



Full wwPDB EM Validation Report ⓘ

Mar 17, 2026 – 11:17 PM UTC

PDB ID : 8V9K / pdb_00008v9k
EMDB ID : EMD-43075
Title : Cryo-EM structure of the Mycobacterium smegmatis 70S ribosome in complex with hibernation factor Rv2629 (Balon) (Structure 5)
Authors : Rybak, M.Y.; Helena-Bueno, K.; Hill, C.H.; Melnikov, S.V.; Gagnon, M.G.
Deposited on : 2023-12-08
Resolution : 3.10 Å(reported)
Based on initial model : 5o60

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

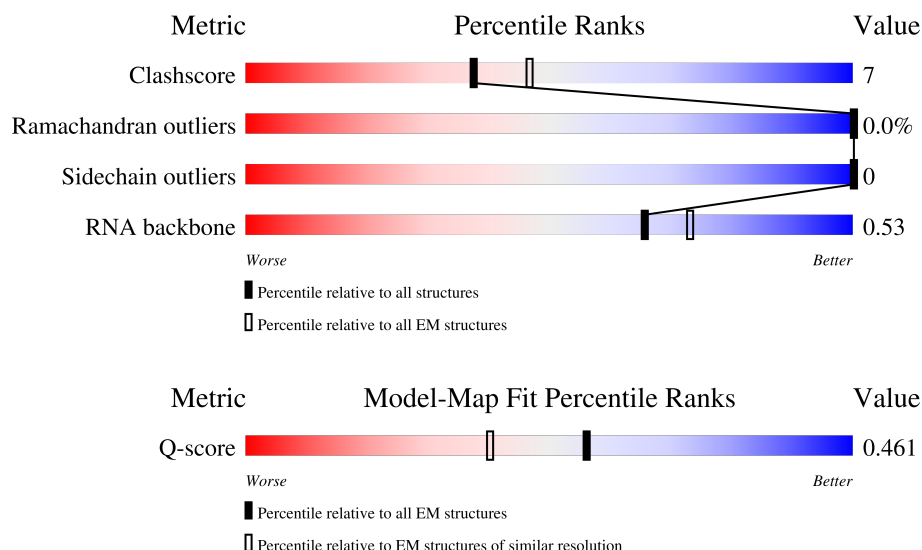
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13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

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 Å.

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



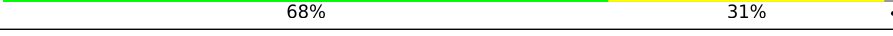
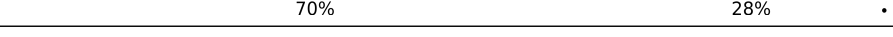
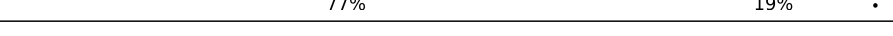
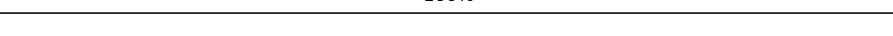
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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

Mol	Chain	Length	Quality of chain
1	a	1528	
2	b	277	
3	c	275	

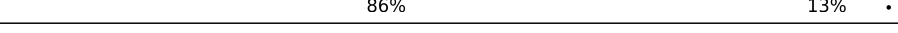
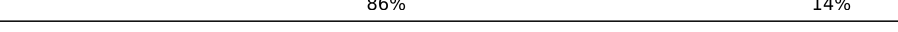
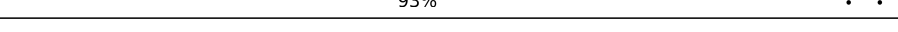
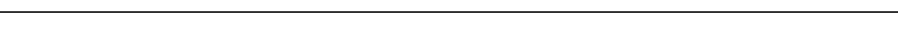
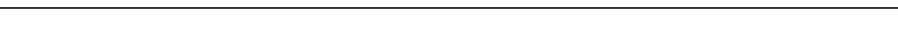
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Mol	Chain	Length	Quality of chain
4	d	201	
5	e	214	
6	f	96	
7	g	156	
8	h	132	
9	i	150	
10	j	101	
11	k	138	
12	l	124	
13	m	124	
14	n	61	
15	o	89	
16	p	156	
17	q	98	
18	r	84	
19	s	93	
20	t	86	
21	u	33	
22	v	3	
23	y	76	
24	z	374	
25	A	3164	
26	B	118	
27	C	278	
28	D	217	

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Mol	Chain	Length	Quality of chain
29	E	215	
30	F	187	
31	G	179	
32	H	151	
33	I	175	
34	J	142	
35	K	235	
36	L	147	
37	M	122	
38	N	147	
39	O	137	
40	P	199	
41	Q	127	
42	R	113	
43	S	129	
44	T	103	
45	U	153	
46	V	100	
47	W	105	
48	X	215	
49	Y	88	
50	Z	64	
51	1	77	
52	2	61	
53	3	75	

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Mol	Chain	Length	Quality of chain
54	4	57	 82%12%5%
55	5	55	 84%5%11%
56	6	47	 91%6%.
57	7	64	 75%23%.
58	8	37	 78%22%
59	9	24	 75%21%.

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 153253 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	1511	Total	C	N	O	P	0	0
			32439	14448	5930	10550	1511		

- Molecule 2 is a protein called 30S Ribosomal Protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	b	228	Total	C	N	O	S	0	0
			1793	1132	322	330	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	c	208	Total	C	N	O	S	0	0
			1660	1036	322	298	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	d	200	Total	C	N	O	S	0	0
			1641	1028	316	295	2		

- Molecule 5 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	e	180	Total	C	N	O	S	0	0
			1296	812	245	235	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	f	96	Total	C	N	O	S	0	0
			771	486	138	145	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	g	155	Total	C	N	O	S	0	0
			1232	768	241	221	2		

- Molecule 8 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	h	131	Total	C	N	O	S	0	0
			1010	633	189	187	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	i	126	Total	C	N	O	S	0	0
			994	630	194	170			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	j	99	Total	C	N	O	S	0	0
			788	495	146	144	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	k	115	Total	C	N	O	S	0	0
			855	528	170	156	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	l	122	Total	C	N	O	S	0	0
			958	594	197	165	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	m	116	Total	C	N	O	S	0	0
			935	572	191	169	3		

- Molecule 14 is a protein called Small ribosomal subunit protein uS14B.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	n	60	Total	C	N	O	S	0	0
			477	302	97	73	5		

- Molecule 15 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	o	88	Total	C	N	O		0	0
			720	449	147	124			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	p	113	Total	C	N	O		0	0
			891	570	162	159			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	q	94	Total	C	N	O	S	0	0
			748	469	142	135	2		

- Molecule 18 is a protein called Small ribosomal subunit protein bS18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	r	65	Total	C	N	O	S	0	0
			513	318	102	90	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	s	82	Total	C	N	O	S	0	0
			650	418	122	109	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	t	85	Total	C	N	O		0	0
			660	402	139	119			

- Molecule 21 is a protein called 30S Ribosomal Protein S22.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	u	32	Total	C	N	O	S	0	0
			280	172	71	36	1		

- Molecule 22 is a RNA chain called poly-U mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	v	3	Total	C	N	O	P	0	0
			60	27	6	24	3		

- Molecule 23 is a RNA chain called pe/E deacylated phenylalanine-tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	y	74	Total	C	N	O	P	S	0	0
			1581	707	285	515	73	1		

- Molecule 24 is a protein called Ribosome hibernation factor Balon (Rv2629).

Mol	Chain	Residues	Atoms					AltConf	Trace
24	z	364	Total	C	N	O	S	0	0
			2800	1740	511	543	6		

- Molecule 25 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	A	3081	Total	C	N	O	P	0	0
			66171	29494	12172	21424	3081		

- Molecule 26 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	B	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

- Molecule 27 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	C	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 28 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	D	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 29 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	E	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 30 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	F	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

- Molecule 31 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	G	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 32 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	H	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 33 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	I	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 34 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	J	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 35 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	K	102	Total	C	N	O	0	0
			531	316	109	106		

- Molecule 36 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	L	146	Total	C	N	O	S	0
			1130	722	207	200	1	0

- Molecule 37 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	M	122	Total	C	N	O	S	0
			938	586	179	170	3	0

- Molecule 38 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	N	145	Total	C	N	O	S	0
			1078	676	205	194	3	0

- Molecule 39 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	O	136	Total	C	N	O	S	0
			1092	690	213	187	2	0

- Molecule 40 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	P	118	Total	C	N	O	S	0
			928	583	180	163	2	0

- Molecule 41 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	Q	126	Total	C	N	O	0	0
			956	586	199	171		

- Molecule 42 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	R	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 43 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	S	124	Total	C	N	O		0	0
			988	613	203	172			

- Molecule 44 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	T	100	Total	C	N	O		0	0
			754	478	137	139			

- Molecule 45 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	U	114	Total	C	N	O		0	0
			873	543	171	159			

- Molecule 46 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	V	97	Total	C	N	O		0	0
			756	479	138	139			

- Molecule 47 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	W	97	Total	C	N	O	S	0	0
			732	456	137	137	2		

- Molecule 48 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	X	192	Total	C	N	O		0	0
			1428	881	255	292			

- Molecule 49 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	Y	85	Total	C	N	O	0	0
			628	387	133	108		

- Molecule 50 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Z	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 51 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	1	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 52 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	2	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 53 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	3	59	Total	C	N	O	S	0	0
			432	269	73	85	5		

- Molecule 54 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	4	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 55 is a protein called Large ribosomal subunit protein bL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	5	49	Total	C	N	O	S	0	0
			405	248	82	71	4		

- Molecule 56 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	6	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 57 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	7	63	Total	C	N	O		0	0
			502	302	115	85			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
58	8	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

- Molecule 59 is a protein called 50S Ribosomal Protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	9	23	Total	C	N	O		0	0
			189	111	50	28			

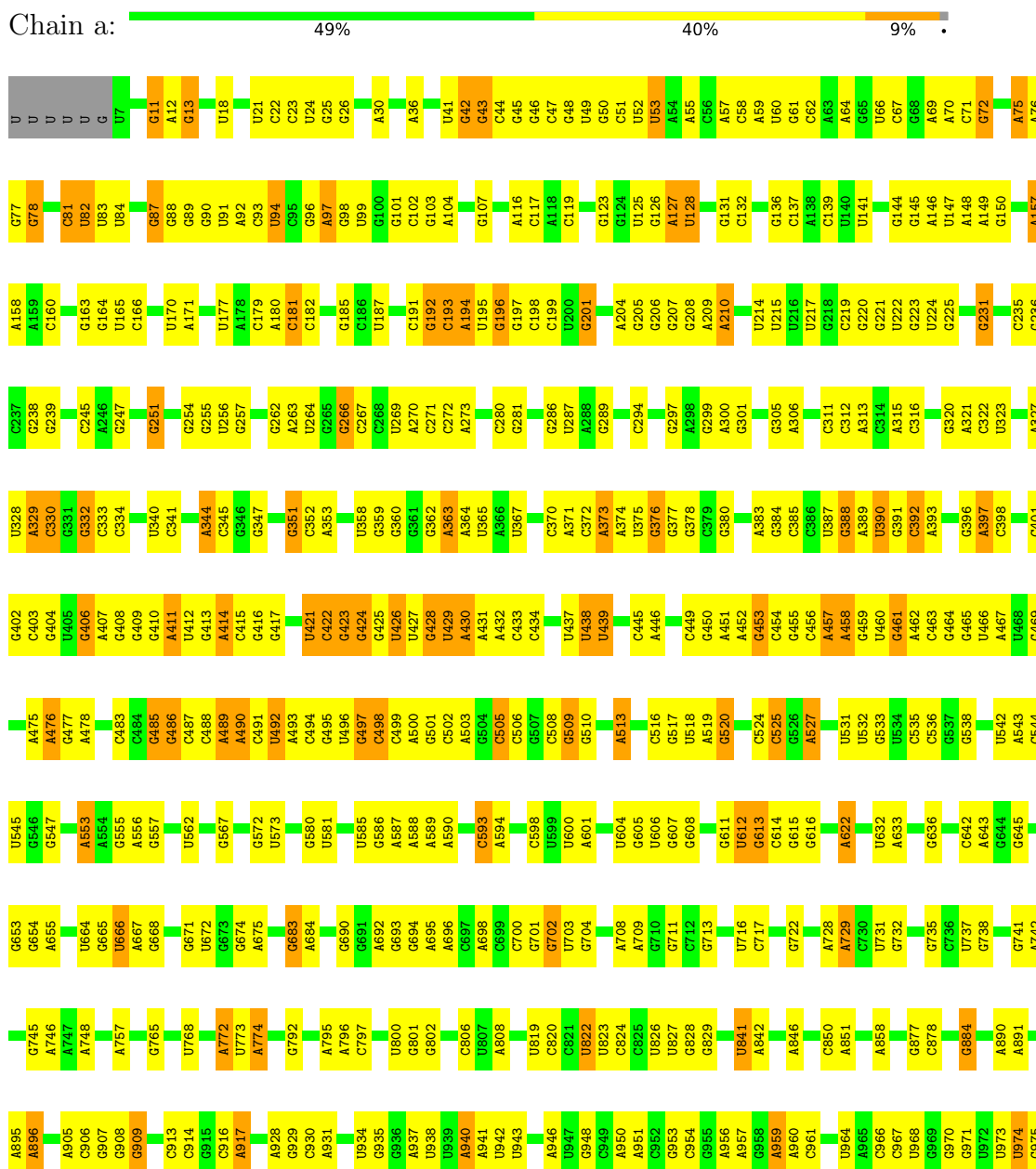
- Molecule 60 is ZINC ION (CCD ID: ZN) (formula: Zn).

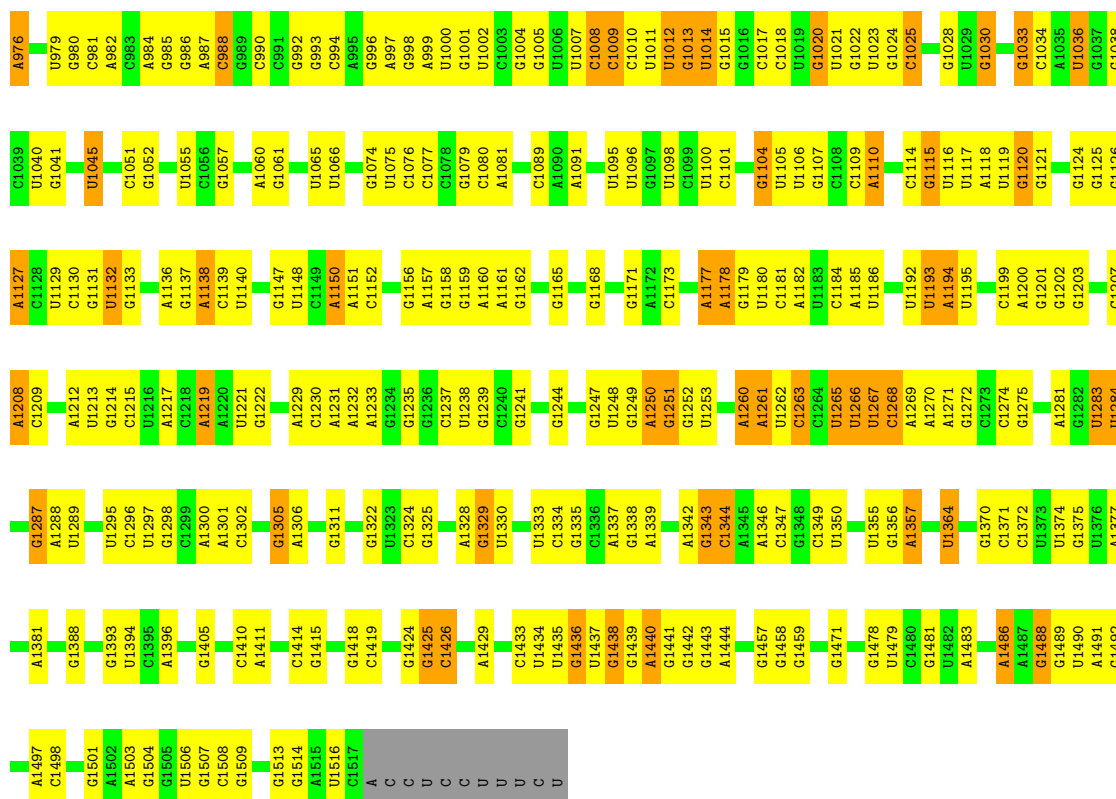
Mol	Chain	Residues	Atoms		AltConf
60	Z	1	Total	Zn	0
			1	1	
60	5	1	Total	Zn	0
			1	1	

3 Residue-property plots

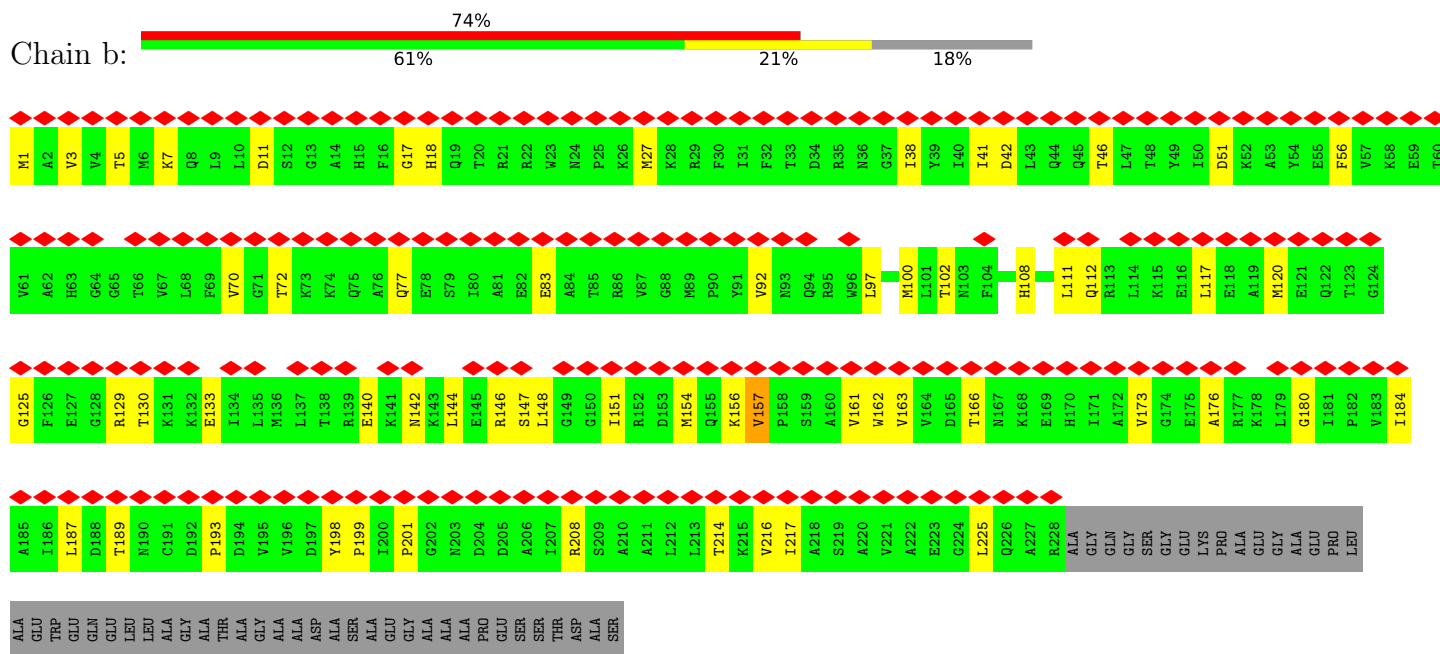
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 16S Ribosomal RNA

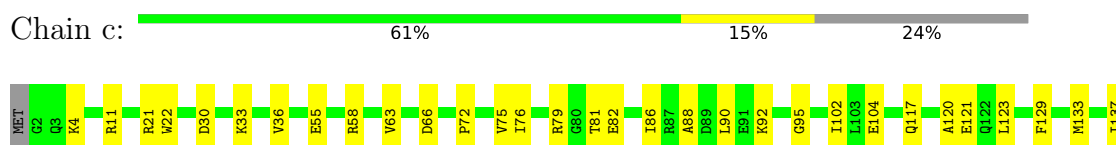


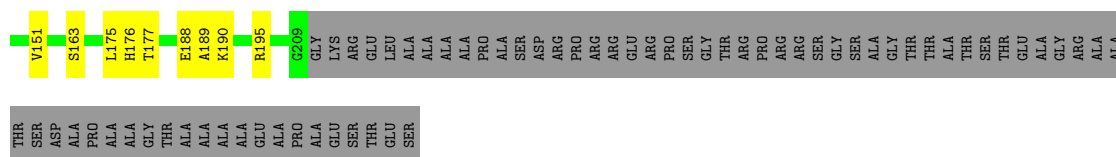


• Molecule 2: 30S Ribosomal Protein S2



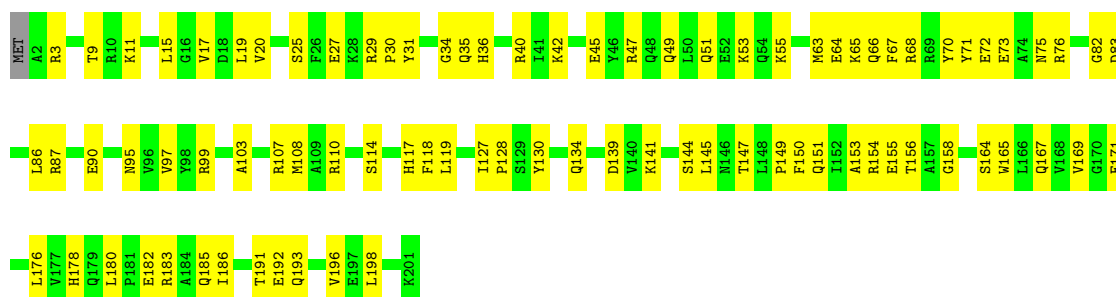
• Molecule 3: 30S ribosomal protein S3





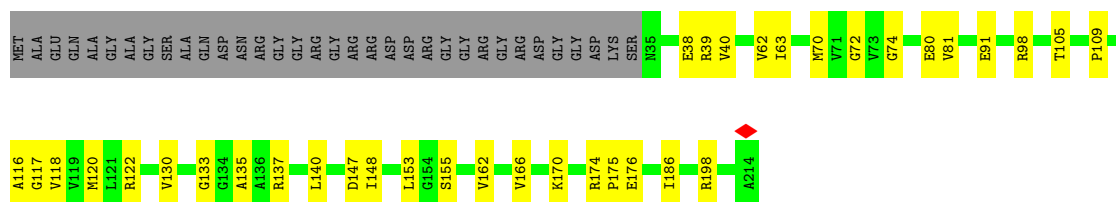
• Molecule 4: 30S ribosomal protein S4

Chain d: 57% 42%



• Molecule 5: Small ribosomal subunit protein uS5

Chain e: 67% 17% 16%



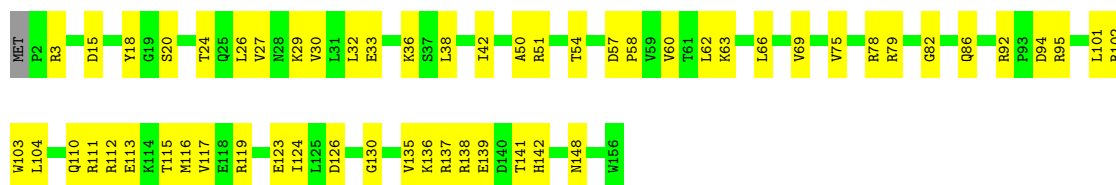
• Molecule 6: 30S ribosomal protein S6

Chain f: 73% 27%



• Molecule 7: 30S ribosomal protein S7

Chain g: 63% 36%



• Molecule 8: Small ribosomal subunit protein uS8

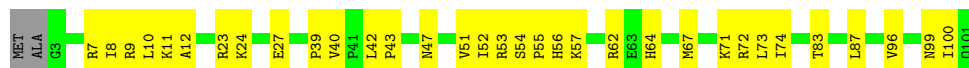
Chain h: 77% 22%



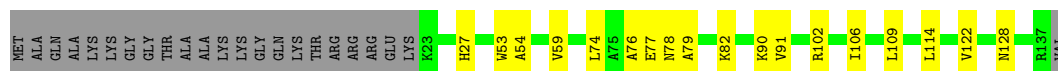
• Molecule 9: 30S ribosomal protein S9



• Molecule 10: 30S ribosomal protein S10



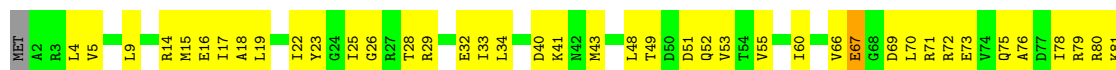
• Molecule 11: 30S ribosomal protein S11



• Molecule 12: 30S ribosomal protein S12



• Molecule 13: 30S ribosomal protein S13



• Molecule 14: Small ribosomal subunit protein uS14B

Chain n:  70% 28% .



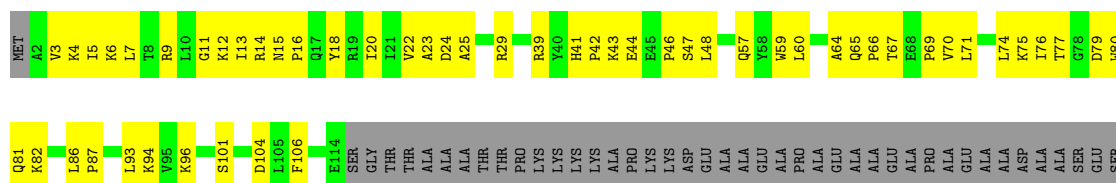
- Molecule 15: Small ribosomal subunit protein uS15

Chain o:  79% 20% .



- Molecule 16: 30S ribosomal protein S16

Chain p:  38% 34% 28%



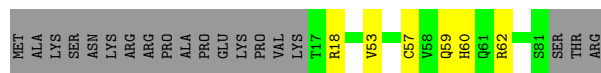
- Molecule 17: 30S ribosomal protein S17

Chain q:  77% 19% .



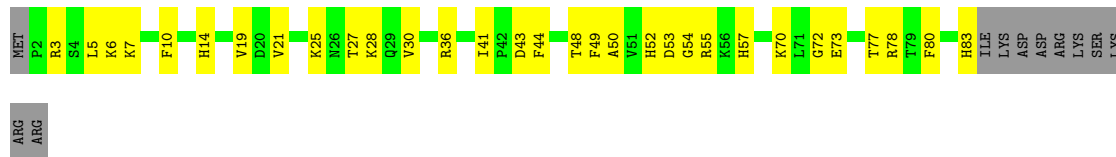
- Molecule 18: Small ribosomal subunit protein bS18B

Chain r:  70% 7% 23%



- Molecule 19: 30S ribosomal protein S19

Chain s:  55% 33% 12%

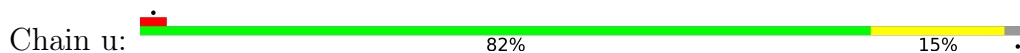


- Molecule 20: 30S ribosomal protein S20

Chain t:  66% 33% .



- Molecule 21: 30S Ribosomal Protein S22

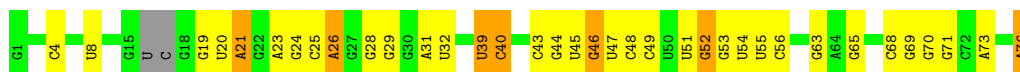


- Molecule 22: poly-U mRNA

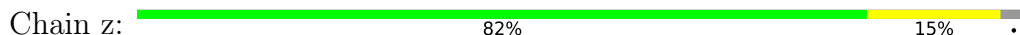


There are no outlier residues recorded for this chain.

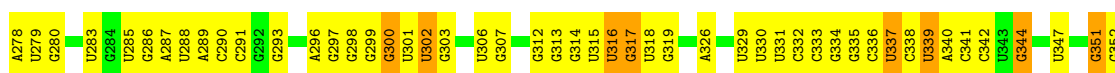
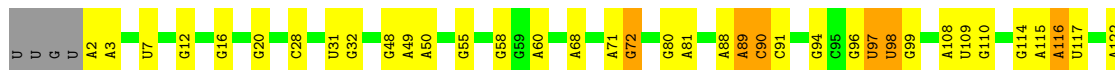
- Molecule 23: pe/E deacylated phenylalanine-tRNA



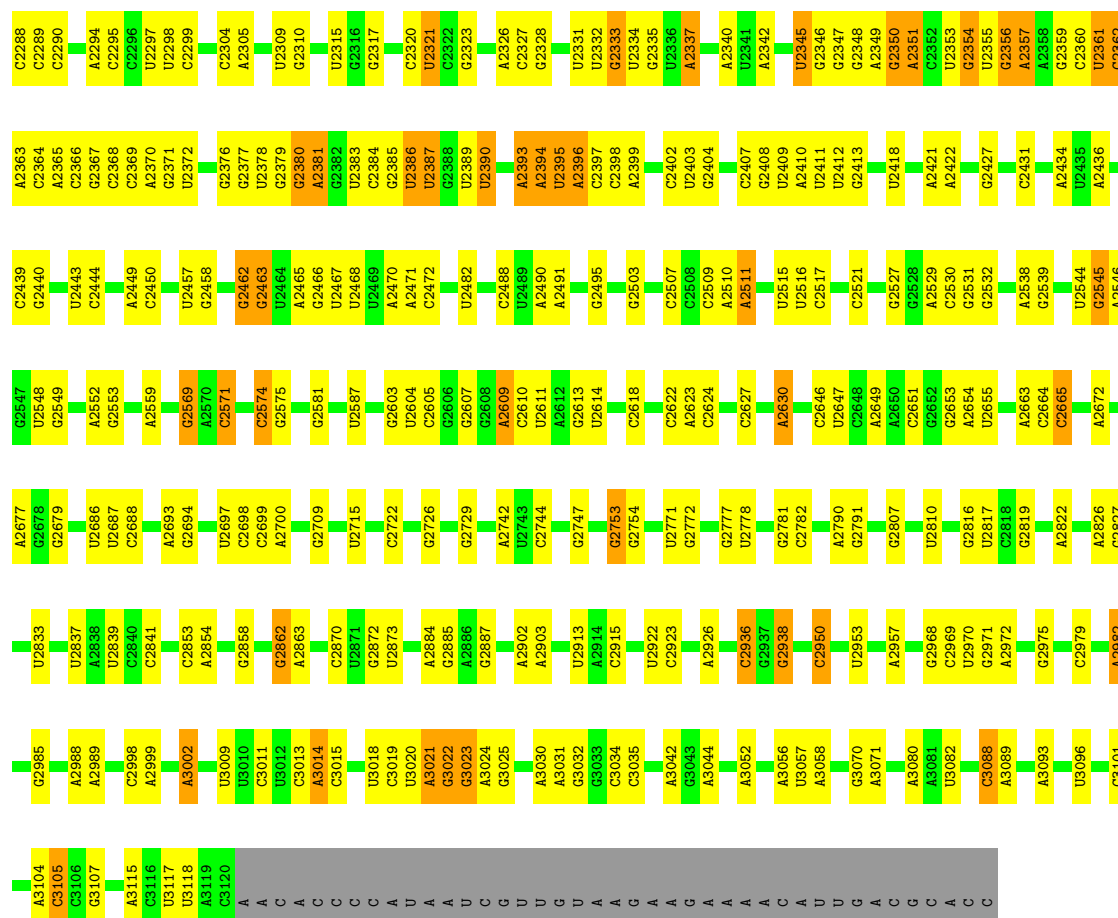
- Molecule 24: Ribosome hibernation factor Balon (Rv2629)



- Molecule 25: 23S Ribosomal RNA

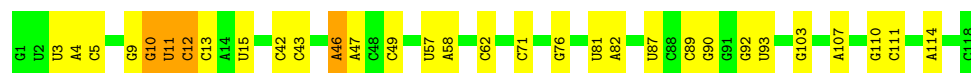


U2167	G2034	G1885	A1737	G1626	A1566	C1472	G1306	A1204	G1087	U966	A830	U709	G474
U2168	U2035	G1892	G1738	U1627	C	A1473	C1311	G1205	U1088	G967	A831	C718	U487
G2178	A2042	G1892	G1746	A1628	A	A1474	C1312	A1206	G1092	A972	G832	C719	G488
U2179	C2043	G1892	G1755	A1629	C	G1475	U1313	G1209	A1093	G973	U839	C720	A489
U2180	A2046	C1900	G1755	U1630	C	G1476	C1314	G1212	G1094	G974	C845	C721	G494
A2184	G2061	C1901	G1756	G1632	G	C1477	G1335	U1213	A1099	U975	C846	C722	G499
G2188	G2062	C1904	U1757	G1637	G	G1478	G1336	A1214	G1100	A978	U857	C723	G499
G2191	A2065	G1905	G1758	U1640	A	A1480	G1339	U1215	A1101	C990	A858	A726	C618
A2194	G2075	C1927	A1759	U1641	C	U1494	G1344	G1220	G1102	U981	U862	G728	C502
U2195	G2075	G1938	G1762	G1642	C	A1499	A1344	A1221	G1107	A982	C868	G730	A503
U2196	U2086	U1939	G1763	A1648	C	A1500	G1363	C1222	G1114	A994	U871	A731	G512
C2087	C2087	C1944	U1767	C1649	A	C1501	U995	G1223	U995	G996	A871	G732	A517
C2088	C2088	U1945	G1768	G1653	C	G1502	G1365	G1224	A1118	G996	G872	U733	G634
C2089	U1946	G1946	G1769	G1654	U	U1507	G1371	U1226	A1119	G997	G875	C734	G635
U2090	U1947	G1947	G1780	A1655	U	A1508	G1379	C1227	C1122	C998	A876	U735	G637
U2091	A1948	A1948	C1784	G1658	C	U1509	A1380	A1228	A1127	C1000	U877	G736	U638
U2092	C1949	C1949	C1785	G1658	G	A1510	G1381	G1230	A1128	C1001	G878	A737	C639
G2093	C1952	C1952	G1786	G1670	G	U1511	A1382	U1231	G1129	C1002	A879	U738	G640
G2094	C1953	C1953	G1787	G1671	C	G1524	G1384	G1232	C1130	A1003	G880	A740	U641
G2095	C1956	C1956	G1788	G1674	G	G1524	G1385	G1233	C1131	C1004	G643	G741	G643
G2096	U1956	U1956	U1675	U1675	U	G1528	G1386	G1238	G1131	A1005	G891	G745	U544
G2097	U1956	U1956	U1676	U1676	G	U1529	U1387	A1246	G1140	G1006	G891	U746	A545
U2098	G1961	G1961	A1790	G1676	U	G1530	U1388	G1249	U1141	G1007	A897	A747	A546
G2099	G1962	G1962	A1791	A1679	G	C1531	U1389	U1250	A1144	U1009	A898	C750	U547
G2100	G1963	G1963	A1792	A1680	C	G1532	G1392	U1251	A1145	U1010	G899	C751	G551
A2106	U1964	U1964	U1798	U1681	G	U1533	C1393	G1252	U1151	A1011	C912	A753	A554
G2107	U1964	U1964	U1798	U1681	U	C1534	A1394	G1253	U1152	A1012	A904	C752	G557
A2244	C1973	C1973	C1801	G1688	U	U1535	A1395	G1254	U1153	U1013	U911	G757	G561
C2245	A1974	A1974	G1802	U1688	G	A1536	G1396	G1255	G1162	G1022	A917	A758	G665
U2246	A1975	A1975	A1803	U1689	U	G1537	G1397	G1256	A1163	A1025	U918	G759	G662
C2129	U1975	U1975	G1804	A1691	G	U1538	U1397	G1257	G1164	C1030	A919	U760	A666
G2130	U1981	U1981	G1805	A1691	U	A1539	G1400	G1258	G1165	U1033	G920	U764	A667
G2131	A1990	A1990	A1808	G1703	G	U1540	A1415	C1260	U1178	A1033	C921	G768	G669
C2138	U1996	U1996	U1809	U1704	G1605	G1541	A1416	A1261	U1179	A1033	C927	C672	A579
A2255	U1996	U1996	A1810	C1705	G1606	A1542	A1416	G1272	G1180	C1045	U928	U772	G580
U2141	A2001	A2001	C1825	G1707	U1607	A1543	C1421	G1273	U1183	C1046	C929	G773	G581
A2142	C2007	C2007	A1826	U1710	G1608	U1544	A1422	A1274	U1183	A1047	A935	G774	G582
A2143	A2008	A2008	A1827	G1711	U1611	G1549	G1426	C1283	A1188	G1048	U942	C781	U566
C2144	C2008	C2008	A1828	G1712	U1612	G1550	G1434	A1284	A1188	G1049	U943	U782	G567
C2148	C1829	C1829	U1713	A1714	G1613	U1551	C1435	G1285	A1191	G1063	U947	G783	A588
U2015	C1830	C1830	A1715	A1715	G1614	A1552	G1443	C1286	G1192	A1064	G948	G784	A589
G2016	G1840	G1840	U1716	U1716	G1615	C1553	G1455	C1287	A1195	A1065	C949	A785	A590
C2017	G2018	G2018	U1717	U1717	C1617	A1556	G1465	A1288	U1199	A1076	A950	U801	A592
G2018	A2019	A2019	C1718	G1718	U1618	A1559	G1466	A1289	U1200	G1077	G951	G785	G593
A2020	U1864	U1864	C1719	G1719	U1619	U1560	U1467	G1293	G1193	G1078	C705	C786	U594
G2026	A1865	A1865	G1720	G1720	U1620	C1561	G1468	G1296	C1194	G1085	G706	G787	A595
C2027	C1866	C1866	G1724	G1724	G1621	C1562	U1468	A1297	A1195	G1085	A1202	U829	C597
G2028	U1870	U1870	A1731	A1731	G1622	A1563	A1469	C1298	U1199	G1085	G960	U818	U594
A2284	G2031	G2031	G1871	A1871	U1623	A1564	A1469	G1298	U1200	G1085	U961	G819	A595
G2285	A2032	A2032	A1872	A1872	G1625	A1565	A1469	C1298	G1201	G1085	G960	U819	C596
A2286	C2165	C2165	A1872	A1872	G1625	A1565	A1469	C1298	A1202	G1085	U961	U829	C597
C2287	C2166	C2166	A1872	A1872	G1625	A1565	A1469	C1298	A1202	G1085	U961	U829	C597



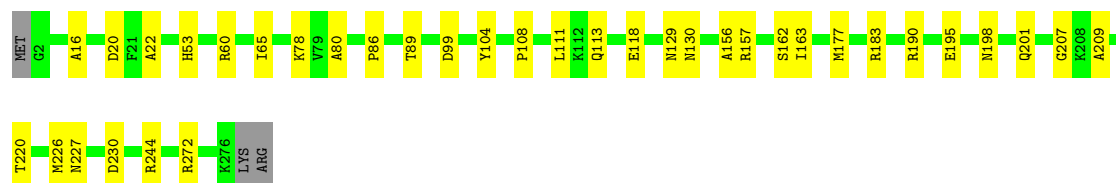
• Molecule 26: 5S Ribosomal RNA

Chain B: 74% 23%



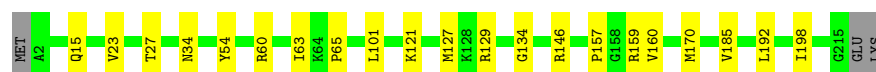
• Molecule 27: 50S ribosomal protein L2

Chain C: 86% 13%



• Molecule 28: 50S ribosomal protein L3

Chain D: 89% 10%



- Molecule 29: Large ribosomal subunit protein uL4

Chain E:  87% 11%



- Molecule 30: Large ribosomal subunit protein uL5

Chain F:  74% 23%



- Molecule 31: 50S ribosomal protein L6

Chain G:  84% 14%



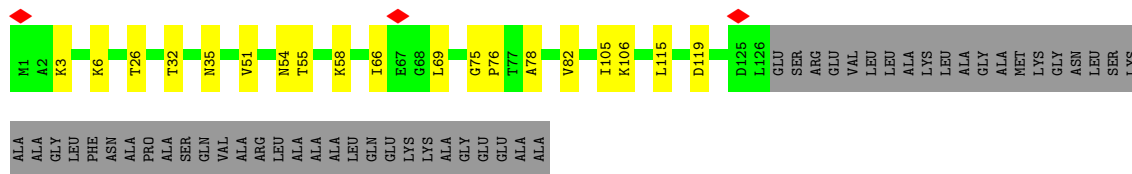
- Molecule 32: 50S ribosomal protein L9

Chain H:  89% 11%



- Molecule 33: 50S ribosomal protein L10

Chain I:  61% 11% 28%



- Molecule 34: 50S ribosomal protein L11

Chain J:  75% 19% 6%



- Molecule 35: Large ribosomal subunit protein uL1

Chain Q:  86% 13%



- Molecule 42: 50S ribosomal protein L19

Chain R:  86% 14%



- Molecule 43: Large ribosomal subunit protein bL20

Chain S:  88% 9%



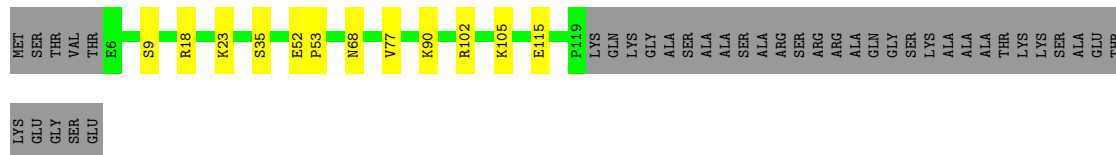
- Molecule 44: Large ribosomal subunit protein bL21

Chain T:  93%



- Molecule 45: Large ribosomal subunit protein uL22

Chain U:  67% 8% 25%



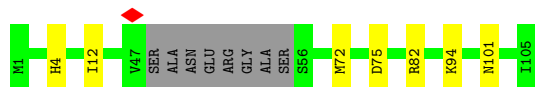
- Molecule 46: Large ribosomal subunit protein uL23

Chain V:  83% 14%



- Molecule 47: 50S ribosomal protein L24

Chain W:  86% 7% 8%



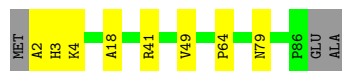
- Molecule 48: 50S ribosomal protein L25

Chain X:  76% 13% 11%



- Molecule 49: 50S ribosomal protein L27

Chain Y:  88% 9% .



- Molecule 50: Large ribosomal subunit protein bL28

Chain Z:  75% 23% .



- Molecule 51: 50S ribosomal protein L29

Chain 1:  70% 13% 17%



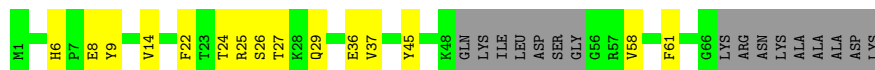
- Molecule 52: 50S ribosomal protein L30

Chain 2:  95% . .



- Molecule 53: Large ribosomal subunit protein bL31

Chain 3:  59% 20% 21%



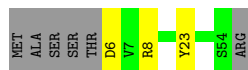
- Molecule 54: 50S ribosomal protein L32

Chain 4:  82% 12% 5%



- Molecule 55: Large ribosomal subunit protein bL33A

Chain 5: 84% 5% 11%



- Molecule 56: 50S ribosomal protein L34

Chain 6: 91% 6% .



- Molecule 57: 50S ribosomal protein L35

Chain 7: 75% 23% .



- Molecule 58: 50S ribosomal protein L36

Chain 8: 78% 22%



- Molecule 59: 50S Ribosomal Protein L37

Chain 9: 75% 21% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	147778	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 ($e^-/\text{\AA}^2$)	40.18	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	96000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	1.418	Depositor
Minimum map value	-0.439	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.083	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	435.2, 435.2, 435.2	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 4SU, ZN, PSU, 5MU, 7MG

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	a	0.11	0/36309	0.26	0/56657
2	b	0.11	0/1822	0.31	0/2457
3	c	0.13	0/1684	0.34	0/2261
4	d	0.14	0/1672	0.39	0/2251
5	e	0.13	0/1312	0.32	0/1772
6	f	0.13	0/782	0.32	0/1059
7	g	0.13	0/1252	0.38	0/1690
8	h	0.13	0/1025	0.30	0/1385
9	i	0.13	0/1012	0.37	0/1362
10	j	0.12	0/802	0.37	0/1086
11	k	0.13	0/873	0.33	0/1180
12	l	0.17	0/969	0.37	0/1294
13	m	0.16	0/942	0.53	1/1260 (0.1%)
14	n	0.13	0/488	0.35	0/650
15	o	0.17	0/729	0.34	0/977
16	p	0.17	0/908	0.46	0/1226
17	q	0.10	0/759	0.31	0/1016
18	r	0.10	0/518	0.28	0/693
19	s	0.10	0/668	0.29	0/901
20	t	0.16	0/663	0.36	0/882
21	u	0.15	0/280	0.34	0/359
22	v	0.08	0/65	0.14	0/98
23	y	0.18	1/1628 (0.1%)	0.23	0/2536
24	z	0.13	0/2848	0.32	0/3874
25	A	0.14	0/74096	0.28	0/115613
26	B	0.12	0/2821	0.26	0/4396
27	C	0.14	0/2153	0.29	0/2895
28	D	0.15	0/1609	0.32	0/2165
29	E	0.13	0/1592	0.27	0/2153
30	F	0.12	0/1467	0.30	0/1973
31	G	0.12	0/1369	0.28	0/1848
32	H	0.10	0/1027	0.32	0/1398

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.09	0/925	0.28	0/1246
34	J	0.11	0/1006	0.30	0/1364
35	K	0.08	0/530	0.22	0/731
36	L	0.16	0/1157	0.30	1/1567 (0.1%)
37	M	0.12	0/946	0.26	0/1268
38	N	0.15	0/1091	0.37	0/1457
39	O	0.13	0/1118	0.29	0/1506
40	P	0.14	0/945	0.27	0/1267
41	Q	0.12	0/966	0.24	0/1298
42	R	0.14	0/921	0.32	0/1236
43	S	0.15	0/1000	0.24	0/1341
44	T	0.12	0/764	0.25	0/1030
45	U	0.13	0/887	0.28	0/1204
46	V	0.14	0/766	0.28	0/1030
47	W	0.12	0/738	0.27	0/987
48	X	0.12	0/1443	0.28	0/1970
49	Y	0.13	0/638	0.24	0/854
50	Z	0.15	0/478	0.29	0/641
51	1	0.12	0/534	0.21	0/713
52	2	0.13	0/477	0.23	0/640
53	3	0.10	0/441	0.27	0/597
54	4	0.14	0/427	0.28	0/572
55	5	0.14	0/413	0.33	0/553
56	6	0.14	0/380	0.24	0/500
57	7	0.14	0/507	0.27	0/672
58	8	0.13	0/303	0.29	0/401
59	9	0.14	0/191	0.31	0/247
All	All	0.13	1/166136 (0.0%)	0.28	2/248259 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	y	8	4SU	O3'-P	6.08	1.62	1.56

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	L	2	PRO	CA-N-CD	-5.68	104.05	112.00
13	m	67	GLU	CB-CA-C	-5.23	108.98	115.89

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	a	32439	0	16321	567	0
2	b	1793	0	1839	37	0
3	c	1660	0	1707	31	0
4	d	1641	0	1668	77	0
5	e	1296	0	1360	22	0
6	f	771	0	797	20	0
7	g	1232	0	1282	46	0
8	h	1010	0	1046	19	0
9	i	994	0	1050	33	0
10	j	788	0	819	31	0
11	k	855	0	863	13	0
12	l	958	0	1045	28	0
13	m	935	0	986	45	0
14	n	477	0	503	13	0
15	o	720	0	760	13	0
16	p	891	0	935	57	0
17	q	748	0	795	17	0
18	r	513	0	540	3	0
19	s	650	0	656	27	0
20	t	660	0	712	20	0
21	u	280	0	342	4	0
22	v	60	0	31	0	0
23	y	1581	0	808	24	0
24	z	2800	0	2769	35	0
25	A	66171	0	33292	540	0
26	B	2522	0	1285	14	0
27	C	2110	0	2165	26	0
28	D	1587	0	1630	15	0
29	E	1569	0	1607	14	0
30	F	1445	0	1476	32	0
31	G	1348	0	1399	16	0
32	H	1018	0	988	13	0
33	I	918	0	959	14	0
34	J	990	0	1021	21	0
35	K	531	0	271	2	0
36	L	1130	0	1167	13	0
37	M	938	0	1000	12	0

Continued on next page...

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	N	1078	0	1151	15	0
39	O	1092	0	1128	18	0
40	P	928	0	972	11	0
41	Q	956	0	991	13	0
42	R	907	0	938	11	0
43	S	988	0	1038	8	0
44	T	754	0	802	2	0
45	U	873	0	909	8	0
46	V	756	0	802	11	0
47	W	732	0	782	5	0
48	X	1428	0	1443	18	0
49	Y	628	0	647	8	0
50	Z	470	0	480	12	0
51	1	531	0	541	9	0
52	2	474	0	500	1	0
53	3	432	0	392	11	0
54	4	423	0	463	8	0
55	5	405	0	407	3	0
56	6	377	0	411	3	0
57	7	502	0	541	11	0
58	8	299	0	324	4	0
59	9	189	0	205	4	0
60	5	1	0	0	0	0
60	Z	1	0	0	0	0
All	All	153253	0	103761	1878	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 7.

All (1878) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:177:U:H3	1:a:209:A:N6	1.57	1.03
25:A:337:U:H3	25:A:344:G:H1	1.00	0.96
1:a:1244:G:H1	1:a:1253:U:H3	1.04	0.95
1:a:49:U:H3	1:a:396:G:H1	1.10	0.94
23:y:51:U:H3	23:y:63:G:H1	1.06	0.94
25:A:334:G:H1	25:A:347:U:H3	1.12	0.92
13:m:25:ILE:HG23	13:m:29:ARG:HB2	1.53	0.91
1:a:177:U:H3	1:a:209:A:H62	0.96	0.91
25:A:273:A:H62	25:A:313:G:N2	1.69	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:72:G:H1	1:a:97:A:N6	1.74	0.85
25:A:1541:G:N1	25:A:1631:A:N6	2.25	0.85
25:A:1380:A:H3'	54:4:16:ARG:HH12	1.42	0.84
28:D:63:ILE:HG22	28:D:65:PRO:HD2	1.58	0.84
1:a:60:U:H2'	1:a:61:G:H8	1.42	0.84
1:a:417:G:H1	1:a:426:U:H3	1.27	0.82
1:a:424:G:H2'	1:a:425:G:H8	1.43	0.81
25:A:444:U:H5''	25:A:446:G:H4'	1.61	0.81
25:A:351:G:H1	25:A:444:U:H3	1.26	0.81
1:a:728:A:O2'	1:a:729:A:N7	2.14	0.81
25:A:1540:U:H3	25:A:1632:G:H1	1.28	0.81
25:A:1550:G:H1	25:A:1620:U:H3	1.26	0.80
25:A:273:A:N6	25:A:313:G:H21	1.80	0.80
25:A:273:A:N6	25:A:313:G:N2	2.30	0.80
25:A:998:G:H1	25:A:1009:U:H3	0.85	0.79
1:a:884:G:H5'	21:u:18:ARG:HH12	1.47	0.79
1:a:407:A:H5''	4:d:107:ARG:HD2	1.64	0.79
1:a:82:U:H3	1:a:87:G:H1	0.82	0.79
40:P:11:GLY:HA3	40:P:16:HIS:HD2	1.49	0.78
25:A:1379:G:OP1	54:4:16:ARG:NH2	2.17	0.78
14:n:47:MET:HE3	14:n:53:LEU:HD21	1.64	0.77
48:X:39:GLY:HA3	48:X:99:VAL:HG22	1.67	0.77
1:a:72:G:N1	1:a:97:A:N6	2.32	0.76
1:a:376:G:O6	1:a:387:U:C4	2.38	0.76
23:y:39:PSU:H3'	23:y:40:C:H5''	1.67	0.76
13:m:16:GLU:HG3	13:m:17:ILE:HD12	1.67	0.76
1:a:438:U:H3	1:a:476:A:H8	1.34	0.75
1:a:376:G:N1	1:a:387:U:C2	2.55	0.75
38:N:44:LYS:HG3	38:N:45:ASN:H	1.51	0.75
25:A:1754:G:H1	25:A:1759:A:N6	1.85	0.75
1:a:653:G:H2'	1:a:654:G:C8	2.22	0.75
6:f:2:ARG:HH12	6:f:69:PRO:HG3	1.50	0.75
30:F:87:ARG:H	30:F:90:MET:HE2	1.50	0.74
1:a:1295:U:OP1	19:s:6:LYS:NZ	2.21	0.74
1:a:485:G:H2'	1:a:486:G:C8	2.21	0.74
24:z:77:ILE:HB	24:z:85:VAL:HB	1.68	0.74
1:a:144:G:H2'	1:a:145:G:C8	2.22	0.74
25:A:326:A:H2	25:A:449:G:H1	1.36	0.73
1:a:772:A:O2'	1:a:774:A:N7	2.21	0.73
1:a:60:U:H2'	1:a:61:G:C8	2.24	0.73
1:a:375:U:H5'	16:p:69:PRO:HG3	1.68	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:p:41:HIS:HD2	16:p:48:LEU:HD23	1.53	0.73
25:A:919:A:OP1	38:N:44:LYS:NZ	2.18	0.73
30:F:147:GLU:OE1	53:3:27:THR:OG1	2.06	0.73
1:a:1338:G:H2'	1:a:1339:A:H8	1.54	0.73
1:a:1066:U:H3	1:a:1079:G:H22	1.36	0.72
25:A:994:A:N6	25:A:1014:G:O2'	2.22	0.72
25:A:287:A:N6	25:A:299:G:O2'	2.22	0.72
25:A:1720:G:N2	27:C:99:ASP:O	2.22	0.72
23:y:49:C:H42	23:y:65:G:H1	1.35	0.72
25:A:289:A:N7	25:A:299:G:N2	2.38	0.72
1:a:297:G:N2	1:a:300:A:OP2	2.21	0.72
23:y:26:A:H61	23:y:44:G:H1	1.37	0.72
38:N:84:ASN:ND2	38:N:117:LYS:O	2.23	0.72
16:p:41:HIS:HB2	16:p:48:LEU:HB3	1.71	0.71
1:a:1300:A:OP1	19:s:7:LYS:NZ	2.21	0.71
1:a:411:A:N6	1:a:430:A:N7	2.38	0.71
25:A:329:U:O2	25:A:446:G:O6	2.08	0.71
1:a:187:U:O2	1:a:201:G:O6	2.09	0.70
4:d:90:GLU:HA	4:d:95:ASN:HD22	1.55	0.70
25:A:337:U:O2	25:A:344:G:N2	2.20	0.70
25:A:1754:G:N1	25:A:1759:A:N6	2.38	0.70
1:a:1338:G:H2'	1:a:1339:A:C8	2.26	0.70
1:a:1405:G:H5'	37:M:48:PRO:HB3	1.72	0.70
25:A:2587:U:OP2	57:7:43:ARG:NH2	2.24	0.70
13:m:29:ARG:O	13:m:33:ILE:HG12	1.91	0.70
25:A:329:U:O2	25:A:447:A:N6	2.24	0.70
1:a:358:U:H2'	1:a:359:G:H8	1.55	0.70
1:a:940:A:N6	19:s:77:THR:O	2.24	0.70
1:a:374:A:OP1	1:a:453:G:N2	2.25	0.70
1:a:1104:G:N2	1:a:1105:U:O4	2.22	0.70
25:A:2380:G:O2'	25:A:2381:A:N7	2.25	0.70
25:A:544:U:H1'	46:V:71:THR:HG23	1.73	0.70
1:a:593:C:OP2	4:d:76:ARG:NH2	2.25	0.70
25:A:1541:G:N2	25:A:1631:A:N1	2.40	0.69
1:a:996:G:N2	1:a:999:A:OP2	2.21	0.69
25:A:747:A:N6	25:A:768:G:O2'	2.25	0.69
1:a:426:U:H4'	4:d:34:GLY:H	1.58	0.69
8:h:74:ILE:HD12	8:h:77:LEU:HD11	1.73	0.69
12:l:71:GLY:O	12:l:99:ARG:NH2	2.26	0.69
30:F:141:GLU:HG3	30:F:143:SER:H	1.56	0.69
1:a:92:A:H1'	1:a:93:C:H5	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:s:36:ARG:NH1	19:s:52:HIS:O	2.26	0.69
37:M:88:LYS:HE2	37:M:92:ASP:HB2	1.74	0.69
51:1:22:LEU:HD21	51:1:58:TYR:HE1	1.58	0.69
1:a:66:U:O2	1:a:101:G:N2	2.23	0.69
1:a:424:G:H2'	1:a:425:G:C8	2.28	0.69
25:A:752:C:H2'	25:A:753:A:H8	1.58	0.69
25:A:1533:U:OP2	25:A:1535:C:N4	2.25	0.69
1:a:438:U:O2	1:a:476:A:N7	2.26	0.68
25:A:1164:A:O2'	33:I:6:LYS:NZ	2.24	0.68
1:a:426:U:H2'	1:a:427:U:C6	2.28	0.68
7:g:138:ARG:HG2	7:g:142:HIS:CE1	2.28	0.68
25:A:2819:G:N2	25:A:2822:A:OP2	2.26	0.68
37:M:93:PRO:HG3	37:M:114:ILE:HG12	1.74	0.68
4:d:42:LYS:O	4:d:47:ARG:NH2	2.26	0.68
25:A:759:G:H1	49:Y:64:PRO:HB3	1.58	0.68
1:a:82:U:O2	1:a:87:G:N2	2.23	0.68
1:a:502:C:H41	12:l:50:ARG:HH22	1.42	0.68
25:A:1710:A:N6	25:A:1716:A:OP2	2.26	0.68
25:A:326:A:N1	25:A:449:G:O6	2.26	0.68
1:a:181:C:O2	1:a:208:G:N2	2.26	0.68
18:r:57:CYS:SG	18:r:60:HIS:ND1	2.67	0.67
50:Z:33:ILE:HA	50:Z:52:CYS:HA	1.75	0.67
1:a:376:G:N1	1:a:387:U:N3	2.41	0.67
1:a:654:G:H2'	1:a:655:A:H8	1.58	0.67
13:m:69:ASP:OD1	13:m:70:LEU:N	2.28	0.67
25:A:1863:G:H5''	25:A:1864:U:H5'	1.76	0.67
32:H:124:ILE:HG22	32:H:125:LYS:H	1.59	0.67
34:J:45:ASN:OD1	34:J:52:ARG:NH2	2.27	0.67
1:a:518:U:H2'	1:a:519:A:H8	1.59	0.67
25:A:1561:C:H42	25:A:1610:C:H42	1.40	0.67
16:p:74:LEU:HD22	16:p:79:ASP:HB3	1.75	0.67
1:a:272:C:H2'	1:a:273:A:H8	1.60	0.67
40:P:37:THR:HG22	40:P:39:PRO:HD2	1.76	0.67
4:d:19:LEU:HG	4:d:20:VAL:HG23	1.76	0.67
1:a:415:C:N4	1:a:428:G:O6	2.28	0.66
9:i:75:VAL:HG21	9:i:107:LEU:HD23	1.75	0.66
13:m:52:GLN:HA	13:m:55:VAL:HG22	1.75	0.66
17:q:37:VAL:HG22	17:q:60:LYS:HG2	1.76	0.66
25:A:1628:A:N3	25:A:1630:U:N3	2.42	0.66
4:d:154:ARG:NH2	4:d:171:GLU:O	2.28	0.66
9:i:32:ARG:HG3	9:i:33:LYS:HG2	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:351:G:O6	25:A:444:U:O2	2.14	0.66
25:A:1002:C:OP1	25:A:1006:G:N2	2.28	0.66
13:m:69:ASP:HA	13:m:72:ARG:HE	1.60	0.66
33:I:51:VAL:HG12	33:I:78:ALA:HA	1.77	0.66
1:a:392:C:P	16:p:9:ARG:HH12	2.18	0.66
42:R:2:ASN:HB3	42:R:5:ASP:HB3	1.78	0.66
1:a:42:G:H22	1:a:397:A:H5''	1.60	0.66
25:A:2361:U:H3	25:A:2376:G:H1	1.42	0.66
1:a:72:G:N2	1:a:97:A:N1	2.43	0.66
30:F:52:ARG:HH12	30:F:85:LYS:HB2	1.61	0.66
30:F:117:ARG:NH2	30:F:143:SER:O	2.29	0.66
4:d:11:LYS:NZ	4:d:55:LYS:HA	2.10	0.66
23:y:4:C:H42	23:y:69:G:H1	1.44	0.66
54:4:31:SER:OG	54:4:36:GLN:NE2	2.29	0.66
25:A:1754:G:N2	25:A:1759:A:N1	2.43	0.65
1:a:1209:C:OP1	13:m:108:ARG:NH2	2.29	0.65
1:a:451:A:N6	1:a:461:G:OP2	2.28	0.65
1:a:1438:G:H2'	1:a:1439:G:C8	2.31	0.65
30:F:70:GLN:NE2	30:F:97:THR:O	2.30	0.65
1:a:693:G:H2'	1:a:694:G:C8	2.31	0.65
3:c:188:GLU:OE1	3:c:195:ARG:NH2	2.29	0.65
16:p:6:LYS:HD3	16:p:23:ALA:HB3	1.77	0.65
25:A:899:G:H5'	27:C:227:ASN:HD21	1.62	0.65
1:a:1289:U:O2'	13:m:110:ARG:NH2	2.28	0.65
1:a:1329:G:N2	1:a:1357:A:OP2	2.25	0.65
48:X:178:VAL:HG12	48:X:179:VAL:HG23	1.77	0.65
13:m:79:ARG:HA	13:m:82:ILE:HG12	1.78	0.65
25:A:1938:G:H21	25:A:1956:A:H62	1.43	0.65
1:a:66:U:H3	1:a:101:G:H1	1.44	0.65
1:a:979:U:H2'	1:a:980:G:H8	1.62	0.65
4:d:49:GLN:HB3	4:d:198:LEU:HB2	1.78	0.65
10:j:51:VAL:HG13	14:n:41:ARG:HB2	1.78	0.65
1:a:496:U:H3	1:a:513:A:H62	1.45	0.65
1:a:722:G:OP2	15:o:35:ARG:NH2	2.30	0.65
3:c:11:ARG:NH2	3:c:175:LEU:O	2.30	0.65
38:N:58:HIS:O	57:7:13:ARG:NH1	2.29	0.64
1:a:1284:U:O4	13:m:14:ARG:NH1	2.30	0.64
7:g:130:GLY:O	7:g:136:LYS:NZ	2.30	0.64
16:p:71:LEU:O	16:p:75:LYS:HG2	1.98	0.64
25:A:2350:G:O2'	25:A:2351:A:N7	2.26	0.64
1:a:1203:G:H5''	19:s:78:ARG:HH21	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:g:32:LEU:HG	7:g:33:GLU:HG2	1.78	0.64
25:A:137:G:H21	25:A:1524:G:H1'	1.63	0.64
25:A:1530:G:N2	25:A:1805:G:H1	1.95	0.64
1:a:375:U:N3	1:a:376:G:N7	2.46	0.64
1:a:986:G:N2	1:a:987:A:N3	2.46	0.64
2:b:166:THR:HG23	2:b:173:VAL:HG21	1.80	0.64
42:R:51:GLY:HA2	42:R:56:GLU:HG3	1.79	0.64
1:a:698:A:H5'	11:k:128:ASN:HB2	1.79	0.64
1:a:746:A:OP2	1:a:792:G:N2	2.30	0.64
1:a:1231:A:H2'	1:a:1232:A:C8	2.33	0.64
1:a:222:U:H2'	1:a:223:G:H8	1.62	0.64
12:l:72:HIS:HD2	12:l:74:LEU:HB2	1.63	0.64
16:p:7:LEU:HD22	16:p:18:TYR:HB3	1.80	0.64
1:a:586:G:N2	1:a:612:U:OP1	2.28	0.64
28:D:129:ARG:HG3	28:D:170:MET:HB3	1.78	0.64
1:a:1051:C:H2'	1:a:1052:G:H8	1.62	0.64
25:A:389:G:N1	25:A:392:A:OP2	2.27	0.64
6:f:15:ASP:OD2	6:f:17:ARG:NH1	2.31	0.63
55:5:6:ASP:O	55:5:8:ARG:N	2.30	0.63
1:a:87:G:H2'	1:a:88:G:H8	1.62	0.63
1:a:196:G:H2'	1:a:197:G:H8	1.63	0.63
13:m:49:THR:H	13:m:52:GLN:NE2	1.96	0.63
1:a:1356:G:OP1	7:g:36:LYS:NZ	2.30	0.63
4:d:90:GLU:OE1	4:d:99:ARG:NH1	2.32	0.63
19:s:41:ILE:HG22	19:s:43:ASP:H	1.62	0.63
25:A:947:U:H2'	25:A:948:G:H8	1.61	0.63
10:j:56:HIS:O	10:j:57:LYS:HG2	1.99	0.63
23:y:26:A:N6	23:y:44:G:H1	1.96	0.63
24:z:288:ASP:HB2	24:z:362:ARG:HG3	1.79	0.63
25:A:58:G:OP2	51:1:51:ARG:NH2	2.31	0.63
4:d:90:GLU:OE1	4:d:95:ASN:ND2	2.30	0.63
13:m:108:ARG:HH21	13:m:114:LYS:HA	1.64	0.63
25:A:277:U:H2'	25:A:278:A:C8	2.34	0.63
30:F:81:ILE:HG22	30:F:86:LEU:HB3	1.81	0.63
1:a:107:G:H1	1:a:330:C:H41	1.44	0.63
1:a:219:C:H2'	1:a:220:G:H8	1.64	0.63
7:g:79:ARG:HH12	7:g:82:GLY:H	1.46	0.63
20:t:7:GLN:O	20:t:11:ILE:HG13	1.98	0.63
25:A:1229:A:H8	25:A:1230:G:H1'	1.62	0.63
1:a:694:G:H2'	1:a:695:A:C8	2.34	0.63
2:b:27:MET:HG2	2:b:193:PRO:HG3	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:g:26:LEU:HA	7:g:101:LEU:HD21	1.80	0.63
25:A:273:A:N6	25:A:313:G:C2	2.66	0.63
2:b:1:MET:N	2:b:51:ASP:OD2	2.30	0.62
25:A:1544:U:O4	25:A:1626:G:O6	2.16	0.62
1:a:24:U:O2'	1:a:553:A:N6	2.31	0.62
1:a:1186:U:H4'	3:c:195:ARG:HD3	1.81	0.62
25:A:1788:G:H5'	27:C:60:ARG:HA	1.80	0.62
25:A:2359:G:H1	25:A:2378:U:H3	1.36	0.62
1:a:380:G:N2	1:a:383:A:OP2	2.27	0.62
1:a:1199:C:H2'	1:a:1200:A:H8	1.63	0.62
25:A:499:G:OP2	25:A:2630:A:O2'	2.17	0.62
1:a:407:A:H2'	1:a:408:G:C8	2.34	0.62
4:d:164:SER:OG	4:d:185:GLN:NE2	2.31	0.62
6:f:17:ARG:NH2	25:A:1560:U:O2	2.33	0.62
1:a:1120:G:H4'	1:a:1121:G:H5'	1.82	0.62
6:f:37:VAL:HB	6:f:66:LYS:HB3	1.81	0.62
25:A:2220:C:OP1	37:M:31:ARG:NH1	2.32	0.62
25:A:1426:G:OP2	25:A:1426:G:N2	2.30	0.62
44:T:60:VAL:HG22	44:T:102:ILE:HG12	1.82	0.62
1:a:222:U:H2'	1:a:223:G:C8	2.34	0.62
7:g:116:MET:HA	7:g:119:ARG:HB2	1.82	0.62
4:d:145:LEU:HD12	4:d:150:PHE:HE2	1.63	0.62
19:s:3:ARG:HE	19:s:7:LYS:HB2	1.64	0.62
25:A:745:G:OP1	57:7:19:THR:OG1	2.17	0.62
1:a:632:U:O4	1:a:732:G:O2'	2.18	0.62
25:A:1690:A:H2'	25:A:1691:A:C8	2.35	0.62
1:a:25:G:H2'	1:a:26:G:H8	1.64	0.61
25:A:2394:A:O2'	25:A:2396:A:OP1	2.17	0.61
57:7:29:ARG:NH1	57:7:41:THR:O	2.33	0.61
13:m:40:ASP:HB3	13:m:43:MET:HG2	1.82	0.61
17:q:27:VAL:HG22	17:q:72:ASP:H	1.65	0.61
18:r:18:ARG:NH2	18:r:53:VAL:O	2.33	0.61
25:A:81:A:OP1	47:W:4:HIS:NE2	2.33	0.61
25:A:1094:G:HO2'	25:A:1274:A:HO2'	1.49	0.61
1:a:416:G:N2	1:a:427:U:O2	2.29	0.61
4:d:15:LEU:HD22	4:d:51:GLN:HG2	1.82	0.61
3:c:58:ARG:HG3	3:c:63:VAL:HG22	1.81	0.61
16:p:57:GLN:NE2	16:p:79:ASP:OD1	2.33	0.61
25:A:1540:U:O4	25:A:1632:G:O6	2.18	0.61
48:X:158:THR:HB	48:X:161:GLN:HE22	1.64	0.61
5:e:109:PRO:HB3	5:e:122:ARG:HG2	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:l:111:LYS:O	12:l:114:ARG:NH1	2.33	0.61
24:z:205:ARG:HE	24:z:222:GLN:HE21	1.48	0.61
1:a:50:G:O2'	1:a:365:U:O2'	2.13	0.61
1:a:407:A:H2'	1:a:408:G:H8	1.65	0.61
34:J:103:THR:OG1	34:J:106:GLN:OE1	2.16	0.61
41:Q:87:LEU:HD22	41:Q:91:ARG:HH21	1.65	0.61
1:a:437:U:H5'	4:d:147:THR:HG23	1.83	0.61
1:a:531:U:O2'	12:l:83:ARG:NH1	2.34	0.61
1:a:1106:U:O4	10:j:9:ARG:NH1	2.33	0.61
25:A:2178:G:O2'	25:A:2180:U:O4	2.16	0.61
25:A:2248:C:H2'	25:A:2249:G:H8	1.66	0.61
25:A:2571:C:O2'	55:5:23:TYR:OH	2.18	0.61
58:8:2:LYS:NZ	58:8:31:ARG:O	2.34	0.61
25:A:1541:G:H1	25:A:1631:A:N6	1.98	0.61
11:k:59:VAL:HG11	11:k:74:LEU:HB3	1.83	0.61
25:A:1201:G:N2	25:A:1204:A:OP2	2.22	0.61
1:a:505:C:H2'	1:a:506:C:C6	2.36	0.60
1:a:401:C:O2'	1:a:601:A:N3	2.33	0.60
1:a:1410:C:H2'	1:a:1411:A:H8	1.67	0.60
3:c:137:ILE:HD11	3:c:151:VAL:HG12	1.81	0.60
8:h:12:THR:HG22	8:h:15:ARG:HH12	1.67	0.60
26:B:9:G:OP1	41:Q:26:ARG:NH1	2.34	0.60
25:A:996:G:H2'	25:A:997:G:C8	2.36	0.60
1:a:979:U:H2'	1:a:980:G:C8	2.36	0.60
25:A:1022:C:OP1	39:O:24:GLY:N	2.33	0.60
25:A:2255:A:N3	25:A:2679:G:O2'	2.31	0.60
4:d:183:ARG:NH1	4:d:183:ARG:O	2.35	0.60
20:t:35:PHE:HD1	20:t:50:LEU:HD12	1.66	0.60
20:t:58:LEU:HD13	20:t:72:ALA:HB1	1.84	0.60
53:3:9:TYR:CD1	53:3:25:ARG:HD2	2.37	0.60
1:a:53:U:H3	1:a:362:G:H1'	1.66	0.60
10:j:42:LEU:HB2	10:j:71:LYS:HG3	1.84	0.60
16:p:5:ILE:HG22	16:p:70:VAL:HG21	1.84	0.60
23:y:49:C:N4	23:y:65:G:H1	2.00	0.60
25:A:290:C:N4	25:A:298:G:H1	1.99	0.60
25:A:1000:C:H3'	25:A:1001:C:H5''	1.84	0.60
50:Z:41:ARG:HG3	50:Z:43:GLY:H	1.65	0.60
1:a:598:C:N4	1:a:601:A:OP2	2.35	0.60
1:a:1208:A:N7	19:s:83:HIS:ND1	2.46	0.60
9:i:41:LEU:HD21	9:i:81:PHE:HD1	1.67	0.60
16:p:75:LYS:HZ2	16:p:80:TRP:CD1	2.19	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:1078:G:O6	59:9:8:LYS:NZ	2.35	0.60
25:A:1533:U:H5''	25:A:1535:C:H42	1.66	0.60
34:J:10:LEU:HD22	34:J:61:THR:HA	1.83	0.60
4:d:107:ARG:HA	4:d:110:ARG:HG2	1.84	0.59
16:p:86:LEU:HG	16:p:87:PRO:HD3	1.84	0.59
25:A:1273:G:OP2	43:S:58:ARG:NH1	2.34	0.59
26:B:5:C:OP1	26:B:62:C:O2'	2.20	0.59
30:F:118:ILE:HB	30:F:121:PHE:HB2	1.82	0.59
1:a:1000:U:H2'	1:a:1001:G:H8	1.68	0.59
7:g:103:TRP:CG	7:g:137:ARG:HH22	2.19	0.59
25:A:929:C:H1'	25:A:1339:G:H21	1.66	0.59
25:A:2552:A:H2'	25:A:2553:G:C8	2.37	0.59
4:d:141:LYS:O	4:d:145:LEU:N	2.35	0.59
6:f:2:ARG:NH1	6:f:69:PRO:HG3	2.16	0.59
19:s:70:LYS:HB2	19:s:73:GLU:HB2	1.83	0.59
1:a:209:A:O2'	1:a:210:A:O4'	2.20	0.59
1:a:980:G:N2	1:a:1023:U:O2	2.33	0.59
2:b:125:GLY:O	2:b:129:ARG:NH2	2.30	0.59
5:e:175:PRO:HB2	5:e:186:ILE:HD11	1.83	0.59
3:c:22:TRP:NE1	14:n:54:PRO:HG3	2.18	0.59
25:A:1996:U:OP2	25:A:2001:A:N6	2.25	0.59
25:A:2317:G:H1	25:A:2418:U:H3	1.51	0.59
1:a:1129:U:H1'	9:i:38:ARG:HH21	1.67	0.59
25:A:1653:G:H2'	25:A:1654:G:C8	2.38	0.59
1:a:1130:C:H2'	1:a:1131:G:C8	2.37	0.59
2:b:140:GLU:O	2:b:144:LEU:HD23	2.02	0.59
25:A:1541:G:C6	25:A:1631:A:N6	2.70	0.59
34:J:39:GLU:HA	34:J:42:LYS:HE3	1.84	0.59
19:s:36:ARG:HG2	19:s:72:GLY:HA3	1.83	0.59
25:A:1552:A:N6	25:A:1616:A:OP2	2.36	0.59
25:A:2350:G:N2	25:A:2384:C:O2'	2.35	0.59
45:U:90:LYS:HG2	45:U:102:ARG:HH21	1.68	0.59
1:a:402:G:H5'	1:a:601:A:H1'	1.85	0.58
30:F:23:LEU:HD13	30:F:36:PRO:HG2	1.84	0.58
51:1:14:THR:HG22	51:1:17:GLU:HG2	1.83	0.58
3:c:76:ILE:HG13	3:c:102:ILE:HD12	1.85	0.58
25:A:1212:U:H2'	25:A:1213:A:H5''	1.84	0.58
1:a:1266:U:H2'	1:a:1267:U:H5''	1.85	0.58
4:d:165:TRP:HD1	4:d:185:GLN:HG2	1.68	0.58
8:h:103:VAL:HG13	8:h:114:THR:HG23	1.85	0.58
25:A:997:G:H1	25:A:1010:U:H3	1.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:2467:U:H2'	25:A:2468:U:C6	2.38	0.58
1:a:397:A:N7	1:a:527:A:O2'	2.35	0.58
25:A:996:G:H2'	25:A:997:G:H8	1.68	0.58
25:A:1809:U:H2'	25:A:1810:A:H8	1.68	0.58
25:A:2386:U:H2'	25:A:2387:U:H4'	1.84	0.58
25:A:3096:U:H1'	42:R:1:MET:H3	1.69	0.58
1:a:316:C:OP2	1:a:351:G:O2'	2.18	0.58
1:a:1199:C:H2'	1:a:1200:A:C8	2.38	0.58
4:d:182:GLU:H	4:d:185:GLN:HB3	1.69	0.58
38:N:44:LYS:HG3	38:N:45:ASN:N	2.18	0.58
7:g:94:ASP:OD1	7:g:95:ARG:N	2.36	0.58
13:m:71:ARG:O	13:m:75:GLN:NE2	2.36	0.58
24:z:301:VAL:HG12	24:z:326:VAL:HG22	1.86	0.58
25:A:978:A:OP1	39:O:22:SER:OG	2.19	0.58
25:A:1306:G:OP2	38:N:29:LYS:NZ	2.36	0.58
1:a:49:U:O4	1:a:396:G:O6	2.20	0.58
1:a:858:A:H1'	8:h:12:THR:HG21	1.85	0.58
39:O:59:LYS:HB3	39:O:60:ARG:HD2	1.86	0.58
1:a:1337:A:H2'	1:a:1338:G:H8	1.67	0.58
25:A:1476:G:H2'	25:A:1477:C:C6	2.39	0.58
26:B:76:G:H1'	48:X:36:VAL:HG21	1.84	0.58
1:a:1105:U:O2'	1:a:1106:U:O5'	2.16	0.58
25:A:1640:A:H2'	25:A:1642:G:N7	2.19	0.57
1:a:322:C:H42	1:a:329:A:H62	1.52	0.57
8:h:80:VAL:HG12	8:h:87:VAL:HG11	1.86	0.57
25:A:380:A:N3	25:A:401:C:O2'	2.33	0.57
1:a:654:G:H2'	1:a:655:A:C8	2.37	0.57
4:d:154:ARG:NH1	4:d:155:GLU:OE2	2.37	0.57
11:k:76:ALA:HB1	11:k:109:LEU:HD12	1.86	0.57
24:z:102:ASP:O	24:z:306:ARG:NH2	2.37	0.57
25:A:2862:G:O2'	25:A:3002:A:N6	2.37	0.57
10:j:64:HIS:HB3	14:n:59:SER:HB2	1.84	0.57
1:a:1000:U:H2'	1:a:1001:G:C8	2.39	0.57
25:A:451:U:H2'	25:A:452:G:C8	2.40	0.57
25:A:1706:A:H2'	25:A:1707:G:H8	1.69	0.57
25:A:2089:C:O2'	25:A:2090:U:O4'	2.22	0.57
1:a:450:G:H4'	16:p:42:PRO:HB3	1.86	0.57
12:l:3:THR:HG22	12:l:5:GLN:H	1.68	0.57
24:z:305:ALA:HB3	24:z:308:THR:HG22	1.86	0.57
25:A:1621:C:H2'	25:A:1622:G:C8	2.39	0.57
1:a:373:A:N3	1:a:462:A:N6	2.53	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:928:A:H2'	1:a:929:G:H8	1.68	0.57
1:a:185:G:O6	1:a:204:A:N6	2.38	0.57
4:d:67:PHE:HA	4:d:70:TYR:HD2	1.70	0.57
13:m:91:ARG:HG2	13:m:98:VAL:HA	1.87	0.57
19:s:36:ARG:HH12	19:s:53:ASP:HA	1.69	0.57
51:1:22:LEU:HD21	51:1:58:TYR:CE1	2.37	0.57
1:a:1184:C:OP1	14:n:2:ALA:N	2.38	0.57
7:g:138:ARG:O	7:g:141:THR:OG1	2.15	0.57
13:m:73:GLU:O	13:m:76:ALA:HB3	2.04	0.57
25:A:263:G:O2'	25:A:517:A:N3	2.36	0.57
7:g:27:VAL:HA	7:g:30:VAL:HG12	1.85	0.56
12:l:23:ALA:HB1	12:l:61:VAL:HG21	1.86	0.56
39:O:42:ILE:HD12	39:O:97:VAL:HG21	1.87	0.56
1:a:998:G:H2'	1:a:999:A:C8	2.40	0.56
33:I:54:ASN:OD1	33:I:55:THR:N	2.33	0.56
1:a:332:G:OP2	20:t:3:ASN:N	2.39	0.56
1:a:344:A:H5''	1:a:345:C:H5	1.69	0.56
1:a:414:A:N6	1:a:431:A:O2'	2.37	0.56
1:a:518:U:H2'	1:a:519:A:C8	2.39	0.56
1:a:1014:U:H2'	1:a:1015:G:C8	2.39	0.56
5:e:135:ALA:HB1	5:e:162:VAL:HG23	1.87	0.56
25:A:604:C:OP2	54:4:10:ARG:NH2	2.38	0.56
25:A:960:G:OP2	25:A:960:G:N2	2.25	0.56
24:z:116:ARG:NH1	24:z:241:THR:OG1	2.38	0.56
25:A:2043:C:O2'	25:A:2195:U:OP2	2.23	0.56
1:a:449:C:N3	16:p:43:LYS:NZ	2.39	0.56
1:a:499:C:H4'	24:z:39:ARG:HH22	1.71	0.56
1:a:993:G:H1	1:a:1002:U:H3	1.53	0.56
1:a:1274:C:H2'	1:a:1275:G:H8	1.71	0.56
1:a:1457:G:H2'	1:a:1458:G:C8	2.41	0.56
2:b:72:THR:O	2:b:77:GLN:NE2	2.38	0.56
25:A:329:U:H2'	25:A:446:G:H1	1.70	0.56
25:A:1162:G:OP2	33:I:3:LYS:NZ	2.38	0.56
46:V:7:PRO:HG3	46:V:48:LYS:HD3	1.87	0.56
1:a:21:U:H2'	1:a:22:C:C6	2.41	0.56
1:a:695:A:H2'	1:a:696:A:C8	2.40	0.56
1:a:1305:G:H2'	1:a:1306:A:C8	2.41	0.56
23:y:28:G:H2'	23:y:29:G:C8	2.40	0.56
25:A:706:G:O2'	29:E:160:ARG:NH2	2.38	0.56
25:A:740:A:O2'	25:A:741:G:OP2	2.21	0.56
33:I:66:ILE:HB	33:I:69:LEU:HD12	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:410:G:N2	1:a:431:A:N7	2.53	0.56
1:a:1260:A:OP2	10:j:11:LYS:NZ	2.39	0.56
4:d:90:GLU:HG3	4:d:186:ILE:HD13	1.88	0.56
20:t:51:LEU:HD12	20:t:83:LEU:HD22	1.87	0.56
1:a:25:G:H2'	1:a:26:G:C8	2.40	0.56
1:a:376:G:N2	1:a:387:U:O2	2.38	0.56
9:i:54:THR:HG23	9:i:56:GLU:H	1.70	0.56
30:F:27:PHE:CE2	30:F:172:GLU:HG3	2.40	0.56
1:a:177:U:N3	1:a:209:A:N6	2.31	0.56
1:a:1036:U:H5'	3:c:163:SER:HB2	1.88	0.56
1:a:1203:G:OP1	19:s:78:ARG:NH2	2.39	0.56
25:A:1455:U:OP2	46:V:62:ARG:NH2	2.39	0.56
25:A:2106:A:H3'	25:A:2107:G:H5''	1.88	0.56
1:a:1251:G:H2'	1:a:1252:G:C8	2.41	0.55
1:a:1440:A:H3'	1:a:1441:G:H8	1.71	0.55
8:h:51:THR:HG22	8:h:58:LYS:HD2	1.88	0.55
34:J:16:GLN:HA	34:J:55:VAL:HA	1.87	0.55
39:O:30:GLY:O	39:O:134:ARG:NH1	2.39	0.55
1:a:11:G:H1	5:e:122:ARG:HH11	1.54	0.55
1:a:49:U:H2'	1:a:50:G:C8	2.41	0.55
1:a:737:U:H2'	1:a:738:G:O4'	2.07	0.55
1:a:1269:A:H2	1:a:1335:G:H1'	1.70	0.55
1:a:1337:A:H2'	1:a:1338:G:C8	2.41	0.55
5:e:40:VAL:HG12	5:e:62:VAL:HG22	1.87	0.55
25:A:1001:C:N4	25:A:1006:G:O6	2.38	0.55
4:d:167:GLN:HB3	4:d:169:VAL:HG23	1.88	0.55
5:e:70:MET:HE2	5:e:98:ARG:HH11	1.70	0.55
25:A:81:A:N1	25:A:96:G:O2'	2.29	0.55
25:A:999:C:H2'	25:A:1000:C:C6	2.41	0.55
1:a:976:A:N1	14:n:4:LYS:NZ	2.55	0.55
4:d:164:SER:O	4:d:167:GLN:NE2	2.39	0.55
24:z:148:GLY:HA2	49:Y:3:HIS:HB3	1.88	0.55
25:A:80:G:OP1	47:W:94:LYS:NZ	2.32	0.55
25:A:935:A:H4'	25:A:951:G:N2	2.21	0.55
25:A:1704:U:H2'	25:A:1705:C:C6	2.41	0.55
27:C:198:ASN:ND2	27:C:201:GLN:OE1	2.39	0.55
1:a:163:G:H2'	1:a:164:G:H8	1.70	0.55
1:a:562:U:OP2	1:a:738:G:N1	2.28	0.55
1:a:1311:G:H5''	13:m:26:GLY:H	1.71	0.55
11:k:27:HIS:HD2	11:k:90:LYS:HB3	1.72	0.55
25:A:287:A:N1	25:A:300:G:N1	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:2611:U:O4'	49:Y:41:ARG:NH1	2.40	0.55
1:a:98:G:H21	1:a:148:A:H2	1.55	0.55
1:a:1230:C:H42	1:a:1271:A:H62	1.53	0.55
23:y:69:G:H2'	23:y:70:G:H8	1.70	0.55
24:z:311:ARG:H	24:z:315:MET:HE2	1.71	0.55
25:A:1195:A:N1	25:A:1206:A:O2'	2.35	0.55
25:A:2249:G:H2'	25:A:2250:A:C8	2.42	0.55
25:A:2357:A:H8	25:A:2380:G:H21	1.54	0.55
25:A:2527:G:H21	30:F:136:THR:HG21	1.72	0.55
30:F:14:ARG:NH2	30:F:179:ALA:O	2.39	0.55
1:a:87:G:H2'	1:a:88:G:C8	2.41	0.55
1:a:1506:U:H2'	1:a:1507:G:H8	1.70	0.55
5:e:130:VAL:O	5:e:137:ARG:NH2	2.40	0.55
5:e:140:LEU:HD13	5:e:148:ILE:HG21	1.88	0.55
25:A:2389:U:O4	25:A:2393:A:N6	2.39	0.55
34:J:114:LYS:HB3	34:J:118:LEU:HD13	1.89	0.55
16:p:48:LEU:HD13	16:p:96:LYS:HE2	1.89	0.55
25:A:306:U:H5''	32:H:41:ARG:HG2	1.88	0.55
25:A:2359:G:N1	25:A:2378:U:N3	2.41	0.55
31:G:103:ASN:HB3	31:G:115:LEU:HD11	1.89	0.55
32:H:126:SER:OG	32:H:130:HIS:NE2	2.38	0.55
36:L:77:HIS:CD2	36:L:79:GLY:H	2.25	0.55
43:S:47:TYR:OH	43:S:51:ARG:NH2	2.37	0.55
53:3:14:VAL:HB	53:3:22:PHE:HB2	1.87	0.55
1:a:146:A:H2'	1:a:147:U:H6	1.72	0.55
1:a:819:U:H3	1:a:829:G:H1	1.55	0.55
7:g:15:ASP:OD2	7:g:18:TYR:N	2.39	0.55
9:i:42:VAL:HG12	9:i:44:GLY:H	1.70	0.55
25:A:1809:U:H2'	25:A:1810:A:C8	2.42	0.55
1:a:429:U:H4'	4:d:9:THR:HG21	1.89	0.55
1:a:503:A:H2	12:l:88:LYS:HE2	1.70	0.55
1:a:970:G:H1'	1:a:998:G:H22	1.72	0.55
20:t:80:ALA:O	20:t:84:ASN:ND2	2.40	0.55
25:A:1548:C:N4	25:A:1549:G:O6	2.40	0.55
1:a:1350:U:H5'	10:j:62:ARG:NH1	2.22	0.54
15:o:74:ASP:OD1	15:o:75:VAL:N	2.40	0.54
16:p:66:PRO:HG2	16:p:80:TRP:CZ3	2.43	0.54
1:a:45:G:H2'	1:a:46:G:H8	1.71	0.54
1:a:642:C:H2'	1:a:643:A:C8	2.42	0.54
23:y:76:A:O2'	25:A:2618:C:N3	2.35	0.54
25:A:256:A:H2'	25:A:257:A:H8	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:3024:A:H2'	25:A:3025:G:H8	1.71	0.54
1:a:320:G:H2'	1:a:321:A:C8	2.43	0.54
25:A:1288:A:H2'	25:A:1289:A:C8	2.42	0.54
1:a:145:G:H2'	1:a:146:A:C8	2.43	0.54
1:a:254:G:O6	1:a:273:A:N6	2.40	0.54
1:a:1040:U:H2'	1:a:1041:G:H8	1.72	0.54
1:a:1274:C:H2'	1:a:1275:G:C8	2.43	0.54
13:m:75:GLN:HA	13:m:78:ILE:HD13	1.90	0.54
37:M:115:VAL:HG13	37:M:121:VAL:HG21	1.88	0.54
6:f:82:ASN:ND2	6:f:84:SER:OG	2.40	0.54
25:A:857:U:H2'	25:A:858:A:C8	2.42	0.54
50:Z:46:LYS:NZ	50:Z:64:ALA:O	2.40	0.54
1:a:146:A:H2'	1:a:147:U:C6	2.43	0.54
1:a:555:G:O2'	1:a:801:G:OP2	2.25	0.54
1:a:980:G:H1	1:a:1023:U:H3	1.55	0.54
1:a:1156:G:H2'	1:a:1157:A:H8	1.73	0.54
10:j:43:PRO:O	10:j:71:LYS:NZ	2.39	0.54
24:z:118:THR:HG23	24:z:193:PRO:HA	1.89	0.54
25:A:668:U:H2'	25:A:669:G:C8	2.43	0.54
30:F:178:ARG:HE	30:F:184:PHE:HB2	1.72	0.54
34:J:57:PRO:HG2	34:J:73:LYS:HB2	1.89	0.54
1:a:605:G:O2'	16:p:39:ARG:NH1	2.40	0.54
1:a:745:G:N1	1:a:792:G:O2'	2.30	0.54
25:A:2288:C:H2'	25:A:2289:C:C6	2.43	0.54
1:a:1296:C:H2'	1:a:1297:U:C6	2.43	0.54
25:A:72:G:H22	25:A:108:A:H2	1.55	0.54
25:A:1529:U:H3'	25:A:1530:G:C8	2.43	0.54
1:a:98:G:H2'	1:a:99:U:C6	2.43	0.54
1:a:1148:U:OP1	1:a:1150:A:N6	2.34	0.54
1:a:1180:U:H4'	10:j:56:HIS:CD2	2.42	0.54
1:a:1329:G:O6	9:i:32:ARG:NH2	2.41	0.54
2:b:83:GLU:OE2	2:b:214:THR:HB	2.08	0.54
2:b:184:ILE:HG12	2:b:198:TYR:HB2	1.88	0.54
7:g:51:ARG:HD2	7:g:58:PRO:HG3	1.90	0.54
25:A:357:U:H4'	25:A:358:G:O5'	2.06	0.54
25:A:406:A:N6	25:A:420:G:O2'	2.40	0.54
1:a:1349:C:O2'	10:j:62:ARG:NH1	2.40	0.54
3:c:190:LYS:HB3	3:c:195:ARG:NH1	2.23	0.54
25:A:935:A:H4'	25:A:951:G:H22	1.71	0.54
25:A:1544:U:H3	25:A:1626:G:H1	1.54	0.54
1:a:294:C:OP1	1:a:590:A:O2'	2.20	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1055:U:H5'	2:b:102:THR:HG21	1.89	0.53
8:h:10:PHE:HB2	8:h:33:LYS:HD3	1.90	0.53
8:h:15:ARG:NH2	8:h:77:LEU:O	2.25	0.53
45:U:35:SER:HA	45:U:77:VAL:HA	1.90	0.53
4:d:27:GLU:HA	4:d:30:PRO:HG3	1.90	0.53
16:p:101:SER:OG	16:p:104:ASP:OD2	2.26	0.53
25:A:995:U:H2'	25:A:996:G:C8	2.43	0.53
25:A:997:G:H22	25:A:1010:U:H3	1.55	0.53
25:A:1178:U:OP2	34:J:114:LYS:NZ	2.42	0.53
40:P:70:ILE:HD11	40:P:76:VAL:HG22	1.90	0.53
1:a:21:U:H2'	1:a:22:C:H6	1.74	0.53
1:a:421:U:H5''	1:a:422:C:H5	1.73	0.53
8:h:3:MET:HE1	8:h:9:ASP:HB2	1.90	0.53
20:t:4:ILE:HB	20:t:7:GLN:HB2	1.90	0.53
20:t:35:PHE:CE2	20:t:79:LEU:HD22	2.44	0.53
25:A:1560:U:H2'	25:A:1561:C:C6	2.43	0.53
25:A:2747:G:O2'	25:A:2988:A:O2'	2.26	0.53
25:A:2863:A:O2'	36:L:99:ARG:NH2	2.41	0.53
1:a:636:G:O2'	15:o:28:GLN:NE2	2.42	0.53
1:a:846:A:H5'	5:e:116:ALA:HB2	1.90	0.53
4:d:67:PHE:HA	4:d:70:TYR:CD2	2.43	0.53
25:A:3018:U:H2'	25:A:3019:C:C6	2.43	0.53
53:3:36:GLU:OE1	53:3:37:VAL:HG23	2.09	0.53
1:a:269:U:H2'	1:a:270:A:C8	2.43	0.53
1:a:438:U:C2	1:a:476:A:N7	2.76	0.53
1:a:674:G:H22	1:a:768:U:H5'	1.74	0.53
1:a:1235:G:OP1	10:j:47:ASN:ND2	2.42	0.53
24:z:56:ASP:HA	24:z:59:GLU:OE1	2.08	0.53
25:A:998:G:N2	25:A:1009:U:O2	2.27	0.53
25:A:2359:G:O6	25:A:2378:U:O4	2.27	0.53
1:a:1267:U:H3'	1:a:1268:C:H5'	1.90	0.53
10:j:39:PRO:HA	10:j:73:LEU:O	2.08	0.53
4:d:63:MET:HE2	4:d:66:GLN:HE22	1.73	0.53
25:A:218:A:N3	25:A:234:U:O2'	2.40	0.53
25:A:502:C:H2'	25:A:503:A:H8	1.74	0.53
25:A:1122:C:H2'	25:A:1129:G:H2'	1.91	0.53
25:A:1927:C:O2'	25:A:3080:A:N3	2.38	0.53
1:a:231:G:H22	1:a:262:G:N2	2.06	0.53
1:a:401:C:H2'	1:a:402:G:C8	2.44	0.53
25:A:995:U:H2'	25:A:996:G:H8	1.74	0.53
25:A:2359:G:N2	25:A:2378:U:O2	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:G:157:PRO:HB2	31:G:173:LYS:HG2	1.91	0.53
1:a:148:A:H3'	1:a:149:A:H8	1.73	0.53
1:a:1232:A:H2'	1:a:1233:A:C8	2.44	0.53
25:A:1544:U:C4	25:A:1626:G:O6	2.62	0.53
25:A:2530:C:H5''	25:A:2531:G:H2'	1.90	0.53
7:g:24:THR:HA	7:g:27:VAL:HG12	1.91	0.53
25:A:1183:U:OP1	34:J:89:LYS:NZ	2.40	0.53
28:D:121:LYS:HB2	28:D:170:MET:HG3	1.91	0.53
1:a:946:A:O2'	10:j:57:LYS:NZ	2.24	0.52
1:a:986:G:N3	1:a:987:A:H1'	2.24	0.52
1:a:1249:G:O2'	1:a:1250:A:O5'	2.25	0.52
15:o:18:HIS:CD2	15:o:20:THR:H	2.27	0.52
20:t:48:SER:O	20:t:52:HIS:ND1	2.40	0.52
25:A:2709:G:OP1	39:O:46:GLN:NE2	2.39	0.52
3:c:75:VAL:HG13	3:c:76:ILE:HD12	1.91	0.52
16:p:24:ASP:OD1	16:p:25:ALA:N	2.42	0.52
25:A:752:C:H2'	25:A:753:A:C8	2.40	0.52
1:a:692:A:H2'	1:a:693:G:C8	2.44	0.52
1:a:1375:G:N2	1:a:1486:A:H8	2.07	0.52
7:g:115:THR:HG22	7:g:117:VAL:HG12	1.92	0.52
19:s:30:VAL:HG13	19:s:48:THR:HG23	1.92	0.52
25:A:217:G:H22	25:A:235:U:H4'	1.74	0.52
25:A:1283:C:H2'	25:A:1284:A:H8	1.75	0.52
1:a:985:G:H2'	1:a:986:G:C8	2.45	0.52
4:d:144:SER:HA	4:d:147:THR:OG1	2.09	0.52
23:y:20:U:H2'	23:y:21:A:H4'	1.91	0.52
25:A:774:G:OP1	29:E:101:ARG:NH1	2.40	0.52
48:X:111:THR:HA	48:X:130:THR:HG22	1.92	0.52
1:a:225:G:O2'	17:q:10:THR:O	2.27	0.52
1:a:1138:A:H62	1:a:1159:G:H21	1.55	0.52
1:a:1329:G:H5''	9:i:129:ARG:HG3	1.90	0.52
1:a:1438:G:H2'	1:a:1439:G:H8	1.74	0.52
2:b:42:ASP:O	2:b:46:THR:OG1	2.23	0.52
3:c:79:ARG:HG2	3:c:81:THR:H	1.73	0.52
16:p:46:PRO:HG2	16:p:96:LYS:HZ2	1.74	0.52
25:A:947:U:H2'	25:A:948:G:C8	2.43	0.52
59:9:14:SER:HB2	59:9:17:ASN:HD22	1.75	0.52
1:a:192:G:H2'	1:a:193:C:H2'	1.91	0.52
1:a:532:U:H2'	1:a:533:G:H8	1.75	0.52
24:z:281:ALA:HB1	24:z:361:LEU:HD11	1.92	0.52
25:A:1550:G:O6	25:A:1620:U:O4	2.28	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:2294:A:H2'	25:A:2295:C:C6	2.45	0.52
25:A:2398:C:H2'	25:A:2399:A:C8	2.45	0.52
25:A:2470:A:H2'	25:A:2471:A:C8	2.45	0.52
32:H:32:PRO:HB3	50:Z:64:ALA:HA	1.92	0.52
2:b:176:ALA:O	2:b:180:GLY:N	2.42	0.52
11:k:102:ARG:O	11:k:106:ILE:HG12	2.10	0.52
25:A:339:U:H2'	25:A:340:A:C8	2.44	0.52
38:N:84:ASN:HD21	38:N:118:LEU:HA	1.73	0.52
1:a:23:C:H2'	1:a:24:U:H6	1.75	0.52
6:f:2:ARG:HD3	6:f:92:ARG:NE	2.25	0.52
25:A:1087:G:H2'	25:A:1088:U:C6	2.45	0.52
39:O:74:LEU:HD12	39:O:92:TRP:HE1	1.75	0.52
1:a:196:G:H2'	1:a:197:G:C8	2.43	0.52
1:a:262:G:H2'	1:a:263:A:C8	2.44	0.52
1:a:1410:C:H2'	1:a:1411:A:C8	2.44	0.52
25:A:2245:C:OP1	43:S:25:ARG:NH1	2.43	0.52
27:C:65:ILE:HD13	27:C:104:TYR:HB3	1.90	0.52
28:D:15:GLN:HE21	28:D:23:VAL:HG21	1.73	0.52
37:M:7:ARG:HG2	37:M:20:LEU:HD12	1.90	0.52
1:a:69:A:H2	1:a:219:C:H1'	1.75	0.52
1:a:165:U:H2'	1:a:166:C:C6	2.45	0.52
12:l:25:LYS:HE3	12:l:59:SER:HB3	1.92	0.52
46:V:69:THR:HG23	46:V:71:THR:H	1.74	0.52
1:a:702:G:H1	1:a:713:G:H1	1.58	0.51
1:a:716:U:H2'	1:a:717:C:H6	1.75	0.51
1:a:961:C:O2	14:n:19:ARG:NE	2.41	0.51
1:a:988:C:H4'	1:a:1018:C:H1'	1.91	0.51
7:g:69:VAL:HA	7:g:138:ARG:HD3	1.93	0.51
13:m:19:LEU:O	13:m:22:ILE:HG22	2.10	0.51
16:p:74:LEU:HA	16:p:77:THR:HG22	1.92	0.51
25:A:2922:U:H2'	25:A:2923:C:C6	2.44	0.51
29:E:61:GLY:HA3	29:E:80:ARG:HG2	1.91	0.51
41:Q:73:ILE:HG22	41:Q:75:GLY:H	1.75	0.51
6:f:44:GLY:HA3	6:f:59:ILE:HG23	1.90	0.51
25:A:928:U:H2'	25:A:929:C:C6	2.45	0.51
25:A:1530:G:H21	25:A:1805:G:H1	1.57	0.51
25:A:1938:G:N2	25:A:1956:A:H62	2.08	0.51
26:B:81:U:H2'	26:B:82:A:C8	2.45	0.51
1:a:57:A:N6	1:a:359:G:O6	2.44	0.51
1:a:1051:C:H2'	1:a:1052:G:C8	2.45	0.51
13:m:16:GLU:HB3	13:m:34:LEU:HD13	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:q:74:VAL:HG12	17:q:93:ILE:HG13	1.92	0.51
25:A:1706:A:H2'	25:A:1707:G:C8	2.45	0.51
25:A:2364:C:H2'	25:A:2365:A:H8	1.74	0.51
25:A:2515:U:H2'	25:A:2516:U:C6	2.45	0.51
32:H:77:ASP:OD1	32:H:145:SER:OG	2.16	0.51
1:a:425:G:N2	4:d:35:GLN:HE21	2.08	0.51
1:a:483:C:O2'	1:a:490:A:N6	2.44	0.51
1:a:690:G:H5''	6:f:54:LYS:NZ	2.25	0.51
1:a:917:A:N1	7:g:3:ARG:NH2	2.58	0.51
25:A:190:A:H2'	25:A:191:G:N3	2.25	0.51
25:A:2777:G:C2	25:A:2807:G:H1'	2.45	0.51
25:A:2902:A:H2'	25:A:2903:A:C8	2.45	0.51
39:O:108:TYR:CD1	39:O:109:PRO:HD2	2.46	0.51
41:Q:18:ARG:NH1	41:Q:105:GLY:O	2.43	0.51
1:a:960:A:N7	1:a:1300:A:N6	2.59	0.51
10:j:12:ALA:HB2	10:j:96:VAL:HA	1.91	0.51
19:s:36:ARG:HH22	19:s:53:ASP:HA	1.75	0.51
25:A:2396:A:H2'	25:A:2397:C:O4'	2.11	0.51
25:A:2470:A:H2'	25:A:2471:A:H8	1.75	0.51
25:A:2622:C:H2'	25:A:2623:A:H8	1.75	0.51
28:D:27:THR:HG21	28:D:198:ILE:HG12	1.93	0.51
37:M:71:ARG:HH12	37:M:104:ARG:HB3	1.76	0.51
39:O:18:ARG:HG3	39:O:18:ARG:HH11	1.75	0.51
1:a:236:G:O3'	17:q:57:LYS:NZ	2.43	0.51
17:q:46:HIS:HD2	17:q:48:LEU:H	1.57	0.51
25:A:334:G:H2'	25:A:335:G:C8	2.46	0.51
41:Q:77:LYS:HB3	41:Q:112:ARG:HD3	1.93	0.51
1:a:358:U:H2'	1:a:359:G:C8	2.41	0.51
9:i:119:LYS:HA	9:i:124:LEU:HD22	1.92	0.51
16:p:41:HIS:O	16:p:47:SER:HA	2.11	0.51
25:A:1225:G:OP1	33:I:54:ASN:N	2.44	0.51
25:A:1790:A:H2'	25:A:1791:A:C8	2.46	0.51
1:a:890:A:H2'	1:a:891:A:H8	1.76	0.51
1:a:1091:A:N6	3:c:176:HIS:O	2.41	0.51
11:k:91:VAL:HG21	11:k:114:LEU:HD13	1.92	0.51
25:A:705:C:H2'	25:A:706:G:H5''	1.92	0.51
33:I:26:THR:HG22	33:I:105:ILE:HA	1.93	0.51
1:a:193:C:O2	1:a:194:A:N6	2.44	0.51
1:a:376:G:C6	1:a:387:U:C4	2.99	0.51
1:a:1414:C:H2'	1:a:1415:G:O4'	2.11	0.51
25:A:3105:C:O2'	25:A:3107:G:OP2	2.27	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:G:23:ASN:HD21	31:G:34:THR:HG23	1.75	0.51
1:a:177:U:C2	1:a:209:A:N6	2.79	0.51
1:a:370:C:H2'	1:a:371:A:C8	2.45	0.51
1:a:496:U:H2'	1:a:497:G:O4'	2.11	0.51
1:a:535:C:H2'	1:a:536:C:C6	2.45	0.51
1:a:606:U:H2'	1:a:607:G:C8	2.45	0.51
1:a:615:G:H2'	1:a:616:G:H8	1.76	0.51
25:A:998:G:O6	25:A:1009:U:O4	2.29	0.51
25:A:1611:A:H2'	25:A:1612:U:C6	2.46	0.51
25:A:2035:U:H2'	27:C:157:ARG:HB2	1.92	0.51
40:P:7:GLY:O	40:P:9:ARG:NH1	2.44	0.51
4:d:11:LYS:HZ1	4:d:55:LYS:HA	1.75	0.50
16:p:13:ILE:HG23	16:p:14:ARG:HG2	1.92	0.50
25:A:279:U:H3	25:A:307:G:H1	1.59	0.50
25:A:1532:G:O2'	25:A:1803:A:N1	2.42	0.50
25:A:1703:G:H2'	25:A:1704:U:C6	2.44	0.50
25:A:2061:U:H2'	25:A:2062:G:H8	1.77	0.50
27:C:80:ALA:O	27:C:113:GLN:NE2	2.44	0.50
48:X:119:THR:O	48:X:122:THR:OG1	2.26	0.50
1:a:1028:G:O2'	1:a:1030:G:OP1	2.28	0.50
13:m:34:LEU:HD11	13:m:41:LYS:HA	1.93	0.50
28:D:127:MET:HE3	28:D:146:ARG:HA	1.92	0.50
48:X:139:SER:O	48:X:139:SER:OG	2.26	0.50
1:a:413:G:H22	1:a:429:U:H5''	1.77	0.50
1:a:452:A:N1	16:p:47:SER:HB2	2.26	0.50
8:h:5:ASP:OD2	8:h:79:ARG:NE	2.38	0.50
24:z:171:GLU:HG3	24:z:175:MET:HE3	1.91	0.50
25:A:3071:A:N7	25:A:3089:A:O2'	2.38	0.50
25:A:2288:C:H2'	25:A:2289:C:H6	1.76	0.50
25:A:2376:G:H2'	25:A:2377:G:H8	1.76	0.50
45:U:18:ARG:HH21	45:U:105:LYS:HD2	1.76	0.50
5:e:117:GLY:HA2	5:e:155:SER:HB2	1.93	0.50
5:e:166:VAL:O	5:e:170:LYS:HG2	2.12	0.50
7:g:79:ARG:HH12	7:g:82:GLY:N	2.09	0.50
13:m:70:LEU:O	13:m:73:GLU:HG3	2.11	0.50
29:E:61:GLY:O	29:E:78:SER:OG	2.28	0.50
38:N:49:MET:HB2	38:N:58:HIS:CE1	2.46	0.50
50:Z:28:ARG:HE	50:Z:30:ASN:ND2	2.09	0.50
1:a:1109:C:O2'	1:a:1110:A:O5'	2.30	0.50
1:a:1508:C:H2'	1:a:1509:G:H8	1.77	0.50
2:b:70:VAL:HA	2:b:92:VAL:HB	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:E:23:GLU:HG3	29:E:24:LEU:HG	1.93	0.50
58:8:1:MET:HE3	58:8:33:LYS:HE3	1.93	0.50
1:a:61:G:N2	1:a:388:G:N7	2.58	0.50
1:a:384:G:H2'	1:a:385:C:C6	2.46	0.50
1:a:928:A:H2'	1:a:929:G:C8	2.45	0.50
3:c:82:GLU:O	3:c:86:ILE:HD12	2.11	0.50
24:z:111:ASP:OD1	24:z:112:LEU:N	2.44	0.50
57:7:31:HIS:CD2	57:7:32:LEU:HG	2.46	0.50
1:a:127:A:C8	17:q:80:ARG:HG3	2.47	0.50
1:a:264:U:H4'	17:q:80:ARG:HH11	1.77	0.50
12:l:107:VAL:HG13	12:l:110:ARG:HB2	1.92	0.50
23:y:23:A:H2'	23:y:24:G:C8	2.47	0.50
24:z:5:ARG:HH12	24:z:115:ARG:HE	1.60	0.50
25:A:290:C:H42	25:A:298:G:H1	1.58	0.50
25:A:1033:A:N3	26:B:81:U:O2'	2.44	0.50
30:F:130:ASP:HB3	30:F:134:ASN:HB2	1.94	0.50
1:a:390:U:H2'	1:a:391:G:C8	2.46	0.50
1:a:580:G:H2'	1:a:581:U:C6	2.47	0.50
3:c:21:ARG:HH12	3:c:55:GLU:HG2	1.77	0.50
7:g:110:GLN:O	7:g:112:ARG:NH1	2.45	0.50
13:m:69:ASP:HA	13:m:72:ARG:NE	2.27	0.50
1:a:1011:U:H4'	1:a:1013:G:H22	1.76	0.49
9:i:91:GLY:O	9:i:95:GLN:HG3	2.12	0.49
25:A:88:A:H1'	25:A:89:A:C8	2.47	0.49
25:A:621:U:H2'	25:A:622:C:C6	2.47	0.49
25:A:2031:G:OP2	25:A:2032:A:O2'	2.25	0.49
25:A:2299:C:OP2	25:A:2462:G:N2	2.45	0.49
42:R:99:LEU:HD11	42:R:109:ILE:HD11	1.94	0.49
46:V:81:ARG:HG3	46:V:81:ARG:HH11	1.75	0.49
1:a:485:G:O2'	1:a:486:G:OP1	2.30	0.49
8:h:108:THR:OG1	8:h:111:GLY:O	2.27	0.49
25:A:502:C:H2'	25:A:503:A:C8	2.46	0.49
25:A:751:A:H2'	25:A:752:C:C6	2.46	0.49
43:S:24:TYR:HB2	43:S:29:SER:HB3	1.93	0.49
1:a:45:G:H2'	1:a:46:G:C8	2.47	0.49
1:a:960:A:N6	1:a:1300:A:N7	2.60	0.49
4:d:40:ARG:HH12	4:d:42:LYS:HD2	1.77	0.49
9:i:111:GLN:NE2	9:i:113:GLU:OE2	2.44	0.49
24:z:134:TYR:CD2	24:z:139:ILE:HD12	2.48	0.49
25:A:829:U:O2'	25:A:831:A:N7	2.32	0.49
25:A:979:G:H2'	25:A:980:C:C6	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:1131:G:H21	43:S:122:ASN:ND2	2.10	0.49
25:A:2622:C:H2'	25:A:2623:A:C8	2.48	0.49
25:A:3096:U:H1'	42:R:1:MET:N	2.27	0.49
27:C:226:MET:HE2	27:C:230:ASP:HB3	1.93	0.49
36:L:64:VAL:HG21	36:L:69:LEU:HD13	1.92	0.49
1:a:1436:G:H4'	1:a:1437:U:H4'	1.95	0.49
10:j:9:ARG:HB2	10:j:99:ASN:OD1	2.11	0.49
25:A:1561:C:H42	25:A:1610:C:N4	2.09	0.49
25:A:1944:C:H2'	25:A:1945:U:H6	1.77	0.49
25:A:2337:A:N7	25:A:2390:U:O2'	2.38	0.49
25:A:2872:G:H2'	25:A:2873:U:C6	2.46	0.49
29:E:68:GLN:HG3	29:E:69:LYS:HG3	1.93	0.49
1:a:136:G:H21	17:q:8:LYS:HA	1.76	0.49
1:a:438:U:P	4:d:117:HIS:HE2	2.36	0.49
1:a:940:A:C2	19:s:55:ARG:HG3	2.48	0.49
1:a:1334:C:H2'	1:a:1335:G:C8	2.46	0.49
2:b:146:ARG:NH1	2:b:147:SER:HB3	2.27	0.49
3:c:66:ASP:OD2	3:c:66:ASP:N	2.45	0.49
25:A:277:U:H2'	25:A:278:A:H8	1.76	0.49
25:A:384:G:H2'	25:A:385:G:H8	1.76	0.49
25:A:561:G:H2'	25:A:562:G:H5'	1.94	0.49
25:A:750:C:H2'	25:A:751:A:H8	1.77	0.49
25:A:1612:U:H2'	25:A:1613:G:C8	2.48	0.49
27:C:118:GLU:O	27:C:129:ASN:ND2	2.45	0.49
33:I:76:PRO:O	33:I:106:LYS:NZ	2.34	0.49
53:3:58:VAL:HA	53:3:61:PHE:HB3	1.94	0.49
1:a:205:G:H2'	1:a:206:G:C8	2.48	0.49
1:a:1017:C:H2'	1:a:1018:C:C6	2.48	0.49
25:A:1153:U:H5'	31:G:60:ARG:HH11	1.77	0.49
25:A:2332:U:H2'	25:A:2333:G:C8	2.47	0.49
33:I:115:LEU:HG	33:I:119:ASP:HB2	1.95	0.49
46:V:4:ILE:HD13	51:1:22:LEU:HD23	1.95	0.49
57:7:16:ARG:HG2	57:7:22:ILE:HD13	1.94	0.49
1:a:543:A:H2'	1:a:547:G:C8	2.48	0.49
1:a:716:U:H2'	1:a:717:C:C6	2.47	0.49
1:a:819:U:H3	1:a:829:G:H22	1.60	0.49
25:A:1825:C:N4	25:A:1840:G:OP2	2.44	0.49
30:F:125:SER:O	30:F:135:TYR:OH	2.24	0.49
1:a:78:G:O6	1:a:91:U:O4	2.30	0.49
4:d:3:ARG:HH21	4:d:110:ARG:HB2	1.77	0.49
16:p:3:VAL:HG13	16:p:64:ALA:HA	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:z:310:ALA:HB3	24:z:316:LEU:HD12	1.95	0.49
25:A:1537:U:H2'	25:A:1538:G:H8	1.78	0.49
25:A:2096:G:H2'	25:A:2097:G:H8	1.77	0.49
25:A:3057:U:H2'	25:A:3058:A:H8	1.78	0.49
30:F:116:PRO:HB3	53:3:45:TYR:HE2	1.78	0.49
34:J:79:LYS:HA	34:J:82:LEU:HD12	1.94	0.49
1:a:1231:A:H4'	9:i:90:GLY:N	2.27	0.49
25:A:1107:G:OP2	52:2:11:SER:OG	2.27	0.49
25:A:1900:C:H2'	25:A:1901:C:C6	2.48	0.49
25:A:2902:A:H2'	25:A:2903:A:H8	1.78	0.49
57:7:29:ARG:NH1	57:7:45:ASP:HB3	2.28	0.49
1:a:11:G:H1	5:e:122:ARG:NH1	2.11	0.49
25:A:543:U:H3'	25:A:544:U:H5''	1.95	0.49
31:G:45:ARG:NH1	31:G:50:ALA:O	2.45	0.49
57:7:50:VAL:HG11	57:7:58:ILE:HD12	1.94	0.49
1:a:1010:C:H42	1:a:1014:U:H3	1.61	0.48
25:A:453:U:H2'	25:A:454:U:C6	2.48	0.48
25:A:1961:G:H2'	25:A:1962:A:C8	2.48	0.48
25:A:2364:C:H2'	25:A:2365:A:C8	2.48	0.48
25:A:3070:G:H22	25:A:3088:C:H4'	1.77	0.48
50:Z:2:ALA:C	50:Z:33:ILE:HD11	2.38	0.48
25:A:337:U:O4	25:A:344:G:O6	2.30	0.48
25:A:2131:G:O6	25:A:2148:C:N4	2.46	0.48
25:A:2510:A:H4'	25:A:2511:A:O4'	2.13	0.48
26:B:15:U:OP2	26:B:71:C:O2'	2.30	0.48
46:V:69:THR:HG22	46:V:72:GLY:O	2.13	0.48
50:Z:28:ARG:HE	50:Z:30:ASN:HD21	1.60	0.48
1:a:895:A:H4'	1:a:896:A:O5'	2.14	0.48
4:d:17:VAL:HB	4:d:55:LYS:HE2	1.94	0.48
4:d:151:GLN:HA	4:d:154:ARG:HG2	1.95	0.48
24:z:125:ASP:O	24:z:127:THR:N	2.40	0.48
25:A:966:U:H2'	25:A:967:G:H8	1.78	0.48
25:A:2610:C:O2'	49:Y:41:ARG:NH1	2.46	0.48
25:A:3052:A:OP1	28:D:60:ARG:NH2	2.37	0.48
36:L:37:ARG:NH1	36:L:110:PRO:HG2	2.29	0.48
36:L:41:LYS:NZ	36:L:50:GLY:O	2.37	0.48
47:W:75:ASP:OD2	47:W:101:ASN:ND2	2.46	0.48
48:X:109:GLU:OE2	48:X:130:THR:OG1	2.20	0.48
1:a:44:C:H2'	1:a:45:G:C8	2.49	0.48
1:a:1442:G:OP1	20:t:30:THR:OG1	2.27	0.48
3:c:33:LYS:HA	3:c:36:VAL:HG12	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:g:86:GLN:HB2	7:g:148:ASN:ND2	2.29	0.48
10:j:40:VAL:HG12	10:j:73:LEU:HB2	1.95	0.48
14:n:24:CYS:SG	14:n:40:CYS:N	2.85	0.48
24:z:16:PHE:HB2	24:z:101:SER:O	2.14	0.48
25:A:72:G:H2'	25:A:72:G:N3	2.28	0.48
25:A:672:C:H2'	25:A:673:C:C6	2.48	0.48
25:A:2378:U:C2	25:A:2379:G:C8	3.01	0.48
25:A:2781:G:H2'	25:A:2782:C:C6	2.49	0.48
37:M:63:VAL:HG12	37:M:106:LEU:HD11	1.95	0.48
1:a:1057:G:N2	1:a:1060:A:OP2	2.41	0.48
4:d:110:ARG:O	4:d:114:SER:HB2	2.13	0.48
7:g:57:ASP:HB2	7:g:60:VAL:HG22	1.93	0.48
20:t:21:ASN:HA	20:t:24:VAL:HG12	1.96	0.48
25:A:228:A:H3'	25:A:229:U:H5''	1.95	0.48
25:A:429:A:H2'	25:A:430:A:C8	2.48	0.48
25:A:1311:C:C2	25:A:1312:G:C8	3.02	0.48
25:A:1606:G:H2'	25:A:1607:C:C6	2.49	0.48
25:A:1870:U:C4	40:P:8:PRO:HG2	2.49	0.48
58:8:3:VAL:HG22	58:8:35:ARG:HG2	1.96	0.48
1:a:532:U:H2'	1:a:533:G:C8	2.48	0.48
1:a:937:A:H2'	1:a:938:U:H6	1.79	0.48
1:a:1179:G:H2'	1:a:1180:U:C6	2.48	0.48
1:a:1297:U:H2'	1:a:1298:G:O4'	2.14	0.48
16:p:66:PRO:HB2	16:p:71:LEU:HD22	1.96	0.48
25:A:1193:C:H5''	39:O:60:ARG:HH21	1.78	0.48
1:a:488:C:H1'	1:a:489:A:C2	2.49	0.48
1:a:642:C:OP2	6:f:95:LYS:NZ	2.37	0.48
1:a:967:C:H2'	1:a:968:U:C6	2.48	0.48
4:d:45:GLU:OE1	4:d:45:GLU:N	2.47	0.48
4:d:87:ARG:HD2	4:d:180:LEU:HD13	1.95	0.48
37:M:97:ARG:HE	37:M:97:ARG:HB3	1.54	0.48
46:V:11:ILE:HD12	46:V:49:ILE:HD12	1.94	0.48
1:a:30:A:H61	1:a:538:G:H1'	1.79	0.48
1:a:312:C:H2'	1:a:313:A:C8	2.49	0.48
1:a:1418:G:H2'	1:a:1419:C:C6	2.49	0.48
2:b:5:THR:HG22	2:b:7:LYS:H	1.78	0.48
25:A:646:U:H2'	25:A:647:G:O4'	2.14	0.48
25:A:2357:A:H8	25:A:2380:G:N2	2.10	0.48
25:A:2361:U:O2'	25:A:2362:C:O5'	2.32	0.48
42:R:19:PHE:O	42:R:49:ARG:NH1	2.46	0.48
1:a:257:G:O6	1:a:270:A:N6	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:323:U:H3	1:a:327:A:H62	1.62	0.48
1:a:1091:A:N1	3:c:177:THR:HG22	2.29	0.48
10:j:24:LYS:O	10:j:27:GLU:HG3	2.14	0.48
16:p:12:LYS:HB3	16:p:15:ASN:OD1	2.14	0.48
25:A:159:A:N3	25:A:2431:C:O2'	2.45	0.48
25:A:897:A:N1	27:C:226:MET:HE3	2.29	0.48
25:A:1393:C:H2'	25:A:1394:A:H8	1.78	0.48
25:A:3034:C:H2'	25:A:3035:C:H6	1.79	0.48
28:D:34:ASN:HB2	28:D:101:LEU:HB2	1.95	0.48
1:a:119:C:OP1	1:a:311:C:O2'	2.32	0.48
1:a:255:G:H2'	1:a:256:U:C6	2.49	0.48
1:a:501:G:H2'	1:a:502:C:H6	1.79	0.48
1:a:993:G:H2'	1:a:994:C:C6	2.49	0.48
1:a:1296:C:H2'	1:a:1297:U:H6	1.79	0.48
25:A:1500:A:O2'	25:A:1511:U:O2	2.32	0.48
25:A:2357:A:P	25:A:2380:G:H22	2.35	0.48
25:A:2463:G:OP1	27:C:244:ARG:NH2	2.39	0.48
1:a:76:A:N1	1:a:94:U:O2'	2.34	0.47
1:a:445:C:H2'	1:a:446:A:C8	2.48	0.47
4:d:53:LYS:NZ	4:d:64:GLU:OE2	2.39	0.47
9:i:100:ARG:HE	9:i:123:PHE:HD1	1.61	0.47
14:n:8:HIS:HA	14:n:11:ASN:HD22	1.79	0.47
25:A:2771:U:H2'	25:A:2772:G:H8	1.79	0.47
31:G:12:PRO:HD2	31:G:15:VAL:HG21	1.96	0.47
1:a:48:G:H2'	1:a:49:U:H6	1.79	0.47
3:c:88:ALA:O	3:c:92:LYS:HG2	2.14	0.47
4:d:191:THR:HG22	4:d:193:GLN:H	1.79	0.47
13:m:9:LEU:HD22	13:m:18:ALA:HB1	1.96	0.47
15:o:3:LEU:HB2	15:o:8:LYS:HE3	1.96	0.47
20:t:44:LYS:HA	20:t:47:ALA:HB3	1.96	0.47
25:A:818:U:H2'	25:A:819:G:O4'	2.14	0.47
25:A:2304:C:H2'	25:A:2305:A:H8	1.79	0.47
1:a:593:C:H2'	1:a:594:A:C8	2.48	0.47
1:a:1265:U:OP2	1:a:1266:U:O2'	2.22	0.47
1:a:1497:A:H2'	1:a:1498:C:C6	2.49	0.47
12:l:79:MET:HG2	12:l:102:LEU:HD13	1.95	0.47
12:l:99:ARG:HH21	12:l:107:VAL:HB	1.77	0.47
15:o:78:TYR:O	15:o:82:ILE:HG12	2.14	0.47
19:s:50:ALA:HB1	19:s:57:HIS:HB3	1.95	0.47
25:A:2982:A:C4	31:G:68:LEU:HD21	2.49	0.47
25:A:3117:U:H2'	25:A:3118:U:C6	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:O:35:GLN:HE21	39:O:130:ARG:HE	1.62	0.47
1:a:422:C:H4'	1:a:423:G:O5'	2.13	0.47
1:a:438:U:N3	1:a:476:A:C8	2.63	0.47
1:a:606:U:H2'	1:a:607:G:H8	1.80	0.47
1:a:1184:C:H2'	1:a:1185:A:C8	2.49	0.47
1:a:1374:U:H2'	1:a:1375:G:C8	2.48	0.47
7:g:111:ARG:NH2	7:g:123:GLU:OE1	2.48	0.47
25:A:302:U:O2'	25:A:303:G:N7	2.47	0.47
30:F:147:GLU:OE2	53:3:26:SER:OG	2.19	0.47
36:L:72:LYS:HD3	36:L:89:ILE:HG13	1.96	0.47
39:O:108:TYR:HB3	39:O:114:ALA:HB2	1.95	0.47
1:a:23:C:H2'	1:a:24:U:C6	2.49	0.47
1:a:157:A:H2'	1:a:158:A:O4'	2.15	0.47
1:a:1393:G:H2'	1:a:1394:U:C6	2.49	0.47
5:e:74:GLY:HA2	5:e:91:GLU:OE1	2.14	0.47
25:A:297:G:H2'	25:A:298:G:C8	2.49	0.47
25:A:334:G:N2	25:A:347:U:O2	2.30	0.47
33:I:3:LYS:HA	33:I:6:LYS:HE3	1.96	0.47
36:L:4:TYR:OH	36:L:10:ASP:OD2	2.33	0.47
5:e:80:GLU:OE2	5:e:81:VAL:HG12	2.14	0.47
25:A:138:A:H2'	25:A:139:U:O2	2.14	0.47
25:A:1562:C:H2'	25:A:1563:A:C8	2.50	0.47
35:K:43:GLU:HA	35:K:175:ILE:H	1.80	0.47
1:a:123:G:O2'	17:q:21:LYS:NZ	2.46	0.47
1:a:323:U:O4	1:a:327:A:N7	2.48	0.47
1:a:1214:G:H2'	1:a:1215:C:C6	2.49	0.47
4:d:29:ARG:HD3	4:d:31:TYR:OH	2.15	0.47
4:d:103:ALA:HB1	4:d:108:MET:HB2	1.97	0.47
4:d:147:THR:HG22	4:d:149:PRO:HD2	1.96	0.47
6:f:38:ASP:OD1	6:f:39:LYS:N	2.48	0.47
7:g:137:ARG:O	7:g:141:THR:HG23	2.14	0.47
9:i:72:LEU:HB3	9:i:78:VAL:HG12	1.97	0.47
9:i:139:LYS:HB2	9:i:143:LYS:HG2	1.97	0.47
25:A:122:A:OP2	56:6:22:ARG:NH1	2.38	0.47
25:A:1619:U:H2'	25:A:1620:U:O4'	2.15	0.47
25:A:2297:U:H2'	25:A:2298:U:C6	2.49	0.47
25:A:2422:A:N1	25:A:2450:C:N4	2.56	0.47
25:A:2686:U:H2'	25:A:2687:U:C6	2.49	0.47
32:H:109:GLY:N	32:H:110:PRO:HD2	2.30	0.47
32:H:115:ARG:HH22	50:Z:42:PRO:HB2	1.78	0.47
1:a:128:U:H3	1:a:231:G:H1	1.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:271:C:H2'	1:a:272:C:C6	2.50	0.47
1:a:376:G:C6	1:a:387:U:N3	2.82	0.47
11:k:54:ALA:HB3	11:k:79:ALA:HB2	1.97	0.47
13:m:25:ILE:HD11	13:m:66:VAL:HG11	1.97	0.47
25:A:2465:A:H2'	25:A:2466:G:C8	2.50	0.47
25:A:3024:A:H2'	25:A:3025:G:C8	2.49	0.47
1:a:519:A:H2'	1:a:520:G:C8	2.50	0.47
1:a:604:U:H4'	16:p:11:GLY:HA2	1.96	0.47
1:a:1342:A:H2'	1:a:1343:G:C8	2.50	0.47
7:g:15:ASP:HB3	7:g:20:SER:H	1.79	0.47
15:o:36:ILE:HG23	15:o:56:LEU:HD11	1.96	0.47
20:t:81:LEU:HB3	20:t:85:LYS:NZ	2.30	0.47
21:u:14:LYS:O	21:u:18:ARG:HG2	2.14	0.47
23:y:25:C:H3'	23:y:26:A:H5''	1.97	0.47
25:A:2354:G:H1'	25:A:2356:G:N3	2.30	0.47
25:A:2393:A:O2'	25:A:2394:A:H5''	2.15	0.47
1:a:44:C:H2'	1:a:45:G:H8	1.79	0.47
1:a:934:U:H2'	1:a:935:G:H8	1.80	0.47
11:k:27:HIS:CD2	11:k:90:LYS:HB3	2.50	0.47
25:A:382:A:OP2	47:W:82:ARG:NH2	2.43	0.47
25:A:782:U:H2'	25:A:783:G:O4'	2.14	0.47
25:A:2007:C:H2'	25:A:2008:A:C8	2.50	0.47
25:A:2356:G:H2'	25:A:2380:G:C2	2.50	0.47
26:B:49:C:OP1	41:Q:42:ARG:NH1	2.37	0.47
44:T:53:ASP:OD1	44:T:54:ASP:N	2.48	0.47
1:a:125:U:O2'	1:a:127:A:H2'	2.16	0.46
1:a:223:G:H2'	1:a:224:U:O4'	2.15	0.46
1:a:1089:C:OP2	3:c:176:HIS:ND1	2.46	0.46
1:a:1106:U:P	10:j:7:ARG:HH22	2.39	0.46
1:a:1125:G:N2	1:a:1127:A:H62	2.13	0.46
1:a:1200:A:H2'	1:a:1201:G:H8	1.81	0.46
2:b:17:GLY:H	2:b:38:ILE:HG12	1.80	0.46
2:b:162:TRP:HA	2:b:184:ILE:O	2.15	0.46
3:c:120:ALA:HB1	3:c:189:ALA:HB2	1.96	0.46
10:j:9:ARG:HG2	10:j:73:LEU:HD23	1.96	0.46
16:p:70:VAL:O	16:p:74:LEU:HG	2.15	0.46
25:A:487:U:H2'	25:A:488:G:O4'	2.15	0.46
25:A:1004:C:H3'	25:A:1005:A:H8	1.80	0.46
25:A:1127:A:N3	25:A:1272:C:O2'	2.43	0.46
25:A:2439:C:H2'	25:A:2440:G:H8	1.80	0.46
25:A:2530:C:H3'	25:A:2531:G:H8	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:N:55:MET:O	38:N:60:ARG:NH1	2.47	0.46
50:Z:18:VAL:HG22	50:Z:24:ARG:HG2	1.97	0.46
1:a:163:G:H2'	1:a:164:G:C8	2.50	0.46
1:a:968:U:H1'	19:s:54:GLY:O	2.15	0.46
1:a:1115:G:H1'	1:a:1121:G:C2	2.51	0.46
1:a:1244:G:O6	1:a:1253:U:O4	2.32	0.46
2:b:117:LEU:HA	2:b:120:MET:HE2	1.96	0.46
4:d:97:VAL:HG21	4:d:118:PHE:HE2	1.80	0.46
12:l:39:THR:OG1	24:z:33:ARG:NE	2.49	0.46
25:A:1005:A:H3'	25:A:1006:G:C8	2.50	0.46
25:A:1102:G:H2'	59:9:22:PRO:HB3	1.97	0.46
25:A:3030:A:H2'	25:A:3031:A:C8	2.50	0.46
27:C:16:ALA:HB2	27:C:207:GLY:HA3	1.97	0.46
41:Q:26:ARG:NH1	41:Q:37:ARG:HH12	2.13	0.46
1:a:254:G:H4'	17:q:35:THR:HG21	1.97	0.46
1:a:937:A:H2'	1:a:938:U:C6	2.51	0.46
1:a:993:G:N2	1:a:1002:U:O2	2.45	0.46
1:a:1173:C:OP2	3:c:4:LYS:NZ	2.47	0.46
1:a:1219:A:N3	1:a:1219:A:H2'	2.30	0.46
3:c:30:ASP:O	3:c:33:LYS:HG2	2.16	0.46
13:m:88:GLN:O	13:m:92:HIS:ND1	2.45	0.46
23:y:4:C:N4	23:y:69:G:H1	2.10	0.46
25:A:529:U:H2'	25:A:530:G:C8	2.50	0.46
25:A:1756:G:H1'	25:A:1758:G:O6	2.16	0.46
25:A:2516:U:H2'	25:A:2517:C:C6	2.50	0.46
1:a:238:G:H2'	1:a:239:G:C8	2.50	0.46
1:a:270:A:H2'	1:a:271:C:C6	2.51	0.46
1:a:315:A:N7	1:a:328:U:H5	2.14	0.46
1:a:429:U:OP2	4:d:25:SER:HB3	2.15	0.46
1:a:432:A:C2	1:a:433:C:H1'	2.50	0.46
1:a:748:A:H4'	1:a:1507:G:N2	2.30	0.46
1:a:877:G:H2'	1:a:878:C:C6	2.51	0.46
12:l:114:ARG:HG2	12:l:119:ALA:HB3	1.97	0.46
23:y:51:U:O2	23:y:63:G:N2	2.37	0.46
25:A:28:C:O2'	25:A:1353:G:OP1	2.33	0.46
25:A:329:U:O2	25:A:446:G:C6	2.68	0.46
25:A:781:C:H2'	25:A:782:U:C6	2.49	0.46
25:A:1201:G:N2	25:A:1203:A:H3'	2.30	0.46
25:A:2088:C:H2'	25:A:2089:C:C5	2.50	0.46
30:F:39:VAL:HB	30:F:164:VAL:HG23	1.98	0.46
1:a:30:A:N6	1:a:538:G:H1'	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:145:G:H2'	1:a:146:A:H8	1.78	0.46
1:a:407:A:H4'	4:d:107:ARG:HB3	1.96	0.46
1:a:486:G:N7	1:a:487:C:N4	2.63	0.46
1:a:1008:C:N3	1:a:1009:C:N4	2.62	0.46
2:b:41:ILE:HG21	2:b:201:PRO:HB3	1.96	0.46
17:q:91:VAL:HG12	17:q:92:GLU:HG3	1.98	0.46
25:A:334:G:H2'	25:A:335:G:H8	1.80	0.46
25:A:1705:C:H2'	25:A:1706:A:H8	1.79	0.46
25:A:1791:A:H2'	25:A:1792:A:H8	1.80	0.46
26:B:11:U:O2'	26:B:12:C:H5'	2.15	0.46
1:a:75:A:N3	1:a:75:A:H2'	2.31	0.46
1:a:89:G:H2'	1:a:90:G:H8	1.81	0.46
1:a:127:A:O4'	17:q:80:ARG:NH1	2.49	0.46
1:a:985:G:N2	1:a:1018:C:N3	2.63	0.46
1:a:997:A:OP2	19:s:14:HIS:NE2	2.49	0.46
1:a:1040:U:H4'	10:j:54:SER:HB2	1.97	0.46
12:l:50:ARG:HB3	12:l:66:TYR:HE1	1.81	0.46
24:z:118:THR:HA	24:z:134:TYR:O	2.16	0.46
25:A:718:C:O2'	25:A:772:U:OP1	2.34	0.46
25:A:1624:U:O2'	25:A:1625:G:N7	2.33	0.46
53:3:24:THR:OG1	53:3:25:ARG:N	2.49	0.46
1:a:524:C:H2'	1:a:525:C:C6	2.50	0.46
3:c:133:MET:HB2	3:c:151:VAL:HG11	1.97	0.46
6:f:30:ILE:O	6:f:36:THR:OG1	2.23	0.46
20:t:10:ARG:HA	20:t:13:THR:HG22	1.98	0.46
25:A:551:G:N2	25:A:554:A:OP2	2.42	0.46
25:A:1229:A:C8	25:A:1230:G:H1'	2.48	0.46
25:A:1537:U:H2'	25:A:1538:G:C8	2.51	0.46
25:A:1658:G:O2'	25:A:1738:G:O2'	2.31	0.46
25:A:2398:C:O2'	35:K:217:THR:O	2.20	0.46
25:A:2816:G:H2'	25:A:2817:U:C6	2.51	0.46
42:R:14:ASP:O	42:R:16:ILE:HD12	2.15	0.46
1:a:102:C:H2'	1:a:103:G:O4'	2.16	0.46
1:a:150:G:H1	1:a:165:U:H3	1.64	0.46
1:a:406:G:N7	1:a:475:A:O2'	2.38	0.46
1:a:450:G:H4'	16:p:42:PRO:CB	2.46	0.46
1:a:457:A:O2'	1:a:458:A:O5'	2.32	0.46
1:a:708:A:H2'	1:a:709:A:C8	2.50	0.46
1:a:1221:U:OP1	7:g:116:MET:HE1	2.15	0.46
1:a:1375:G:H21	1:a:1486:A:H8	1.63	0.46
2:b:111:LEU:HD12	2:b:148:LEU:HD11	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:c:72:PRO:HD3	3:c:104:GLU:OE1	2.16	0.46
8:h:27:LEU:HD12	8:h:60:LEU:HD22	1.97	0.46
10:j:67:MET:HE3	10:j:67:MET:HB2	1.87	0.46
13:m:22:ILE:HG21	13:m:25:ILE:HD13	1.98	0.46
15:o:18:HIS:HD2	15:o:20:THR:H	1.63	0.46
19:s:3:ARG:HH22	19:s:10:PHE:HB2	1.81	0.46
24:z:133:LEU:HB3	24:z:140:SER:OG	2.16	0.46
25:A:384:G:H2'	25:A:385:G:C8	2.51	0.46
25:A:1010:U:O2'	25:A:1011:A:OP1	2.32	0.46
25:A:2007:C:O2'	27:C:209:ALA:HB2	2.16	0.46
1:a:263:A:H2'	1:a:264:U:C6	2.51	0.46
4:d:11:LYS:HZ2	4:d:55:LYS:HA	1.78	0.46
13:m:22:ILE:HG13	13:m:67:GLU:OE2	2.16	0.46
25:A:1791:A:H2'	25:A:1792:A:C8	2.51	0.46
25:A:2309:U:H2'	25:A:2310:G:C8	2.51	0.46
31:G:105:GLU:OE2	31:G:115:LEU:HD13	2.16	0.46
40:P:72:ASP:O	40:P:76:VAL:HG23	2.16	0.46
43:S:91:ASP:OD1	43:S:91:ASP:N	2.49	0.46
53:3:8:GLU:HG3	53:3:29:GLN:HG2	1.98	0.46
1:a:147:U:H2'	1:a:148:A:H8	1.81	0.46
1:a:466:U:H2'	1:a:467:A:C8	2.51	0.46
1:a:1066:U:H3	1:a:1079:G:N2	2.10	0.46
12:l:42:PRO:HB3	12:l:89:ASP:HB3	1.98	0.46
12:l:48:ALA:HB3	12:l:50:ARG:HE	1.80	0.46
13:m:83:GLU:OE1	30:F:119:ARG:NH1	2.49	0.46
16:p:77:THR:HG23	16:p:79:ASP:H	1.80	0.46
23:y:76:A:N6	25:A:2646:C:O4'	2.49	0.46
25:A:90:C:H2'	25:A:91:C:C6	2.51	0.46
25:A:1703:G:H2'	25:A:1704:U:H6	1.81	0.46
36:L:96:HIS:HA	36:L:97:PRO:HD3	1.78	0.46
1:a:1020:G:H2'	1:a:1021:U:C6	2.50	0.45
1:a:1488:G:OP1	1:a:1491:A:H4'	2.16	0.45
7:g:63:LYS:HA	7:g:66:LEU:HG	1.98	0.45
12:l:43:LYS:HG3	12:l:45:PRO:HD2	1.97	0.45
23:y:69:G:H2'	23:y:70:G:C8	2.49	0.45
25:A:736:G:N2	25:A:738:A:H3'	2.31	0.45
25:A:1314:C:H1'	43:S:4:VAL:HG22	1.97	0.45
25:A:2236:G:N7	45:U:23:LYS:NZ	2.64	0.45
29:E:197:SER:OG	29:E:199:GLU:OE1	2.33	0.45
30:F:29:TYR:OH	30:F:172:GLU:HG2	2.15	0.45
33:I:32:THR:H	33:I:35:ASN:HD22	1.63	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:J:14:GLN:HG2	34:J:57:PRO:HB3	1.98	0.45
34:J:95:HIS:ND1	34:J:95:HIS:O	2.49	0.45
46:V:57:VAL:HG22	46:V:84:VAL:HG22	1.98	0.45
51:1:22:LEU:HD13	51:1:57:VAL:HB	1.98	0.45
1:a:363:A:OP2	12:l:31:ARG:NE	2.49	0.45
1:a:1008:C:H2'	1:a:1009:C:C6	2.52	0.45
1:a:1125:G:H2'	1:a:1126:G:H5''	1.98	0.45
4:d:3:ARG:HG3	4:d:3:ARG:NH1	2.31	0.45
9:i:111:GLN:HE22	9:i:113:GLU:HB2	1.81	0.45
11:k:122:VAL:HG23	11:k:122:VAL:O	2.16	0.45
24:z:294:GLU:O	24:z:294:GLU:HG2	2.16	0.45
24:z:312:ASP:N	24:z:312:ASP:OD1	2.47	0.45
25:A:1118:A:H2'	25:A:1119:A:C8	2.50	0.45
25:A:1283:C:H2'	25:A:1284:A:C8	2.50	0.45
29:E:154:VAL:HG23	29:E:193:ASP:HB2	1.98	0.45
58:8:16:VAL:HG22	58:8:25:VAL:HG22	1.97	0.45
1:a:461:G:O2'	1:a:463:C:N4	2.45	0.45
1:a:588:A:C2	1:a:589:A:H1'	2.51	0.45
1:a:1045:U:H5''	1:a:1171:G:N2	2.32	0.45
1:a:1221:U:C5	7:g:116:MET:HE2	2.51	0.45
6:f:4:TYR:HB2	6:f:65:VAL:HG23	1.97	0.45
13:m:15:MET:HE1	13:m:43:MET:HB2	1.97	0.45
19:s:44:PHE:HB3	19:s:49:PHE:HZ	1.82	0.45
25:A:1178:U:C2	25:A:1180:G:H5'	2.52	0.45
25:A:2347:G:H2'	25:A:2348:G:O4'	2.17	0.45
25:A:2490:A:H4'	25:A:2491:A:N3	2.32	0.45
51:1:14:THR:HG23	51:1:16:ASP:H	1.82	0.45
1:a:604:U:H2'	1:a:605:G:H8	1.80	0.45
1:a:941:A:HO2'	1:a:966:C:HO2'	1.55	0.45
1:a:959:A:H1'	1:a:964:U:O4	2.17	0.45
1:a:1033:G:N2	1:a:1038:G:O6	2.50	0.45
1:a:1425:G:OP2	1:a:1426:C:N4	2.46	0.45
1:a:1443:G:H2'	1:a:1444:A:H8	1.81	0.45
25:A:256:A:H2'	25:A:257:A:C8	2.51	0.45
34:J:23:ALA:HB3	34:J:24:PRO:HD3	1.97	0.45
34:J:95:HIS:HE1	48:X:119:THR:HG23	1.82	0.45
38:N:86:ALA:O	38:N:101:LYS:NZ	2.38	0.45
1:a:272:C:H2'	1:a:273:A:C8	2.46	0.45
1:a:508:C:H3'	1:a:509:G:H5''	1.99	0.45
1:a:737:U:OP1	1:a:802:G:O2'	2.35	0.45
4:d:139:ASP:OD1	4:d:139:ASP:N	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:g:29:LYS:NZ	7:g:102:ARG:HB2	2.32	0.45
7:g:139:GLU:HA	7:g:142:HIS:ND1	2.31	0.45
9:i:65:GLN:O	9:i:69:LYS:HG2	2.17	0.45
16:p:75:LYS:HA	16:p:81:GLN:HE22	1.82	0.45
25:A:1396:G:H2'	25:A:1397:U:C6	2.51	0.45
30:F:10:ARG:O	30:F:14:ARG:N	2.42	0.45
4:d:47:ARG:O	4:d:51:GLN:HG3	2.17	0.45
4:d:86:LEU:O	4:d:90:GLU:HG2	2.16	0.45
7:g:50:ALA:O	7:g:54:THR:HG22	2.16	0.45
13:m:101:GLN:OE1	13:m:101:GLN:N	2.50	0.45
25:A:137:G:H2'	25:A:138:A:C8	2.52	0.45
25:A:340:A:H2'	25:A:341:C:C6	2.51	0.45
25:A:2152:A:H2'	25:A:2153:G:O4'	2.16	0.45
25:A:2326:A:H2'	25:A:2327:C:C6	2.51	0.45
25:A:2482:U:O2'	25:A:2651:C:OP2	2.33	0.45
25:A:2884:A:H2'	25:A:2885:G:O4'	2.16	0.45
25:A:3021:A:H4'	25:A:3022:G:C8	2.52	0.45
27:C:53:HIS:CE1	27:C:220:THR:HG23	2.51	0.45
38:N:4:ILE:HG23	38:N:8:ASP:HB2	1.97	0.45
1:a:321:A:H2'	1:a:322:C:H6	1.81	0.45
1:a:401:C:H2'	1:a:402:G:H8	1.80	0.45
1:a:1160:A:H2'	1:a:1161:A:C8	2.51	0.45
1:a:1231:A:H2'	1:a:1232:A:H8	1.81	0.45
1:a:1364:U:H1'	7:g:78:ARG:HE	1.81	0.45
7:g:101:LEU:HA	7:g:104:LEU:HG	1.99	0.45
16:p:79:ASP:HA	16:p:82:LYS:HE2	1.98	0.45
40:P:65:GLU:HA	40:P:68:LYS:HD2	1.98	0.45
57:7:24:ARG:HG2	57:7:50:VAL:HG22	1.98	0.45
1:a:501:G:H2'	1:a:502:C:C6	2.52	0.45
1:a:653:G:H2'	1:a:654:G:H8	1.79	0.45
1:a:1132:U:O2'	1:a:1133:G:H5''	2.17	0.45
1:a:1202:G:O3'	19:s:77:THR:HG21	2.17	0.45
14:n:15:LYS:C	14:n:16:PHE:HD2	2.25	0.45
20:t:16:ARG:O	20:t:20:ARG:HG3	2.17	0.45
23:y:31:A:N1	23:y:39:PSU:O2	2.50	0.45
25:A:1690:A:H2'	25:A:1691:A:H8	1.77	0.45
25:A:2342:A:H4'	25:A:2395:U:C5	2.51	0.45
25:A:2516:U:H2'	25:A:2517:C:H6	1.82	0.45
25:A:3019:C:H3'	25:A:3020:U:C2	2.50	0.45
27:C:177:MET:HE3	27:C:183:ARG:HB3	1.98	0.45
28:D:157:PRO:HB2	28:D:159:ARG:HG2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:91:LEU:HD12	32:H:125:LYS:HA	1.99	0.45
48:X:136:GLU:HG3	48:X:139:SER:HB3	1.98	0.45
48:X:169:ASN:OD1	48:X:170:LEU:N	2.42	0.45
50:Z:39:VAL:HG21	50:Z:64:ALA:HB3	1.98	0.45
1:a:392:C:C2	1:a:393:A:C8	3.04	0.45
1:a:1311:G:H5''	13:m:26:GLY:N	2.32	0.45
1:a:1330:U:OP1	9:i:132:GLU:HG2	2.17	0.45
16:p:44:GLU:OE2	16:p:48:LEU:N	2.37	0.45
25:A:994:A:N6	25:A:1014:G:HO2'	2.13	0.45
25:A:994:A:H2'	25:A:994:A:N3	2.32	0.45
25:A:1468:A:H2'	25:A:1469:A:C8	2.52	0.45
31:G:149:ILE:O	31:G:152:LEU:HD23	2.17	0.45
34:J:103:THR:H	34:J:106:GLN:NE2	2.14	0.45
1:a:401:C:OP2	4:d:65:LYS:NZ	2.24	0.45
1:a:1269:A:C2	1:a:1335:G:H1'	2.52	0.45
2:b:108:HIS:CD2	2:b:112:GLN:HE21	2.35	0.45
13:m:79:ARG:CA	13:m:82:ILE:HG12	2.47	0.45
15:o:12:LEU:HD13	15:o:22:THR:HG22	1.98	0.45
16:p:74:LEU:HB3	16:p:80:TRP:H	1.82	0.45
17:q:15:LYS:HD2	17:q:15:LYS:HA	1.70	0.45
25:A:998:G:H2'	25:A:999:C:C6	2.53	0.45
25:A:2096:G:H2'	25:A:2097:G:C8	2.51	0.45
1:a:49:U:H2'	1:a:50:G:H8	1.81	0.44
1:a:312:C:H2'	1:a:313:A:H8	1.81	0.44
1:a:493:A:H2'	1:a:494:C:C6	2.52	0.44
1:a:1011:U:O2'	1:a:1012:U:O5'	2.29	0.44
2:b:130:THR:HB	2:b:133:GLU:HB2	1.99	0.44
7:g:66:LEU:HA	7:g:69:VAL:HG22	1.99	0.44
25:A:1311:C:H2'	25:A:1312:G:H8	1.82	0.44
25:A:1532:G:H2'	25:A:1533:U:C6	2.52	0.44
25:A:1538:G:H2'	25:A:1539:A:C8	2.52	0.44
25:A:2042:A:H2'	25:A:2043:C:C6	2.53	0.44
25:A:3023:G:OP2	25:A:3023:G:H8	2.00	0.44
25:A:3057:U:H2'	25:A:3058:A:C8	2.51	0.44
48:X:16:ARG:HG2	48:X:48:GLU:HG3	1.99	0.44
1:a:593:C:H2'	1:a:594:A:H8	1.82	0.44
6:f:23:LEU:O	6:f:27:LEU:HD23	2.17	0.44
6:f:45:ARG:H	6:f:59:ILE:HA	1.83	0.44
13:m:80:ARG:O	13:m:83:GLU:HG3	2.17	0.44
14:n:53:LEU:HB2	14:n:56:VAL:HG22	1.98	0.44
15:o:18:HIS:CE1	15:o:21:ASP:HB3	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:p:66:PRO:HG2	16:p:80:TRP:HZ3	1.80	0.44
25:A:2:A:H2'	25:A:3:A:C8	2.52	0.44
25:A:290:C:H42	25:A:298:G:H22	1.64	0.44
25:A:546:G:O2'	25:A:557:G:O6	2.31	0.44
25:A:2248:C:H2'	25:A:2249:G:C8	2.50	0.44
25:A:2679:G:O3'	59:9:4:ARG:NH1	2.50	0.44
25:A:3019:C:N4	25:A:3021:A:H8	2.15	0.44
31:G:22:GLN:HE21	31:G:39:GLU:HA	1.82	0.44
40:P:45:ARG:HB3	40:P:46:PRO:HD3	1.99	0.44
1:a:390:U:O3'	16:p:29:ARG:NH2	2.39	0.44
1:a:445:C:H2'	1:a:446:A:H8	1.82	0.44
1:a:1040:U:H5''	10:j:53:ARG:HG2	1.99	0.44
2:b:97:LEU:HD12	2:b:100:MET:HE2	1.98	0.44
25:A:609:G:H2'	25:A:610:C:C6	2.52	0.44
25:A:2362:C:H2'	25:A:2363:A:C8	2.52	0.44
25:A:3018:U:H2'	25:A:3019:C:H6	1.82	0.44
38:N:81:GLY:HA3	38:N:116:GLY:HA3	2.00	0.44
45:U:18:ARG:NH2	45:U:105:LYS:HD2	2.32	0.44
1:a:78:G:O6	1:a:91:U:C4	2.70	0.44
1:a:340:U:H2'	1:a:341:C:H6	1.82	0.44
1:a:1158:G:OP2	9:i:119:LYS:NZ	2.50	0.44
2:b:3:VAL:HG11	2:b:216:VAL:HG22	1.99	0.44
3:c:90:LEU:HD23	3:c:95:GLY:HA3	1.99	0.44
4:d:68:ARG:O	4:d:72:GLU:OE1	2.34	0.44
11:k:78:ASN:OD1	11:k:82:LYS:HE2	2.18	0.44
20:t:24:VAL:HG11	20:t:66:VAL:HG21	2.00	0.44
25:A:2270:G:O5'	54:4:16:ARG:HB3	2.18	0.44
25:A:2457:U:H2'	25:A:2458:G:H8	1.81	0.44
1:a:98:G:H2'	1:a:99:U:H6	1.80	0.44
1:a:997:A:H5'	19:s:14:HIS:CE1	2.52	0.44
1:a:1329:G:C8	9:i:129:ARG:HG2	2.53	0.44
7:g:62:LEU:HD21	7:g:124:ILE:HD13	1.99	0.44
7:g:115:THR:O	7:g:119:ARG:HG3	2.18	0.44
9:i:138:LEU:HB3	9:i:143:LYS:O	2.17	0.44
10:j:52:ILE:HD13	10:j:62:ARG:HD3	1.99	0.44
13:m:51:ASP:O	13:m:55:VAL:HG13	2.18	0.44
32:H:85:ALA:HB3	32:H:88:THR:HB	2.00	0.44
48:X:126:GLN:HE21	48:X:129:ASN:HA	1.81	0.44
1:a:439:U:O2'	4:d:114:SER:O	2.13	0.44
1:a:496:U:OP2	1:a:497:G:N2	2.50	0.44
1:a:498:C:C5	1:a:509:G:H3'	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1004:G:H2'	1:a:1005:G:C8	2.52	0.44
1:a:1396:A:H2	1:a:1471:G:H22	1.66	0.44
9:i:111:GLN:NE2	9:i:113:GLU:HB2	2.32	0.44
16:p:46:PRO:HB3	16:p:94:LYS:NZ	2.33	0.44
25:A:1963:G:H2'	25:A:1964:U:C6	2.53	0.44
25:A:2495:G:OP1	49:Y:18:ALA:HB1	2.17	0.44
26:B:10:G:HO2'	26:B:11:U:P	2.41	0.44
42:R:2:ASN:O	42:R:5:ASP:N	2.38	0.44
1:a:231:G:H22	1:a:262:G:H22	1.65	0.44
1:a:376:G:OP1	16:p:7:LEU:N	2.50	0.44
1:a:586:G:H5''	1:a:587:A:H5'	2.00	0.44
1:a:1036:U:OP1	3:c:163:SER:N	2.49	0.44
1:a:1185:A:H2'	1:a:1186:U:O4'	2.17	0.44
4:d:176:LEU:HB3	16:p:106:PHE:HE1	1.83	0.44
5:e:176:GLU:OE2	5:e:198:ARG:NH1	2.50	0.44
13:m:23:TYR:HE2	13:m:70:LEU:HB3	1.82	0.44
23:y:26:A:N1	23:y:44:G:N2	2.66	0.44
25:A:90:C:H2'	25:A:91:C:H6	1.81	0.44
25:A:1200:U:H2'	25:A:1201:G:O4'	2.17	0.44
30:F:41:VAL:HG12	30:F:163:VAL:HG22	1.99	0.44
1:a:81:C:H3'	1:a:82:U:H5''	2.00	0.44
1:a:373:A:H61	1:a:391:G:H1'	1.83	0.44
1:a:1192:U:H4'	1:a:1193:U:H4'	2.00	0.44
4:d:176:LEU:HB3	16:p:106:PHE:CE1	2.53	0.44
7:g:138:ARG:HG2	7:g:142:HIS:HE1	1.81	0.44
8:h:107:SER:HA	8:h:112:LEU:HD23	2.00	0.44
12:l:27:SER:OG	12:l:29:GLN:O	2.32	0.44
13:m:28:THR:O	13:m:32:GLU:OE1	2.36	0.44
13:m:49:THR:O	13:m:53:VAL:HG23	2.18	0.44
25:A:49:A:H2'	25:A:50:A:C8	2.53	0.44
25:A:658:U:OP1	38:N:31:LYS:HE2	2.18	0.44
25:A:949:C:C2	25:A:950:A:C8	3.05	0.44
25:A:2465:A:H2'	25:A:2466:G:H8	1.82	0.44
1:a:131:G:H2'	1:a:132:C:O4'	2.17	0.44
1:a:374:A:H2'	1:a:375:U:O4'	2.18	0.44
1:a:1388:G:H4'	21:u:12:MET:HE2	1.99	0.44
2:b:18:HIS:HB2	2:b:189:THR:HB	1.99	0.44
2:b:56:PHE:HD2	2:b:184:ILE:HD11	1.83	0.44
9:i:50:LEU:HD22	9:i:87:LEU:HD11	1.99	0.44
9:i:120:LYS:HA	9:i:120:LYS:HE3	2.00	0.44
10:j:83:THR:O	10:j:87:LEU:HG	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:o:9:LYS:HA	15:o:9:LYS:HD2	1.90	0.44
19:s:21:VAL:O	19:s:25:LYS:HE2	2.18	0.44
24:z:149:TYR:HB2	49:Y:4:LYS:HG2	2.00	0.44
24:z:166:GLN:O	24:z:170:GLU:HG3	2.17	0.44
25:A:114:G:OP2	25:A:116:A:O2'	2.27	0.44
25:A:332:C:H2'	25:A:333:C:C6	2.53	0.44
25:A:539:C:H4'	29:E:53:LYS:NZ	2.32	0.44
25:A:1285:G:H2'	25:A:1286:C:C6	2.52	0.44
25:A:1885:G:O2'	25:A:2215:U:O4	2.36	0.44
25:A:2569:G:N3	25:A:2605:C:H2'	2.32	0.44
34:J:16:GLN:CD	34:J:18:GLY:H	2.26	0.44
40:P:87:TYR:OH	40:P:116:VAL:O	2.33	0.44
1:a:622:A:C5	8:h:109:SER:HA	2.53	0.43
1:a:850:C:H2'	1:a:851:A:O4'	2.18	0.43
1:a:1295:U:H2'	1:a:1296:C:C6	2.53	0.43
2:b:146:ARG:HH11	2:b:147:SER:HB3	1.83	0.43
6:f:4:TYR:CD2	6:f:72:VAL:HG21	2.53	0.43
16:p:20:ILE:HD12	16:p:70:VAL:HG22	1.99	0.43
25:A:193:G:H2'	25:A:194:A:O4'	2.18	0.43
25:A:279:U:H2'	25:A:280:G:H8	1.83	0.43
25:A:1392:G:H2'	25:A:1393:C:C6	2.53	0.43
25:A:1611:A:H2'	25:A:1612:U:H6	1.83	0.43
27:C:108:PRO:HD2	27:C:111:LEU:HD22	1.99	0.43
29:E:40:ALA:HB2	29:E:100:GLN:HE21	1.82	0.43
30:F:132:THR:HG21	41:Q:6:VAL:HG21	2.00	0.43
1:a:454:C:H2'	1:a:455:G:O4'	2.18	0.43
4:d:11:LYS:HE2	4:d:15:LEU:HD12	2.00	0.43
9:i:67:LEU:HD11	9:i:100:ARG:NH1	2.33	0.43
12:l:59:SER:HB2	12:l:61:VAL:HG22	2.00	0.43
12:l:75:GLN:OE1	12:l:75:GLN:N	2.51	0.43
12:l:81:LEU:HD23	12:l:98:ILE:HD11	1.98	0.43
23:y:44:G:N3	23:y:45:U:H1'	2.33	0.43
25:A:978:A:H2'	25:A:979:G:C8	2.54	0.43
25:A:1025:A:N3	25:A:2488:C:O2'	2.46	0.43
25:A:1654:G:H2'	25:A:1655:A:C8	2.53	0.43
25:A:1715:A:N3	25:A:1798:U:O2'	2.38	0.43
25:A:1938:G:N2	25:A:1939:U:O4	2.51	0.43
25:A:2362:C:H2'	25:A:2363:A:H8	1.83	0.43
25:A:2366:C:H2'	25:A:2367:G:O4'	2.19	0.43
41:Q:44:ALA:O	41:Q:77:LYS:NZ	2.47	0.43
45:U:52:GLU:HB2	45:U:53:PRO:HD3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:Y:49:VAL:HG22	49:Y:79:ASN:HD22	1.83	0.43
1:a:612:U:H5'	1:a:613:G:C8	2.52	0.43
1:a:1136:A:H2'	1:a:1137:G:O4'	2.17	0.43
9:i:126:ARG:NH1	9:i:127:ASP:O	2.52	0.43
25:A:1717:U:H5''	25:A:1718:C:H5	1.84	0.43
25:A:2086:U:H3	25:A:2096:G:H1	1.65	0.43
25:A:2331:U:H2'	25:A:2332:U:C6	2.53	0.43
25:A:2439:C:H2'	25:A:2440:G:C8	2.54	0.43
25:A:2975:G:H4'	31:G:4:ILE:HD11	2.00	0.43
26:B:43:C:N3	30:F:97:THR:HG22	2.33	0.43
29:E:196:PHE:HB3	29:E:201:LEU:HB2	2.00	0.43
1:a:359:G:C6	1:a:360:G:C5	3.06	0.43
1:a:426:U:OP2	4:d:29:ARG:NH1	2.52	0.43
1:a:613:G:H2'	1:a:614:C:C6	2.54	0.43
1:a:671:G:H2'	1:a:672:U:C6	2.54	0.43
1:a:1076:C:H2'	1:a:1077:C:H6	1.83	0.43
1:a:1200:A:H2'	1:a:1201:G:C8	2.53	0.43
1:a:1202:G:H2'	1:a:1203:G:H8	1.83	0.43
1:a:1229:A:C6	1:a:1272:G:C6	3.06	0.43
9:i:68:ILE:O	9:i:71:PRO:HD2	2.18	0.43
24:z:165:PHE:HA	24:z:168:THR:HG22	2.00	0.43
25:A:2075:G:O2'	25:A:2107:G:N1	2.37	0.43
25:A:2098:U:H2'	25:A:2099:G:O4'	2.18	0.43
28:D:34:ASN:ND2	28:D:54:TYR:HB2	2.34	0.43
40:P:35:LYS:HE3	40:P:100:VAL:HG21	2.00	0.43
1:a:299:G:N2	1:a:545:U:O2	2.51	0.43
1:a:1269:A:H2'	1:a:1270:A:C8	2.54	0.43
3:c:11:ARG:NH2	3:c:177:THR:O	2.37	0.43
6:f:44:GLY:HA2	6:f:60:TYR:H	1.82	0.43
7:g:92:ARG:HG3	7:g:94:ASP:OD1	2.18	0.43
13:m:4:LEU:HD13	13:m:53:VAL:HG13	1.99	0.43
24:z:302:THR:HB	24:z:309:VAL:HG12	2.01	0.43
25:A:1223:U:H2'	25:A:1224:G:C8	2.52	0.43
25:A:1434:G:H2'	25:A:1435:C:C6	2.53	0.43
25:A:1556:A:N1	25:A:1615:G:O6	2.52	0.43
25:A:1804:G:H2'	25:A:1805:G:C8	2.53	0.43
25:A:2113:A:H2'	25:A:2114:A:C8	2.53	0.43
25:A:2240:U:O2	54:4:4:PRO:HG2	2.19	0.43
25:A:3020:U:O2'	25:A:3021:A:O5'	2.35	0.43
27:C:89:THR:HG22	27:C:201:GLN:HG2	2.00	0.43
1:a:572:G:H2'	1:a:573:U:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:731:U:H2'	1:a:732:G:O4'	2.18	0.43
1:a:1301:A:C8	1:a:1305:G:C5	3.06	0.43
1:a:1491:A:H2'	1:a:1492:G:C8	2.53	0.43
16:p:15:ASN:CB	16:p:43:LYS:HG3	2.49	0.43
25:A:857:U:H2'	25:A:858:A:H8	1.83	0.43
25:A:1421:C:H2'	25:A:1422:A:H8	1.84	0.43
25:A:1756:G:H1'	25:A:1758:G:C6	2.53	0.43
25:A:2015:U:OP2	27:C:272:ARG:NH2	2.52	0.43
25:A:2332:U:H3	25:A:2403:U:H3	1.65	0.43
30:F:47:VAL:HG21	30:F:57:ILE:HD12	2.01	0.43
30:F:130:ASP:O	30:F:132:THR:N	2.42	0.43
1:a:182:C:C2	1:a:207:G:N2	2.87	0.43
1:a:413:G:N2	1:a:429:U:H5''	2.34	0.43
1:a:519:A:OP1	12:l:111:LYS:HE2	2.18	0.43
2:b:161:VAL:HG12	2:b:163:VAL:HG23	2.01	0.43
4:d:153:ALA:HA	4:d:156:THR:HG22	2.00	0.43
10:j:8:ILE:HG22	10:j:100:ILE:HA	2.00	0.43
25:A:911:U:H2'	25:A:912:C:C6	2.54	0.43
47:W:12:ILE:HD11	47:W:72:MET:SD	2.59	0.43
1:a:391:G:H2'	1:a:392:C:O4'	2.19	0.43
1:a:513:A:C6	1:a:516:C:C2	3.06	0.43
1:a:585:U:H2'	1:a:586:G:C8	2.54	0.43
1:a:820:C:N4	1:a:822:U:O4	2.52	0.43
2:b:11:ASP:O	2:b:208:ARG:NH2	2.52	0.43
4:d:70:TYR:HA	4:d:73:GLU:CD	2.42	0.43
4:d:193:GLN:O	4:d:196:VAL:N	2.52	0.43
5:e:174:ARG:HG2	5:e:175:PRO:HD2	2.01	0.43
16:p:9:ARG:CZ	16:p:16:PRO:HB3	2.49	0.43
24:z:59:GLU:HG2	24:z:60:GLU:N	2.33	0.43
25:A:996:G:N1	25:A:1013:U:O4	2.52	0.43
25:A:1225:G:H4'	33:I:75:GLY:C	2.44	0.43
25:A:1296:G:H2'	25:A:1297:G:C8	2.54	0.43
25:A:1610:C:C2	25:A:1611:A:C8	3.07	0.43
25:A:2603:G:H2'	25:A:2604:U:C6	2.54	0.43
30:F:8:LEU:HD22	30:F:12:LYS:HZ2	1.84	0.43
1:a:47:C:H5''	16:p:13:ILE:HG22	2.00	0.43
1:a:1100:U:H2'	1:a:1101:C:C6	2.54	0.43
2:b:154:MET:O	2:b:156:LYS:N	2.45	0.43
25:A:772:U:H2'	25:A:773:G:C8	2.54	0.43
25:A:1048:A:H3'	25:A:1049:G:H4'	2.01	0.43
25:A:1762:C:H2'	25:A:1763:G:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:2239:A:C2	54:4:3:VAL:HG12	2.53	0.43
25:A:2969:C:H2'	25:A:2970:U:C6	2.53	0.43
30:F:10:ARG:NH1	30:F:108:ASP:OD1	2.52	0.43
39:O:35:GLN:HE22	39:O:130:ARG:HH21	1.66	0.43
48:X:146:VAL:HG21	48:X:157:ILE:HG21	2.00	0.43
50:Z:33:ILE:HG22	50:Z:52:CYS:HB3	2.01	0.43
1:a:69:A:C8	1:a:214:U:H1'	2.53	0.43
1:a:376:G:O2'	1:a:377:G:O5'	2.36	0.43
1:a:907:G:C2	1:a:909:G:C8	3.07	0.43
1:a:1194:A:O2'	1:a:1195:U:H2'	2.19	0.43
4:d:83:ASP:OD1	4:d:87:ARG:NH1	2.51	0.43
5:e:120:MET:SD	5:e:122:ARG:HG3	2.59	0.43
7:g:126:ASP:O	7:g:130:GLY:N	2.52	0.43
19:s:19:VAL:HG11	19:s:44:PHE:CE1	2.54	0.43
24:z:32:GLU:HA	24:z:35:GLU:OE2	2.18	0.43
25:A:582:G:N3	45:U:68:ASN:ND2	2.67	0.43
25:A:680:U:H2'	25:A:681:C:C6	2.53	0.43
25:A:2816:G:H2'	25:A:2817:U:H6	1.84	0.43
31:G:99:LEU:HD22	31:G:126:VAL:HB	2.01	0.43
36:L:102:GLU:HG2	36:L:124:VAL:HG21	2.00	0.43
50:Z:36:VAL:HG22	50:Z:63:ARG:NH2	2.34	0.43
1:a:71:C:H2'	1:a:72:G:C8	2.55	0.42
1:a:800:U:H4'	1:a:801:G:OP2	2.19	0.42
2:b:142:ASN:O	2:b:146:ARG:HD2	2.19	0.42
7:g:38:LEU:O	7:g:42:ILE:HG12	2.19	0.42
7:g:130:GLY:HA2	7:g:135:VAL:HG21	2.01	0.42
16:p:22:VAL:HG21	16:p:59:TRP:NE1	2.34	0.42
24:z:125:ASP:C	24:z:127:THR:H	2.27	0.42
25:A:1784:C:H2'	25:A:1785:C:C6	2.53	0.42
25:A:1900:C:H2'	25:A:1901:C:H6	1.83	0.42
32:H:124:ILE:HG22	32:H:125:LYS:N	2.30	0.42
34:J:24:PRO:HD2	34:J:25:PRO:HD3	2.00	0.42
42:R:30:LYS:HG3	42:R:79:ASN:O	2.18	0.42
1:a:104:A:C2	20:t:10:ARG:HG2	2.54	0.42
1:a:191:C:H2'	1:a:192:G:O4'	2.19	0.42
1:a:198:C:H2'	1:a:199:C:C6	2.54	0.42
1:a:806:C:O2	8:h:16:ASN:ND2	2.52	0.42
1:a:1110:A:N6	1:a:1125:G:H1'	2.34	0.42
2:b:156:LYS:O	2:b:157:VAL:HG22	2.19	0.42
9:i:72:LEU:HD23	9:i:107:LEU:HD21	2.01	0.42
13:m:29:ARG:HA	13:m:32:GLU:OE1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:p:67:THR:HG23	16:p:69:PRO:HG2	2.00	0.42
25:A:176:G:OP2	25:A:176:G:N2	2.37	0.42
25:A:899:G:H5'	27:C:227:ASN:ND2	2.30	0.42
25:A:1562:C:H2'	25:A:1563:A:H8	1.84	0.42
25:A:1944:C:H2'	25:A:1945:U:C6	2.53	0.42
25:A:2275:A:H8	25:A:2275:A:OP2	2.03	0.42
25:A:3032:G:H5''	28:D:63:ILE:HG23	2.00	0.42
32:H:75:LEU:H	32:H:75:LEU:HD23	1.83	0.42
41:Q:121:ARG:NE	41:Q:127:PHE:OXT	2.52	0.42
1:a:13:G:H5'	5:e:133:GLY:HA3	2.01	0.42
1:a:235:C:H5'	17:q:87:ARG:HG3	1.99	0.42
1:a:410:G:H21	1:a:432:A:H62	1.67	0.42
1:a:594:A:N6	1:a:607:G:O6	2.52	0.42
3:c:188:GLU:OE2	3:c:195:ARG:HB3	2.19	0.42
4:d:70:TYR:HA	4:d:73:GLU:OE2	2.19	0.42
10:j:23:ARG:HD3	10:j:23:ARG:HA	1.91	0.42
21:u:8:ARG:O	21:u:11:ARG:HG2	2.19	0.42
25:A:326:A:N1	25:A:449:G:C6	2.86	0.42
25:A:1199:U:H2'	25:A:1200:U:C6	2.54	0.42
25:A:1478:C:O2'	25:A:2026:A:N3	2.50	0.42
25:A:1534:C:H3'	25:A:1535:C:O2	2.18	0.42
25:A:1541:G:N1	25:A:1631:A:C6	2.83	0.42
25:A:2771:U:H2'	25:A:2772:G:C8	2.55	0.42
31:G:55:ARG:HD2	31:G:57:ASP:O	2.19	0.42
1:a:82:U:O4	1:a:87:G:O6	2.37	0.42
1:a:251:G:N1	1:a:266:G:O6	2.53	0.42
1:a:286:G:H2'	1:a:287:U:C6	2.54	0.42
1:a:1095:U:H2'	1:a:1096:U:C6	2.55	0.42
1:a:1110:A:C8	1:a:1127:A:C6	3.08	0.42
1:a:1305:G:O2'	1:a:1344:C:O2'	2.36	0.42
2:b:56:PHE:CD2	2:b:184:ILE:HD11	2.54	0.42
7:g:75:VAL:CG2	7:g:86:GLN:HB3	2.50	0.42
9:i:121:ALA:HB1	9:i:123:PHE:HE2	1.85	0.42
19:s:27:THR:O	19:s:28:LYS:HE2	2.19	0.42
25:A:720:C:N4	38:N:105:ARG:HH21	2.18	0.42
25:A:1472:C:H2'	25:A:1473:G:O4'	2.19	0.42
25:A:1618:C:H2'	25:A:1619:U:C6	2.55	0.42
25:A:2289:C:H2'	25:A:2290:C:H6	1.85	0.42
25:A:2443:U:H2'	25:A:2444:C:H6	1.84	0.42
27:C:162:SER:HB3	27:C:195:GLU:HG2	2.01	0.42
28:D:185:VAL:HG22	28:D:192:LEU:HD23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:667:A:H62	1:a:683:G:H21	1.66	0.42
4:d:156:THR:O	4:d:158:GLY:N	2.48	0.42
7:g:116:MET:HE3	7:g:119:ARG:HH21	1.85	0.42
25:A:139:U:H2'	25:A:140:G:O4'	2.19	0.42
25:A:248:G:H5'	25:A:250:G:N7	2.35	0.42
25:A:388:U:H2'	25:A:389:G:O4'	2.20	0.42
25:A:547:U:OP1	56:6:43:ARG:HG2	2.20	0.42
25:A:2094:G:O2'	25:A:2095:G:H8	2.03	0.42
27:C:20:ASP:O	27:C:22:ALA:N	2.53	0.42
31:G:55:ARG:NH1	31:G:58:ASP:OD1	2.53	0.42
43:S:83:LEU:HD22	43:S:88:VAL:HG21	2.01	0.42
1:a:359:G:C4	1:a:360:G:C8	3.06	0.42
1:a:636:G:N2	15:o:23:GLY:HA3	2.34	0.42
2:b:214:THR:HA	2:b:217:ILE:HG22	2.00	0.42
8:h:7:ILE:HD11	8:h:32:LEU:HD23	2.02	0.42
18:r:59:GLN:O	18:r:62:ARG:HG2	2.19	0.42
19:s:5:LEU:HD23	19:s:5:LEU:H	1.84	0.42
24:z:124:VAL:HG11	24:z:208:LEU:HD13	2.01	0.42
25:A:1808:A:H2'	25:A:1809:U:H6	1.85	0.42
25:A:2142:A:O2'	25:A:2144:C:N4	2.53	0.42
25:A:2623:A:H2'	25:A:2624:C:C6	2.55	0.42
25:A:2950:C:H4'	37:M:1:MET:HE1	2.01	0.42
25:A:3021:A:H4'	25:A:3022:G:N7	2.35	0.42
25:A:3023:G:H2'	25:A:3024:A:O4'	2.20	0.42
28:D:160:VAL:HG12	28:D:160:VAL:O	2.20	0.42
30:F:70:GLN:HB2	53:3:6:HIS:CE1	2.54	0.42
34:J:56:ILE:O	34:J:56:ILE:HG13	2.18	0.42
1:a:103:G:C2	1:a:104:A:H1'	2.55	0.42
1:a:408:G:H2'	1:a:409:G:C8	2.55	0.42
1:a:493:A:H2'	1:a:494:C:H6	1.85	0.42
1:a:498:C:H4'	1:a:499:C:H6	1.84	0.42
1:a:600:U:C2	1:a:601:A:C8	3.08	0.42
1:a:604:U:H2'	1:a:605:G:C8	2.55	0.42
1:a:930:C:H2'	1:a:931:A:H8	1.85	0.42
4:d:82:GLY:HA3	4:d:192:GLU:HG3	2.02	0.42
13:m:78:ILE:H	13:m:78:ILE:HD12	1.85	0.42
24:z:102:ASP:OD1	24:z:102:ASP:N	2.51	0.42
25:A:733:U:H2'	25:A:734:C:C6	2.54	0.42
25:A:2086:U:O2	25:A:2096:G:N2	2.41	0.42
25:A:2872:G:H2'	25:A:2873:U:H6	1.84	0.42
27:C:89:THR:CG2	27:C:201:GLN:HG2	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:F:172:GLU:OE2	30:F:172:GLU:N	2.51	0.42
39:O:18:ARG:HG3	39:O:18:ARG:NH1	2.35	0.42
1:a:41:U:OP1	12:l:121:LYS:HE3	2.20	0.42
1:a:459:G:H2'	1:a:460:U:C6	2.55	0.42
1:a:666:U:H1'	11:k:53:TRP:HE1	1.83	0.42
11:k:74:LEU:HD23	11:k:74:LEU:HA	1.85	0.42
20:t:35:PHE:CD2	20:t:79:LEU:HD22	2.55	0.42
25:A:1191:A:C5	25:A:1192:G:C8	3.07	0.42
25:A:1220:C:C2	25:A:1221:A:C8	3.08	0.42
25:A:1549:G:N1	25:A:1622:G:O6	2.53	0.42
26:B:81:U:H2'	26:B:82:A:H8	1.84	0.42
39:O:10:ARG:HG2	39:O:90:PRO:HG3	2.00	0.42
1:a:64:A:N6	1:a:104:A:H5'	2.35	0.42
1:a:429:U:O2'	1:a:430:A:OP2	2.32	0.42
1:a:439:U:H6	1:a:439:U:H2'	1.69	0.42
1:a:495:G:H2'	1:a:496:U:C6	2.55	0.42
1:a:941:A:O2'	1:a:966:C:O2'	2.21	0.42
1:a:1076:C:H2'	1:a:1077:C:C6	2.54	0.42
1:a:1508:C:H2'	1:a:1509:G:C8	2.53	0.42
4:d:71:TYR:O	4:d:75:ASN:ND2	2.53	0.42
16:p:66:PRO:HB3	16:p:70:VAL:HG12	2.01	0.42
25:A:898:A:N3	25:A:899:G:H5''	2.35	0.42
25:A:1532:G:N2	25:A:1804:G:C4	2.88	0.42
25:A:2538:A:H2'	25:A:2539:G:C8	2.55	0.42
25:A:2538:A:H2'	25:A:2539:G:H8	1.85	0.42
25:A:2613:G:H5''	25:A:2614:U:O4'	2.19	0.42
25:A:3013:C:H5'	25:A:3014:A:H5'	2.02	0.42
26:B:46:A:C4	26:B:47:A:C8	3.07	0.42
31:G:99:LEU:HD23	31:G:99:LEU:H	1.85	0.42
38:N:51:GLU:OE2	57:7:57:ARG:NH2	2.44	0.42
1:a:667:A:C2	1:a:684:A:C5	3.07	0.42
1:a:987:A:H2'	1:a:988:C:C6	2.55	0.42
1:a:1098:U:H1'	1:a:1160:A:C5	2.55	0.42
1:a:1219:A:H2	1:a:1222:G:N3	2.18	0.42
8:h:35:ASN:HB3	8:h:112:LEU:HD12	2.02	0.42
16:p:7:LEU:HD23	16:p:20:ILE:HD13	2.00	0.42
25:A:1609:G:H2'	25:A:1610:C:H6	1.84	0.42
25:A:2297:U:H2'	25:A:2298:U:H6	1.85	0.42
26:B:110:G:H2'	26:B:111:C:C6	2.54	0.42
36:L:98:THR:O	36:L:102:GLU:HG3	2.20	0.42
2:b:151:ILE:HG23	2:b:154:MET:SD	2.60	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:b:187:LEU:HD11	2:b:199:PRO:HB2	2.02	0.41
4:d:127:ILE:HB	4:d:130:TYR:HB2	2.02	0.41
11:k:74:LEU:O	11:k:77:GLU:HG3	2.20	0.41
16:p:4:LYS:HG2	16:p:65:GLN:HB2	2.02	0.41
25:A:1226:U:H2'	25:A:1227:C:C6	2.55	0.41
25:A:1952:C:H2'	25:A:1953:C:C6	2.55	0.41
25:A:2320:C:O2'	25:A:2321:U:H6	2.03	0.41
25:A:2393:A:H1'	25:A:2394:A:O4'	2.20	0.41
25:A:2410:A:H2'	25:A:2411:U:C6	2.55	0.41
25:A:2509:C:P	55:5:8:ARG:HH21	2.42	0.41
25:A:2936:C:OP1	25:A:2938:G:H4'	2.19	0.41
46:V:54:VAL:HG13	46:V:84:VAL:HG13	2.02	0.41
1:a:437:U:O3'	4:d:117:HIS:NE2	2.43	0.41
1:a:1436:G:H5'	1:a:1438:G:H5''	2.02	0.41
4:d:107:ARG:HG2	4:d:110:ARG:HD3	2.03	0.41
13:m:78:ILE:O	13:m:81:LYS:HG2	2.19	0.41
25:A:402:G:H4'	25:A:404:A:N7	2.35	0.41
25:A:1528:G:H2'	25:A:1529:U:C6	2.55	0.41
25:A:1542:A:N6	25:A:1629:G:OP2	2.53	0.41
25:A:1560:U:H2'	25:A:1561:C:H6	1.83	0.41
25:A:2581:G:OP2	25:A:2581:G:H8	2.03	0.41
30:F:40:LYS:HD3	30:F:99:ARG:NH2	2.34	0.41
36:L:34:THR:HG23	36:L:39:LYS:HB2	2.01	0.41
1:a:254:G:C6	1:a:273:A:C6	3.08	0.41
1:a:256:U:H2'	1:a:257:G:H8	1.85	0.41
1:a:914:C:H5''	7:g:3:ARG:HG2	2.02	0.41
1:a:1114:C:H2'	1:a:1115:G:H4'	2.03	0.41
3:c:117:GLN:O	3:c:121:GLU:OE1	2.38	0.41
4:d:66:GLN:OE1	4:d:66:GLN:N	2.44	0.41
4:d:119:LEU:HD21	4:d:141:LYS:HE2	2.03	0.41
7:g:113:GLU:CD	7:g:119:ARG:HG2	2.45	0.41
13:m:48:LEU:HA	13:m:52:GLN:HE21	1.85	0.41
15:o:85:LEU:HD23	15:o:85:LEU:HA	1.91	0.41
25:A:682:A:OP1	29:E:96:ARG:NH2	2.54	0.41
25:A:2019:A:H2'	25:A:2020:A:C8	2.55	0.41
25:A:2609:A:H2'	25:A:2610:C:C6	2.55	0.41
41:Q:37:ARG:NH2	41:Q:54:ASP:OD1	2.53	0.41
46:V:53:LYS:HA	46:V:53:LYS:HD2	1.91	0.41
48:X:124:VAL:HG22	48:X:181:VAL:HG22	2.01	0.41
1:a:299:G:H2'	1:a:300:A:C8	2.55	0.41
1:a:389:A:C5	1:a:390:U:H1'	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:674:G:H2'	1:a:675:A:O4'	2.20	0.41
1:a:980:G:H2'	1:a:981:C:H6	1.84	0.41
1:a:1229:A:N6	1:a:1272:G:C6	2.88	0.41
1:a:1371:C:H2'	1:a:1372:C:C6	2.55	0.41
9:i:28:THR:HG21	9:i:105:ARG:HB2	2.02	0.41
10:j:10:LEU:HD23	10:j:72:ARG:O	2.20	0.41
25:A:109:U:H2'	25:A:110:G:O4'	2.20	0.41
25:A:316:U:O2'	25:A:317:G:OP1	2.33	0.41
25:A:919:A:H5''	25:A:920:G:OP1	2.20	0.41
37:M:68:GLU:CD	37:M:68:GLU:H	2.27	0.41
39:O:79:ALA:HB3	49:Y:2:ALA:HA	2.02	0.41
41:Q:43:SER:O	41:Q:112:ARG:NH2	2.43	0.41
42:R:26:ASN:HB3	42:R:43:LYS:HG3	2.03	0.41
48:X:117:ASP:N	48:X:149:GLU:OE2	2.41	0.41
54:4:35:GLN:OE1	54:4:35:GLN:N	2.51	0.41
1:a:402:G:H2'	1:a:403:C:C6	2.56	0.41
1:a:1105:U:C2	1:a:1107:G:C8	3.08	0.41
1:a:1305:G:H2'	1:a:1306:A:H8	1.85	0.41
1:a:1324:C:H2'	1:a:1325:G:H8	1.85	0.41
3:c:123:LEU:HD12	3:c:129:PHE:HA	2.01	0.41
6:f:27:LEU:O	6:f:30:ILE:HG22	2.21	0.41
12:l:4:ILE:HD11	17:q:49:TYR:HB3	2.01	0.41
25:A:639:C:O2'	25:A:640:G:H8	2.03	0.41
25:A:751:A:H2'	25:A:752:C:H6	1.86	0.41
25:A:2315:U:OP1	25:A:2422:A:O2'	2.36	0.41
25:A:2574:C:H2'	25:A:2575:G:O4'	2.20	0.41
25:A:2697:U:O2'	25:A:2698:C:H6	2.02	0.41
34:J:17:ALA:O	34:J:52:ARG:NH2	2.54	0.41
51:1:13:LEU:HB3	51:1:17:GLU:HG3	2.02	0.41
53:3:36:GLU:CD	53:3:37:VAL:HG23	2.46	0.41
1:a:136:G:C6	1:a:225:G:C5	3.09	0.41
1:a:387:U:H5''	1:a:388:G:OP1	2.21	0.41
1:a:741:G:H2'	1:a:742:A:C8	2.55	0.41
1:a:1124:G:H2'	1:a:1125:G:C8	2.55	0.41
2:b:151:ILE:HA	2:b:154:MET:HE3	2.02	0.41
25:A:1400:G:N2	25:A:1443:G:H5''	2.36	0.41
25:A:1787:A:H2'	27:C:86:PRO:HG3	2.03	0.41
25:A:2211:C:H2'	25:A:2212:A:H8	1.85	0.41
25:A:2238:A:H2'	25:A:2239:A:C8	2.55	0.41
25:A:2246:U:O2'	25:A:2841:C:H5'	2.20	0.41
25:A:2998:C:H2'	25:A:2999:A:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:C:156:ALA:HB2	27:C:163:ILE:HG13	2.03	0.41
29:E:127:VAL:HG21	29:E:144:PHE:HE2	1.86	0.41
34:J:30:LEU:HD23	34:J:30:LEU:H	1.86	0.41
1:a:412:U:H5'	1:a:413:G:H5'	2.03	0.41
1:a:492:U:O4'	4:d:36:HIS:HE1	2.04	0.41
1:a:974:U:N3	1:a:1025:C:N3	2.68	0.41
1:a:1105:U:HO2'	1:a:1106:U:P	2.41	0.41
1:a:1301:A:N7	1:a:1305:G:C5	2.89	0.41
1:a:1355:U:OP1	9:i:93:SER:OG	2.30	0.41
6:f:26:PHE:O	6:f:29:VAL:HG12	2.20	0.41
10:j:55:PRO:HB3	14:n:42:ILE:HD11	2.02	0.41
25:A:278:A:H2'	25:A:279:U:C6	2.55	0.41
25:A:681:C:H2'	25:A:682:A:H8	1.84	0.41
25:A:1904:C:H2'	25:A:1905:G:O4'	2.21	0.41
25:A:3011:C:H1'	28:D:65:PRO:HG3	2.02	0.41
28:D:127:MET:HE2	28:D:134:GLY:HA3	2.02	0.41
30:F:10:ARG:H	30:F:10:ARG:HG2	1.73	0.41
48:X:71:ILE:O	48:X:74:THR:HG22	2.21	0.41
1:a:137:C:O2'	17:q:8:LYS:HE3	2.21	0.41
1:a:1333:U:H4'	7:g:33:GLU:OE1	2.20	0.41
3:c:76:ILE:HD11	3:c:102:ILE:HB	2.03	0.41
13:m:60:ILE:HD12	13:m:60:ILE:HA	1.93	0.41
23:y:43:C:H2'	23:y:44:G:C8	2.56	0.41
34:J:80:LEU:HD23	34:J:80:LEU:HA	1.90	0.41
41:Q:26:ARG:CZ	41:Q:37:ARG:HH12	2.34	0.41
1:a:376:G:O6	1:a:387:U:O4	2.38	0.41
1:a:664:U:H2'	1:a:665:G:O4'	2.21	0.41
1:a:806:C:H1'	8:h:16:ASN:HD22	1.86	0.41
1:a:1212:A:H2'	1:a:1213:U:C6	2.56	0.41
1:a:1370:G:H2'	1:a:1371:C:C6	2.56	0.41
2:b:225:LEU:HD23	2:b:225:LEU:HA	1.91	0.41
4:d:107:ARG:O	4:d:110:ARG:HG2	2.21	0.41
5:e:63:ILE:HD12	5:e:72:GLY:O	2.21	0.41
10:j:39:PRO:HB3	10:j:74:ILE:HD11	2.03	0.41
16:p:22:VAL:HG11	16:p:59:TRP:CE2	2.56	0.41
16:p:76:ILE:HG22	16:p:93:LEU:HB2	2.01	0.41
20:t:35:PHE:HE1	20:t:51:LEU:HB2	1.86	0.41
25:A:124:A:H5''	25:A:125:C:C6	2.56	0.41
25:A:543:U:H3'	25:A:544:U:C5'	2.51	0.41
25:A:586:U:H2'	25:A:587:G:O4'	2.21	0.41
25:A:1130:C:C5	36:L:144:GLN:HG3	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:1501:C:H2'	25:A:1502:G:C8	2.56	0.41
25:A:2113:A:H2'	25:A:2114:A:H8	1.86	0.41
25:A:2361:U:O2	25:A:2376:G:N2	2.39	0.41
25:A:2402:C:H2'	25:A:2403:U:C6	2.56	0.41
25:A:2457:U:H2'	25:A:2458:G:C8	2.56	0.41
25:A:2545:G:H5'	25:A:2546:A:OP2	2.21	0.41
25:A:2664:C:H2'	25:A:2665:C:H4'	2.02	0.41
27:C:78:LYS:HE2	27:C:78:LYS:HB3	1.87	0.41
29:E:108:ALA:O	29:E:112:ARG:HG3	2.21	0.41
31:G:90:ILE:HG12	31:G:163:VAL:HG22	2.02	0.41
39:O:35:GLN:NE2	39:O:130:ARG:HE	2.18	0.41
45:U:9:SER:HB3	45:U:115:GLU:HG2	2.03	0.41
48:X:148:VAL:HG13	48:X:148:VAL:O	2.20	0.41
1:a:377:G:H2'	1:a:378:G:C8	2.56	0.41
1:a:519:A:H2'	1:a:520:G:H8	1.85	0.41
1:a:1168:G:N3	14:n:60:SER:OG	2.54	0.41
1:a:1287:G:H2'	1:a:1288:A:H8	1.86	0.41
5:e:38:GLU:C	5:e:39:ARG:HD2	2.46	0.41
12:l:24:LEU:HD12	12:l:26:GLY:H	1.85	0.41
13:m:76:ALA:HA	13:m:79:ARG:NH1	2.35	0.41
16:p:60:LEU:HD21	16:p:66:PRO:HG3	2.03	0.41
16:p:66:PRO:HB3	16:p:70:VAL:CG1	2.51	0.41
23:y:23:A:H2'	23:y:24:G:H8	1.86	0.41
25:A:663:A:H2'	25:A:663:A:N3	2.36	0.41
25:A:728:G:H2'	25:A:729:C:C6	2.56	0.41
25:A:875:G:H2'	25:A:876:A:O4'	2.21	0.41
25:A:1393:C:H2'	25:A:1394:A:C8	2.56	0.41
25:A:2530:C:H3'	25:A:2531:G:C8	2.56	0.41
27:C:130:ASN:OD1	27:C:190:ARG:HD3	2.21	0.41
32:H:124:ILE:CG2	32:H:125:LYS:H	2.31	0.41
40:P:10:LEU:HB3	40:P:17:GLN:HG3	2.02	0.41
1:a:43:G:C6	1:a:404:G:C6	3.09	0.40
1:a:403:C:H5''	4:d:128:PRO:HD2	2.02	0.40
1:a:485:G:O2'	1:a:486:G:P	2.80	0.40
1:a:499:C:H2'	1:a:500:A:C8	2.56	0.40
1:a:586:G:C2	1:a:611:G:H2'	2.56	0.40
1:a:593:C:N4	1:a:608:G:O6	2.54	0.40
1:a:1229:A:C2	1:a:1272:G:C2	3.09	0.40
1:a:1261:A:OP1	10:j:9:ARG:NH2	2.54	0.40
1:a:1295:U:H2'	1:a:1296:C:H6	1.85	0.40
4:d:134:GLN:HB2	4:d:178:HIS:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:i:50:LEU:HD23	9:i:85:ALA:HB3	2.03	0.40
10:j:8:ILE:CG1	10:j:74:ILE:HB	2.50	0.40
25:A:722:G:H2'	25:A:723:C:C6	2.56	0.40
25:A:2753:G:H5''	25:A:2754:G:H5''	2.02	0.40
1:a:177:U:O4	1:a:209:A:N7	2.54	0.40
1:a:375:U:OP1	16:p:69:PRO:HB3	2.21	0.40
1:a:929:G:H2'	1:a:930:C:C6	2.56	0.40
1:a:1115:G:H1'	1:a:1121:G:N2	2.37	0.40
1:a:1177:A:O2'	1:a:1178:A:OP1	2.37	0.40
1:a:1207:C:H4'	19:s:80:PHE:CZ	2.56	0.40
1:a:1281:A:N3	1:a:1281:A:H2'	2.35	0.40
5:e:105:THR:HG22	5:e:147:ASP:HB2	2.02	0.40
8:h:65:LYS:O	8:h:73:SER:OG	2.34	0.40
23:y:52:G:C2	23:y:53:G:C8	3.09	0.40
25:A:231:U:H5'	25:A:232:G:OP2	2.21	0.40
25:A:579:A:H2'	25:A:580:G:O4'	2.21	0.40
25:A:1287:C:H2'	25:A:1288:A:H8	1.86	0.40
25:A:1475:G:C8	25:A:1476:G:C8	3.09	0.40
25:A:2345:U:H2'	25:A:2346:G:C8	2.56	0.40
36:L:102:GLU:O	36:L:106:ILE:HG12	2.22	0.40
1:a:333:C:C2	1:a:334:C:C5	3.10	0.40
1:a:967:C:H2'	1:a:968:U:H6	1.83	0.40
1:a:1281:A:C5	1:a:1283:U:H1'	2.56	0.40
7:g:58:PRO:O	7:g:62:LEU:HD23	2.21	0.40
12:l:16:ILE:O	12:l:16:ILE:HG13	2.21	0.40
25:A:97:U:H4'	25:A:98:U:O5'	2.21	0.40
25:A:726:A:H2'	25:A:727:A:C8	2.56	0.40
25:A:1808:A:H2'	25:A:1809:U:C6	2.56	0.40
25:A:2552:A:H2'	25:A:2553:G:H8	1.83	0.40
25:A:2971:G:O6	25:A:2979:C:H5''	2.22	0.40
25:A:3022:G:H2'	25:A:3023:G:O4'	2.21	0.40
26:B:92:G:H2'	26:B:93:U:C6	2.56	0.40
37:M:122:LEU:HD13	42:R:69:VAL:HG11	2.03	0.40
1:a:305:G:H4'	1:a:306:A:H5''	2.04	0.40
1:a:495:G:H2'	1:a:496:U:H6	1.86	0.40
1:a:517:G:C6	1:a:518:U:C4	3.10	0.40
1:a:841:U:C2	1:a:842:A:C8	3.10	0.40
1:a:905:A:H2'	1:a:906:C:C6	2.57	0.40
1:a:913:C:H2'	1:a:914:C:H6	1.87	0.40
1:a:1262:U:H2'	1:a:1263:C:H5	1.86	0.40
1:a:1265:U:H5''	1:a:1266:U:H4'	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1442:G:OP1	20:t:27:SER:HA	2.21	0.40
6:f:36:THR:HB	6:f:66:LYS:O	2.22	0.40
9:i:33:LYS:O	9:i:34:GLU:HG3	2.21	0.40
16:p:7:LEU:HD22	16:p:18:TYR:CB	2.49	0.40
24:z:209:LEU:HA	24:z:212:LEU:HD12	2.02	0.40
25:A:448:U:H2'	25:A:449:G:C8	2.56	0.40
25:A:1654:G:H2'	25:A:1655:A:H8	1.86	0.40
25:A:1705:C:H2'	25:A:1706:A:C8	2.56	0.40
33:I:82:VAL:HG23	33:I:82:VAL:O	2.21	0.40
39:O:75:THR:HA	39:O:90:PRO:HA	2.03	0.40
51:1:7:PRO:O	51:1:11:ARG:HG3	2.21	0.40
1:a:421:U:H3'	1:a:422:C:H6	1.87	0.40
5:e:118:VAL:HG13	5:e:153:LEU:HB2	2.03	0.40
16:p:22:VAL:HG11	16:p:59:TRP:CD2	2.57	0.40
23:y:70:G:H2'	23:y:71:G:C8	2.57	0.40
25:A:1064:A:H2'	25:A:1065:C:C6	2.57	0.40
25:A:1256:G:H2'	25:A:1257:G:O4'	2.22	0.40
25:A:1830:C:H5'	56:6:10:PRO:HG3	2.04	0.40
25:A:2327:C:H2'	25:A:2328:G:H8	1.87	0.40
25:A:2411:U:H2'	25:A:2412:U:O4'	2.21	0.40
25:A:2471:A:H2'	25:A:2472:C:H6	1.86	0.40
32:H:9:VAL:HG23	32:H:12:LEU:HB2	2.04	0.40
33:I:54:ASN:O	33:I:58:LYS:HG3	2.21	0.40
57:7:32:LEU:O	57:7:36:LYS:NZ	2.42	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
2	b	226/277 (82%)	212 (94%)	13 (6%)	1 (0%)	30 61

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	c	206/275 (75%)	192 (93%)	14 (7%)	0	100	100
4	d	198/201 (98%)	189 (96%)	9 (4%)	0	100	100
5	e	178/214 (83%)	169 (95%)	9 (5%)	0	100	100
6	f	94/96 (98%)	92 (98%)	2 (2%)	0	100	100
7	g	153/156 (98%)	149 (97%)	4 (3%)	0	100	100
8	h	129/132 (98%)	127 (98%)	2 (2%)	0	100	100
9	i	124/150 (83%)	115 (93%)	9 (7%)	0	100	100
10	j	97/101 (96%)	89 (92%)	8 (8%)	0	100	100
11	k	113/138 (82%)	104 (92%)	9 (8%)	0	100	100
12	l	120/124 (97%)	113 (94%)	7 (6%)	0	100	100
13	m	114/124 (92%)	104 (91%)	9 (8%)	1 (1%)	14	44
14	n	58/61 (95%)	51 (88%)	7 (12%)	0	100	100
15	o	86/89 (97%)	86 (100%)	0	0	100	100
16	p	111/156 (71%)	106 (96%)	5 (4%)	0	100	100
17	q	92/98 (94%)	89 (97%)	3 (3%)	0	100	100
18	r	63/84 (75%)	62 (98%)	1 (2%)	0	100	100
19	s	80/93 (86%)	78 (98%)	2 (2%)	0	100	100
20	t	83/86 (96%)	81 (98%)	2 (2%)	0	100	100
21	u	30/33 (91%)	30 (100%)	0	0	100	100
24	z	362/374 (97%)	348 (96%)	14 (4%)	0	100	100
27	C	273/278 (98%)	258 (94%)	15 (6%)	0	100	100
28	D	212/217 (98%)	202 (95%)	10 (5%)	0	100	100
29	E	207/215 (96%)	202 (98%)	5 (2%)	0	100	100
30	F	180/187 (96%)	175 (97%)	5 (3%)	0	100	100
31	G	174/179 (97%)	173 (99%)	1 (1%)	0	100	100
32	H	149/151 (99%)	139 (93%)	10 (7%)	0	100	100
33	I	124/175 (71%)	120 (97%)	4 (3%)	0	100	100
34	J	131/142 (92%)	121 (92%)	10 (8%)	0	100	100
35	K	98/235 (42%)	90 (92%)	8 (8%)	0	100	100
36	L	144/147 (98%)	137 (95%)	7 (5%)	0	100	100
37	M	120/122 (98%)	119 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	N	143/147 (97%)	128 (90%)	15 (10%)	0	100	100
39	O	134/137 (98%)	126 (94%)	8 (6%)	0	100	100
40	P	116/199 (58%)	113 (97%)	3 (3%)	0	100	100
41	Q	124/127 (98%)	123 (99%)	1 (1%)	0	100	100
42	R	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
43	S	122/129 (95%)	121 (99%)	1 (1%)	0	100	100
44	T	98/103 (95%)	95 (97%)	3 (3%)	0	100	100
45	U	112/153 (73%)	109 (97%)	3 (3%)	0	100	100
46	V	95/100 (95%)	90 (95%)	5 (5%)	0	100	100
47	W	93/105 (89%)	88 (95%)	5 (5%)	0	100	100
48	X	190/215 (88%)	184 (97%)	6 (3%)	0	100	100
49	Y	83/88 (94%)	80 (96%)	3 (4%)	0	100	100
50	Z	61/64 (95%)	59 (97%)	2 (3%)	0	100	100
51	1	62/77 (80%)	61 (98%)	1 (2%)	0	100	100
52	2	57/61 (93%)	55 (96%)	2 (4%)	0	100	100
53	3	55/75 (73%)	53 (96%)	2 (4%)	0	100	100
54	4	52/57 (91%)	52 (100%)	0	0	100	100
55	5	47/55 (86%)	46 (98%)	1 (2%)	0	100	100
56	6	44/47 (94%)	44 (100%)	0	0	100	100
57	7	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
58	8	35/37 (95%)	32 (91%)	3 (9%)	0	100	100
59	9	21/24 (88%)	20 (95%)	1 (5%)	0	100	100
All	All	6445/7287 (88%)	6164 (96%)	279 (4%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	b	157	VAL
13	m	5	VAL

5.3.2 Protein sidechains ⓘ

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

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	b	191/218 (88%)	191 (100%)	0	100	100
3	c	170/212 (80%)	170 (100%)	0	100	100
4	d	175/176 (99%)	175 (100%)	0	100	100
5	e	127/147 (86%)	127 (100%)	0	100	100
6	f	85/85 (100%)	85 (100%)	0	100	100
7	g	131/132 (99%)	131 (100%)	0	100	100
8	h	107/108 (99%)	107 (100%)	0	100	100
9	i	102/125 (82%)	102 (100%)	0	100	100
10	j	89/90 (99%)	89 (100%)	0	100	100
11	k	89/105 (85%)	89 (100%)	0	100	100
12	l	103/105 (98%)	103 (100%)	0	100	100
13	m	99/104 (95%)	99 (100%)	0	100	100
14	n	49/50 (98%)	49 (100%)	0	100	100
15	o	76/77 (99%)	76 (100%)	0	100	100
16	p	92/118 (78%)	92 (100%)	0	100	100
17	q	80/83 (96%)	80 (100%)	0	100	100
18	r	55/72 (76%)	55 (100%)	0	100	100
19	s	70/84 (83%)	70 (100%)	0	100	100
20	t	69/70 (99%)	69 (100%)	0	100	100
21	u	30/31 (97%)	30 (100%)	0	100	100
24	z	290/298 (97%)	290 (100%)	0	100	100
27	C	215/218 (99%)	215 (100%)	0	100	100
28	D	160/163 (98%)	160 (100%)	0	100	100
29	E	169/173 (98%)	169 (100%)	0	100	100
30	F	151/156 (97%)	151 (100%)	0	100	100
31	G	148/150 (99%)	148 (100%)	0	100	100
32	H	90/116 (78%)	90 (100%)	0	100	100
33	I	89/120 (74%)	89 (100%)	0	100	100
34	J	102/108 (94%)	102 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	K	6/184 (3%)	6 (100%)	0	100	100
36	L	119/120 (99%)	119 (100%)	0	100	100
37	M	100/100 (100%)	100 (100%)	0	100	100
38	N	112/114 (98%)	112 (100%)	0	100	100
39	O	114/115 (99%)	114 (100%)	0	100	100
40	P	97/158 (61%)	97 (100%)	0	100	100
41	Q	93/94 (99%)	93 (100%)	0	100	100
42	R	100/100 (100%)	100 (100%)	0	100	100
43	S	97/99 (98%)	97 (100%)	0	100	100
44	T	81/83 (98%)	81 (100%)	0	100	100
45	U	90/117 (77%)	90 (100%)	0	100	100
46	V	83/85 (98%)	83 (100%)	0	100	100
47	W	81/86 (94%)	81 (100%)	0	100	100
48	X	155/168 (92%)	155 (100%)	0	100	100
49	Y	61/63 (97%)	61 (100%)	0	100	100
50	Z	50/51 (98%)	50 (100%)	0	100	100
51	1	58/66 (88%)	58 (100%)	0	100	100
52	2	52/54 (96%)	52 (100%)	0	100	100
53	3	46/63 (73%)	46 (100%)	0	100	100
54	4	43/46 (94%)	43 (100%)	0	100	100
55	5	47/52 (90%)	47 (100%)	0	100	100
56	6	35/36 (97%)	35 (100%)	0	100	100
57	7	53/54 (98%)	53 (100%)	0	100	100
58	8	35/35 (100%)	35 (100%)	0	100	100
59	9	18/19 (95%)	18 (100%)	0	100	100
All	All	5229/5856 (89%)	5229 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (103) such sidechains are listed below:

Mol	Chain	Res	Type
2	b	108	HIS

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Mol	Chain	Res	Type
2	b	167	ASN
3	c	8	HIS
3	c	68	HIS
4	d	35	GLN
4	d	75	ASN
4	d	84	ASN
4	d	115	HIS
4	d	185	GLN
6	f	82	ASN
6	f	96	HIS
7	g	148	ASN
8	h	16	ASN
8	h	29	HIS
9	i	64	HIS
10	j	64	HIS
11	k	31	HIS
11	k	49	ASN
11	k	84	GLN
11	k	110	GLN
12	l	5	GLN
12	l	72	HIS
13	m	31	ASN
14	n	11	ASN
15	o	18	HIS
15	o	28	GLN
15	o	37	GLN
15	o	46	HIS
15	o	48	HIS
16	p	41	HIS
17	q	46	HIS
19	s	47	HIS
20	t	3	ASN
20	t	21	ASN
20	t	71	GLN
20	t	84	ASN
24	z	44	HIS
24	z	126	HIS
24	z	152	HIS
24	z	167	HIS
24	z	222	GLN
24	z	259	GLN
27	C	53	HIS

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Mol	Chain	Res	Type
27	C	113	GLN
27	C	129	ASN
27	C	227	ASN
28	D	15	GLN
28	D	51	GLN
28	D	179	ASN
28	D	202	ASN
29	E	76	GLN
29	E	91	HIS
29	E	100	GLN
29	E	151	ASN
29	E	171	ASN
29	E	202	ASN
30	F	28	ASN
31	G	23	ASN
31	G	112	HIS
31	G	144	GLN
32	H	147	ASN
33	I	16	GLN
33	I	35	ASN
34	J	121	ASN
36	L	103	ASN
36	L	132	HIS
37	M	89	ASN
38	N	58	HIS
39	O	35	GLN
40	P	62	ASN
41	Q	8	GLN
42	R	76	HIS
43	S	41	HIS
43	S	72	ASN
43	S	94	ASN
43	S	122	ASN
44	T	67	HIS
44	T	76	HIS
44	T	85	HIS
44	T	93	GLN
45	U	66	GLN
47	W	31	ASN
47	W	67	HIS
47	W	70	ASN
48	X	46	HIS

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Mol	Chain	Res	Type
48	X	61	HIS
48	X	94	HIS
48	X	161	GLN
49	Y	3	HIS
49	Y	12	ASN
49	Y	19	GLN
49	Y	29	GLN
49	Y	79	ASN
50	Z	30	ASN
53	3	20	HIS
53	3	29	GLN
54	4	36	GLN
55	5	22	ASN
55	5	44	ASN
57	7	31	HIS
57	7	59	ASN
59	9	17	ASN
59	9	23	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1510/1528 (98%)	292 (19%)	0
22	v	2/3 (66%)	0	0
23	y	72/76 (94%)	12 (16%)	0
25	A	3079/3164 (97%)	500 (16%)	13 (0%)
26	B	117/118 (99%)	15 (12%)	1 (0%)
All	All	4780/4889 (97%)	819 (17%)	14 (0%)

All (819) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	11	G
1	a	12	A
1	a	13	G
1	a	18	U
1	a	36	A
1	a	42	G
1	a	43	G
1	a	51	C
1	a	52	U

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Mol	Chain	Res	Type
1	a	53	U
1	a	55	A
1	a	58	C
1	a	59	A
1	a	62	C
1	a	67	C
1	a	70	A
1	a	72	G
1	a	75	A
1	a	77	G
1	a	78	G
1	a	81	C
1	a	82	U
1	a	83	U
1	a	84	U
1	a	87	G
1	a	94	U
1	a	96	G
1	a	97	A
1	a	116	A
1	a	117	C
1	a	126	G
1	a	127	A
1	a	128	U
1	a	139	C
1	a	141	U
1	a	157	A
1	a	160	C
1	a	170	U
1	a	171	A
1	a	179	C
1	a	180	A
1	a	181	C
1	a	192	G
1	a	193	C
1	a	194	A
1	a	195	U
1	a	196	G
1	a	201	G
1	a	210	A
1	a	215	U
1	a	217	U

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Mol	Chain	Res	Type
1	a	221	G
1	a	231	G
1	a	245	C
1	a	247	G
1	a	251	G
1	a	266	G
1	a	267	C
1	a	280	C
1	a	281	G
1	a	289	G
1	a	301	G
1	a	329	A
1	a	330	C
1	a	332	G
1	a	344	A
1	a	347	G
1	a	351	G
1	a	352	C
1	a	353	A
1	a	363	A
1	a	364	A
1	a	367	U
1	a	372	C
1	a	373	A
1	a	376	G
1	a	388	G
1	a	390	U
1	a	392	C
1	a	397	A
1	a	398	C
1	a	406	G
1	a	411	A
1	a	414	A
1	a	421	U
1	a	422	C
1	a	423	G
1	a	424	G
1	a	426	U
1	a	428	G
1	a	429	U
1	a	430	A
1	a	434	C

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Mol	Chain	Res	Type
1	a	438	U
1	a	439	U
1	a	453	G
1	a	456	C
1	a	457	A
1	a	458	A
1	a	461	G
1	a	464	G
1	a	465	G
1	a	469	G
1	a	476	A
1	a	477	G
1	a	478	A
1	a	485	G
1	a	486	G
1	a	489	A
1	a	490	A
1	a	491	C
1	a	492	U
1	a	497	G
1	a	498	C
1	a	505	C
1	a	509	G
1	a	510	G
1	a	513	A
1	a	520	G
1	a	525	C
1	a	527	A
1	a	542	U
1	a	544	C
1	a	553	A
1	a	556	A
1	a	557	G
1	a	567	G
1	a	593	C
1	a	612	U
1	a	613	G
1	a	622	A
1	a	633	A
1	a	645	G
1	a	666	U
1	a	668	G

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Mol	Chain	Res	Type
1	a	683	G
1	a	700	C
1	a	701	G
1	a	702	G
1	a	703	U
1	a	704	G
1	a	711	G
1	a	729	A
1	a	735	G
1	a	757	A
1	a	765	G
1	a	772	A
1	a	773	U
1	a	774	A
1	a	795	A
1	a	796	A
1	a	797	C
1	a	808	A
1	a	822	U
1	a	823	U
1	a	824	C
1	a	826	U
1	a	827	U
1	a	828	G
1	a	841	U
1	a	884	G
1	a	896	A
1	a	908	G
1	a	909	G
1	a	916	C
1	a	917	A
1	a	940	A
1	a	942	U
1	a	943	U
1	a	948	G
1	a	950	A
1	a	951	A
1	a	953	G
1	a	954	C
1	a	956	A
1	a	957	A
1	a	959	A

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Mol	Chain	Res	Type
1	a	971	G
1	a	973	U
1	a	974	U
1	a	975	G
1	a	976	A
1	a	982	A
1	a	984	A
1	a	988	C
1	a	990	C
1	a	992	G
1	a	1007	U
1	a	1008	C
1	a	1009	C
1	a	1012	U
1	a	1013	G
1	a	1014	U
1	a	1020	G
1	a	1022	G
1	a	1024	G
1	a	1025	C
1	a	1030	G
1	a	1033	G
1	a	1034	C
1	a	1036	U
1	a	1045	U
1	a	1061	G
1	a	1065	U
1	a	1074	G
1	a	1075	U
1	a	1080	C
1	a	1081	A
1	a	1104	G
1	a	1110	A
1	a	1115	G
1	a	1116	U
1	a	1117	U
1	a	1118	A
1	a	1119	U
1	a	1120	G
1	a	1127	A
1	a	1132	U
1	a	1138	A

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Mol	Chain	Res	Type
1	a	1139	C
1	a	1140	U
1	a	1147	G
1	a	1150	A
1	a	1151	A
1	a	1152	C
1	a	1162	G
1	a	1165	G
1	a	1177	A
1	a	1178	A
1	a	1181	C
1	a	1182	A
1	a	1193	U
1	a	1194	A
1	a	1208	A
1	a	1217	A
1	a	1219	A
1	a	1237	C
1	a	1238	U
1	a	1239	G
1	a	1241	G
1	a	1247	G
1	a	1248	U
1	a	1250	A
1	a	1251	G
1	a	1260	A
1	a	1261	A
1	a	1263	C
1	a	1265	U
1	a	1266	U
1	a	1267	U
1	a	1268	C
1	a	1283	U
1	a	1284	U
1	a	1287	G
1	a	1302	C
1	a	1305	G
1	a	1322	G
1	a	1328	A
1	a	1329	G
1	a	1343	G
1	a	1344	C

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Mol	Chain	Res	Type
1	a	1346	A
1	a	1347	C
1	a	1357	A
1	a	1364	U
1	a	1377	A
1	a	1381	A
1	a	1424	G
1	a	1425	G
1	a	1426	C
1	a	1429	A
1	a	1433	C
1	a	1434	U
1	a	1435	U
1	a	1436	G
1	a	1438	G
1	a	1440	A
1	a	1459	G
1	a	1478	G
1	a	1479	U
1	a	1481	G
1	a	1483	A
1	a	1486	A
1	a	1488	G
1	a	1489	G
1	a	1490	U
1	a	1501	G
1	a	1503	A
1	a	1504	G
1	a	1513	G
1	a	1514	G
1	a	1516	U
23	y	19	G
23	y	21	A
23	y	26	A
23	y	40	C
23	y	46	7MG
23	y	47	U
23	y	48	C
23	y	52	G
23	y	56	C
23	y	68	C
23	y	73	A

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Mol	Chain	Res	Type
23	y	76	A
25	A	7	U
25	A	12	G
25	A	16	G
25	A	20	G
25	A	31	U
25	A	32	G
25	A	48	G
25	A	55	G
25	A	60	A
25	A	68	A
25	A	71	A
25	A	72	G
25	A	89	A
25	A	90	C
25	A	94	G
25	A	98	U
25	A	99	G
25	A	115	A
25	A	116	A
25	A	117	U
25	A	125	C
25	A	164	A
25	A	195	A
25	A	198	A
25	A	212	A
25	A	214	G
25	A	215	A
25	A	221	A
25	A	227	A
25	A	228	A
25	A	229	U
25	A	230	G
25	A	231	U
25	A	248	G
25	A	264	G
25	A	265	A
25	A	274	C
25	A	275	C
25	A	283	U
25	A	285	U
25	A	286	G

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Mol	Chain	Res	Type
25	A	288	U
25	A	291	C
25	A	293	G
25	A	296	A
25	A	300	G
25	A	301	U
25	A	302	U
25	A	312	G
25	A	314	G
25	A	315	U
25	A	317	G
25	A	318	U
25	A	319	G
25	A	330	U
25	A	331	U
25	A	336	C
25	A	337	U
25	A	338	C
25	A	339	U
25	A	342	C
25	A	344	G
25	A	351	G
25	A	352	G
25	A	357	U
25	A	358	G
25	A	361	A
25	A	364	A
25	A	369	G
25	A	370	U
25	A	371	G
25	A	384	G
25	A	393	U
25	A	399	G
25	A	412	A
25	A	413	G
25	A	424	G
25	A	434	G
25	A	445	U
25	A	446	G
25	A	447	A
25	A	450	G
25	A	452	G

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Mol	Chain	Res	Type
25	A	453	U
25	A	454	U
25	A	460	G
25	A	474	G
25	A	489	A
25	A	494	G
25	A	512	G
25	A	537	A
25	A	543	U
25	A	544	U
25	A	562	G
25	A	566	A
25	A	569	G
25	A	589	A
25	A	591	G
25	A	592	A
25	A	594	U
25	A	595	A
25	A	596	C
25	A	597	C
25	A	614	C
25	A	617	U
25	A	618	C
25	A	619	C
25	A	620	G
25	A	634	C
25	A	635	G
25	A	636	U
25	A	637	G
25	A	638	U
25	A	639	C
25	A	640	G
25	A	642	G
25	A	644	G
25	A	655	G
25	A	665	G
25	A	666	A
25	A	667	A
25	A	678	A
25	A	679	G
25	A	684	G
25	A	685	G

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Mol	Chain	Res	Type
25	A	696	A
25	A	706	G
25	A	707	G
25	A	708	G
25	A	709	U
25	A	721	A
25	A	728	G
25	A	731	A
25	A	738	A
25	A	740	A
25	A	753	A
25	A	757	G
25	A	758	A
25	A	760	U
25	A	764	U
25	A	768	G
25	A	784	G
25	A	785	A
25	A	801	U
25	A	832	G
25	A	839	U
25	A	845	C
25	A	862	U
25	A	868	C
25	A	871	A
25	A	872	G
25	A	878	G
25	A	879	A
25	A	880	G
25	A	890	G
25	A	891	G
25	A	897	A
25	A	899	G
25	A	904	A
25	A	917	A
25	A	920	G
25	A	921	C
25	A	927	C
25	A	942	U
25	A	961	U
25	A	972	A
25	A	974	G

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Mol	Chain	Res	Type
25	A	975	U
25	A	981	U
25	A	982	A
25	A	994	A
25	A	1001	C
25	A	1003	A
25	A	1006	G
25	A	1007	G
25	A	1011	A
25	A	1012	C
25	A	1014	G
25	A	1025	A
25	A	1030	C
25	A	1045	C
25	A	1046	C
25	A	1047	A
25	A	1049	G
25	A	1063	G
25	A	1076	A
25	A	1078	G
25	A	1085	G
25	A	1092	G
25	A	1099	A
25	A	1101	A
25	A	1114	G
25	A	1131	G
25	A	1140	G
25	A	1141	U
25	A	1144	A
25	A	1151	U
25	A	1165	G
25	A	1188	A
25	A	1191	A
25	A	1202	A
25	A	1205	G
25	A	1206	A
25	A	1209	G
25	A	1213	A
25	A	1215	U
25	A	1229	A
25	A	1230	G
25	A	1232	G

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Mol	Chain	Res	Type
25	A	1238	G
25	A	1246	A
25	A	1250	U
25	A	1251	A
25	A	1253	C
25	A	1254	G
25	A	1260	C
25	A	1261	A
25	A	1292	U
25	A	1293	G
25	A	1298	C
25	A	1335	G
25	A	1344	A
25	A	1353	G
25	A	1365	G
25	A	1371	G
25	A	1384	G
25	A	1386	G
25	A	1387	A
25	A	1389	U
25	A	1415	A
25	A	1416	A
25	A	1456	G
25	A	1465	C
25	A	1467	U
25	A	1480	A
25	A	1494	U
25	A	1499	A
25	A	1507	G
25	A	1508	A
25	A	1510	A
25	A	1511	U
25	A	1531	C
25	A	1532	G
25	A	1533	U
25	A	1534	C
25	A	1538	G
25	A	1540	U
25	A	1543	A
25	A	1549	G
25	A	1550	G
25	A	1551	U

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Mol	Chain	Res	Type
25	A	1553	C
25	A	1559	A
25	A	1560	U
25	A	1564	A
25	A	1565	A
25	A	1625	G
25	A	1628	A
25	A	1629	G
25	A	1630	U
25	A	1631	A
25	A	1637	G
25	A	1640	A
25	A	1641	U
25	A	1648	A
25	A	1649	C
25	A	1654	G
25	A	1670	G
25	A	1674	G
25	A	1676	G
25	A	1679	A
25	A	1680	A
25	A	1681	U
25	A	1688	G
25	A	1703	G
25	A	1710	A
25	A	1711	G
25	A	1713	U
25	A	1714	A
25	A	1716	A
25	A	1717	U
25	A	1724	G
25	A	1731	A
25	A	1737	A
25	A	1738	G
25	A	1746	G
25	A	1754	G
25	A	1755	A
25	A	1756	G
25	A	1757	U
25	A	1758	G
25	A	1759	A
25	A	1767	U

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Mol	Chain	Res	Type
25	A	1769	G
25	A	1780	G
25	A	1786	G
25	A	1789	A
25	A	1798	U
25	A	1801	C
25	A	1803	A
25	A	1826	A
25	A	1828	A
25	A	1864	U
25	A	1866	C
25	A	1870	U
25	A	1871	G
25	A	1872	A
25	A	1892	G
25	A	1947	U
25	A	1949	C
25	A	1973	C
25	A	1975	A
25	A	1981	U
25	A	1990	A
25	A	2001	A
25	A	2017	C
25	A	2018	G
25	A	2026	A
25	A	2033	U
25	A	2046	A
25	A	2065	A
25	A	2075	G
25	A	2086	U
25	A	2087	C
25	A	2088	C
25	A	2089	C
25	A	2091	U
25	A	2092	U
25	A	2093	G
25	A	2094	G
25	A	2095	G
25	A	2096	G
25	A	2107	G
25	A	2129	C
25	A	2130	G

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Mol	Chain	Res	Type
25	A	2138	C
25	A	2141	U
25	A	2153	G
25	A	2154	G
25	A	2160	A
25	A	2162	A
25	A	2163	U
25	A	2164	U
25	A	2166	C
25	A	2168	U
25	A	2179	U
25	A	2184	A
25	A	2188	G
25	A	2191	C
25	A	2194	A
25	A	2195	U
25	A	2196	G
25	A	2215	U
25	A	2216	G
25	A	2217	U
25	A	2220	C
25	A	2221	A
25	A	2244	A
25	A	2247	A
25	A	2255	A
25	A	2256	G
25	A	2257	A
25	A	2263	G
25	A	2267	C
25	A	2279	C
25	A	2280	G
25	A	2284	A
25	A	2285	G
25	A	2286	A
25	A	2321	U
25	A	2323	G
25	A	2333	G
25	A	2334	U
25	A	2335	G
25	A	2337	A
25	A	2340	A
25	A	2345	U

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Mol	Chain	Res	Type
25	A	2349	A
25	A	2350	G
25	A	2351	A
25	A	2353	U
25	A	2354	G
25	A	2355	U
25	A	2356	G
25	A	2357	A
25	A	2360	C
25	A	2361	U
25	A	2362	C
25	A	2368	C
25	A	2369	C
25	A	2370	A
25	A	2371	G
25	A	2372	U
25	A	2380	G
25	A	2381	A
25	A	2383	U
25	A	2385	G
25	A	2386	U
25	A	2387	U
25	A	2390	U
25	A	2393	A
25	A	2394	A
25	A	2395	U
25	A	2396	A
25	A	2404	G
25	A	2407	C
25	A	2408	G
25	A	2409	U
25	A	2413	G
25	A	2421	A
25	A	2427	G
25	A	2434	A
25	A	2436	A
25	A	2449	A
25	A	2462	G
25	A	2463	G
25	A	2503	G
25	A	2507	C
25	A	2511	A

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Mol	Chain	Res	Type
25	A	2521	C
25	A	2529	A
25	A	2532	G
25	A	2544	U
25	A	2545	G
25	A	2548	U
25	A	2549	G
25	A	2559	A
25	A	2569	G
25	A	2571	C
25	A	2574	C
25	A	2607	G
25	A	2609	A
25	A	2627	C
25	A	2630	A
25	A	2647	U
25	A	2649	A
25	A	2653	G
25	A	2654	A
25	A	2655	U
25	A	2663	A
25	A	2665	C
25	A	2672	A
25	A	2677	A
25	A	2688	C
25	A	2693	A
25	A	2694	G
25	A	2699	C
25	A	2700	A
25	A	2715	U
25	A	2722	C
25	A	2726	G
25	A	2729	G
25	A	2742	A
25	A	2744	C
25	A	2753	G
25	A	2778	U
25	A	2790	A
25	A	2791	G
25	A	2810	U
25	A	2826	A
25	A	2827	G

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Mol	Chain	Res	Type
25	A	2833	U
25	A	2837	U
25	A	2839	U
25	A	2853	C
25	A	2854	A
25	A	2858	G
25	A	2862	G
25	A	2870	C
25	A	2887	G
25	A	2913	U
25	A	2915	C
25	A	2926	A
25	A	2936	C
25	A	2938	G
25	A	2950	C
25	A	2953	U
25	A	2957	A
25	A	2968	G
25	A	2972	A
25	A	2982	A
25	A	2985	G
25	A	2989	A
25	A	3002	A
25	A	3009	U
25	A	3014	A
25	A	3015	C
25	A	3021	A
25	A	3022	G
25	A	3023	G
25	A	3042	A
25	A	3044	A
25	A	3056	A
25	A	3082	U
25	A	3088	C
25	A	3093	A
25	A	3101	C
25	A	3104	A
25	A	3105	C
25	A	3115	A
26	B	3	U
26	B	4	A
26	B	11	U

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Mol	Chain	Res	Type
26	B	12	C
26	B	13	C
26	B	42	C
26	B	46	A
26	B	57	U
26	B	58	A
26	B	87	U
26	B	89	C
26	B	90	G
26	B	103	G
26	B	107	A
26	B	114	A

All (14) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	A	89	A
25	A	97	U
25	A	316	U
25	A	357	U
25	A	445	U
25	A	643	G
25	A	974	G
25	A	980	C
25	A	981	U
25	A	1010	U
25	A	1249	G
25	A	1510	A
25	A	2094	G
26	B	10	G

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

6 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
23	PSU	y	32	23	18,21,22	1.37	2 (11%)	21,30,33	2.05	4 (19%)
23	PSU	y	39	23	18,21,22	1.33	2 (11%)	21,30,33	2.30	3 (14%)
23	4SU	y	8	23	18,21,22	1.86	4 (22%)	25,30,33	2.21	4 (16%)
23	5MU	y	54	23	19,22,23	1.41	6 (31%)	27,32,35	2.01	6 (22%)
23	PSU	y	55	23	18,21,22	1.37	2 (11%)	21,30,33	2.06	4 (19%)
23	7MG	y	46	23	23,26,27	1.34	3 (13%)	27,39,42	2.74	7 (25%)

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
23	PSU	y	32	23	-	0/7/25/26	0/2/2/2
23	PSU	y	39	23	-	0/7/25/26	0/2/2/2
23	4SU	y	8	23	-	0/7/25/26	0/2/2/2
23	5MU	y	54	23	-	0/7/25/26	0/2/2/2
23	PSU	y	55	23	-	0/7/25/26	0/2/2/2
23	7MG	y	46	23	-	6/7/37/38	0/3/3/3

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	y	8	4SU	C4-S4	-5.05	1.59	1.68
23	y	8	4SU	C4-N3	-3.42	1.34	1.37
23	y	46	7MG	C5-C4	3.40	1.48	1.37
23	y	55	PSU	C6-C5	3.33	1.39	1.35
23	y	32	PSU	C6-C5	3.23	1.38	1.35
23	y	39	PSU	C6-C5	3.06	1.38	1.35
23	y	8	4SU	C5-C4	-2.73	1.39	1.42
23	y	54	5MU	C4-N3	-2.69	1.33	1.38
23	y	54	5MU	C6-C5	2.69	1.39	1.34
23	y	55	PSU	C4-N3	-2.68	1.33	1.38
23	y	32	PSU	C4-N3	-2.68	1.33	1.38
23	y	46	7MG	C6-N1	-2.57	1.34	1.38
23	y	54	5MU	C6-N1	-2.29	1.34	1.38
23	y	54	5MU	C4-C5	2.28	1.48	1.44
23	y	8	4SU	C2-N3	-2.26	1.34	1.38
23	y	39	PSU	C4-N3	-2.22	1.34	1.38
23	y	54	5MU	C2-N1	2.21	1.41	1.38
23	y	46	7MG	C4-N9	-2.21	1.35	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	y	54	5MU	C2-N3	-2.07	1.34	1.38

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	y	46	7MG	N9-C4-N3	9.79	139.81	125.46
23	y	39	PSU	N1-C2-N3	7.07	122.62	115.17
23	y	8	4SU	C4-N3-C2	-6.59	121.00	127.31
23	y	55	PSU	N1-C2-N3	6.45	121.97	115.17
23	y	32	PSU	N1-C2-N3	6.43	121.95	115.17
23	y	46	7MG	C5-C4-N3	-5.95	116.97	128.13
23	y	8	4SU	C5-C4-N3	5.94	120.28	114.75
23	y	39	PSU	C4-N3-C2	-4.88	119.65	126.37
23	y	54	5MU	C4-N3-C2	-4.84	121.00	127.34
23	y	54	5MU	N3-C2-N1	4.83	121.18	114.89
23	y	46	7MG	N9-C8-N7	-4.70	96.72	103.37
23	y	46	7MG	C2-N3-C4	4.67	120.34	112.30
23	y	39	PSU	O2-C2-N1	-4.38	118.27	122.79
23	y	54	5MU	C5-C4-N3	4.15	118.93	115.32
23	y	32	PSU	C4-N3-C2	-4.15	120.66	126.37
23	y	55	PSU	C4-N3-C2	-4.12	120.69	126.37
23	y	8	4SU	C5-C4-S4	-4.01	119.72	124.31
23	y	54	5MU	O4-C4-C5	-3.91	120.45	124.92
23	y	8	4SU	N3-C2-N1	3.79	119.83	114.89
23	y	55	PSU	O2-C2-N1	-3.57	119.11	122.79
23	y	32	PSU	O2-C2-N1	-3.55	119.13	122.79
23	y	54	5MU	C5-C6-N1	-3.34	119.69	123.31
23	y	46	7MG	C5-C6-N1	2.83	115.93	110.94
23	y	46	7MG	C5-C4-N9	-2.43	103.23	106.33
23	y	46	7MG	O6-C6-C5	-2.19	122.25	127.62
23	y	55	PSU	C5-C6-N1	-2.14	119.17	122.14
23	y	54	5MU	O2-C2-N1	-2.10	120.06	122.80
23	y	32	PSU	C5-C6-N1	-2.09	119.23	122.14

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
23	y	46	7MG	O4'-C4'-C5'-O5'
23	y	46	7MG	C3'-C4'-C5'-O5'
23	y	46	7MG	C2'-C1'-N9-C8
23	y	46	7MG	O4'-C1'-N9-C4

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Mol	Chain	Res	Type	Atoms
23	y	46	7MG	C4'-C5'-O5'-P
23	y	46	7MG	O4'-C1'-N9-C8

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	y	39	PSU	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

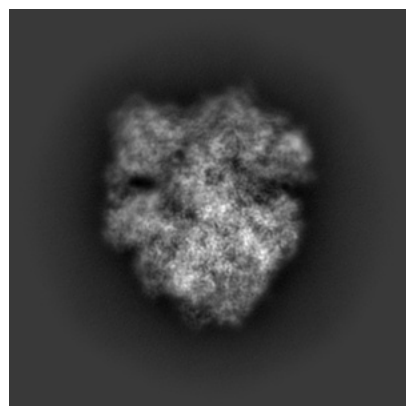
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43075. These allow visual inspection of the internal detail of the map and identification of artifacts.

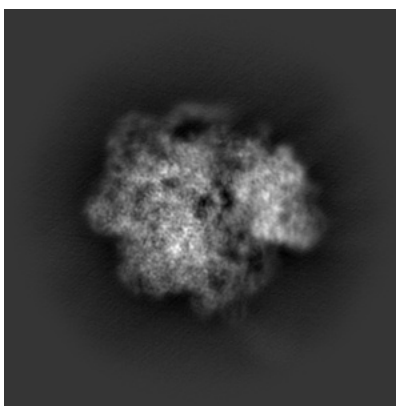
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

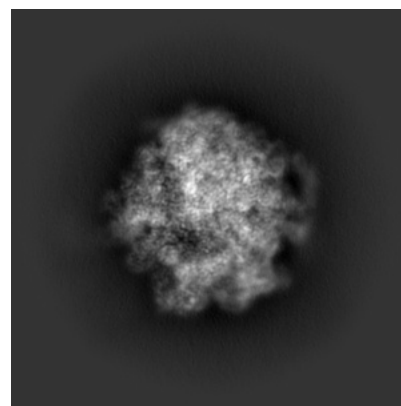
6.1.1 Primary map



X

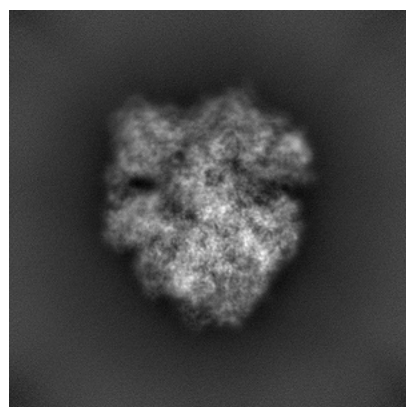


Y

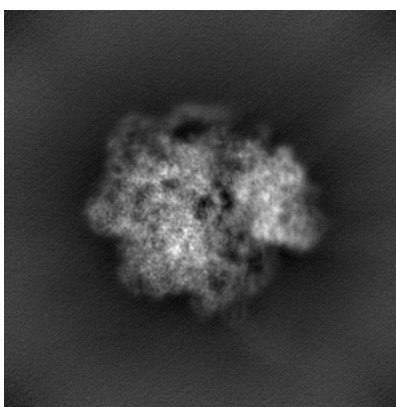


Z

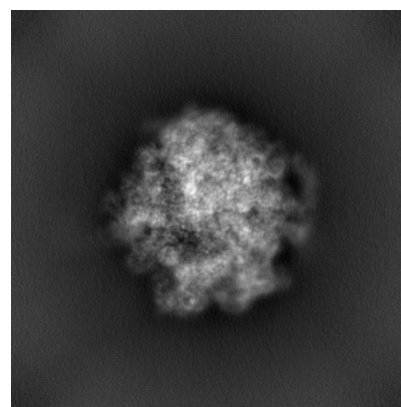
6.1.2 Raw map



X



Y

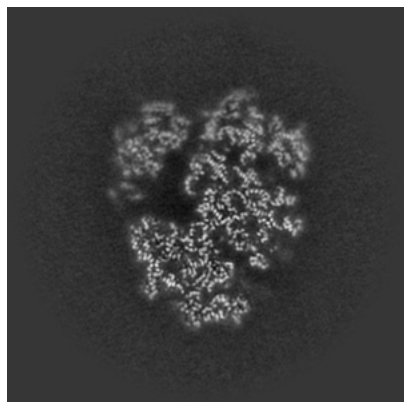


Z

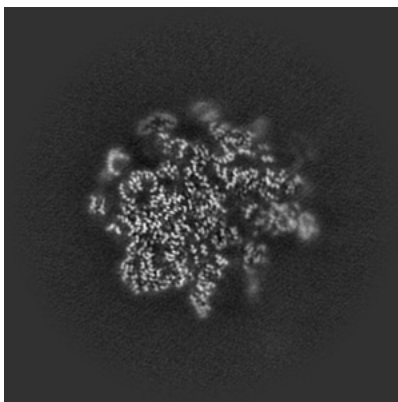
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

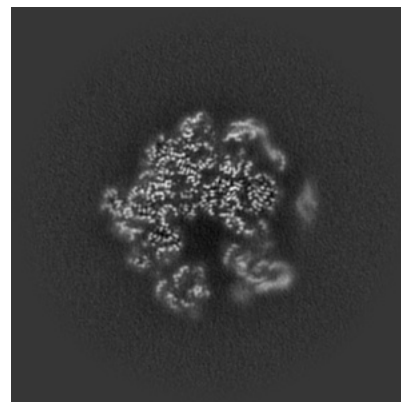
6.2.1 Primary map



X Index: 256

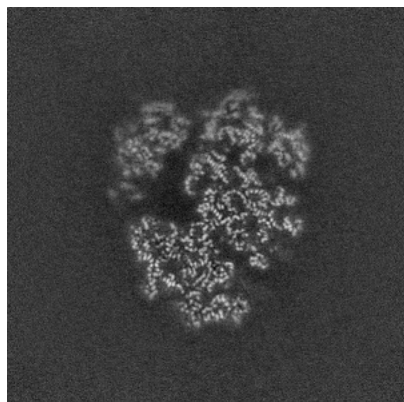


Y Index: 256

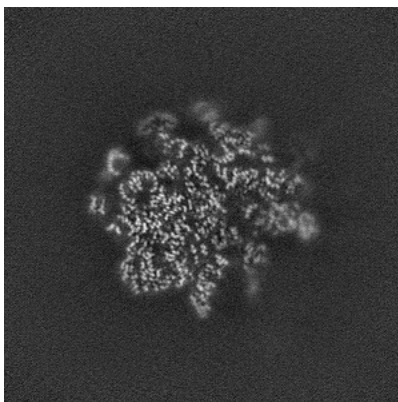


Z Index: 256

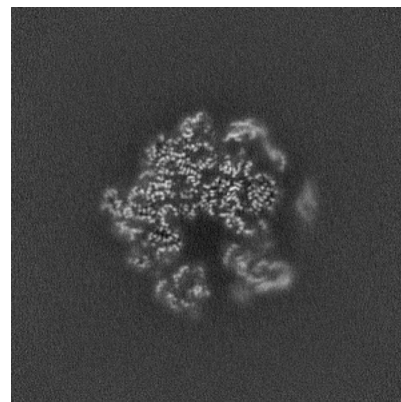
6.2.2 Raw map



X Index: 256



Y Index: 256

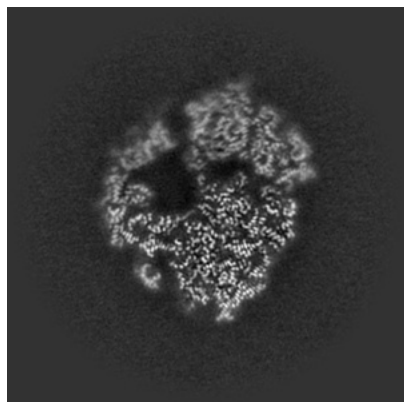


Z Index: 256

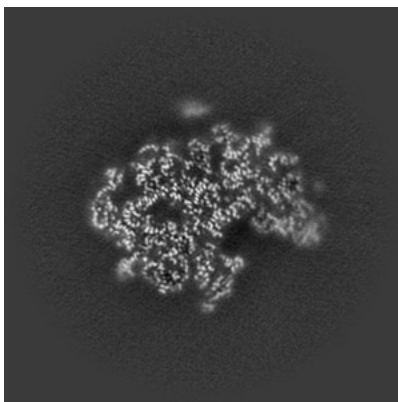
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

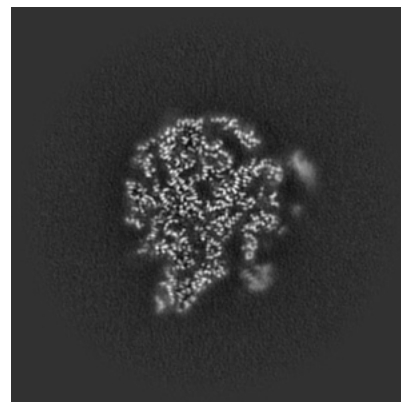
6.3.1 Primary map



X Index: 233

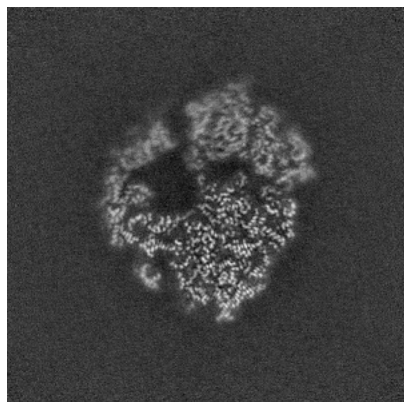


Y Index: 278

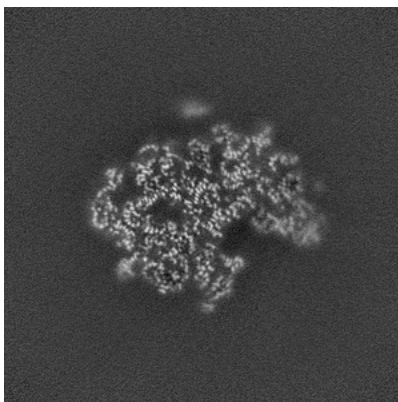


Z Index: 219

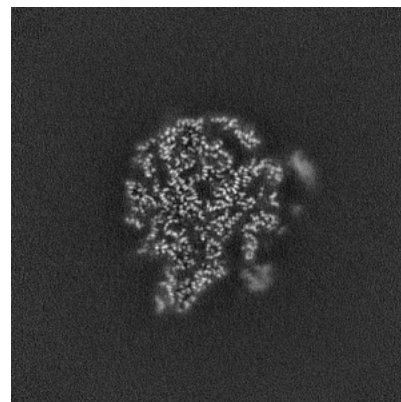
6.3.2 Raw map



X Index: 233



Y Index: 278

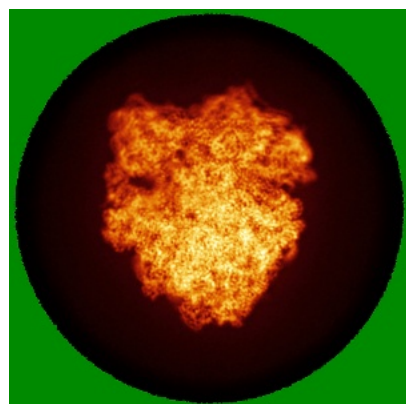


Z Index: 219

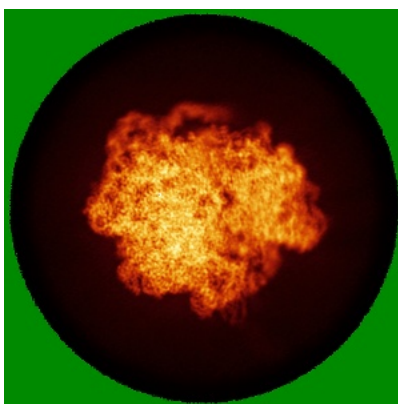
The images above show the largest variance slices of the map in three orthogonal directions.

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

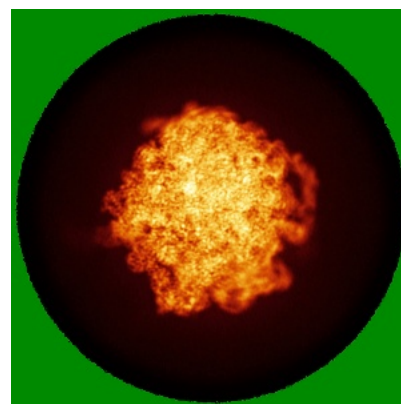
6.4.1 Primary map



X

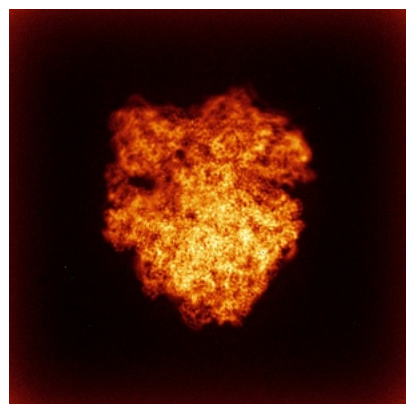


Y

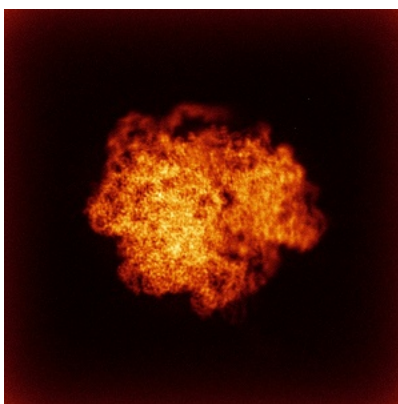


Z

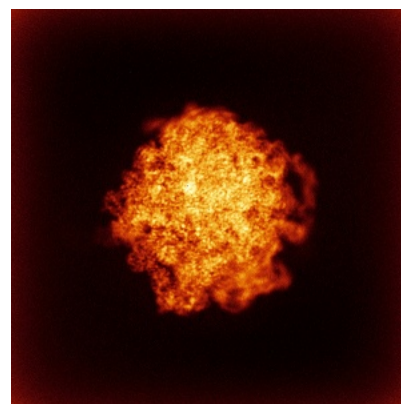
6.4.2 Raw map



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



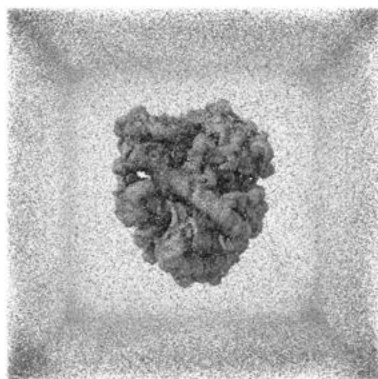
Y



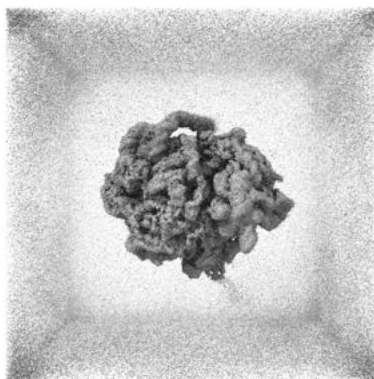
Z

The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

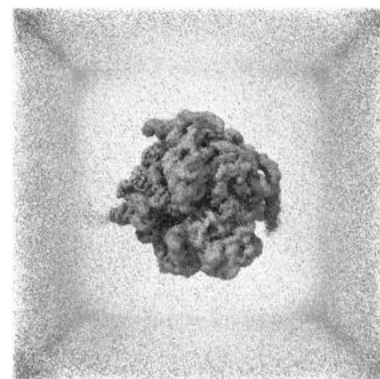
6.5.2 Raw map



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.

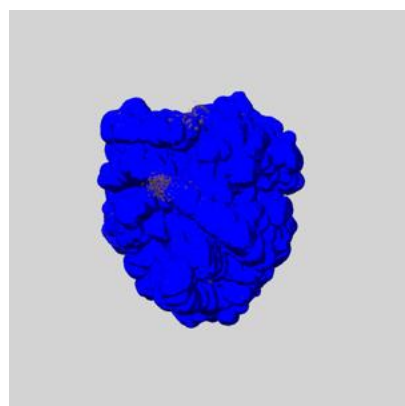
6.6 Mask visualisation [i](#)

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

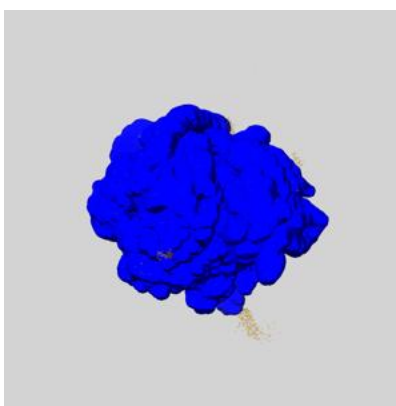
A mask typically either:

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

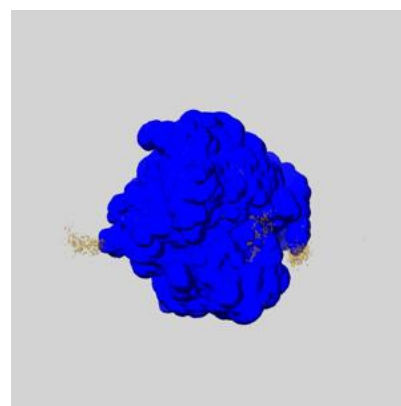
6.6.1 emd_43075_msk_1.map [i](#)



X



Y

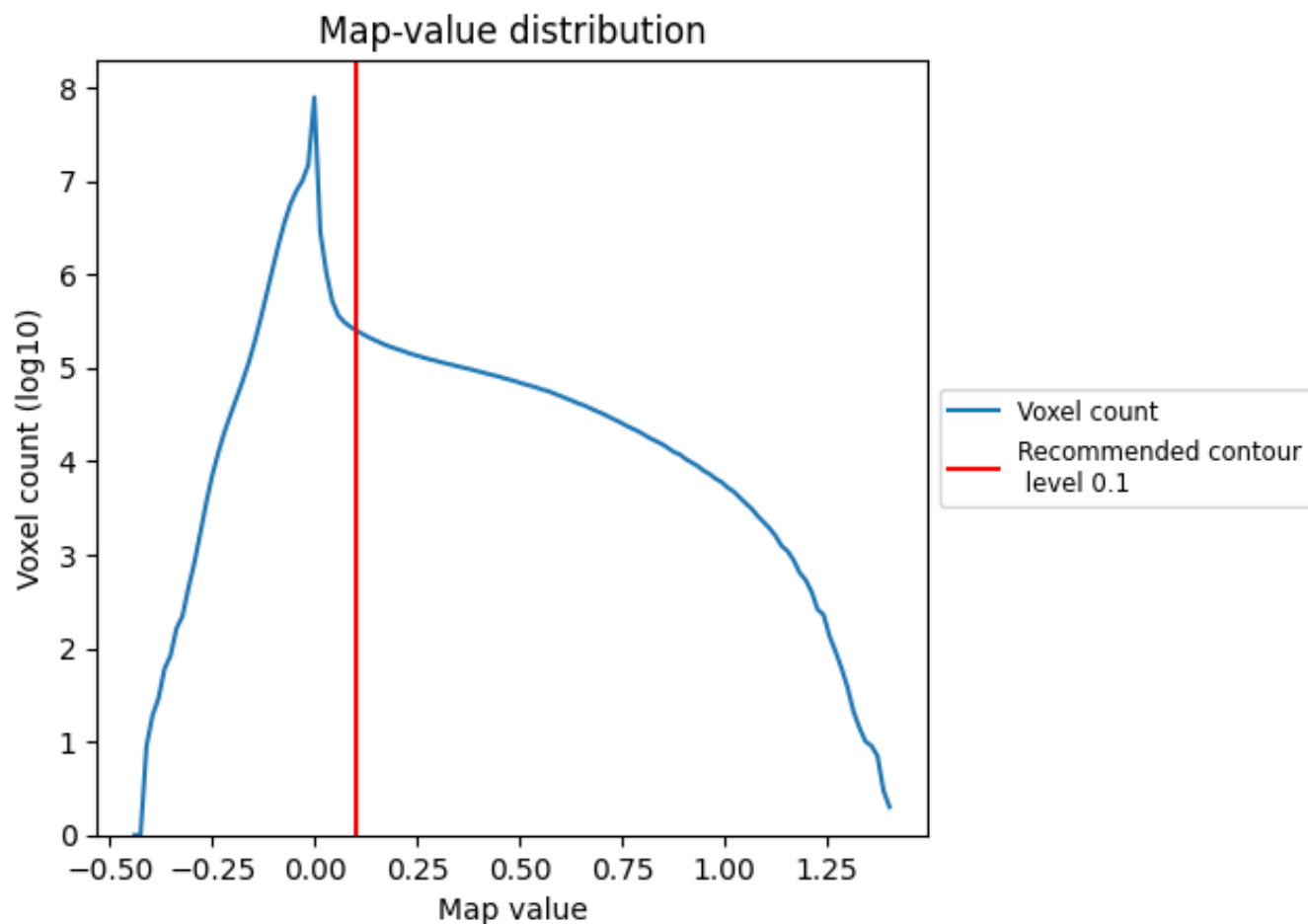


Z

7 Map analysis [i](#)

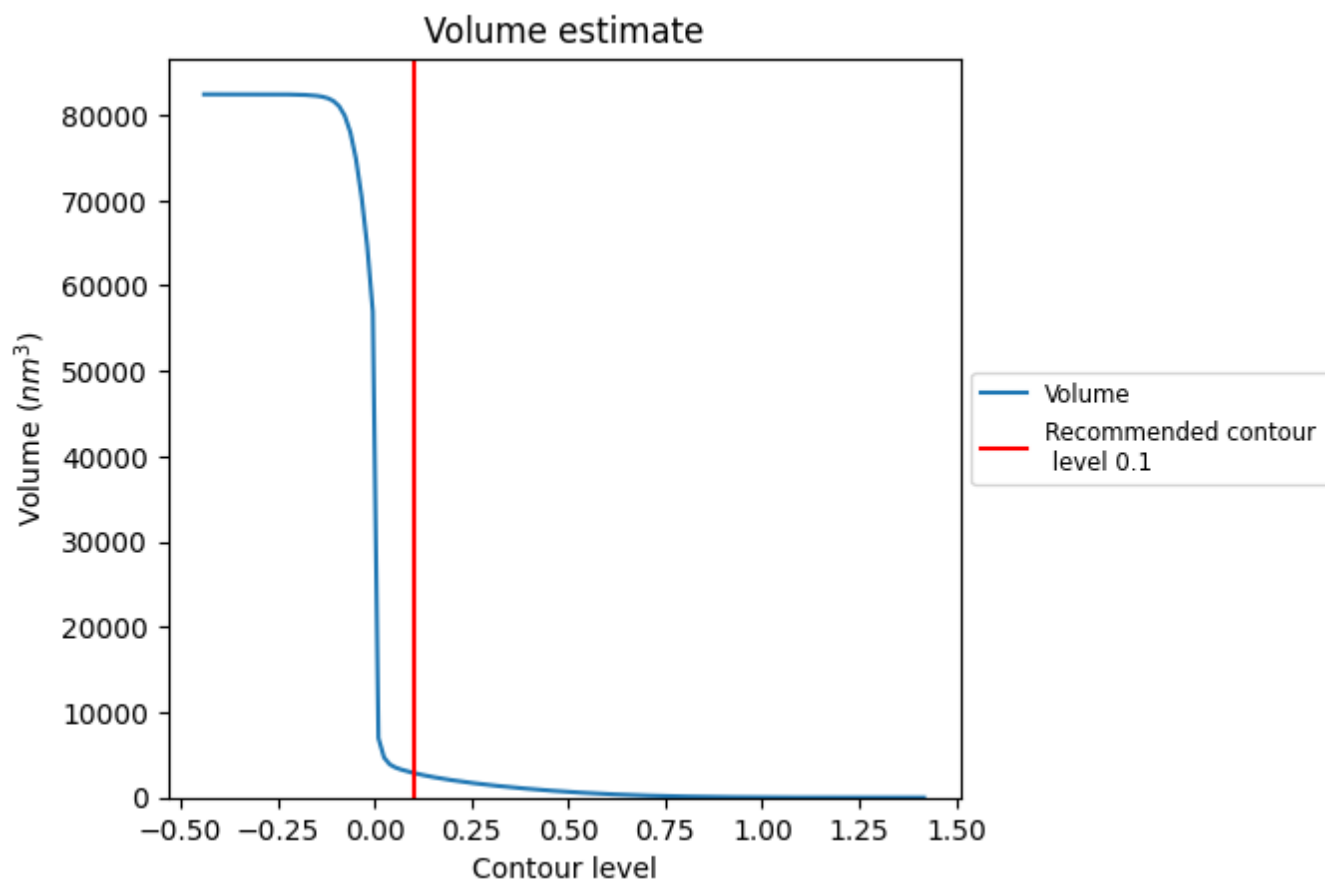
This section contains the results of statistical analysis of the map.

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.

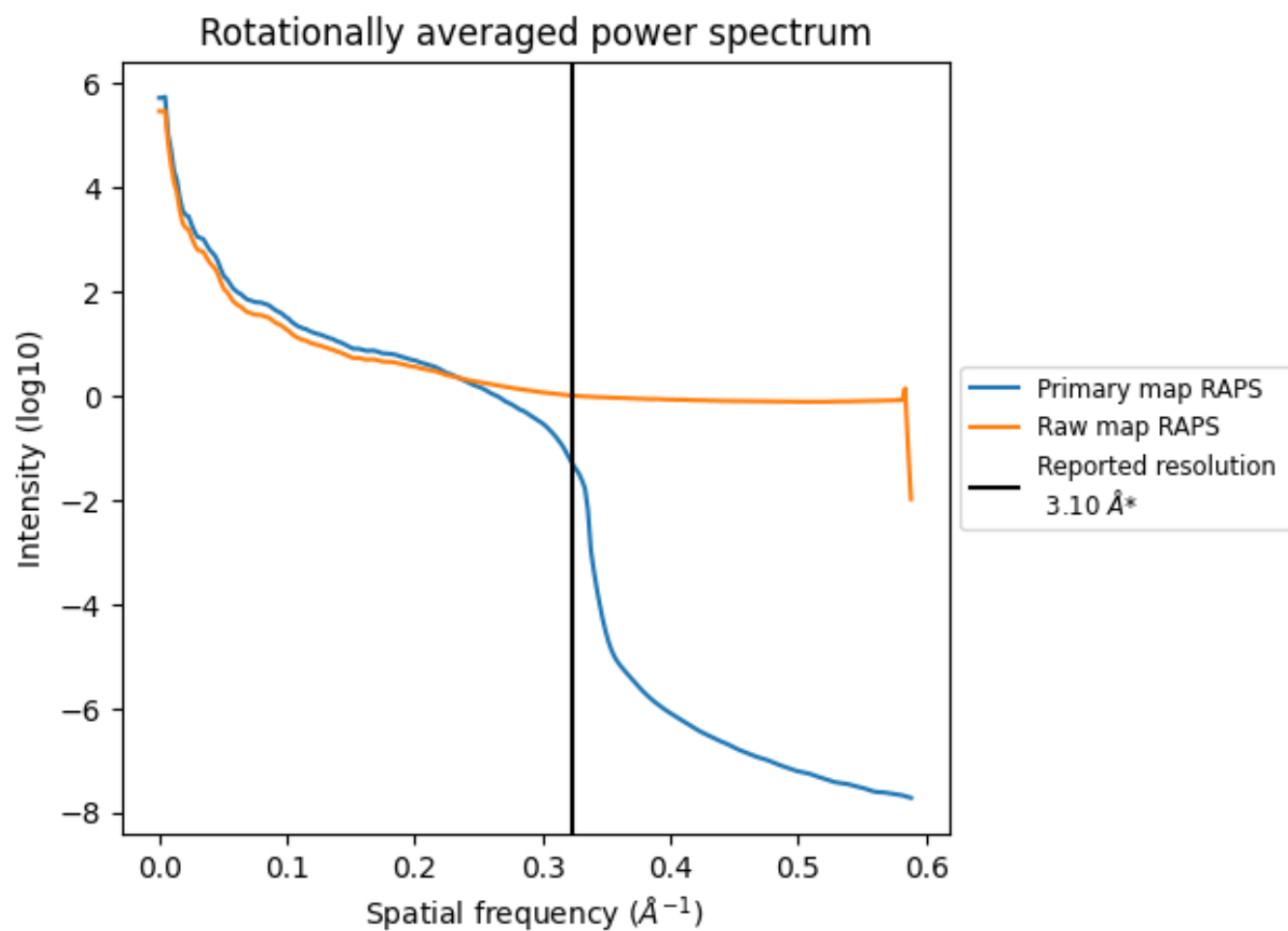
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2897 nm^3 ; this corresponds to an approximate mass of 2617 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 ⓘ

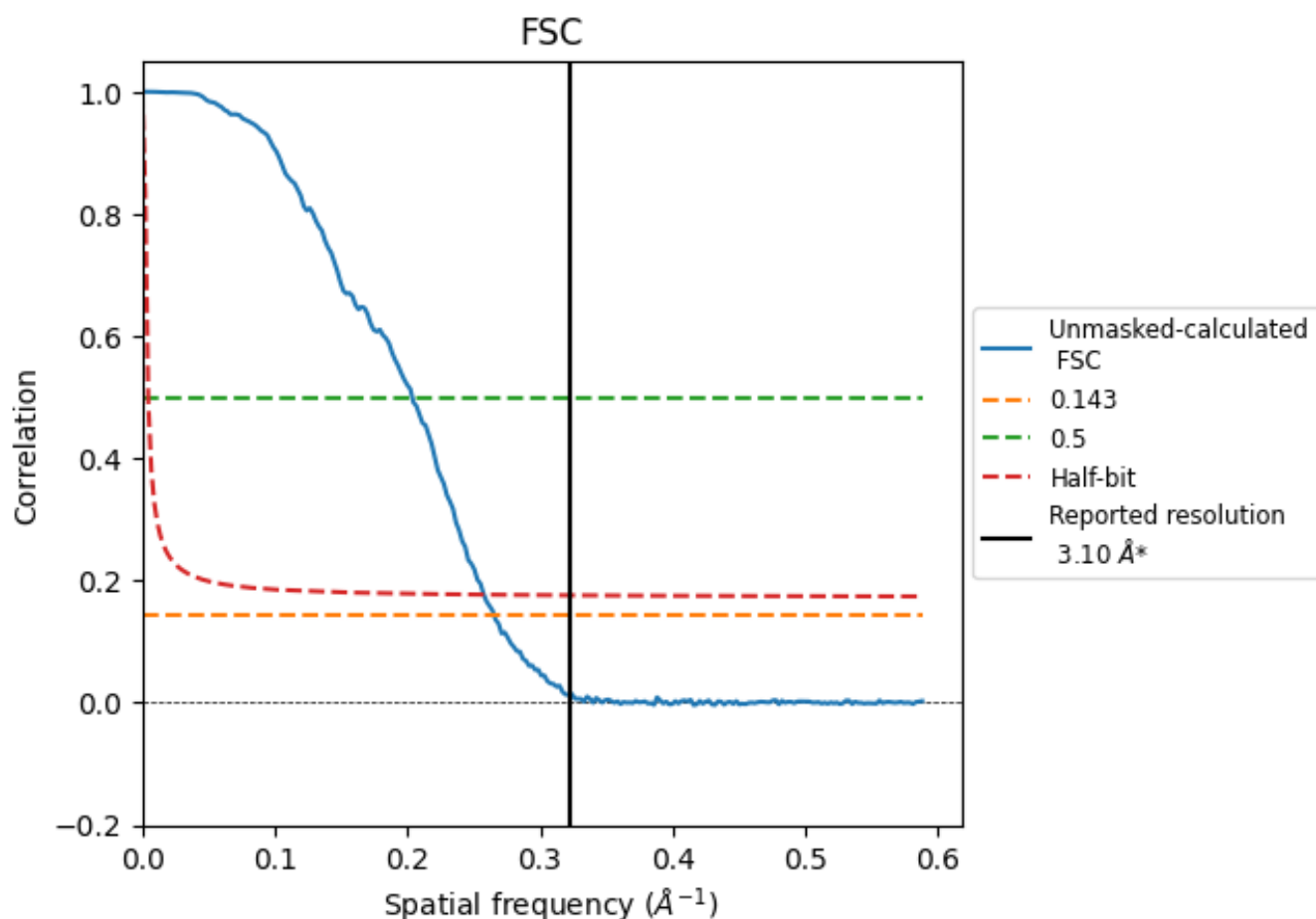


*Reported resolution corresponds to spatial frequency of 0.323 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

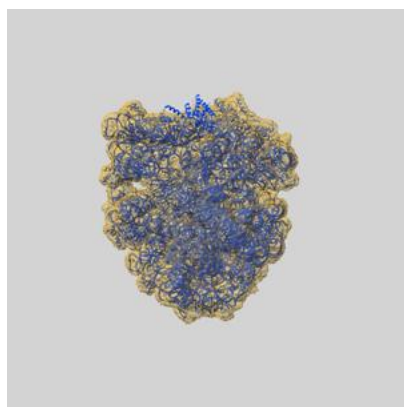
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.77	4.91	3.88

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

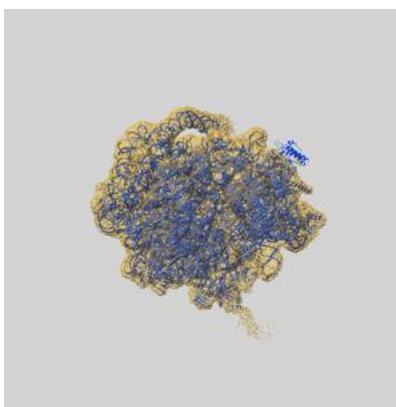
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-43075 and PDB model 8V9K. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

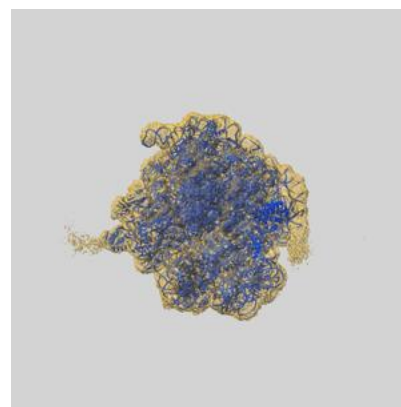
9.1 Map-model overlay [i](#)



X



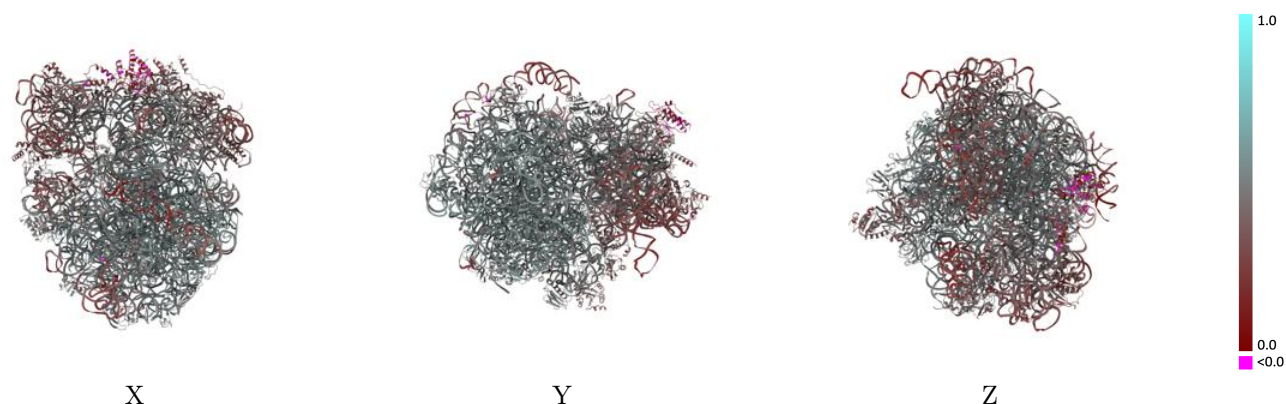
Y



Z

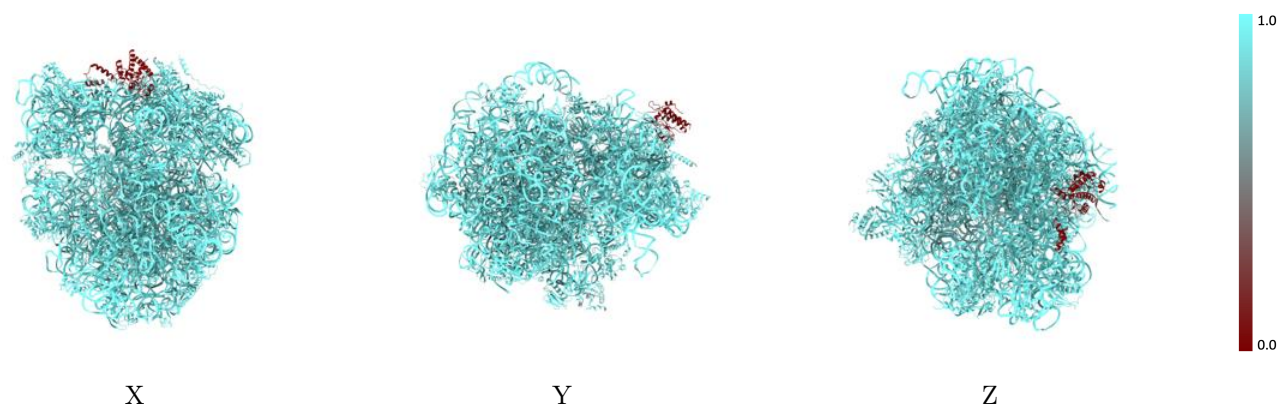
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



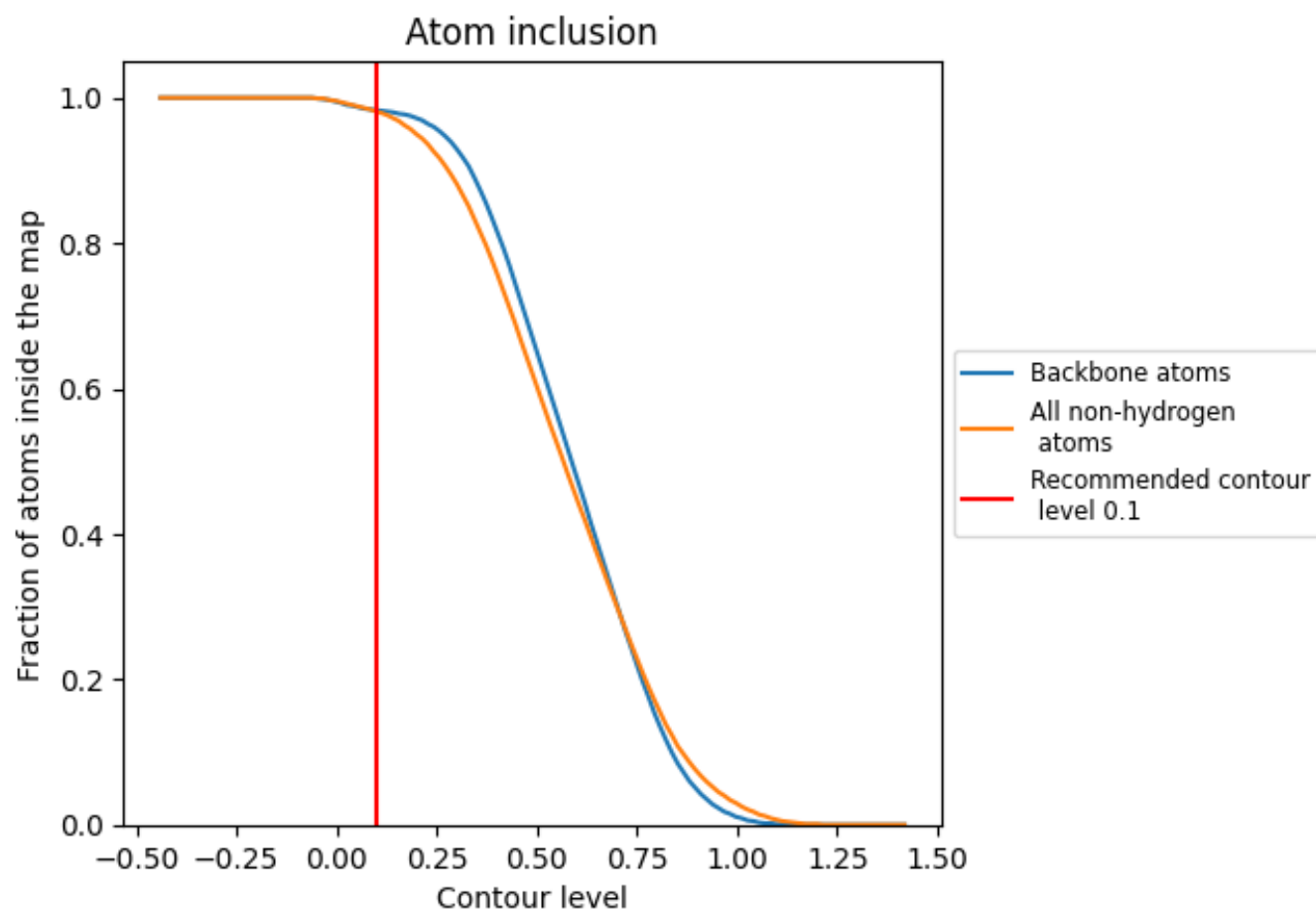
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 98% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9810	 0.4610
1	 0.9920	 0.4880
2	 0.9890	 0.5390
3	 0.9950	 0.4110
4	 0.9900	 0.5400
5	 0.9950	 0.5310
6	 0.9740	 0.5480
7	 0.9850	 0.5530
8	 0.9860	 0.5330
9	 0.9780	 0.5510
A	 0.9980	 0.4950
B	 0.9990	 0.4900
C	 0.9700	 0.5390
D	 0.9900	 0.5320
E	 0.9930	 0.5210
F	 0.9850	 0.4420
G	 0.9880	 0.4800
H	 0.9190	 0.4480
I	 0.8580	 0.3500
J	 0.9930	 0.3880
K	 0.9960	 0.4240
L	 0.9860	 0.5300
M	 0.9540	 0.5260
N	 0.9880	 0.5330
O	 0.9720	 0.5280
P	 0.9910	 0.5390
Q	 0.9960	 0.4940
R	 0.9670	 0.5190
S	 0.9920	 0.5310
T	 0.9990	 0.5480
U	 0.9870	 0.5360
V	 0.9850	 0.5210
W	 0.9850	 0.4940
X	 0.9730	 0.4900
Y	 0.9840	 0.5380



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Chain	Atom inclusion	Q-score
Z	 0.9930	 0.5440
a	 0.9990	 0.4080
b	 0.1040	 0.1510
c	 0.9830	 0.3880
d	 0.9890	 0.3370
e	 0.9740	 0.4480
f	 0.9770	 0.4600
g	 0.9810	 0.3220
h	 0.9960	 0.4740
i	 0.9920	 0.3620
j	 0.9820	 0.3780
k	 0.9810	 0.4800
l	 0.9420	 0.4130
m	 0.9840	 0.3260
n	 0.9760	 0.4230
o	 0.9830	 0.4650
p	 0.9850	 0.3610
q	 0.9790	 0.4200
r	 0.9960	 0.4630
s	 0.9910	 0.3550
t	 0.9750	 0.3360
u	 0.8850	 0.4780
v	 1.0000	 0.4870
y	 0.9980	 0.4330
z	 0.9610	 0.4600