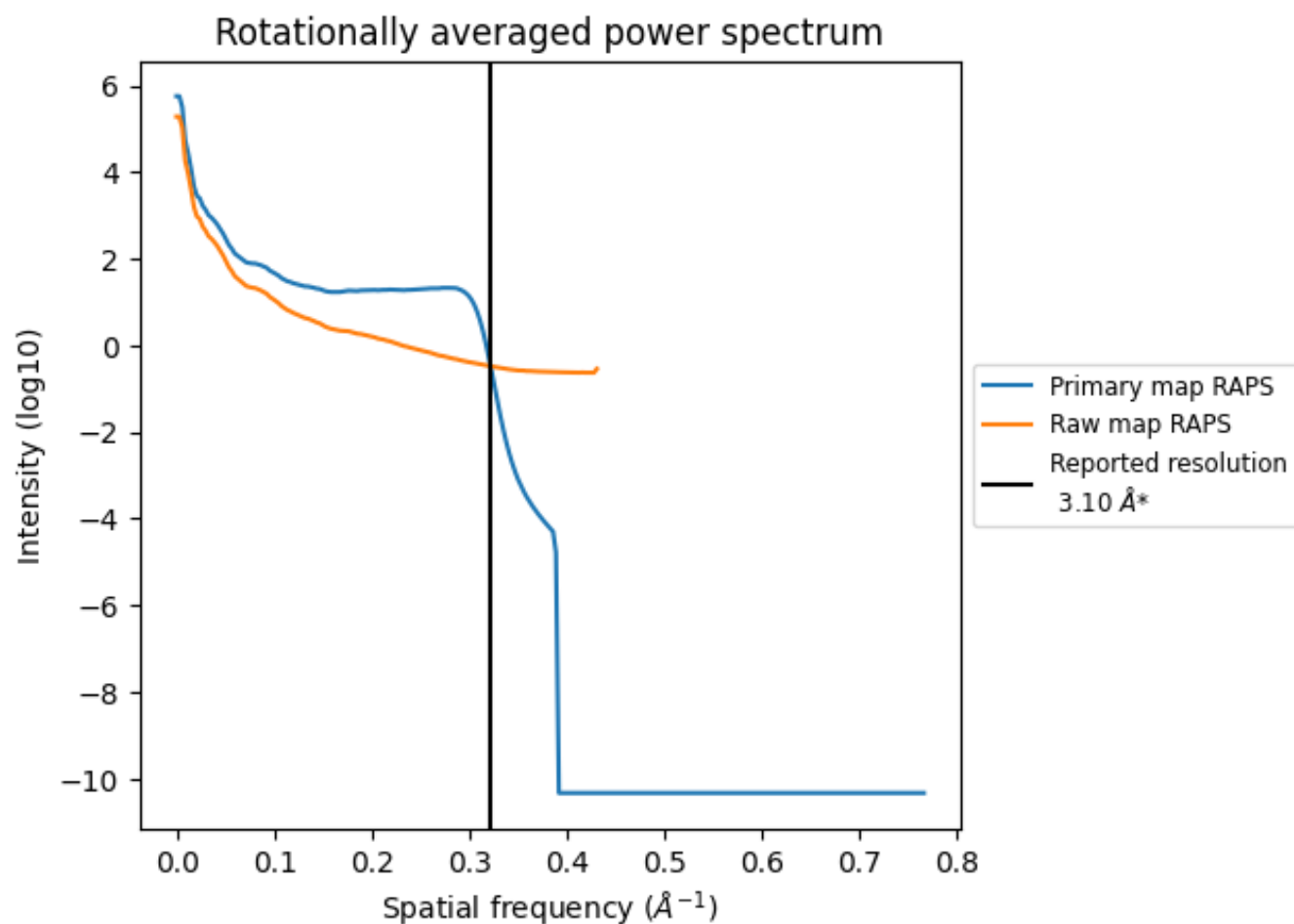
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 10850 nm^3 ; this corresponds to an approximate mass of 9801 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

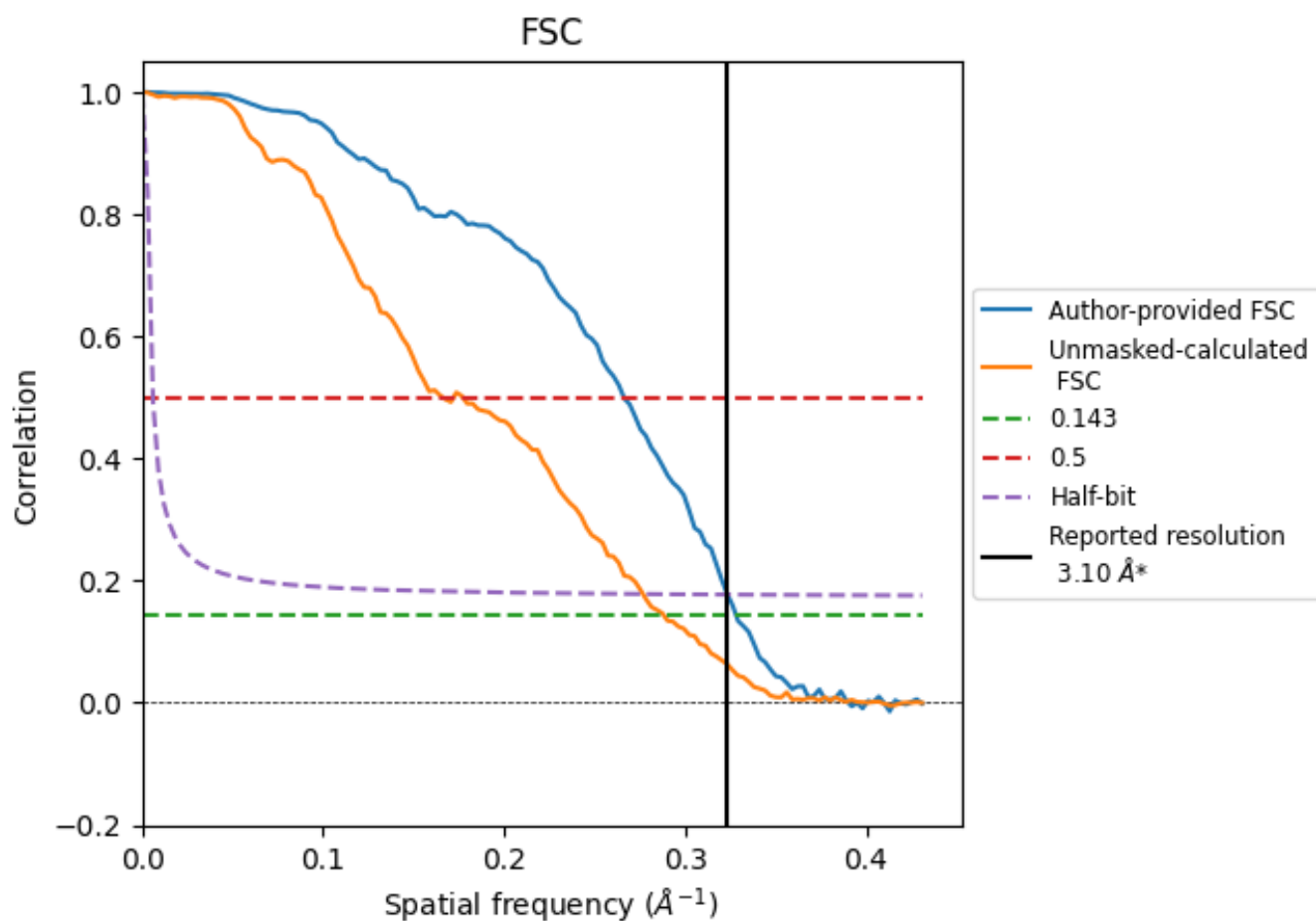


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.323 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

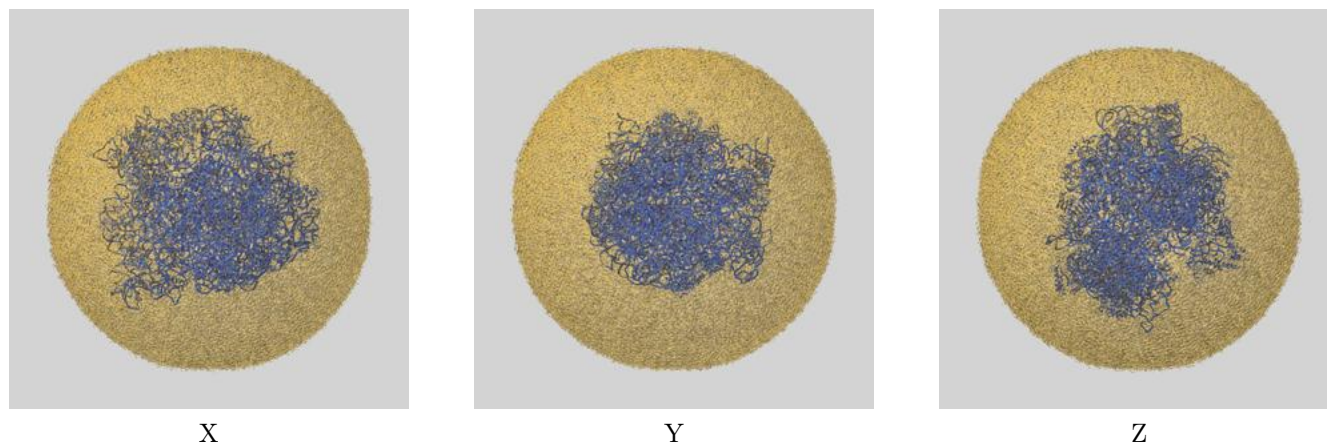
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.05	3.76	3.09
Unmasked-calculated*	3.47	6.02	3.61

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.47 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

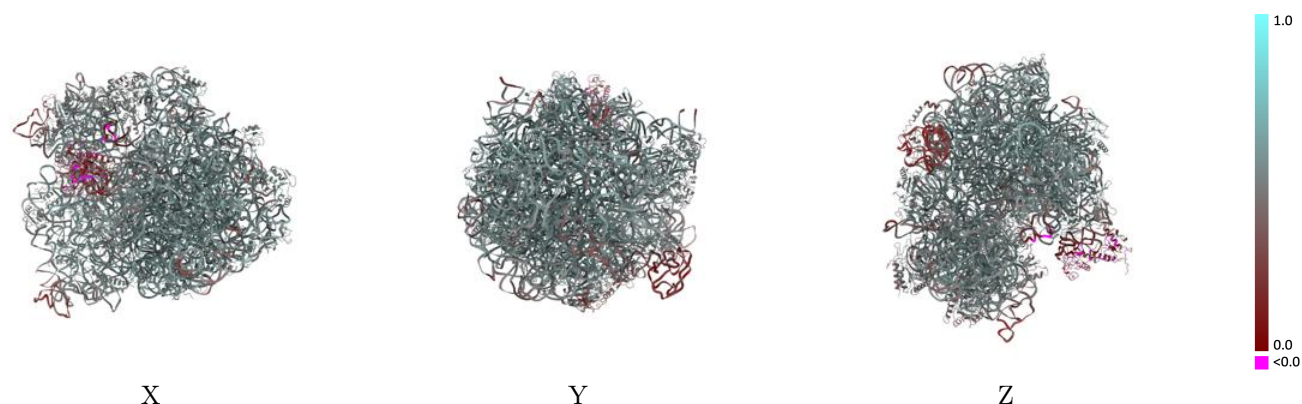
This section contains information regarding the fit between EMDB map EMD-10905 and PDB model 6YSR. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



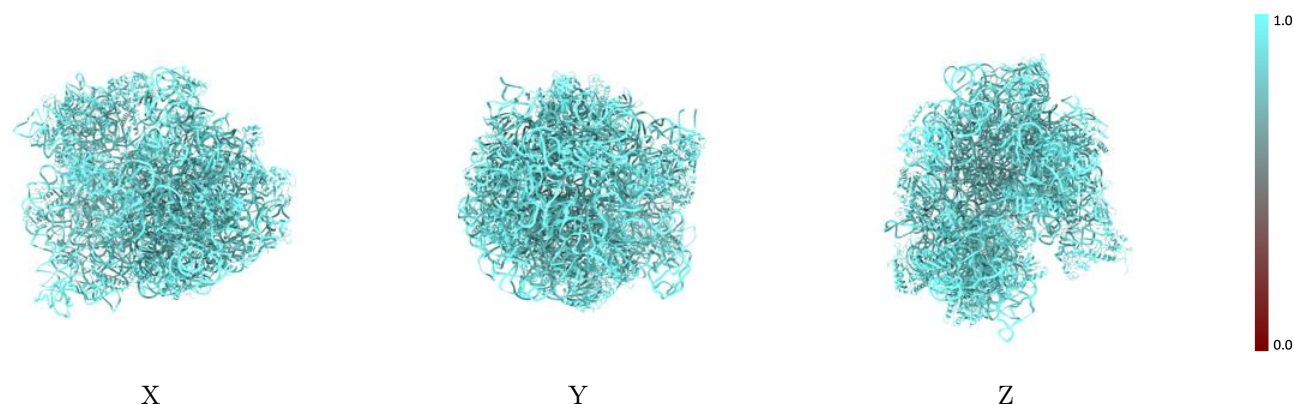
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



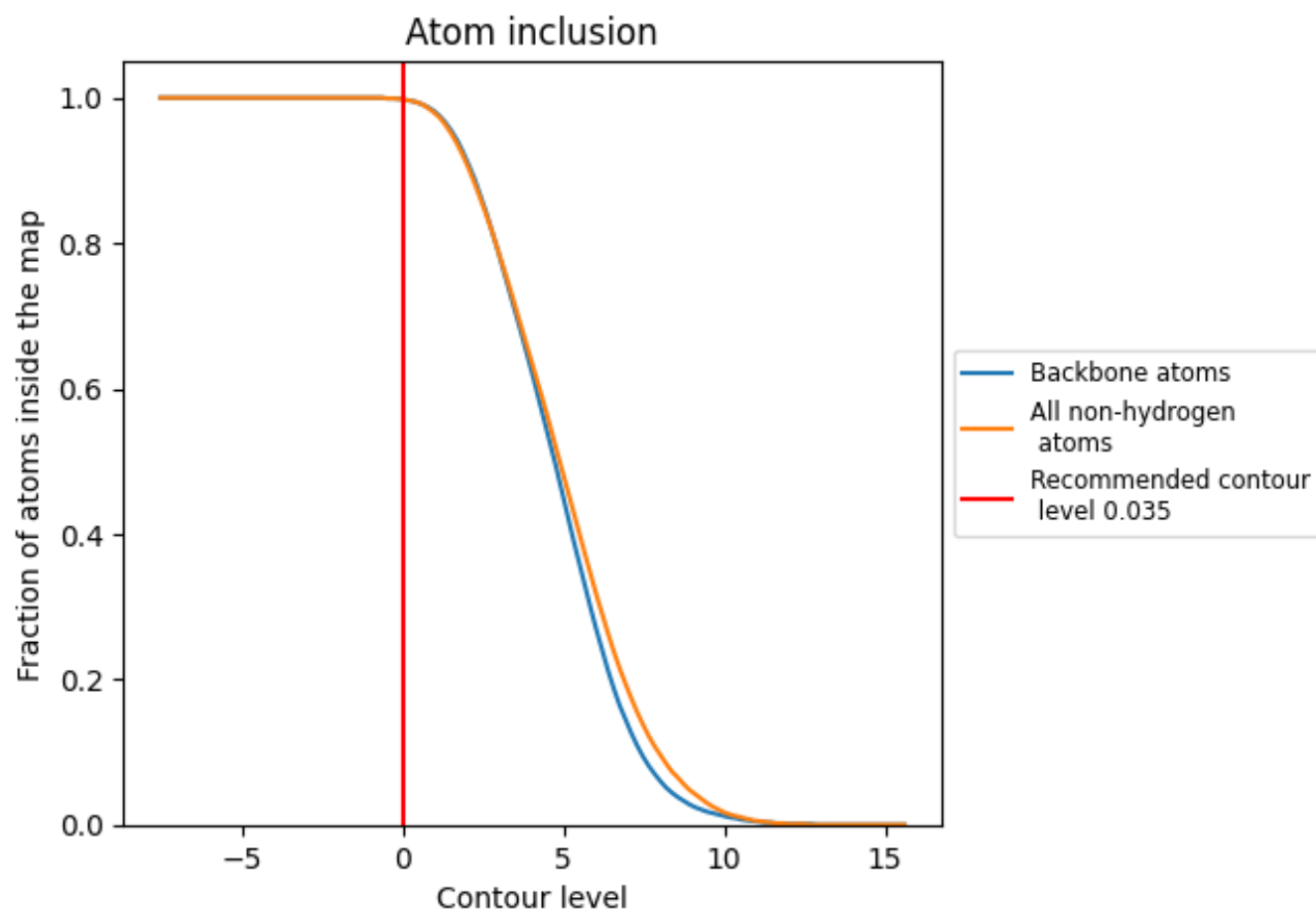
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.035).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 100% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9980	 0.5280
0	 0.9980	 0.5690
1	 1.0000	 0.5540
2	 0.9940	 0.5880
3	 0.9960	 0.5880
4	 0.9930	 0.5740
5	 0.9710	 0.1920
6	 0.9920	 0.4440
A	 0.9980	 0.5340
B	 1.0000	 0.5360
C	 0.9980	 0.5750
D	 0.9970	 0.5730
E	 0.9990	 0.5390
F	 0.9960	 0.5020
G	 0.9970	 0.5040
H	 0.9750	 0.4040
I	 0.9670	 0.1730
J	 1.0000	 0.5740
K	 0.9970	 0.5640
L	 0.9960	 0.5580
M	 0.9990	 0.5600
N	 1.0000	 0.5730
O	 0.9990	 0.5330
P	 0.9990	 0.5700
Q	 0.9970	 0.5690
R	 1.0000	 0.5650
S	 0.9950	 0.5640
T	 1.0000	 0.5370
U	 0.9990	 0.5170
V	 0.9970	 0.5380
W	 0.9930	 0.5800
X	 0.9970	 0.5650
Y	 0.9980	 0.5010
Z	 1.0000	 0.5580
a	 1.0000	 0.5300



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Chain	Atom inclusion	Q-score
b	 0.9920	 0.4770
c	 0.9980	 0.5190
d	 0.9970	 0.5090
e	 0.9990	 0.5460
f	 0.9960	 0.4930
g	 0.9970	 0.4810
h	 0.9960	 0.5560
i	 1.0000	 0.5020
j	 0.9970	 0.4820
k	 0.9950	 0.5300
l	 0.9910	 0.5430
m	 0.9990	 0.5160
n	 1.0000	 0.5260
o	 0.9970	 0.5360
p	 0.9980	 0.5260
q	 0.9980	 0.5230
r	 0.9960	 0.5210
s	 0.9980	 0.5260
t	 0.9950	 0.5250
u	 0.9960	 0.4620
v	 0.8420	 0.4770
w	 1.0000	 0.4820
x	 0.9780	 0.4350