



Full wwPDB EM Validation Report ⓘ

Jun 25, 2026 – 04:41 AM EDT

PDB ID : 8SYL / pdb_00008syl
EMDB ID : EMD-40882
Title : Cryo-EM structure of the Escherichia coli 70S ribosome in complex with amikacin, mRNA, and A-, P-, and E-site tRNAs
Authors : Seely, S.M.; Gagnon, M.G.
Deposited on : 2023-05-25
Resolution : 2.90 Å(reported)
Based on initial model : 8EKC

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:

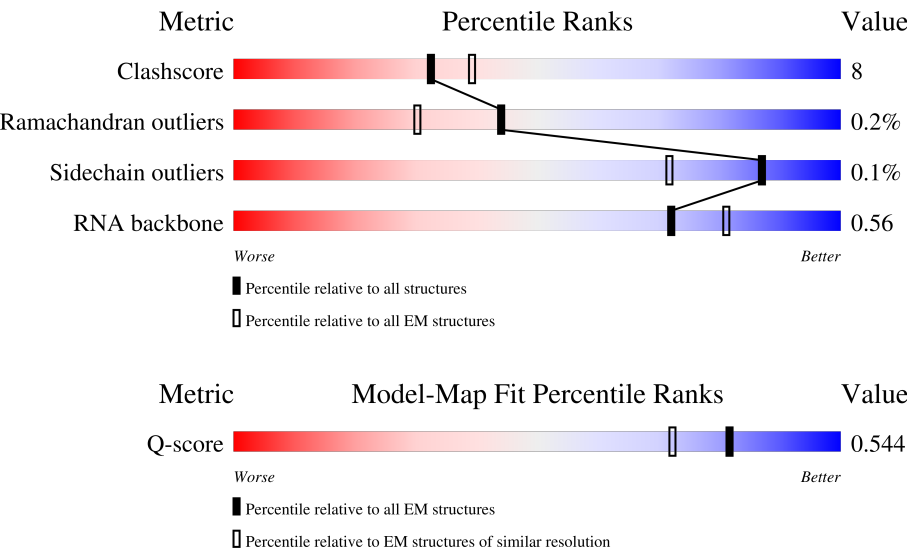
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 i

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

The reported resolution of this entry is 2.90 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.



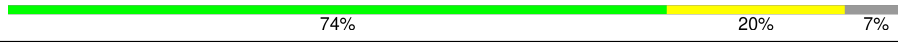
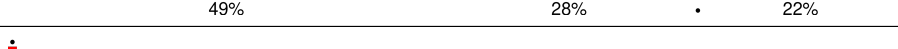
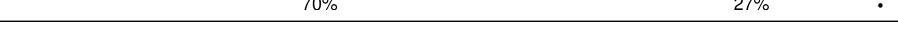
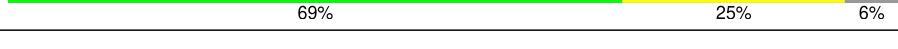
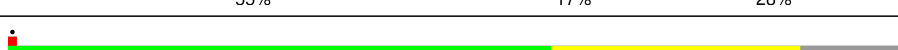
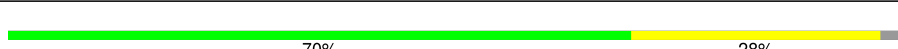
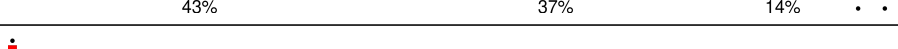
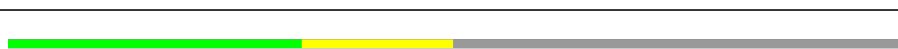
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	1542	54% 41% .
2	b	241	29% 76% 17% 7%
3	c	233	61% 27% 12%

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Mol	Chain	Length	Quality of chain
4	d	206	
5	e	167	
6	f	131	
7	g	156	
8	h	130	
9	i	130	
10	j	103	
11	k	129	
12	l	124	
13	m	118	
14	n	101	
15	o	89	
16	p	82	
17	q	84	
18	r	75	
19	s	92	
20	t	87	
21	u	71	
22	w	76	
22	y	76	
23	x	77	
24	v	24	
25	A	2904	
26	B	120	
27	C	273	

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Mol	Chain	Length	Quality of chain
28	D	209	
29	E	201	
30	F	179	
31	G	177	
32	H	149	
33	L	142	
34	M	123	
35	N	144	
36	O	136	
37	P	127	
38	Q	117	
39	R	115	
40	S	118	
41	T	103	
42	U	110	
43	V	100	
44	W	104	
45	X	94	
46	Y	85	
47	Z	78	
48	1	63	
49	2	59	
50	3	70	
51	4	57	
52	5	55	

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Mol	Chain	Length	Quality of chain
53	6	46	83% 17%
54	7	65	85% 14%
55	8	38	82% 18%

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 144591 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	1528	Total	C	N	O	P	0	0
			32803	14637	6019	10619	1528		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	b	224	Total	C	N	O	S	0	0
			1514	963	279	267	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	c	206	Total	C	N	O	S	0	0
			1613	1023	305	282	3		

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

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

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	e	156	Total	C	N	O	S	0	0
			1117	695	213	203	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	f	102	Total	C	N	O	S	0	0
			778	497	133	143	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	g	152	Total	C	N	O	S	0	0
			1054	656	204	190	4		

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	h	129	Total	C	N	O	S	0	0
			969	611	169	183	6		

- 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
			937	586	183	166	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
10	j	97	Total	C	N	O	0	0
			673	428	130	115		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	k	117	Total	C	N	O	S	0	0
			860	531	168	158	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	119	IAS	ASN	modified residue	UNP A0A0H3PWX2

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	l	121	Total	C	N	O	S	0	0
			924	570	187	162	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	m	113	Total	C	N	O	S	0	0
			823	510	166	145	2		

- Molecule 14 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	n	100	Total	C	N	O	S	0	0
			792	492	162	135	3		

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	o	88	Total	C	N	O	S	0	0
			703	434	141	127	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	p	80	Total	C	N	O	S	0	0
			613	385	123	104	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	q	79	Total	C	N	O	S	0	0
			630	400	116	111	3		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	r	54	Total	C	N	O	0	0
			441	280	83	78		

- 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
			641	411	120	108	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	t	85	Total	C	N	O	S	0	0
			648	400	134	111	3		

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	u	55	Total	C	N	O	S	0	0
			373	241	72	59	1		

- Molecule 22 is a RNA chain called phenylalanine tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	w	74	Total	C	N	O	P	S	0	0
			1591	713	285	517	74	2		
22	y	74	Total	C	N	O	P	S	0	0
			1585	707	285	518	74	1		

- Molecule 23 is a RNA chain called P-site initiator tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	x	76	Total	C	N	O	P	S	0	0
			1625	725	294	529	76	1		

- Molecule 24 is a RNA chain called M-F-Stop mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	v	12	Total	C	N	O	P	0	0
			255	115	46	82	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	A	2845	Total	C	N	O	P	0	0
			61097	27261	11245	19746	2845		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	B	120	Total	C	N	O	P	0	0
			2572	1145	470	837	120		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	C	271	Total	C	N	O	S	0	0
			2069	1282	417	363	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	D	209	Total	C	N	O	S	0	0
			1559	976	288	292	3		

- Molecule 29 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	E	201	Total	C	N	O	S	0	0
			1538	966	282	285	5		

- Molecule 30 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	F	177	Total	C	N	O	S	0	0
			1401	895	245	255	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	G	175	Total	C	N	O	S	0	0
			1299	818	237	242	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	H	41	Total	C	N	O	S	0	0
			303	194	54	54	1		

- Molecule 33 is a protein called 50S ribosomal protein L13.

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

- Molecule 34 is a protein called 50S ribosomal protein L14.

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

- Molecule 35 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	N	144	Total	C	N	O	S	0	0
			1048	651	207	188	2		

- Molecule 36 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	O	136	Total	C	N	O	S	0	0
			1075	686	205	177	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	82	MS6	MET	modified residue	UNP E6BI61

- Molecule 37 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	P	118	Total	C	N	O	S	0	0
			945	585	194	161	5		

- Molecule 38 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	Q	116	Total	C	N	O	0	0
			876	541	175	160		

- Molecule 39 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	R	114	Total	C	N	O	S	0	0
			913	573	178	161	1		

- Molecule 40 is a protein called 50S ribosomal protein L20.

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

- Molecule 41 is a protein called Ribosomal protein L21.

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

- Molecule 42 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	U	110	Total	C	N	O	S	0	0
			850	529	163	155	3		

- Molecule 43 is a protein called 50S ribosomal protein L23.

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

- Molecule 44 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	W	102	Total	C	N	O	0	0
			769	486	144	139		

- Molecule 45 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	X	94	Total	C	N	O	S	0	0
			750	477	137	134	2		

- Molecule 46 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Y	84	Total	C	N	O	S	0	0
			634	391	129	113	1		

- Molecule 47 is a protein called 50S ribosomal protein L28.

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

- Molecule 48 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	1	61	Total	C	N	O	S	0	0
			495	305	97	92	1		

- Molecule 49 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	2	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	3	60	Total	C	N	O	S	0	0
			468	290	87	85	6		

- Molecule 51 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	4	55	Total	C	N	O	S	0	0
			434	263	92	78	1		

- Molecule 52 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	5	51	Total	C	N	O	0	0
			417	269	76	72		

- Molecule 53 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	6	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 54 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	7	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

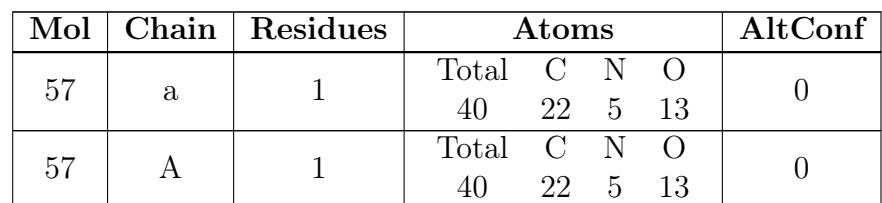
- Molecule 55 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	8	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	a	98	Total	Mg	0
			98	98	
56	x	3	Total	Mg	0
			3	3	
56	v	1	Total	Mg	0
			1	1	
56	A	359	Total	Mg	0
			359	359	
56	B	6	Total	Mg	0
			6	6	
56	C	1	Total	Mg	0
			1	1	
56	D	1	Total	Mg	0
			1	1	
56	P	1	Total	Mg	0
			1	1	
56	S	1	Total	Mg	0
			1	1	
56	X	1	Total	Mg	0
			1	1	
56	Y	1	Total	Mg	0
			1	1	
56	4	1	Total	Mg	0
			1	1	

- Molecule 57 is (2S)-N-[(1R,2S,3S,4R,5S)-4-[(2R,3R,4S,5S,6R)-6-(aminomethyl)-3,4,5-tris(oxidanyl)oxan-2-yl]oxy-5-azanyl-2-[(2S,3R,4S,5S,6R)-4-azanyl-6-(hydroxymethyl)-3,5-bis(oxidanyl)oxan-2-yl]oxy-3-oxidanyl-cyclohexyl]-4-azanyl-2-oxidanyl-butanamide (CCD ID: AKN) (formula: C₂₂H₄₃N₅O₁₃).



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- Chemical structure of Phenylalanine (PHE) is shown. The structure includes a benzene ring (labeled CE1, CE2, CZ, CD1, CD2, CG) attached to a chiral carbon (CA(S)). The chiral carbon is also bonded to an amino group (NH2, labeled N, H2N), a carboxyl group (COOH, labeled C, O, OH), and a hydrogen atom (H). The amino group is shown with a dashed bond, indicating stereochemistry.

Mol	Chain	Residues	Atoms				AltConf
58	w	1	Total	C	N	O	0
			11	9	1	1	

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Mol	Chain	Residues	Atoms		AltConf
59	3	1	Total 1	Zn 1	0
59	8	1	Total 1	Zn 1	0

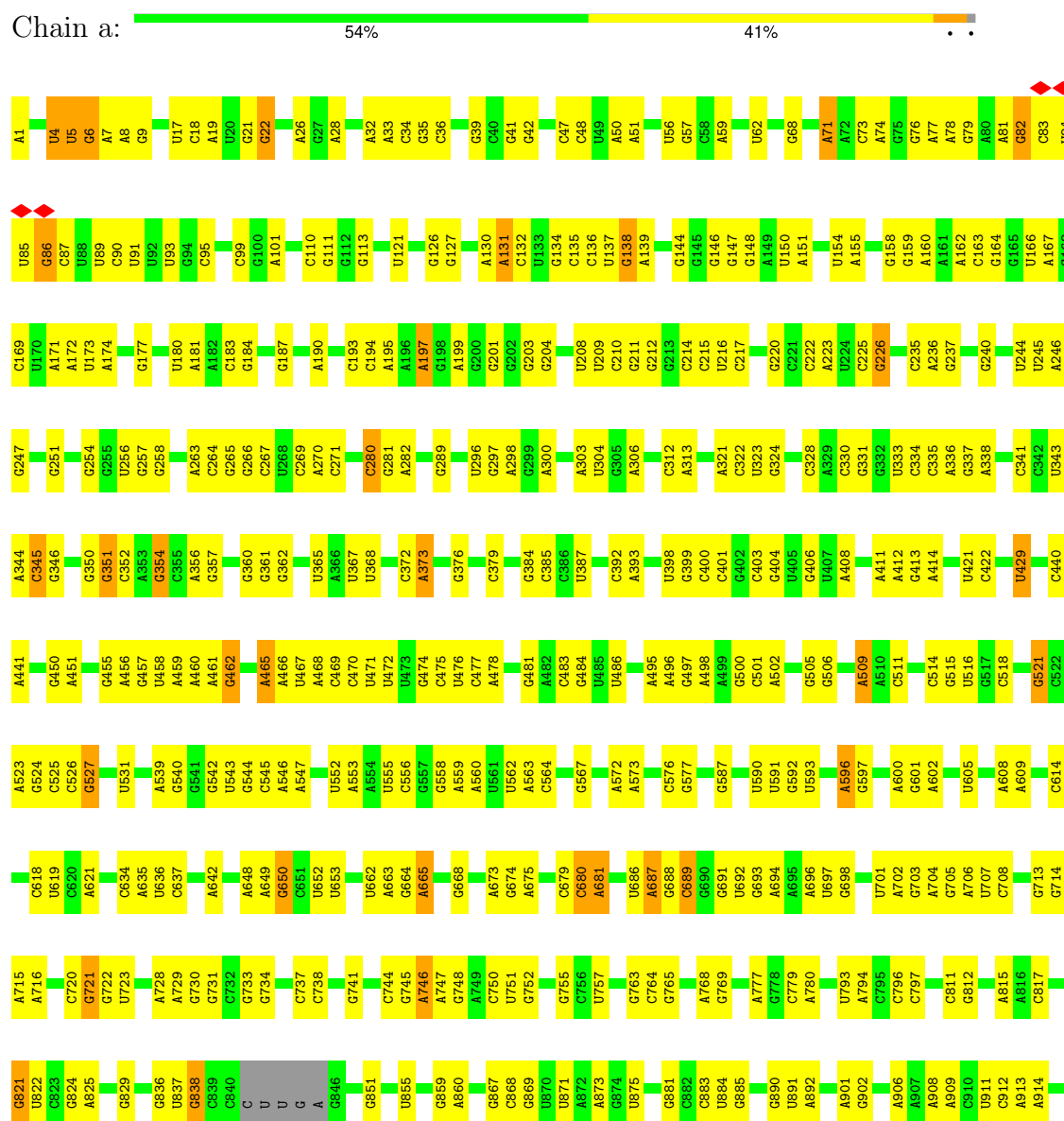
- Molecule 60 is water.

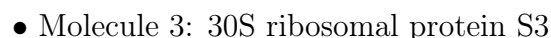
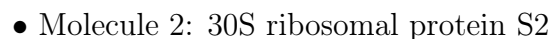
Mol	Chain	Residues	Atoms		AltConf
60	a	11	Total 11	O 11	0
60	n	1	Total 1	O 1	0
60	x	1	Total 1	O 1	0
60	A	60	Total 60	O 60	0
60	N	1	Total 1	O 1	0

3 Residue-property plots

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

• Molecule 1: 16S Ribosomal RNA

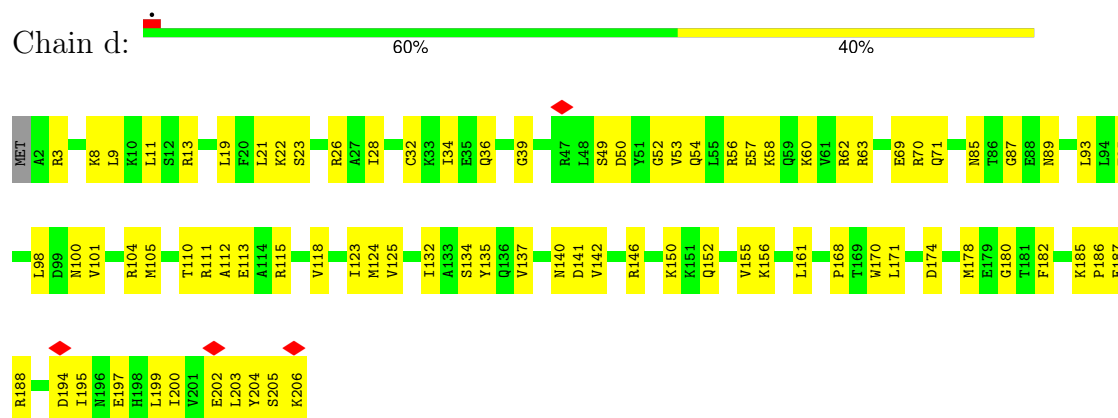




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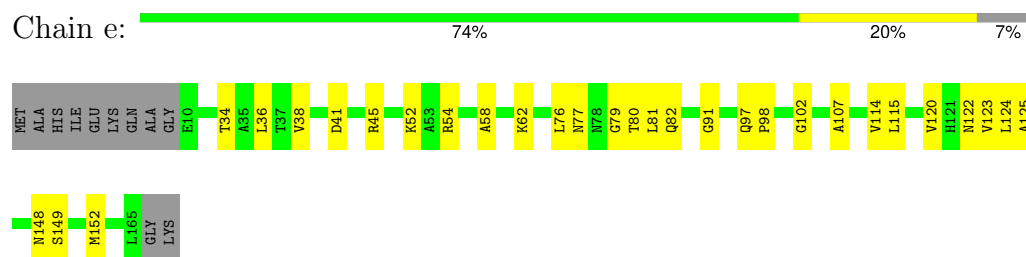
• Molecule 4: 30S ribosomal protein S4

Chain d:



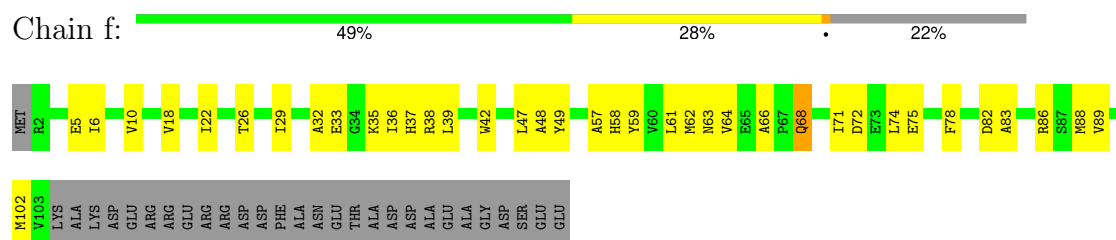
• Molecule 5: 30S ribosomal protein S5

Chain e:



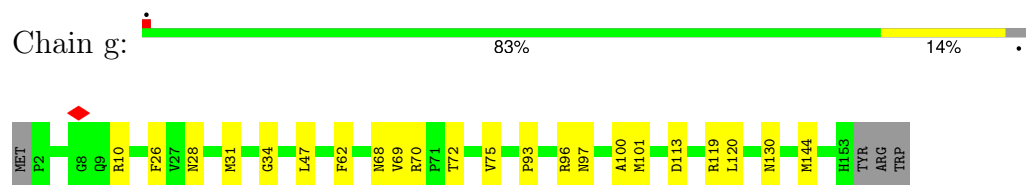
• Molecule 6: 30S ribosomal protein S6

Chain f:



• Molecule 7: 30S ribosomal protein S7

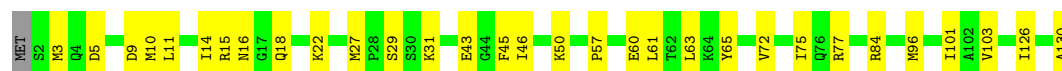
Chain g:



• Molecule 8: 30S ribosomal protein S8

Chain h:

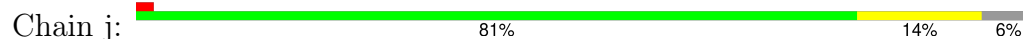




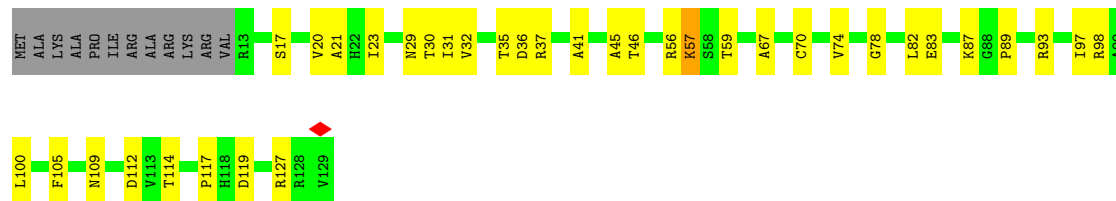
• Molecule 9: 30S ribosomal protein S9



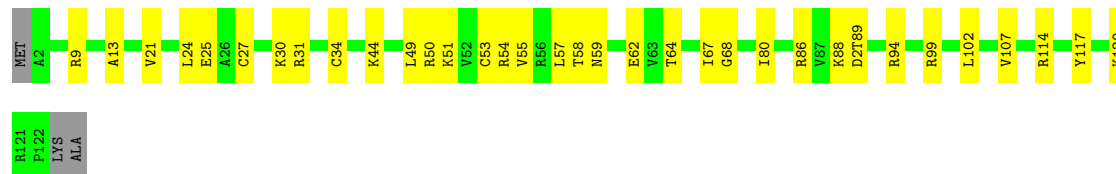
• Molecule 10: 30S ribosomal protein S10



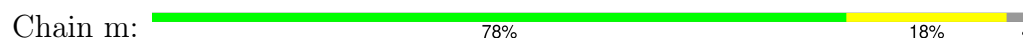
• Molecule 11: 30S ribosomal protein S11



• Molecule 12: 30S ribosomal protein S12



• Molecule 13: 30S ribosomal protein S13



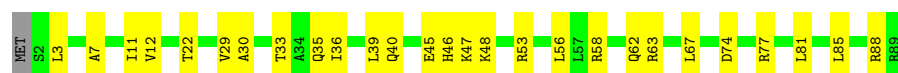
• Molecule 14: 30S ribosomal protein S14

Chain n:  76% 23%



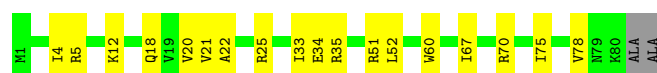
- Molecule 15: 30S ribosomal protein S15

Chain o:  69% 30%



- Molecule 16: 30S ribosomal protein S16

Chain p:  76% 22%



- Molecule 17: 30S ribosomal protein S17

Chain q:  69% 25% 6%



- Molecule 18: 30S ribosomal protein S18

Chain r:  55% 17% 28%



- Molecule 19: 30S ribosomal protein S19

Chain s:  61% 28% 11%

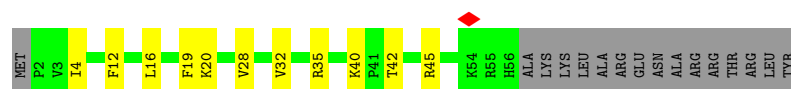


- Molecule 20: 30S ribosomal protein S20

Chain t:  70% 28%



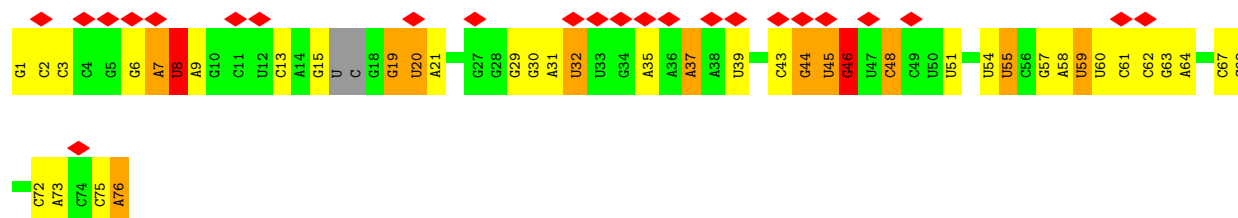
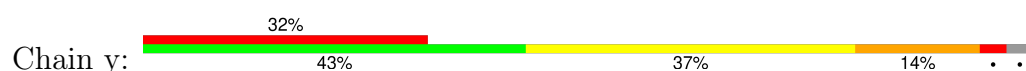
- Molecule 21: 30S ribosomal protein S21



- Molecule 22: phenylalanine tRNA



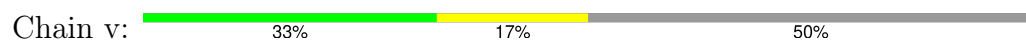
- Molecule 22: phenylalanine tRNA



- Molecule 23: P-site initiator tRNA



- Molecule 24: M-F-Stop mRNA

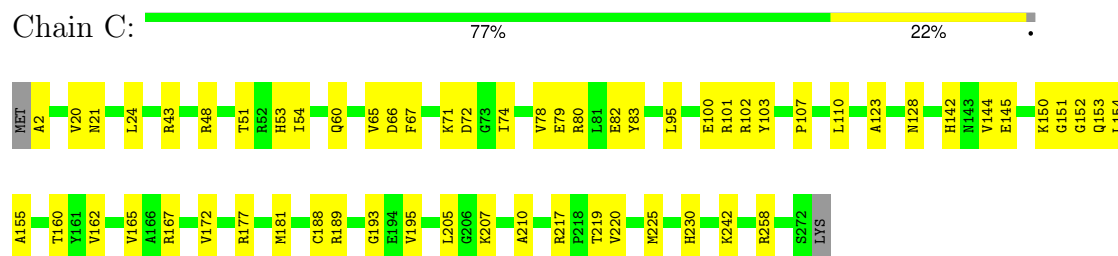


- Molecule 25: 23S Ribosomal RNA

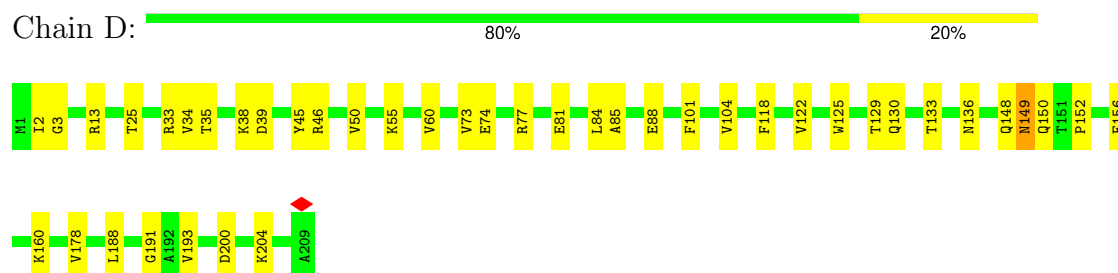


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A1668	U1563	A1453	A1354	U1240	A1126	C964	U871	A782	U667	A582	C476	A340	A222
A1669	C1564	U1460	G1360	G1248	A1127	G964	U872	A783	U668	G583	C475	A341	A223
A1672	C1565	U1469	G1361	U1249	U1130	G974	C873	G784	C671	G585	A479	C353	U224
G1673	A1566	A1469	G1362	G1250	G1131	A974	G874	G785	C672	A586	A480	A354	C225
G1674	G1567	A1470	C1363	G1251	U1132	G978	C875	A788	U675	C587	G481	U355	A226
C1675	G1568	G1475	G1364	G1252	A1133	G978	C876	A789	U676	U588	A481	G356	A227
A1676	A1569	U1477	A1365	A1253	A1134	G984	C877	C791	U677	U589	G482	C228	C228
A1677	U1570	G1478	A1378	U1254	C1135	A984	U877	C792	U678	U590	A491	G359	A233
A1678	A1571	U1479	U1379	U1255	U1141	A984	G880	A792	U679	U591	A492	U360	U234
A1679	G1572	G1482	U1380	G1256	A1142	A988	G881	A793	G682	U592	A493	G361	A244
G1681	U1573	G1483	A1383	U1263	G1149	G989	G882	A794	U686	U593	A494	A362	U244
G1682	U1578	U1484	A1384	A1264	A1150	C995	C888	U807	C687	U594	U499	G363	A244
U1683	A1579	U1485	A1385	G1265	C1150	C996	C889	G808	G697	U595	U499	G363	A244
A1580	A1580	U1486	C1386	G1266	U1153	C997	C890	G809	G698	U596	U499	U365	G248
A1581	U1581	U1487	A1387	U1267	C1153	C998	C891	A892	U700	U597	A503	G372	G249
U1582	U1582	U1488	A1388	G1271	G1158	U999	C892	C812	G703	U598	A504	U373	G250
U1583	U1583	U1489	A1389	U1272	A1169	C999	C893	C813	U704	U599	A505	U374	A251
U1584	U1584	U1490	A1390	U1273	C1170	A1000	C894	C814	G705	A603	C509	A382	C267
U1585	U1585	U1491	A1391	U1274	G1171	A1001	C895	C815	G706	A604	G512	A383	C268
U1586	U1586	U1492	A1392	U1275	C1172	G1002	C896	C816	U707	A605	G513	A384	C269
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U1590	U1590	U1496	A1396	U1279	U1176	G1006	C900	C820	U711	A609	A517	A388	A273
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U1592	U1592	U1498	A1398	U1281	U1178	C1008	C902	C822	U713	A611	A519	A390	C275
U1593	U1593	U1499	A1399	U1282	C1178	A1009	C903	C823	U714	A612	A520	A391	C276
U1594	U1594	U1500	A1400	U1283	U1179	A1010	C904	C824	U715	A613	A521	A392	C277
U1595	U1595	U1501	A1401	U1284	U1180	G1011	C905	C825	U716	A614	A522	A393	C278
U1596	U1596	U1502	A1402	U1285	U1181	C1012	C906	C826	U717	A615	A523	A394	C279
U1597	U1597	U1503	A1403	U1286	U1182	C1013	C907	C827	U718	A616	A524	A395	C280
U1598	U1598	U1504	A1404	U1287	U1183	C1014	C908	C828	U719	A617	A525	A396	C281
U1599	U1599	U1505	A1405	U1288	U1184	C1015	C909	C829	U720	A618	A526	A397	C282
U1600	U1600	U1506	A1406	U1289	U1185	C1016	C910	C830	U721	A619	A527	A398	C283
U1601	U1601	U1507	A1407	U1290	U1186	C1017	C911	C831	U722	A620	A528	A399	C284
U1602	U1602	U1508	A1408	U1291	U1187	C1018	C912	C832	U723	A621	A529	A400	C285
U1603	U1603	U1509	A1409	U1292	U1188	C1019	C913	C833	U724	A622	A530	A401	C286
U1604	U1604	U1510	A1410	U1293	U1189	C1020	C914	C834	U725	A623	A531	A402	C287
U1605	U1605	U1511	A1411	U1294	U1190	C1021	C915	C835	U726	A624	A532	A403	C288
U1606	U1606	U1512	A1412	U1295	U1191	C1022	C916	C836	U727	A625	A533	A404	C289
U1607	U1607	U1513	A1413	U1296	U1192	C1023	C917	C837	U728	A626	A534	A405	C290
U1608	U1608	U1514	A1414	U1297	U1193	C1024	C918	C838	U729	A627	A535	A406	C291
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U1610	U1610	U1516	A1416	U1299	U1195	C1026	C920	C840	U731	A629	A537	A408	C293
U1611	U1611	U1517	A1417	U1300	U1196	C1027	C921	C841	U732	A630	A538	A409	C294
U1612	U1612	U1518	A1418	U1301	U1197	C1028	C922	C842	U733	A631	A539	A410	C295
U1613	U1613	U1519	A1419	U1302	U1198	C1029	C923	C843	U734	A632	A540	A411	C296
U1614	U1614	U1520	A1420	U1303	U1199	C1030	C924	C844	U735	A633	A541	A412	C297
U1615	U1615	U1521	A1421	U1304	U1200	C1031	C925	C845	U736	A634	A542	A413	C298
U1616	U1616	U1522	A1422	U1305	U1201	C1032	C926	C846	U737	A635	A543	A414	C299
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U1618	U1618	U1524	A1424	U1307	U1203	C1034	C928	C848	U739	A637	A545	A416	C301
U1619	U1619	U1525	A1425	U1308	U1204	C1035	C929	C849	U740	A638	A546	A417	C302
U1620	U1620	U1526	A1426	U1309	U1205	C1036	C930	C850	U741	A639	A547	A418	C303
U1621	U1621	U1527	A1427	U1310	U1206	C1037	C931	C851	U742	A640	A548	A419	C304
U1622	U1622	U1528	A1428	U1311	U1207	C1038	C932	C852	U743	A641	A549	A420	C305
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U1624	U1624	U1530	A1430	U1313	U1209	C1040	C934	C854	U745	A643	A551	A422	C307
U1625	U1625	U1531	A1431	U1314	U1210	C1041	C935	C855	U746	A644	A552	A423	C308
U1626	U1626	U1532	A1432	U1315	U1211	C1042	C936	C856	U747	A645	A553	A424	C309
U1627	U1627	U1533	A1433	U1316	U1212	C1043	C937	C857	U748	A646	A554	A425	C310
U1628	U1628	U1534	A1434	U1317	U1213	C1044	C938	C858	U749	A647	A555	A426	C311
U1629	U1629	U1535	A1435	U1318	U1214	C1045	C939	C859	U750	A648	A556	A427	C312
U1630	U1630	U1536	A1436	U1319	U1215	C1046	C940	C860	U751	A649	A557	A428	C313
U1631	U1631	U1537	A1437	U1320	U1216	C1047	C941	C861	U752	A650	A558	A429	C314
U1632	U1632	U1538	A1438	U1321	U1217	C1048	C942	C862	U753	A651	A559	A430	C315
U1633	U1633	U1539	A1439	U1322	U1218	C1049	C943	C863	U754	A652	A560	A431	C316
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U1638	U1638	U1544	A1444	U1327	U1223	C1054	C948	C868	U759	A657	A565	A436	C321
U1639	U1639	U1545	A1445	U1328	U1224	C1055	C949	C869	U760	A658	A566	A437	C322
U1640	U1640	U1546	A1446	U1329	U1225	C1056	C950	C870	U761	A659	A567	A438	C323
U1641	U1641	U1547	A1447	U1330	U1226	C1057	C951	C871	U762	A660	A568	A439	C324
U1642	U1642	U1548	A1448	U1331	U1227	C1058	C952	C872	U763	A661	A569	A440	C325
U1643	U1643	U1549	A1449	U1332	U1228	C1059	C953	C873	U764	A662	A570	A441	C326
U1644	U1644	U1550	A1450	U1333	U1229	C1060	C954	C874	U765	A663	A571	A442	C327
U1645	U1645	U1551	A1451	U1334	U1230	C1061	C955	C875	U766	A664	A572	A443	C328
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U1654	U1654	U1560	A1460	U1343	U1239	C1070	C964	C884	U775	A673	A581	A452	C337
U1655	U1655	U1561	A1461	U1344	U1240	C1071	C965	C885	U776	A674	A582	A453	C338
U1656	U1656	U1562	A1462	U1345	U1241	C1072	C966	C886	U777	A675	A583	A454	C339
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U1658	U1658	U1564	A1464	U1347	U1243	C1074	C968	C888	U779	A677	A585	A456	C341
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U1660	U1660	U1566	A1466	U1349	U1245	C1076	C970	C890	U781	A679	A587	A458	C343
U1661	U1661	U1567	A1467	U1350									

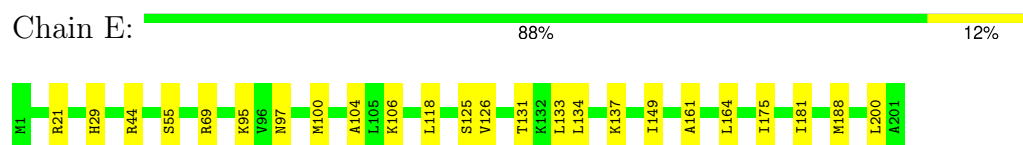
- Molecule 27: 50S ribosomal protein L2



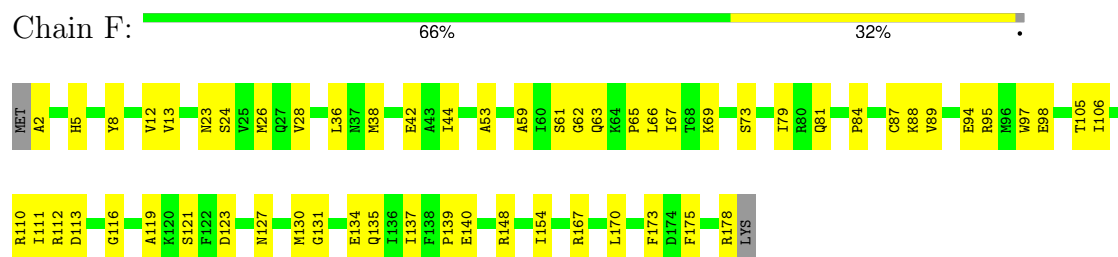
- Molecule 28: 50S ribosomal protein L3



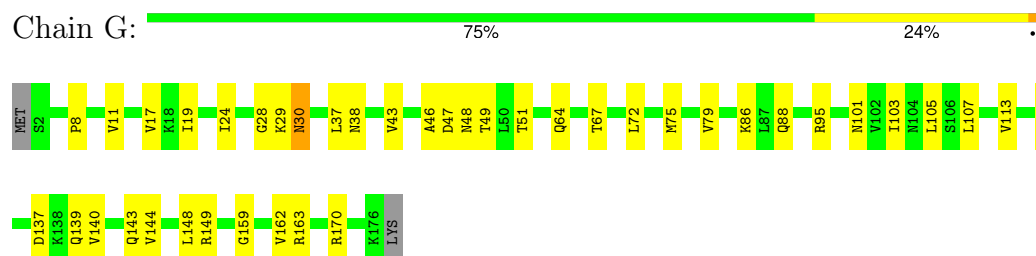
- Molecule 29: 50S ribosomal protein L4



- Molecule 30: 50S ribosomal protein L5



- Molecule 31: 50S ribosomal protein L6



- Molecule 32: 50S ribosomal protein L9

WORLDWIDE
PDB
PROTEIN DATA BANK

Chain Q:  74% 26%



- Molecule 39: 50S ribosomal protein L19

Chain R:  83% 17%



- Molecule 40: 50S ribosomal protein L20

Chain S:  83% 16%



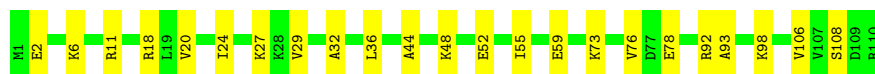
- Molecule 41: Ribosomal protein L21

Chain T:  89% 11%



- Molecule 42: 50S ribosomal protein L22

Chain U:  79% 21%



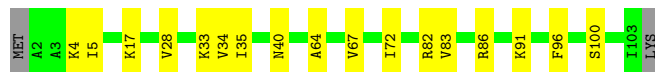
- Molecule 43: 50S ribosomal protein L23

Chain V:  77% 16% 7%



- Molecule 44: 50S ribosomal protein L24

Chain W:  82% 16%



- Molecule 45: 50S ribosomal protein L25

Chain X:  71% 29%



- Molecule 46: 50S ribosomal protein L27

Chain Y:  84% 14%



- Molecule 47: 50S ribosomal protein L28

Chain Z:  79% 19%



- Molecule 48: 50S ribosomal protein L29

Chain 1:  70% 27%



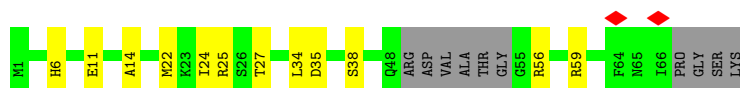
- Molecule 49: 50S ribosomal protein L30

Chain 2:  78% 20%



- Molecule 50: 50S ribosomal protein L31

Chain 3:  69% 17% 14%



- Molecule 51: 50S ribosomal protein L32

Chain 4:  70% 26%



- Molecule 52: 50S ribosomal protein L33

Chain 5:  76% 16% 7%



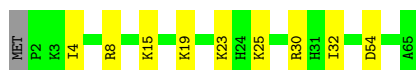
- Molecule 53: 50S ribosomal protein L34

Chain 6:  83% 17%



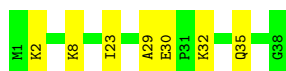
- Molecule 54: 50S ribosomal protein L35

Chain 7:  85% 14%



- Molecule 55: 50S ribosomal protein L36

Chain 8:  82% 18%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	234339	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 ($e^-/\text{\AA}^2$)	40.5852	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.699	Depositor
Minimum map value	-0.330	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.027	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	424.96, 424.96, 424.96	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MIA, 3TD, 5MU, 6MZ, OMC, 4OC, ZN, IAS, MS6, 4D4, AKN, G7M, OMG, 5MC, 4SU, MG, D2T, 2MA, H2U, 2MG, 7MG, MA6, MEQ, 1MG, OMU, UR3, PSU

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	a	0.17	0/36450	0.26	0/56856
2	b	0.13	0/1542	0.32	0/2108
3	c	0.17	0/1640	0.34	0/2211
4	d	0.18	0/1665	0.40	0/2227
5	e	0.19	0/1130	0.35	0/1527
6	f	0.16	0/796	0.43	0/1086
7	g	0.15	0/1068	0.32	0/1452
8	h	0.17	0/979	0.33	0/1314
9	i	0.15	0/949	0.37	0/1276
10	j	0.14	0/682	0.31	0/933
11	k	0.34	0/867	0.50	0/1171
12	l	0.18	0/927	0.33	0/1249
13	m	0.12	0/831	0.28	0/1118
14	n	0.15	0/804	0.31	0/1072
15	o	0.18	0/711	0.32	0/952
16	p	0.15	0/623	0.33	0/842
17	q	0.17	0/639	0.39	0/859
18	r	0.15	0/447	0.26	0/601
19	s	0.14	0/658	0.33	0/889
20	t	0.19	0/654	0.36	0/871
21	u	0.12	0/380	0.37	0/518
22	w	0.24	0/1605	0.40	1/2494 (0.0%)
22	y	0.15	0/1606	0.24	0/2497
23	x	0.19	0/1725	0.24	0/2689
24	v	0.18	0/285	0.18	0/441
25	A	0.23	0/67852	0.28	0/105848
26	B	0.19	0/2876	0.28	0/4483
27	C	0.23	0/2108	0.32	0/2837
28	D	0.22	0/1569	0.32	0/2111
29	E	0.19	0/1557	0.28	0/2095
30	F	0.17	0/1425	0.32	0/1915

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	G	0.16	0/1319	0.37	1/1789 (0.1%)
32	H	0.10	0/306	0.29	0/413
33	L	0.21	0/1152	0.28	0/1551
34	M	0.21	0/955	0.29	0/1279
35	N	0.21	0/1057	0.32	0/1407
36	O	0.21	0/1073	0.29	0/1433
37	P	0.22	0/958	0.35	0/1281
38	Q	0.16	0/886	0.35	0/1192
39	R	0.20	0/925	0.27	0/1238
40	S	0.23	0/960	0.28	0/1278
41	T	0.21	0/829	0.31	0/1107
42	U	0.21	0/857	0.27	0/1149
43	V	0.17	0/744	0.27	0/994
44	W	0.18	0/777	0.33	0/1038
45	X	0.18	0/763	0.35	0/1022
46	Y	0.19	0/642	0.31	0/848
47	Z	0.20	0/635	0.24	0/848
48	1	0.17	0/496	0.31	0/660
49	2	0.21	0/453	0.26	0/605
50	3	0.10	0/475	0.22	0/633
51	4	0.21	0/440	0.28	0/588
52	5	0.16	0/424	0.27	0/565
53	6	0.22	0/380	0.29	0/498
54	7	0.20	0/513	0.31	0/676
55	8	0.22	0/303	0.31	0/397
All	All	0.20	0/155372	0.29	2/233031 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
36	O	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	w	75	C	OP1-P-O3'	13.05	147.14	108.00
31	G	30	ASN	N-CA-C	-6.15	106.75	114.56

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
36	O	81	4D4	Mainchain

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	32803	0	16528	474	0
2	b	1514	0	1322	27	0
3	c	1613	0	1686	43	0
4	d	1643	0	1707	73	0
5	e	1117	0	1132	23	0
6	f	778	0	731	26	0
7	g	1054	0	979	14	0
8	h	969	0	1014	22	0
9	i	937	0	921	35	0
10	j	673	0	628	12	0
11	k	860	0	854	28	0
12	l	924	0	955	23	0
13	m	823	0	838	15	0
14	n	792	0	817	21	0
15	o	703	0	719	19	0
16	p	613	0	608	21	0
17	q	630	0	657	17	0
18	r	441	0	467	13	0
19	s	641	0	648	20	0
20	t	648	0	677	20	0
21	u	373	0	339	11	0
22	w	1591	0	818	25	0
22	y	1585	0	804	26	0
23	x	1625	0	829	14	0
24	v	255	0	129	1	0
25	A	61097	0	30754	680	0
26	B	2572	0	1301	34	0
27	C	2069	0	2129	41	0
28	D	1559	0	1607	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	E	1538	0	1598	18	0
30	F	1401	0	1429	47	0
31	G	1299	0	1332	31	0
32	H	303	0	327	3	0
33	L	1129	0	1162	21	0
34	M	946	0	1023	18	0
35	N	1048	0	1123	27	0
36	O	1075	0	1146	25	0
37	P	945	0	989	19	0
38	Q	876	0	886	21	0
39	R	913	0	958	19	0
40	S	947	0	1019	18	0
41	T	816	0	839	9	0
42	U	850	0	911	15	0
43	V	738	0	807	10	0
44	W	769	0	812	14	0
45	X	750	0	773	20	0
46	Y	634	0	653	10	0
47	Z	625	0	652	12	0
48	1	495	0	526	15	0
49	2	449	0	488	11	0
50	3	468	0	460	11	0
51	4	434	0	445	12	0
52	5	417	0	451	7	0
53	6	377	0	418	8	0
54	7	504	0	572	8	0
55	8	302	0	340	7	0
56	4	1	0	0	0	0
56	A	359	0	0	0	0
56	B	6	0	0	0	0
56	C	1	0	0	0	0
56	D	1	0	0	0	0
56	P	1	0	0	0	0
56	S	1	0	0	0	0
56	X	1	0	0	0	0
56	Y	1	0	0	0	0
56	a	98	0	0	0	0
56	v	1	0	0	0	0
56	x	3	0	0	0	0
57	A	40	0	43	0	0
57	a	40	0	43	1	0
58	w	11	0	8	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	3	1	0	0	0	0
59	8	1	0	0	0	0
60	A	60	0	0	1	0
60	N	1	0	0	0	0
60	a	11	0	0	0	0
60	n	1	0	0	0	0
60	x	1	0	0	0	0
All	All	144591	0	94831	1966	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (1966) 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)
25:A:1047:G:HO2'	25:A:1110:G:H1	1.10	0.99
1:a:180:U:H3	1:a:195:A:H62	1.00	0.96
27:C:71:LYS:HD3	27:C:74:ILE:HD11	1.48	0.94
22:y:15:G:H22	22:y:48:C:H42	1.15	0.93
25:A:881:G:H1	25:A:895:U:H3	0.98	0.91
1:a:1009:U:H3	1:a:1020:G:H1	0.91	0.90
1:a:458:U:H3	1:a:474:G:H1	1.22	0.87
27:C:167:ARG:HG2	27:C:172:VAL:HG12	1.55	0.87
33:L:95:ARG:HD2	33:L:96:ARG:HG2	1.57	0.86
9:i:22:LYS:O	9:i:62:ASP:HB2	1.76	0.85
19:s:11:ILE:HD12	19:s:38:SER:HB3	1.60	0.84
22:y:15:G:N2	22:y:48:C:H42	1.76	0.83
1:a:1031:C:H5'	1:a:1032:G:H5'	1.58	0.83
35:N:91:ASP:OD1	35:N:92:LEU:N	2.13	0.82
22:y:15:G:H22	22:y:48:C:N4	1.78	0.81
1:a:1350:A:OP1	9:i:123:ARG:NH1	2.14	0.81
25:A:1153:C:OP1	40:S:92:ARG:NH2	2.14	0.80
1:a:160:A:N6	1:a:343:U:O2'	2.15	0.80
3:c:111:LEU:HD11	3:c:146:ALA:HB2	1.65	0.79
29:E:21:ARG:HD3	29:E:106:LYS:HB3	1.65	0.79
1:a:450:G:N2	1:a:483:C:O2	2.16	0.78
26:B:42:C:O2'	30:F:63:GLN:OE1	1.99	0.78
36:O:66:ARG:NH1	36:O:104:GLU:OE2	2.16	0.78
1:a:913:A:OP1	12:l:88:LYS:NZ	2.18	0.77
25:A:2343:U:HO2'	25:A:2373:G:HO2'	1.31	0.77
15:o:45:GLU:HG3	15:o:46:HIS:HD1	1.49	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:2153:C:H2'	25:A:2154:A:H8	1.49	0.77
39:R:14:LYS:H	39:R:77:HIS:HD2	1.32	0.76
5:e:115:LEU:HD13	5:e:123:VAL:HG11	1.69	0.76
25:A:1250:G:H5''	40:S:6:ARG:HD3	1.68	0.76
3:c:35:SER:OG	3:c:59:ARG:NH2	2.19	0.75
1:a:664:G:H22	1:a:741:G:H1	1.34	0.75
26:B:41:G:O6	30:F:69:LYS:NZ	2.17	0.75
9:i:21:ILE:HG23	9:i:61:LEU:HD11	1.68	0.75
1:a:673:A:H2'	1:a:674:G:C8	2.21	0.74
17:q:46:VAL:HG12	17:q:73:TRP:HB2	1.69	0.74
25:A:2144:G:N2	25:A:2146:C:O2'	2.21	0.74
6:f:47:LEU:O	18:r:66:SER:OG	2.06	0.74
40:S:48:ARG:NH1	40:S:49:ASP:OD1	2.21	0.74
25:A:475:C:O2	25:A:479:A:N6	2.20	0.73
4:d:57:GLU:HG2	4:d:199:LEU:HD23	1.71	0.73
11:k:93:ARG:NH2	11:k:112:ASP:OD2	2.21	0.73
17:q:20:SER:OG	17:q:71:LYS:NZ	2.22	0.73
43:V:11:LEU:O	48:1:29:ARG:NH1	2.22	0.73
28:D:2:ILE:HD11	28:D:84:LEU:HD23	1.69	0.72
1:a:1071:C:H2'	1:a:1072:G:H8	1.54	0.72
4:d:11:LEU:HG	4:d:63:ARG:HD3	1.72	0.72
1:a:1106:G:O2'	3:c:169:ARG:NH1	2.23	0.72
10:j:66:GLU:HB2	14:n:99:ALA:HB2	1.70	0.72
50:3:11:GLU:HA	50:3:25:ARG:HA	1.70	0.72
25:A:2349:G:O2'	25:A:2350:C:O5'	2.05	0.72
36:O:64:TRP:HB2	36:O:104:GLU:HB2	1.72	0.71
25:A:2183:A:H2'	25:A:2184:A:C8	2.24	0.71
25:A:1779:U:OP2	25:A:1784:A:N6	2.23	0.71
9:i:106:ARG:NH1	9:i:107:ASP:O	2.24	0.71
4:d:150:LYS:O	4:d:156:LYS:NZ	2.23	0.71
1:a:501:C:OP1	12:l:114:ARG:NH2	2.24	0.70
37:P:103:ARG:HD3	37:P:110:MET:HE2	1.73	0.70
9:i:84:THR:HG23	9:i:98:LEU:HD21	1.72	0.70
1:a:1218:C:H2'	1:a:1219:A:H8	1.57	0.70
25:A:2180:U:H2'	25:A:2181:U:C6	2.27	0.70
1:a:150:U:H2'	1:a:151:A:H8	1.57	0.69
1:a:450:G:N1	1:a:483:C:N3	2.38	0.69
25:A:566:U:H5''	35:N:29:LYS:HE3	1.74	0.69
25:A:2126:A:H2'	25:A:2162:G:H21	1.57	0.69
48:1:54:LYS:HA	48:1:57:LEU:HB2	1.74	0.69
1:a:1086:U:H3	1:a:1099:G:H22	1.40	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:848:C:H2'	25:A:849:A:H8	1.57	0.69
33:L:45:THR:HB	33:L:48:VAL:HG12	1.73	0.69
1:a:1311:A:H5'	50:3:59:ARG:HH22	1.58	0.69
4:d:19:LEU:HB2	4:d:21:LEU:HD22	1.75	0.69
8:h:103:VAL:HG13	8:h:126:ILE:HB	1.73	0.69
9:i:52:LEU:HD11	9:i:61:LEU:HD23	1.75	0.69
25:A:2328:A:H2'	25:A:2329:U:C6	2.28	0.69
25:A:2134:A:H61	25:A:2156:G:H2'	1.57	0.69
1:a:138:G:N2	1:a:225:C:O2	2.19	0.68
11:k:35:THR:HG22	11:k:41:ALA:HA	1.75	0.68
30:F:119:ALA:O	30:F:167:ARG:NH1	2.25	0.68
34:M:63:VAL:HG12	34:M:107:LEU:HD21	1.75	0.68
40:S:50:ARG:O	40:S:54:LYS:NZ	2.25	0.68
30:F:98:GLU:OE2	50:3:25:ARG:HB2	1.91	0.68
25:A:1032:A:H1'	55:8:23:ILE:HD13	1.74	0.68
22:y:29:G:H2'	22:y:30:G:H8	1.58	0.68
25:A:2498:OMC:HM22	25:A:2499:C:H5'	1.74	0.68
7:g:69:VAL:HG13	7:g:100:ALA:HB1	1.75	0.68
22:y:9:A:H1'	22:y:45:U:H2'	1.75	0.68
37:P:30:ARG:NH1	37:P:74:GLU:OE2	2.27	0.68
25:A:2467:C:OP1	55:8:8:LYS:NZ	2.27	0.67
1:a:674:G:H2'	1:a:675:A:H8	1.58	0.67
25:A:568:U:H1'	25:A:2030:6MZ:H9C1	1.76	0.67
28:D:13:ARG:NH2	39:R:75:GLN:OE1	2.26	0.67
36:O:41:LEU:HD13	36:O:96:ILE:HG13	1.74	0.67
2:b:70:VAL:HG12	2:b:92:VAL:HB	1.77	0.67
1:a:1218:C:H2'	1:a:1219:A:C8	2.29	0.67
22:y:15:G:N2	22:y:59:U:O4	2.28	0.67
1:a:1152:A:OP1	10:j:70:HIS:ND1	2.28	0.67
5:e:97:GLN:HE21	5:e:124:LEU:HD23	1.60	0.67
25:A:219:A:N3	25:A:234:U:O2'	2.25	0.67
1:a:201:G:H21	1:a:469:C:H1'	1.59	0.67
1:a:401:C:O2'	1:a:621:A:N3	2.26	0.67
25:A:534:U:O2'	40:S:49:ASP:OD2	2.12	0.67
3:c:65:ARG:HB2	3:c:100:GLN:HE21	1.60	0.67
10:j:8:ILE:HD13	10:j:25:ILE:HD11	1.77	0.67
39:R:14:LYS:HD2	39:R:77:HIS:HA	1.77	0.66
28:D:33:ARG:HH12	28:D:74:GLU:HB3	1.60	0.66
36:O:57:VAL:HG11	36:O:105:MET:HE1	1.76	0.66
1:a:403:C:OP2	4:d:71:GLN:NE2	2.27	0.66
1:a:138:G:N1	1:a:225:C:N3	2.34	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:k:31:ILE:HG12	11:k:46:THR:HG22	1.76	0.66
22:y:75:C:H5''	22:y:76:A:H5'	1.78	0.66
20:t:28:MET:O	20:t:32:ILE:HD12	1.95	0.66
26:B:48:U:H4'	38:Q:100:HIS:HD2	1.59	0.66
40:S:49:ASP:HA	40:S:52:GLN:HG2	1.77	0.66
28:D:46:ARG:NH2	28:D:88:GLU:O	2.29	0.66
27:C:79:GLU:OE2	27:C:101:ARG:NH1	2.28	0.65
48:1:49:ASP:OD1	48:1:52:ARG:NH1	2.30	0.65
3:c:14:ILE:HG22	3:c:15:VAL:HG23	1.76	0.65
18:r:32:TYR:CG	18:r:55:LEU:HD21	2.32	0.65
1:a:544:G:OP1	4:d:56:ARG:NH2	2.29	0.65
20:t:17:ALA:O	20:t:21:ASN:ND2	2.29	0.65
26:B:1:U:H2'	26:B:2:G:H8	1.61	0.65
1:a:8:A:N6	4:d:202:GLU:O	2.21	0.65
1:a:713:G:H2'	1:a:714:G:C8	2.32	0.65
20:t:35:VAL:HG21	20:t:54:MET:HG2	1.77	0.65
11:k:21:ALA:HB2	11:k:82:LEU:HD11	1.77	0.65
26:B:1:U:H2'	26:B:2:G:C8	2.32	0.65
1:a:1317:C:O5'	14:n:24:ARG:NH2	2.30	0.65
58:w:101:PHE:N	23:x:76:A:HO2'	1.95	0.65
33:L:49:ASP:OD1	33:L:121:LYS:NZ	2.26	0.65
1:a:401:C:OP2	4:d:70:ARG:NH2	2.30	0.64
4:d:53:VAL:HG12	4:d:199:LEU:HD21	1.78	0.64
20:t:59:ASP:OD1	20:t:76:LYS:NZ	2.23	0.64
44:W:72:ILE:HD12	44:W:83:VAL:HG21	1.79	0.64
49:2:9:GLN:NE2	49:2:11:ARG:O	2.29	0.64
25:A:2134:A:N1	25:A:2136:G:N2	2.46	0.64
30:F:67:ILE:HA	30:F:87:CYS:H	1.62	0.64
25:A:2107:G:N1	25:A:2183:A:C6	2.66	0.64
25:A:2564:A:OP1	25:A:2648:G:O2'	2.13	0.64
1:a:562:U:O2'	12:l:13:ALA:O	2.15	0.64
1:a:946:A:H2'	1:a:947:G:C8	2.33	0.64
16:p:5:ARG:HH22	16:p:22:ALA:HB3	1.62	0.64
25:A:2547:A:H2'	25:A:2548:U:C6	2.33	0.64
31:G:170:ARG:NH1	55:8:29:ALA:O	2.31	0.64
5:e:34:THR:HG22	5:e:52:LYS:HG2	1.79	0.64
38:Q:30:ARG:HB3	38:Q:35:ILE:HG13	1.79	0.64
8:h:50:LYS:NZ	8:h:60:GLU:OE1	2.30	0.63
25:A:2348:U:H3	25:A:2369:A:H62	1.45	0.63
25:A:2848:G:O2'	25:A:2867:G:N2	2.27	0.63
45:X:51:GLN:OE1	45:X:57:TYR:OH	2.16	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:g:68:ASN:ND2	7:g:130:ASN:OD1	2.31	0.63
1:a:1151:A:HO2'	1:a:1152:A:H8	1.47	0.63
15:o:36:ILE:HD12	15:o:56:LEU:HD11	1.80	0.63
1:a:1124:G:N2	1:a:1125:U:O4	2.26	0.63
3:c:19:ASN:O	3:c:40:ARG:NH2	2.31	0.63
4:d:100:ASN:OD1	4:d:111:ARG:NH1	2.32	0.63
25:A:2377:A:HO2'	25:A:2378:A:H8	1.46	0.63
1:a:50:A:O2'	1:a:360:G:N2	2.32	0.63
1:a:1402:4OC:HM22	1:a:1403:C:H5'	1.81	0.63
25:A:1802:A:H2'	25:A:1803:A:C8	2.33	0.63
36:O:76:LYS:NZ	36:O:83:GLY:O	2.30	0.63
34:M:108:ARG:HH12	39:R:34:GLU:HG2	1.64	0.62
43:V:54:GLU:H	43:V:91:GLN:HG3	1.63	0.62
1:a:28:A:O2'	1:a:296:U:OP1	2.14	0.62
13:m:24:GLY:O	13:m:29:ARG:NH1	2.27	0.62
25:A:1248:G:OP1	29:E:44:ARG:NH1	2.27	0.62
31:G:105:LEU:HD21	31:G:148:LEU:HD11	1.81	0.62
1:a:333:U:OP1	20:t:2:ALA:N	2.32	0.62
1:a:337:G:H2'	1:a:338:A:C8	2.34	0.62
1:a:1356:G:H2'	1:a:1357:A:C8	2.33	0.62
22:y:8:4SU:O2'	22:y:46:7MG:N2	2.32	0.62
25:A:2107:G:N1	25:A:2183:A:N6	2.47	0.62
25:A:1434:A:H2'	25:A:1435:G:H8	1.64	0.62
1:a:180:U:H3	1:a:195:A:N6	1.85	0.62
1:a:811:C:O2'	1:a:901:A:N1	2.31	0.62
1:a:1347:G:O6	9:i:12:ARG:NH2	2.32	0.62
3:c:191:THR:HG23	3:c:193:TYR:H	1.64	0.62
7:g:93:PRO:HA	7:g:96:ARG:HG2	1.82	0.62
25:A:2144:G:H1'	25:A:2147:A:H61	1.64	0.62
32:H:1:MET:N	32:H:21:VAL:O	2.33	0.62
1:a:1251:A:N3	1:a:1369:C:O2'	2.31	0.62
14:n:54:ASP:HA	14:n:59:ARG:HG2	1.80	0.62
39:R:14:LYS:HZ2	39:R:81:VAL:HG23	1.64	0.62
1:a:974:A:OP1	14:n:69:ARG:NH2	2.33	0.61
25:A:2536:G:HO2'	25:A:2537:U:H6	1.47	0.61
39:R:85:SER:OG	39:R:87:LYS:NZ	2.33	0.61
41:T:14:VAL:HG12	41:T:20:VAL:HG11	1.82	0.61
46:Y:11:ARG:O	46:Y:14:ARG:NH1	2.33	0.61
9:i:55:VAL:HG11	9:i:94:LEU:HD12	1.80	0.61
12:l:34:CYS:HA	12:l:55:VAL:HG12	1.81	0.61
25:A:1315:C:O2'	25:A:1392:A:N3	2.29	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:1992:G:N2	25:A:1996:C:O2'	2.33	0.61
25:A:2102:G:H1	25:A:2187:U:H3	1.47	0.61
37:P:114:GLU:OE1	37:P:118:ARG:NH1	2.32	0.61
1:a:1266:G:N2	1:a:1269:A:OP2	2.32	0.61
37:P:86:ARG:NE	37:P:117:ASP:OD2	2.28	0.61
3:c:50:ALA:HA	3:c:75:ILE:HD11	1.82	0.61
27:C:165:VAL:HG21	27:C:181:MET:HE1	1.83	0.61
22:y:19:G:H1'	25:A:2112:G:H1'	1.82	0.61
25:A:1796:U:H2'	25:A:1797:G:H8	1.64	0.61
5:e:36:LEU:HD22	5:e:134:ILE:HD13	1.81	0.61
30:F:36:LEU:HB2	30:F:89:VAL:HG22	1.81	0.61
31:G:159:GLY:HA3	31:G:163:ARG:HH21	1.64	0.61
13:m:83:LEU:HD21	19:s:65:GLU:HB3	1.82	0.61
38:Q:30:ARG:HA	38:Q:35:ILE:HA	1.82	0.61
25:A:2107:G:H1	25:A:2183:A:N6	1.98	0.61
25:A:2180:U:H2'	25:A:2181:U:H6	1.66	0.61
25:A:463:G:N2	25:A:466:A:OP2	2.30	0.60
28:D:77:ARG:NH2	28:D:200:ASP:OD1	2.33	0.60
34:M:2:ILE:HD13	34:M:8:LEU:HD21	1.82	0.60
35:N:62:PRO:HB2	54:7:30:ARG:HH21	1.66	0.60
25:A:2304:G:H22	25:A:2312:U:H3	1.50	0.60
25:A:2478:A:H5'	55:8:32:LYS:HE3	1.84	0.60
25:A:10:A:H2	25:A:2629:U:H3	1.48	0.60
25:A:1434:A:H2'	25:A:1435:G:C8	2.36	0.60
1:a:81:A:N7	1:a:82:G:N2	2.49	0.60
25:A:1799:G:OP1	27:C:258:ARG:NH1	2.30	0.60
30:F:42:GLU:OE2	30:F:148:ARG:NH1	2.34	0.60
1:a:668:G:H1'	15:o:46:HIS:HD2	1.67	0.60
8:h:22:LYS:O	8:h:65:TYR:OH	2.18	0.60
12:l:68:GLY:O	12:l:99:ARG:NH1	2.32	0.60
25:A:1392:A:N6	43:V:18:GLU:OE1	2.35	0.60
26:B:37:C:O2	38:Q:100:HIS:NE2	2.33	0.60
1:a:4:U:H2'	1:a:5:U:H5''	1.83	0.60
11:k:98:ARG:NH1	21:u:16:LEU:HD21	2.17	0.60
25:A:643:A:H61	25:A:2369:A:H8	1.49	0.60
11:k:17:SER:H	11:k:78:GLY:HA3	1.66	0.60
33:L:125:TYR:OH	33:L:132:HIS:NE2	2.30	0.60
1:a:1130:A:H61	1:a:1144:G:H1'	1.65	0.60
20:t:35:VAL:O	20:t:39:ILE:HG12	2.01	0.60
27:C:142:HIS:ND1	27:C:193:GLY:O	2.33	0.60
25:A:270:A:H5'	25:A:271:G:H5''	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:639:U:H2'	25:A:640:C:C6	2.37	0.60
25:A:1475:G:O2'	25:A:1514:G:O6	2.20	0.60
26:B:54:G:H21	30:F:26:MET:HE3	1.66	0.60
32:H:2:GLN:NE2	32:H:20:ASN:OD1	2.34	0.60
20:t:68:HIS:CD2	20:t:70:ASN:H	2.20	0.59
1:a:946:A:H2'	1:a:947:G:H8	1.67	0.59
1:a:1029:U:H4'	1:a:1030:U:H5	1.68	0.59
25:A:569:U:O2'	25:A:983:A:N1	2.29	0.59
25:A:1433:A:H2'	25:A:1434:A:C8	2.37	0.59
30:F:123:ASP:OD2	30:F:127:ASN:ND2	2.34	0.59
1:a:1220:G:P	14:n:53:ARG:HH12	2.25	0.59
25:A:1252:G:OP2	40:S:13:ARG:NH2	2.34	0.59
25:A:1432:G:H2'	25:A:1433:A:C8	2.36	0.59
25:A:2204:G:H4'	27:C:150:LYS:HD3	1.84	0.59
28:D:46:ARG:NH1	28:D:85:ALA:O	2.36	0.59
17:q:28:PHE:CE1	17:q:37:PHE:HB3	2.38	0.59
20:t:60:ARG:HG2	20:t:64:LYS:HD2	1.83	0.59
39:R:14:LYS:NZ	39:R:81:VAL:O	2.34	0.59
6:f:36:ILE:O	6:f:38:ARG:N	2.35	0.59
8:h:29:SER:HB3	8:h:57:PRO:HB2	1.85	0.59
25:A:2185:U:H2'	25:A:2186:G:H8	1.67	0.59
30:F:135:GLN:NE2	30:F:148:ARG:O	2.35	0.59
1:a:1287:A:H2'	1:a:1288:A:C8	2.38	0.59
22:y:60:U:OP1	22:y:61:C:N4	2.36	0.59
25:A:30:G:O2'	25:A:1214:A:N3	2.32	0.59
1:a:459:A:H2'	1:a:460:A:H8	1.68	0.59
27:C:225:MET:HE2	27:C:230:HIS:HB2	1.84	0.59
22:w:9:A:N3	22:w:45:U:H2'	2.17	0.59
25:A:1266:G:O2'	25:A:2012:G:O6	2.18	0.59
1:a:1026:G:H2'	1:a:1027:C:C6	2.38	0.59
9:i:44:ALA:O	9:i:48:VAL:HG23	2.03	0.59
22:w:64:A:H2'	22:w:65:G:H8	1.67	0.59
23:x:43:A:H2'	23:x:44:A:C8	2.38	0.59
25:A:24:G:O2'	42:U:78:GLU:O	2.21	0.59
25:A:299:A:N3	25:A:319:G:O2'	2.30	0.59
25:A:1469:A:H2'	25:A:1470:A:C8	2.37	0.59
27:C:66:ASP:OD1	27:C:102:ARG:NH1	2.34	0.59
31:G:46:ALA:HB3	31:G:49:THR:HB	1.85	0.59
1:a:404:G:O2'	1:a:498:A:N1	2.30	0.58
35:N:29:LYS:HG3	35:N:30:THR:HG23	1.84	0.58
1:a:134:G:O6	16:p:25:ARG:NH1	2.35	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:d:54:GLN:HB3	4:d:203:LEU:HB2	1.86	0.58
25:A:2595:G:N2	25:A:2598:A:OP2	2.28	0.58
31:G:86:LYS:HG2	31:G:132:VAL:HG22	1.85	0.58
31:G:105:LEU:HD12	31:G:107:LEU:HD21	1.84	0.58
16:p:21:VAL:HG21	16:p:60:TRP:NE1	2.18	0.58
25:A:1386:C:H2'	25:A:1387:A:C8	2.39	0.58
25:A:2216:G:H2'	25:A:2217:G:H8	1.68	0.58
1:a:131:A:H2'	1:a:132:C:C6	2.38	0.58
1:a:335:C:H2'	1:a:336:A:H8	1.69	0.58
25:A:1386:C:H2'	25:A:1387:A:H8	1.69	0.58
25:A:2134:A:O2'	25:A:2159:G:N3	2.36	0.58
27:C:2:ALA:N	27:C:20:VAL:O	2.36	0.58
1:a:137:U:H3	1:a:226:G:H1	1.50	0.58
1:a:1250:A:H2'	1:a:1251:A:C8	2.37	0.58
25:A:630:G:N2	25:A:633:A:OP2	2.34	0.58
25:A:2131:U:H5'	25:A:2132:U:H5''	1.83	0.58
1:a:744:C:H2'	1:a:745:G:H8	1.69	0.58
1:a:976:G:OP2	1:a:1358:U:O2'	2.22	0.58
9:i:19:VAL:HG12	9:i:65:ILE:HG23	1.84	0.58
11:k:45:ALA:HB3	11:k:70:CYS:HB2	1.84	0.58
1:a:82:G:O2'	1:a:83:C:O4'	2.16	0.58
1:a:523:A:C2	12:l:88:LYS:HB3	2.38	0.58
1:a:1073:U:O2	2:b:103:ASN:ND2	2.36	0.58
25:A:2243:U:H2'	25:A:2244:U:C6	2.39	0.58
2:b:31:ILE:HA	2:b:41:ILE:HA	1.84	0.58
25:A:411:G:OP2	25:A:2406:A:O2'	2.22	0.58
25:A:818:G:N1	25:A:1188:U:OP2	2.30	0.58
1:a:411:A:OP1	4:d:26:ARG:NH1	2.33	0.58
14:n:16:LEU:HB3	14:n:55:SER:HB3	1.84	0.58
14:n:27:LEU:O	14:n:31:ILE:HG12	2.03	0.58
25:A:2286:G:N7	52:5:36:LEU:HD11	2.19	0.58
33:L:19:ASP:O	33:L:23:LYS:NZ	2.29	0.58
1:a:459:A:H2'	1:a:460:A:C8	2.39	0.58
11:k:36:ASP:OD1	11:k:37:ARG:N	2.37	0.57
39:R:10:GLN:HA	39:R:13:MET:HG2	1.86	0.57
33:L:32:LEU:HD22	33:L:54:ILE:HG21	1.86	0.57
11:k:20:VAL:HG23	11:k:83:GLU:HG3	1.84	0.57
25:A:568:U:O4	41:T:81:LYS:NZ	2.37	0.57
26:B:103:U:HO2'	45:X:31:TYR:HH	1.52	0.57
19:s:65:GLU:O	50:3:56:ARG:NH1	2.37	0.57
25:A:647:G:N2	25:A:2350:C:O2'	2.36	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:C:144:VAL:HB	27:C:154:LEU:HB2	1.85	0.57
25:A:645:C:H2'	25:A:647:G:N7	2.19	0.57
30:F:44:ILE:HG21	30:F:79:ILE:HG22	1.87	0.57
35:N:77:VAL:HG21	35:N:95:LEU:HD21	1.86	0.57
35:N:132:ARG:HG3	35:N:142:ILE:HD12	1.87	0.57
9:i:52:LEU:HD13	9:i:83:ILE:HD11	1.87	0.57
25:A:18:U:OP1	40:S:30:ARG:NH2	2.38	0.57
25:A:2380:C:HO2'	25:A:2381:A:H8	1.53	0.57
34:M:71:ARG:NH2	34:M:123:LEU:O	2.38	0.57
39:R:14:LYS:H	39:R:77:HIS:CD2	2.19	0.57
49:2:56:LYS:NZ	49:2:58:GLU:OE2	2.38	0.57
1:a:373:A:O2'	1:a:451:A:N7	2.36	0.57
1:a:1088:G:H21	1:a:1167:A:H61	1.52	0.57
22:w:23:A:H2'	22:w:24:G:C8	2.39	0.57
25:A:2514:U:H2'	25:A:2515:C:C6	2.40	0.57
25:A:2646:C:OP2	25:A:2732:G:O2'	2.22	0.57
1:a:981:U:OP1	14:n:9:ARG:NH1	2.37	0.57
1:a:1526:G:OP1	21:u:45:ARG:NH2	2.38	0.57
11:k:98:ARG:HH12	21:u:16:LEU:HD21	1.70	0.57
25:A:881:G:O6	25:A:895:U:O4	2.22	0.57
25:A:2591:C:H2'	25:A:2592:G:C8	2.39	0.57
1:a:5:U:H4'	1:a:6:G:H5'	1.86	0.57
3:c:53:SER:HB2	3:c:115:LEU:HD21	1.86	0.57
4:d:58:LYS:HD2	4:d:204:TYR:OH	2.05	0.57
20:t:68:HIS:HD2	20:t:70:ASN:H	1.53	0.57
44:W:5:ILE:HG22	44:W:72:ILE:HG13	1.85	0.57
1:a:769:G:H4'	1:a:1513:A:H4'	1.87	0.57
1:a:923:A:O2'	1:a:1399:C:OP2	2.21	0.57
1:a:1120:C:H2'	1:a:1121:U:H6	1.67	0.57
25:A:355:U:H2'	25:A:356:G:C8	2.39	0.57
25:A:742:A:H2'	25:A:743:A:C8	2.40	0.57
25:A:1794:A:H2'	25:A:1795:C:C6	2.40	0.57
25:A:1796:U:H2'	25:A:1797:G:C8	2.40	0.57
30:F:2:ALA:HB2	30:F:94:GLU:HG3	1.86	0.57
38:Q:97:PHE:HB3	38:Q:103:VAL:HG21	1.86	0.57
3:c:85:GLU:OE2	3:c:88:ARG:NH2	2.35	0.56
8:h:46:ILE:HD13	8:h:61:LEU:HD23	1.86	0.56
25:A:672:C:OP2	35:N:42:SER:OG	2.20	0.56
25:A:2246:G:H2'	25:A:2247:A:C8	2.40	0.56
25:A:2566:A:N1	34:M:28:SER:OG	2.30	0.56
25:A:2674:G:H4'	34:M:30:ARG:HG3	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:U:24:ILE:HD13	42:U:36:LEU:HD11	1.86	0.56
19:s:30:PRO:HB3	19:s:48:THR:HG23	1.87	0.56
25:A:1721:G:O2'	25:A:1738:G:N2	2.38	0.56
36:O:28:PHE:HB2	36:O:104:GLU:OE1	2.05	0.56
1:a:127:G:O2'	17:q:6:ARG:NH1	2.38	0.56
10:j:59:LYS:HZ3	10:j:62:ARG:HE	1.53	0.56
25:A:729:G:H5''	25:A:730:A:H5''	1.87	0.56
25:A:1918:A:O2'	25:A:1920:C:N4	2.38	0.56
25:A:2079:U:O2'	47:Z:23:ASN:ND2	2.36	0.56
25:A:2728:U:HO2'	25:A:2729:G:H8	1.52	0.56
1:a:86:G:H5'	1:a:87:C:H6	1.71	0.56
25:A:476:G:N1	25:A:479:A:OP2	2.34	0.56
25:A:585:G:N7	40:S:6:ARG:NH2	2.54	0.56
25:A:644:A:H2'	25:A:645:C:O4'	2.04	0.56
25:A:856:G:H2'	25:A:857:G:C8	2.40	0.56
25:A:859:G:O2'	25:A:916:G:O6	2.20	0.56
25:A:2187:U:H2'	25:A:2188:U:C6	2.40	0.56
1:a:1376:U:O4	7:g:10:ARG:NH2	2.39	0.56
25:A:1009:A:N3	25:A:1153:C:O2'	2.38	0.56
33:L:18:VAL:HG21	33:L:142:ILE:HD12	1.87	0.56
25:A:2419:U:H4'	52:5:22:THR:HG21	1.88	0.56
51:4:46:ASP:O	51:4:53:LYS:NZ	2.39	0.56
4:d:9:LEU:HD13	4:d:32:CYS:HB3	1.87	0.56
12:l:54:ARG:HH11	12:l:64:THR:HB	1.71	0.56
14:n:6:MET:HE2	14:n:63:ARG:HH12	1.71	0.56
20:t:39:ILE:HG21	20:t:82:GLN:HB3	1.88	0.56
25:A:1038:G:H2'	25:A:1039:A:C8	2.41	0.56
3:c:6:HIS:HB3	14:n:89:MET:HE3	1.88	0.56
9:i:50:GLN:HE21	9:i:80:ARG:HD2	1.71	0.56
22:w:15:G:N2	22:w:48:C:H42	2.03	0.56
22:w:43:C:H2'	22:w:44:G:C8	2.41	0.56
1:a:542:G:H5'	4:d:39:GLY:HA3	1.88	0.56
16:p:5:ARG:HH12	16:p:22:ALA:HB3	1.70	0.56
25:A:2184:A:H2'	25:A:2185:U:C6	2.41	0.56
25:A:2291:U:H2'	25:A:2292:U:C6	2.40	0.56
42:U:2:GLU:HA	42:U:108:SER:HB3	1.88	0.56
1:a:222:C:H2'	1:a:223:A:H8	1.71	0.56
25:A:1385:A:O2'	25:A:1396:U:O2	2.23	0.56
25:A:1570:A:H2'	25:A:1571:A:C8	2.41	0.56
1:a:501:C:H2'	1:a:502:A:H8	1.70	0.55
25:A:151:C:H2'	25:A:152:A:H8	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:1856:U:H2'	25:A:1857:G:O4'	2.06	0.55
25:A:2071:A:H2'	25:A:2072:C:C6	2.41	0.55
45:X:8:VAL:O	45:X:40:ILE:HA	2.06	0.55
1:a:458:U:O2	1:a:474:G:N2	2.35	0.55
10:j:11:LYS:HD3	10:j:71:LEU:HD21	1.88	0.55
12:l:55:VAL:HG11	12:l:80:ILE:HD11	1.88	0.55
15:o:3:LEU:HD12	15:o:35:GLN:NE2	2.22	0.55
25:A:945:A:N1	60:A:3405:HOH:O	2.33	0.55
25:A:1141:U:OP2	33:L:65:THR:OG1	2.22	0.55
25:A:2113:U:O4	25:A:2119:A:N6	2.40	0.55
1:a:662:U:H2'	1:a:663:A:C8	2.41	0.55
1:a:1456:A:H2'	1:a:1457:G:O4'	2.07	0.55
2:b:114:LEU:HB2	2:b:144:LEU:HD22	1.87	0.55
17:q:13:VAL:HG23	17:q:22:VAL:HG13	1.87	0.55
25:A:871:U:H2'	25:A:872:U:C6	2.41	0.55
25:A:1006:C:O2'	33:L:108:MET:O	2.23	0.55
25:A:1808:A:H3'	25:A:1809:A:C8	2.41	0.55
3:c:152:GLU:HB3	3:c:167:TRP:HB3	1.87	0.55
13:m:67:GLY:HA3	30:F:113:ASP:HB3	1.88	0.55
1:a:501:C:H2'	1:a:502:A:C8	2.41	0.55
1:a:546:A:OP1	4:d:70:ARG:HG2	2.07	0.55
1:a:745:G:H2'	1:a:746:A:C8	2.41	0.55
1:a:1097:C:H2'	1:a:1098:C:C6	2.42	0.55
1:a:1323:G:H2'	1:a:1324:A:C8	2.42	0.55
25:A:651:G:H5'	54:7:19:LYS:HG3	1.88	0.55
1:a:147:G:H2'	1:a:148:G:C8	2.42	0.55
5:e:58:ALA:O	5:e:62:LYS:HG3	2.06	0.55
5:e:82:GLN:HG3	5:e:149:SER:HA	1.89	0.55
25:A:2246:G:H2'	25:A:2247:A:H8	1.72	0.55
35:N:57:LEU:HD22	54:7:54:ASP:HB3	1.89	0.55
1:a:1060:U:H2'	1:a:1061:G:H8	1.70	0.55
25:A:820:A:H4'	25:A:836:G:H22	1.72	0.55
27:C:155:ALA:HB2	27:C:162:VAL:HG23	1.88	0.55
25:A:5:A:H2'	25:A:6:A:C8	2.42	0.55
25:A:81:G:HO2'	25:A:295:G:HO2'	1.50	0.55
51:4:12:LYS:HD3	51:4:15:MET:HE2	1.89	0.55
1:a:1087:G:H2'	1:a:1088:G:C8	2.42	0.55
1:a:1088:G:N2	1:a:1167:A:H61	2.05	0.55
25:A:2117:A:H61	25:A:2170:A:H61	1.54	0.55
30:F:73:SER:HB3	30:F:81:GLN:H	1.72	0.55
31:G:72:LEU:HA	31:G:75:MET:HB3	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:384:G:H2'	1:a:385:C:C6	2.42	0.55
1:a:521:G:N7	12:l:50:ARG:NH1	2.52	0.55
1:a:746:A:H2'	1:a:747:A:C8	2.42	0.55
3:c:33:LEU:HD21	14:n:93:ILE:HG12	1.89	0.55
4:d:132:ILE:HG22	4:d:134:SER:H	1.72	0.55
37:P:56:LYS:NZ	37:P:90:ARG:O	2.39	0.55
25:A:2327:A:H2'	25:A:2328:A:C8	2.43	0.54
25:A:2502:G:H5''	25:A:2503:2MA:H5''	1.89	0.54
36:O:105:MET:HE2	36:O:108:VAL:HG21	1.88	0.54
1:a:1437:A:H5'	20:t:29:ARG:HH12	1.72	0.54
1:a:1447:A:H5''	1:a:1448:C:H5	1.73	0.54
8:h:15:ARG:NH1	8:h:75:ILE:O	2.41	0.54
31:G:28:GLY:O	31:G:29:LYS:HG3	2.06	0.54
25:A:1590:A:H2'	25:A:1591:A:C8	2.43	0.54
25:A:1636:U:H2'	25:A:1637:A:C8	2.42	0.54
25:A:2291:U:O2'	25:A:2374:C:O2	2.25	0.54
49:2:27:LEU:O	49:2:38:ARG:NH1	2.38	0.54
1:a:1074:G:O2'	2:b:102:THR:OG1	2.26	0.54
1:a:1222:G:OP2	1:a:1322:C:N4	2.36	0.54
4:d:60:LYS:NZ	4:d:194:ASP:O	2.40	0.54
6:f:74:LEU:O	6:f:78:PHE:HD1	1.90	0.54
25:A:2295:C:OP2	38:Q:9:ARG:NH2	2.39	0.54
27:C:80:ARG:NH1	27:C:82:GLU:OE1	2.39	0.54
42:U:11:ARG:NH2	42:U:98:LYS:HD3	2.22	0.54
1:a:90:C:H2'	1:a:91:U:C6	2.42	0.54
1:a:166:U:H2'	1:a:167:A:H8	1.72	0.54
1:a:693:G:OP1	11:k:127:ARG:NH2	2.41	0.54
1:a:796:C:O3'	11:k:127:ARG:NH1	2.41	0.54
1:a:1368:A:OP1	10:j:64:GLN:NE2	2.37	0.54
1:a:1412:C:H2'	1:a:1413:A:C8	2.43	0.54
25:A:1682:G:H2'	25:A:1683:U:C6	2.43	0.54
31:G:149:ARG:HA	31:G:162:VAL:HG21	1.89	0.54
1:a:461:A:H2'	1:a:462:G:H8	1.71	0.54
1:a:1316:G:N1	1:a:1319:A:OP2	2.37	0.54
1:a:187:G:N2	1:a:190:A:OP2	2.38	0.54
1:a:539:A:H2'	1:a:540:G:C8	2.43	0.54
1:a:1360:A:OP2	14:n:75:ARG:NH2	2.41	0.54
1:a:1404:C:H2'	1:a:1405:G:C8	2.43	0.54
2:b:47:VAL:O	2:b:51:ASN:ND2	2.41	0.54
4:d:101:VAL:O	4:d:105:MET:HG2	2.07	0.54
8:h:5:ASP:OD1	8:h:77:ARG:NH1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:1353:A:H2'	25:A:1354:A:C8	2.43	0.54
25:A:2025:C:H2'	25:A:2026:U:C6	2.42	0.54
25:A:2064:C:H2'	25:A:2065:C:C6	2.43	0.54
34:M:43:ILE:HD12	34:M:56:ASP:HB2	1.90	0.54
1:a:62:U:O2'	1:a:379:C:O2	2.24	0.54
16:p:20:VAL:HG23	16:p:35:ARG:HA	1.90	0.54
25:A:1746:A:H2'	25:A:1747:U:C6	2.42	0.54
25:A:2153:C:H2'	25:A:2154:A:C8	2.38	0.54
26:B:98:G:H1	45:X:14:LYS:HB2	1.73	0.54
29:E:97:ASN:HB2	29:E:100:MET:HG3	1.90	0.54
35:N:108:ALA:HB3	35:N:125:LEU:HD22	1.90	0.54
1:a:509:A:N3	1:a:543:U:O2'	2.37	0.54
1:a:908:A:H2'	1:a:909:A:C8	2.43	0.54
1:a:1226:C:H2'	13:m:102:THR:HG22	1.90	0.54
6:f:68:GLN:O	6:f:71:ILE:HG22	2.08	0.54
23:x:56:C:O4'	30:F:73:SER:OG	2.26	0.54
25:A:597:G:O2'	35:N:11:GLY:O	2.23	0.54
25:A:2757:A:N1	31:G:67:THR:OG1	2.39	0.54
1:a:821:G:H2'	1:a:822:U:C6	2.42	0.54
1:a:1120:C:H2'	1:a:1121:U:C6	2.43	0.54
25:A:2020:A:H62	51:4:6:ASN:ND2	2.06	0.54
25:A:2328:A:H2'	25:A:2329:U:H6	1.70	0.54
1:a:17:U:H2'	1:a:18:C:C6	2.43	0.53
1:a:56:U:H2'	1:a:57:G:H8	1.73	0.53
25:A:833:A:H2'	25:A:834:G:C8	2.42	0.53
25:A:2187:U:H2'	25:A:2188:U:H6	1.73	0.53
38:Q:111:ARG:NH1	38:Q:117:PHE:OXT	2.41	0.53
1:a:1363:A:O2'	1:a:1365:G:N7	2.34	0.53
1:a:1386:G:H2'	1:a:1387:G:H5''	1.88	0.53
25:A:813:U:H2'	25:A:814:C:C6	2.44	0.53
25:A:1000:A:H2'	25:A:1001:A:C8	2.44	0.53
25:A:1038:G:H2'	25:A:1039:A:H8	1.72	0.53
25:A:1864:U:OP1	25:A:2410:G:O2'	2.24	0.53
25:A:2683:C:H4'	28:D:13:ARG:NH2	2.23	0.53
34:M:1:MET:SD	34:M:67:LYS:NZ	2.79	0.53
1:a:634:C:H2'	1:a:635:A:H8	1.74	0.53
25:A:849:A:H2'	25:A:850:U:H6	1.73	0.53
30:F:23:ASN:OD1	30:F:24:SER:N	2.40	0.53
44:W:96:PHE:O	44:W:100:SER:HA	2.08	0.53
1:a:159:G:N2	1:a:162:A:OP2	2.40	0.53
1:a:875:U:H1'	8:h:16:ASN:HD21	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:n:79:LEU:HB2	14:n:84:VAL:HG23	1.90	0.53
25:A:2189:U:H2'	25:A:2190:G:C8	2.44	0.53
25:A:2788:C:H2'	25:A:2789:C:C6	2.43	0.53
1:a:945:G:C2	1:a:946:A:C8	2.97	0.53
1:a:1071:C:H2'	1:a:1072:G:C8	2.39	0.53
2:b:72:THR:OG1	2:b:169:GLU:OE2	2.17	0.53
16:p:51:ARG:NH1	16:p:52:LEU:O	2.41	0.53
19:s:37:ARG:O	19:s:70:LYS:NZ	2.40	0.53
25:A:1469:A:H2'	25:A:1470:A:H8	1.73	0.53
29:E:29:HIS:HA	35:N:6:LEU:HD13	1.91	0.53
30:F:59:ALA:O	50:3:27:THR:OG1	2.26	0.53
31:G:24:ILE:HD11	31:G:43:VAL:HG11	1.88	0.53
1:a:1314:C:H2'	1:a:1315:U:C6	2.44	0.53
2:b:68:LEU:HD11	2:b:92:VAL:HG23	1.90	0.53
25:A:593:U:H2'	25:A:594:U:C6	2.44	0.53
25:A:910:A:H2'	25:A:911:A:C8	2.44	0.53
25:A:1125:G:OP2	25:A:1126:A:O2'	2.16	0.53
26:B:39:A:O2'	26:B:46:A:N1	2.40	0.53
3:c:57:ILE:HG22	3:c:66:VAL:HG13	1.90	0.53
6:f:26:THR:HA	6:f:29:ILE:HG22	1.89	0.53
25:A:1281:G:H2'	25:A:1282:U:C6	2.44	0.53
55:8:30:GLU:OE2	55:8:32:LYS:HB2	2.09	0.53
1:a:881:G:P	12:l:9:ARG:HH22	2.32	0.53
1:a:1513:A:H2'	1:a:1514:G:C8	2.43	0.53
22:w:15:G:H22	22:w:48:C:H42	1.56	0.53
25:A:930:G:H1'	49:2:25:LEU:HD11	1.89	0.53
25:A:1028:A:N3	25:A:2486:C:O2'	2.40	0.53
25:A:1443:U:H2'	25:A:1444:G:H8	1.74	0.53
25:A:2216:G:H2'	25:A:2217:G:C8	2.43	0.53
25:A:2591:C:H2'	25:A:2592:G:H8	1.73	0.53
41:T:32:THR:HA	41:T:62:GLU:HA	1.91	0.53
1:a:458:U:H2'	1:a:459:A:C8	2.44	0.53
1:a:977:A:O2'	1:a:979:C:OP2	2.24	0.53
14:n:24:ARG:NH1	14:n:55:SER:O	2.41	0.53
25:A:2557:G:H2'	25:A:2558:C:C6	2.44	0.53
1:a:555:U:H2'	1:a:556:C:C6	2.43	0.53
1:a:1518:MA6:H92	1:a:1519:MA6:N6	2.24	0.53
9:i:63:LEU:HD11	9:i:83:ILE:HG13	1.91	0.53
25:A:1429:G:H2'	25:A:1430:G:H8	1.74	0.53
25:A:2074:U:H2'	25:A:2075:U:C6	2.44	0.53
25:A:2895:G:H2'	25:A:2896:C:H6	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:B:48:U:H4'	38:Q:100:HIS:CD2	2.43	0.53
30:F:8:TYR:HA	30:F:12:VAL:HB	1.91	0.53
1:a:1355:G:H2'	1:a:1356:G:H8	1.74	0.52
25:A:1997:C:OP2	28:D:129:THR:OG1	2.21	0.52
25:A:2743:U:H5'	25:A:2744:G:OP2	2.09	0.52
25:A:2895:G:H2'	25:A:2896:C:C6	2.44	0.52
33:L:99:ARG:HH11	33:L:99:ARG:HG3	1.74	0.52
1:a:411:A:OP2	4:d:26:ARG:NH2	2.38	0.52
1:a:1507:A:H2'	1:a:1508:A:C8	2.44	0.52
3:c:108:LYS:HB2	3:c:144:LEU:HD23	1.91	0.52
4:d:8:LYS:HD2	4:d:21:LEU:HD12	1.91	0.52
4:d:85:ASN:OD1	5:e:102:GLY:HA3	2.08	0.52
5:e:38:VAL:HG21	5:e:114:VAL:HG22	1.90	0.52
1:a:460:A:H2'	1:a:461:A:C8	2.44	0.52
25:A:627:A:OP1	35:N:78:ARG:NH2	2.31	0.52
25:A:1794:A:H2'	25:A:1795:C:H6	1.74	0.52
25:A:2107:G:C2	25:A:2183:A:N1	2.77	0.52
25:A:2329:U:H2'	25:A:2330:G:H8	1.73	0.52
34:M:38:ILE:HD11	34:M:112:PHE:HZ	1.74	0.52
1:a:674:G:H2'	1:a:675:A:C8	2.40	0.52
4:d:174:ASP:O	4:d:178:MET:HA	2.09	0.52
8:h:11:LEU:HB2	8:h:75:ILE:HG12	1.90	0.52
22:y:67:C:H2'	22:y:68:C:C6	2.44	0.52
1:a:714:G:H2'	1:a:715:A:C8	2.44	0.52
25:A:64:A:H2'	25:A:65:U:C6	2.44	0.52
25:A:210:C:OP1	53:6:29:GLN:NE2	2.38	0.52
25:A:2086:U:H2'	25:A:2087:G:C8	2.43	0.52
25:A:2698:U:H2'	25:A:2699:C:C6	2.44	0.52
1:a:1399:C:O2	1:a:1502:A:N6	2.43	0.52
2:b:66:LYS:HB3	2:b:90:PHE:HE2	1.74	0.52
22:y:1:G:H2'	22:y:2:C:C6	2.45	0.52
25:A:191:A:H2'	25:A:192:C:H6	1.74	0.52
25:A:598:U:H2'	25:A:599:A:H8	1.74	0.52
28:D:34:VAL:HG12	28:D:50:VAL:HG12	1.91	0.52
39:R:13:MET:HE1	39:R:54:GLY:O	2.09	0.52
44:W:33:LYS:HB3	44:W:64:ALA:HB1	1.92	0.52
48:1:9:LYS:HG3	48:1:14:LEU:HD23	1.92	0.52
1:a:950:U:H2'	1:a:951:G:C8	2.44	0.52
22:y:72:C:H2'	22:y:73:A:H8	1.74	0.52
25:A:1250:G:N7	35:N:18:ARG:NH1	2.52	0.52
25:A:2744:G:H21	31:G:143:GLN:HE22	1.56	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:B:106:G:H2'	26:B:107:G:O4'	2.10	0.52
47:Z:32:ASN:OD1	47:Z:34:HIS:NE2	2.43	0.52
1:a:1078:U:H1'	5:e:135:ASN:HD21	1.74	0.52
4:d:28:ILE:HG13	4:d:34:ILE:HD11	1.92	0.52
13:m:25:VAL:HG12	13:m:29:ARG:HD3	1.91	0.52
13:m:33:ILE:HD13	13:m:60:VAL:HG22	1.91	0.52
18:r:26:ILE:HG23	18:r:68:LEU:HD21	1.92	0.52
25:A:2051:A:H5'	25:A:2578:G:O4'	2.10	0.52
25:A:2578:G:H21	28:D:130:GLN:HE22	1.58	0.52
3:c:91:VAL:HG21	3:c:101:ILE:HD11	1.91	0.52
25:A:494:G:H4'	42:U:6:LYS:HB2	1.92	0.52
25:A:2143:C:H2'	25:A:2144:G:C8	2.44	0.52
40:S:109:LEU:HD13	41:T:49:ILE:HG12	1.91	0.52
1:a:19:A:H5''	5:e:91:GLY:HA3	1.92	0.52
1:a:1013:G:N2	1:a:1016:A:OP2	2.38	0.52
25:A:686:U:O4	53:6:12:ARG:HG3	2.10	0.52
1:a:171:A:H2'	1:a:172:A:C8	2.45	0.51
1:a:1075:U:OP1	2:b:178:ASN:ND2	2.43	0.51
25:A:458:G:O2'	25:A:469:G:O6	2.24	0.51
45:X:47:VAL:HA	45:X:50:MET:HG2	1.92	0.51
6:f:88:MET:HB2	18:r:65:LEU:HD21	1.93	0.51
25:A:2158:A:H4'	25:A:2159:G:O4'	2.10	0.51
27:C:107:PRO:HD2	27:C:110:LEU:HD22	1.92	0.51
41:T:49:ILE:H	41:T:49:ILE:HD12	1.75	0.51
1:a:376:G:H4'	16:p:5:ARG:HD2	1.91	0.51
7:g:47:LEU:HD21	7:g:62:PHE:HB2	1.92	0.51
9:i:65:ILE:HG21	9:i:79:ILE:HG12	1.93	0.51
25:A:84:A:N1	25:A:98:G:O2'	2.33	0.51
38:Q:37:ALA:HB2	38:Q:106:LEU:HD11	1.91	0.51
1:a:216:U:H2'	1:a:217:C:H6	1.75	0.51
1:a:1004:A:H2'	1:a:1005:A:O4'	2.09	0.51
25:A:2314:A:OP1	30:F:88:LYS:NZ	2.44	0.51
1:a:546:A:P	4:d:69:GLU:HB3	2.51	0.51
6:f:6:ILE:HD12	6:f:89:VAL:HG22	1.93	0.51
25:A:514:A:N3	25:A:581:C:O2'	2.37	0.51
25:A:687:C:H1'	53:6:4:THR:HG22	1.93	0.51
25:A:849:A:H2'	25:A:850:U:C6	2.46	0.51
25:A:1353:A:H2'	25:A:1354:A:H8	1.75	0.51
25:A:1798:U:H5''	27:C:258:ARG:HB2	1.92	0.51
30:F:111:ILE:HA	30:F:137:ILE:HD12	1.92	0.51
1:a:203:G:N2	1:a:204:G:O6	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:j:59:LYS:NZ	10:j:62:ARG:HH21	2.09	0.51
20:t:24:ARG:HH21	20:t:27:MET:HE2	1.76	0.51
22:w:18:G:O2'	22:w:57:G:N2	2.36	0.51
25:A:5:A:H2'	25:A:6:A:H8	1.74	0.51
25:A:468:G:N7	53:6:39:ARG:NH2	2.51	0.51
25:A:1417:C:O2'	25:A:1587:G:O2'	2.23	0.51
29:E:131:THR:HG23	29:E:164:LEU:HD11	1.93	0.51
44:W:86:ARG:NH1	44:W:100:SER:OG	2.39	0.51
1:a:33:A:H2'	1:a:34:C:C6	2.46	0.51
1:a:745:G:H2'	1:a:746:A:H8	1.74	0.51
15:o:74:ASP:OD1	15:o:74:ASP:N	2.42	0.51
25:A:1568:G:H5'	27:C:60:GLN:HA	1.93	0.51
30:F:65:PRO:HA	30:F:89:VAL:HG12	1.93	0.51
1:a:73:C:H2'	1:a:74:A:H8	1.76	0.51
1:a:596:A:H2'	1:a:597:G:H8	1.75	0.51
25:A:807:U:O2'	25:A:2060:A:N1	2.40	0.51
25:A:2739:U:H2'	25:A:2740:A:H5'	1.93	0.51
27:C:65:VAL:HG12	27:C:103:TYR:HB3	1.91	0.51
1:a:458:U:H2'	1:a:459:A:H8	1.74	0.51
1:a:821:G:H2'	1:a:822:U:H6	1.76	0.51
7:g:70:ARG:HA	7:g:100:ALA:HB2	1.93	0.51
10:j:22:THR:HG21	10:j:72:ARG:HG2	1.92	0.51
25:A:500:G:N1	25:A:503:A:OP2	2.39	0.51
25:A:1672:A:C2	25:A:2582:G:H5'	2.46	0.51
29:E:125:SER:O	29:E:137:LYS:NZ	2.37	0.51
1:a:34:C:H2'	1:a:35:G:H8	1.76	0.51
1:a:1010:U:H2'	1:a:1011:C:C6	2.45	0.51
8:h:10:MET:HG3	8:h:27:MET:SD	2.52	0.51
25:A:1197:G:H2'	25:A:1198:U:H6	1.76	0.51
25:A:1264:A:OP1	51:4:16:ARG:NH2	2.33	0.51
1:a:323:U:H2'	1:a:324:G:O4'	2.11	0.50
1:a:636:U:H2'	1:a:637:C:C6	2.45	0.50
3:c:7:PRO:O	3:c:11:ARG:NH1	2.43	0.50
11:k:82:LEU:HB3	11:k:105:PHE:HB3	1.93	0.50
25:A:1405:U:H2'	25:A:1406:U:C6	2.47	0.50
25:A:2537:U:H2'	25:A:2538:C:H6	1.76	0.50
1:a:166:U:H2'	1:a:167:A:C8	2.45	0.50
1:a:1356:G:H2'	1:a:1357:A:H8	1.75	0.50
35:N:79:LEU:HB3	35:N:116:VAL:HG23	1.93	0.50
1:a:999:C:N3	1:a:1042:A:N6	2.58	0.50
11:k:32:VAL:HG11	11:k:67:ALA:HA	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:703:U:H2'	25:A:704:G:O4'	2.11	0.50
25:A:1636:U:H2'	25:A:1637:A:H8	1.75	0.50
11:k:17:SER:N	11:k:78:GLY:HA3	2.27	0.50
16:p:22:ALA:HA	16:p:33:ILE:HD12	1.93	0.50
23:x:21:A:H61	23:x:46:G:H2'	1.75	0.50
25:A:848:C:H2'	25:A:849:A:C8	2.43	0.50
1:a:665:A:H1'	1:a:733:G:H5'	1.93	0.50
1:a:911:U:H2'	1:a:912:C:C6	2.46	0.50
1:a:1355:G:H2'	1:a:1356:G:C8	2.46	0.50
25:A:700:G:O2'	25:A:1632:A:N3	2.33	0.50
25:A:2037:A:H2'	25:A:2038:G:C8	2.46	0.50
25:A:2329:U:H2'	25:A:2330:G:C8	2.46	0.50
27:C:51:THR:HG23	27:C:54:ILE:HD12	1.94	0.50
37:P:24:MET:HE1	37:P:40:LYS:HD3	1.94	0.50
44:W:28:VAL:HG22	44:W:34:VAL:HG12	1.93	0.50
1:a:216:U:H2'	1:a:217:C:C6	2.47	0.50
1:a:235:C:H2'	1:a:236:A:C8	2.46	0.50
9:i:5:GLN:HA	9:i:21:ILE:O	2.11	0.50
12:l:31:ARG:HE	12:l:58:THR:HG21	1.76	0.50
19:s:31:LEU:HD23	19:s:31:LEU:H	1.77	0.50
48:1:43:LEU:HA	48:1:46:VAL:HG22	1.94	0.50
49:2:9:GLN:HE21	49:2:54:MET:HE2	1.76	0.50
1:a:392:C:H2'	1:a:393:A:H8	1.76	0.50
1:a:1251:A:H2'	1:a:1252:A:C8	2.47	0.50
13:m:66:GLU:OE1	30:F:112:ARG:NH2	2.44	0.50
14:n:16:LEU:HD23	14:n:19:LYS:HD3	1.94	0.50
18:r:26:ILE:HD11	18:r:67:LEU:HD22	1.93	0.50
25:A:284:U:H2'	25:A:285:G:H8	1.75	0.50
25:A:2537:U:H2'	25:A:2538:C:C6	2.46	0.50
44:W:17:LYS:NZ	44:W:40:ASN:OD1	2.44	0.50
55:8:2:LYS:HB2	55:8:35:GLN:HG2	1.93	0.50
1:a:337:G:H2'	1:a:338:A:H8	1.75	0.50
2:b:32:PHE:HB3	2:b:42:ASN:HB2	1.93	0.50
3:c:132:ARG:HE	3:c:136:ARG:NH2	2.08	0.50
12:l:53:CYS:HB3	12:l:67:ILE:HD11	1.92	0.50
25:A:711:G:H2'	25:A:712:G:H5''	1.94	0.50
25:A:2114:A:N6	25:A:2115:G:N3	2.60	0.50
40:S:52:GLN:HA	40:S:55:ARG:HG3	1.94	0.50
40:S:66:ASN:O	40:S:70:ARG:HG3	2.12	0.50
1:a:461:A:H2'	1:a:462:G:C8	2.47	0.50
1:a:746:A:H2'	1:a:747:A:H8	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:985:C:H2'	1:a:986:U:C6	2.46	0.50
4:d:9:LEU:HD21	4:d:22:LYS:HG3	1.93	0.50
25:A:12:U:O2	25:A:2626:C:H4'	2.12	0.50
25:A:2014:A:O2'	42:U:92:ARG:NH2	2.44	0.50
25:A:2536:G:O2'	25:A:2537:U:H6	1.94	0.50
22:w:63:G:H2'	22:w:64:A:H8	1.77	0.49
25:A:100:U:O2	44:W:91:LYS:NZ	2.45	0.49
25:A:155:A:H2'	25:A:156:A:C8	2.47	0.49
25:A:577:G:O2'	25:A:1254:A:OP1	2.30	0.49
25:A:2038:G:H2'	25:A:2039:U:O4'	2.12	0.49
50:3:14:ALA:HB3	50:3:22:MET:HG3	1.92	0.49
1:a:1374:A:O3'	7:g:28:ASN:ND2	2.46	0.49
1:a:1497:G:H1'	1:a:1518:MA6:H2	1.93	0.49
1:a:1518:MA6:H103	1:a:1519:MA6:H102	1.94	0.49
4:d:178:MET:O	4:d:178:MET:HG2	2.11	0.49
25:A:549:G:H2'	25:A:550:C:C6	2.46	0.49
25:A:729:G:C5	27:C:207:LYS:HB2	2.47	0.49
25:A:2458:G:O2'	25:A:2460:U:O4	2.28	0.49
31:G:37:LEU:HD21	31:G:72:LEU:HD11	1.94	0.49
1:a:77:A:H2'	1:a:78:A:H8	1.78	0.49
1:a:1314:C:H2'	1:a:1315:U:H6	1.77	0.49
1:a:1391:U:H2'	1:a:1392:G:C8	2.47	0.49
3:c:66:VAL:HB	3:c:101:ILE:HG12	1.93	0.49
9:i:19:VAL:HG12	9:i:65:ILE:HG12	1.95	0.49
25:A:151:C:H2'	25:A:152:A:C8	2.47	0.49
25:A:1542:U:H2'	25:A:1543:G:O4'	2.12	0.49
25:A:1818:U:O2'	27:C:153:GLN:O	2.28	0.49
38:Q:59:ALA:HA	38:Q:62:LEU:HD12	1.94	0.49
6:f:86:ARG:NH1	18:r:64:TYR:O	2.45	0.49
25:A:581:C:H2'	25:A:582:A:C8	2.47	0.49
25:A:582:A:H2'	25:A:583:G:C8	2.48	0.49
25:A:2359:C:O2'	54:7:54:ASP:OD2	2.25	0.49
25:A:2615:U:C2	51:4:4:GLN:HA	2.48	0.49
28:D:3:GLY:HA3	28:D:204:LYS:HG2	1.94	0.49
30:F:62:GLY:O	30:F:95:ARG:NH1	2.45	0.49
31:G:149:ARG:HA	31:G:162:VAL:CG2	2.42	0.49
36:O:79:ALA:O	46:Y:5:LYS:HB2	2.13	0.49
1:a:160:A:H8	1:a:160:A:OP1	1.94	0.49
1:a:600:A:H2'	1:a:601:G:H8	1.77	0.49
1:a:908:A:H2'	1:a:909:A:H8	1.76	0.49
25:A:306:U:H2'	25:A:307:G:O4'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:438:G:H2'	25:A:439:A:C8	2.46	0.49
25:A:629:G:N3	25:A:639:U:O2'	2.45	0.49
25:A:648:G:H4'	25:A:2351:G:H5'	1.92	0.49
25:A:1141:U:H4'	25:A:1142:A:O4'	2.12	0.49
25:A:1361:G:H2'	25:A:1362:C:C6	2.48	0.49
25:A:1486:U:H2'	25:A:1487:U:C6	2.47	0.49
37:P:54:LEU:HD22	37:P:66:ALA:HB2	1.95	0.49
2:b:31:ILE:HG21	2:b:39:HIS:HD2	1.77	0.49
8:h:43:GLU:OE1	8:h:101:ILE:HG21	2.12	0.49
22:w:51:U:H2'	22:w:52:G:C8	2.48	0.49
22:y:7:A:H3'	22:y:8:4SU:H5''	1.94	0.49
25:A:2898:U:H2'	25:A:2899:A:H8	1.77	0.49
1:a:440:C:C2	1:a:441:A:C8	3.00	0.49
12:l:24:LEU:HD23	12:l:27:CYS:O	2.12	0.49
13:m:22:ILE:HB	13:m:25:VAL:HG22	1.94	0.49
25:A:2809:A:H2'	25:A:2810:A:C8	2.47	0.49
37:P:79:LEU:HD23	37:P:83:LEU:HD23	1.95	0.49
1:a:768:A:N3	1:a:1512:U:O2'	2.45	0.49
3:c:24:ALA:HB1	3:c:28:GLU:HG3	1.94	0.49
6:f:82:ASP:OD1	6:f:82:ASP:N	2.46	0.49
9:i:55:VAL:HG21	9:i:87:LEU:HD21	1.93	0.49
25:A:1604:C:O2'	25:A:1610:A:N1	2.39	0.49
42:U:18:ARG:HG3	42:U:76:VAL:CG1	2.42	0.49
1:a:71:A:N1	1:a:99:C:O2'	2.40	0.49
1:a:138:G:O6	1:a:225:C:N4	2.35	0.49
1:a:297:G:N2	1:a:300:A:OP2	2.40	0.49
1:a:757:U:OP1	1:a:822:U:O2'	2.30	0.49
4:d:87:GLY:HA3	4:d:197:GLU:OE1	2.13	0.49
11:k:112:ASP:OD1	11:k:114:THR:OG1	2.30	0.49
25:A:2314:A:H2'	25:A:2315:G:C8	2.48	0.49
1:a:1124:G:H1'	1:a:1125:U:H5	1.77	0.49
36:O:34:LYS:HD3	45:X:82:TYR:HA	1.94	0.49
36:O:77:PRO:HG2	36:O:80:VAL:HG11	1.95	0.49
1:a:875:U:O2'	8:h:15:ARG:NE	2.43	0.48
1:a:1043:G:O2'	1:a:1044:A:H5''	2.13	0.48
1:a:1043:G:O2'	1:a:1044:A:H8	1.96	0.48
3:c:138:VAL:HG13	3:c:149:ILE:HG21	1.94	0.48
4:d:9:LEU:HD22	4:d:28:ILE:HD11	1.93	0.48
4:d:124:MET:HE2	4:d:146:ARG:HD2	1.95	0.48
25:A:155:A:H2'	25:A:156:A:H8	1.77	0.48
25:A:742:A:H2'	25:A:743:A:H8	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:892:A:H2'	25:A:893:C:C6	2.48	0.48
25:A:1428:C:C5	25:A:1569:A:H5''	2.48	0.48
25:A:2229:U:H2'	25:A:2230:G:H8	1.78	0.48
25:A:2804:U:H2'	25:A:2805:C:C6	2.48	0.48
27:C:72:ASP:OD1	27:C:189:ARG:NH1	2.45	0.48
51:4:11:SER:O	51:4:15:MET:HG3	2.13	0.48
4:d:101:VAL:HG21	4:d:137:VAL:HG21	1.95	0.48
25:A:300:A:OP2	44:W:82:ARG:NH2	2.46	0.48
25:A:1883:U:H2'	25:A:1884:G:O4'	2.13	0.48
34:M:63:VAL:HG23	34:M:64:ARG:HG3	1.95	0.48
34:M:108:ARG:HE	34:M:113:MET:HE1	1.78	0.48
39:R:14:LYS:NZ	39:R:81:VAL:HG23	2.28	0.48
42:U:55:ILE:O	42:U:59:GLU:HG3	2.12	0.48
52:5:34:LEU:HD21	52:5:36:LEU:HG	1.94	0.48
1:a:8:A:H62	4:d:205:SER:HG	1.61	0.48
1:a:360:G:H2'	1:a:361:G:C8	2.49	0.48
1:a:1323:G:H2'	1:a:1324:A:H8	1.78	0.48
4:d:3:ARG:HE	4:d:115:ARG:HD3	1.77	0.48
25:A:96:C:OP1	48:1:39:GLN:NE2	2.46	0.48
25:A:191:A:H2'	25:A:192:C:C6	2.48	0.48
25:A:580:U:H2'	25:A:581:C:C6	2.48	0.48
25:A:832:U:H2'	25:A:833:A:C8	2.47	0.48
25:A:863:A:H2'	25:A:864:G:C8	2.48	0.48
25:A:2047:C:H2'	25:A:2048:G:H8	1.77	0.48
25:A:2112:G:H5'	25:A:2113:U:C5	2.49	0.48
25:A:2345:G:N3	25:A:2381:A:H2'	2.28	0.48
26:B:8:C:OP1	38:Q:15:ARG:NH2	2.45	0.48
29:E:118:LEU:HD11	29:E:188:MET:HG3	1.95	0.48
1:a:7:A:H2'	5:e:124:LEU:HD11	1.95	0.48
1:a:1166:G:O2'	1:a:1169:A:N6	2.46	0.48
4:d:87:GLY:HA3	4:d:197:GLU:HB2	1.94	0.48
4:d:95:GLU:OE1	4:d:104:ARG:NH1	2.46	0.48
17:q:60:GLU:OE1	17:q:76:VAL:HB	2.13	0.48
25:A:1007:C:OP1	33:L:39:LYS:HD2	2.13	0.48
25:A:1168:G:H2'	25:A:1169:A:H8	1.78	0.48
25:A:2857:G:N2	25:A:2860:A:OP2	2.30	0.48
30:F:5:HIS:HB2	30:F:97:TRP:CG	2.48	0.48
45:X:77:VAL:HG23	45:X:89:ILE:HG12	1.96	0.48
1:a:6:G:H4'	1:a:298:A:H4'	1.95	0.48
1:a:177:G:OP1	20:t:60:ARG:NH1	2.43	0.48
3:c:77:ILE:HD13	3:c:84:VAL:HG21	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:c:153:VAL:HG23	3:c:198:VAL:HG22	1.96	0.48
6:f:29:ILE:CD1	6:f:64:VAL:HG11	2.43	0.48
12:l:107:VAL:HG21	12:l:117:TYR:HD2	1.79	0.48
25:A:784:G:H5'	25:A:785:G:OP1	2.13	0.48
25:A:1447:C:O2'	25:A:1544:A:N3	2.42	0.48
25:A:2144:G:H1'	25:A:2147:A:N6	2.29	0.48
1:a:111:G:H1	1:a:330:C:H42	1.61	0.48
1:a:559:A:H4'	1:a:560:A:H3'	1.96	0.48
1:a:947:G:H2'	1:a:948:C:C6	2.48	0.48
1:a:1157:A:H5'	1:a:1158:C:C6	2.48	0.48
15:o:47:LYS:O	15:o:53:ARG:NH2	2.47	0.48
16:p:4:ILE:HG12	16:p:21:VAL:HB	1.95	0.48
25:A:1839:G:C2	25:A:1840:G:C8	3.02	0.48
30:F:105:THR:HA	50:3:38:SER:HB3	1.95	0.48
1:a:56:U:H2'	1:a:57:G:C8	2.48	0.48
1:a:235:C:H2'	1:a:236:A:H8	1.79	0.48
1:a:1103:C:H4'	2:b:97:LEU:HD13	1.96	0.48
1:a:1346:A:N1	1:a:1374:A:H5''	2.28	0.48
1:a:1405:G:N7	57:a:3099:AKN:N25	2.61	0.48
5:e:76:LEU:HD22	5:e:120:VAL:HG12	1.96	0.48
13:m:98:ARG:HG3	13:m:100:GLN:HE22	1.79	0.48
14:n:64:CYS:HB2	14:n:79:LEU:HA	1.95	0.48
25:A:373:U:H2'	25:A:374:A:H8	1.78	0.48
25:A:1028:A:H2'	25:A:1029:A:C8	2.49	0.48
25:A:1527:G:N1	25:A:1544:A:OP2	2.34	0.48
25:A:1548:A:H2'	25:A:1549:A:C8	2.49	0.48
25:A:2484:G:OP1	36:O:44:ARG:HD2	2.13	0.48
25:A:2812:G:H2'	25:A:2813:A:C8	2.49	0.48
1:a:236:A:H2'	1:a:237:G:C8	2.49	0.48
1:a:1248:A:H2	9:i:72:ILE:HD11	1.79	0.48
1:a:1387:G:H2'	1:a:1388:C:C6	2.48	0.48
3:c:134:MET:HE3	3:c:153:VAL:HG12	1.94	0.48
16:p:21:VAL:HG12	16:p:34:GLU:O	2.13	0.48
25:A:414:C:H2'	25:A:415:A:C8	2.48	0.48
30:F:134:GLU:HB2	30:F:137:ILE:HG12	1.96	0.48
31:G:38:ASN:HD21	31:G:64:GLN:HG3	1.79	0.48
33:L:49:ASP:CG	33:L:121:LYS:HZ3	2.17	0.48
42:U:27:LYS:HB2	42:U:32:ALA:HB2	1.95	0.48
1:a:59:A:H5'	1:a:387:U:H5''	1.96	0.48
1:a:76:G:N1	1:a:93:U:N3	2.61	0.48
1:a:471:U:H2'	1:a:472:U:C6	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:634:C:H2'	1:a:635:A:C8	2.49	0.48
4:d:57:GLU:HG2	4:d:199:LEU:CD2	2.43	0.48
6:f:35:LYS:O	6:f:64:VAL:HG13	2.14	0.48
12:l:49:LEU:O	12:l:51:LYS:NZ	2.43	0.48
15:o:88:ARG:NH2	25:A:714:U:OP2	2.47	0.48
25:A:419:U:H2'	25:A:420:C:C6	2.49	0.48
25:A:1326:U:H2'	25:A:1327:A:H8	1.78	0.48
40:S:94:ILE:O	40:S:98:ILE:HG12	2.14	0.48
1:a:384:G:H2'	1:a:385:C:H6	1.78	0.48
1:a:1330:U:H2'	1:a:1331:G:O4'	2.13	0.48
25:A:880:G:O6	25:A:898:C:N4	2.47	0.48
25:A:1363:C:O2'	25:A:1809:A:N3	2.36	0.48
25:A:1651:G:H4'	37:P:39:PRO:HG2	1.96	0.48
25:A:2157:G:O2'	25:A:2158:A:O4'	2.21	0.48
25:A:2349:G:O2'	25:A:2350:C:O4'	2.32	0.48
25:A:2747:G:O6	25:A:2755:C:H5''	2.13	0.48
33:L:6:ALA:HB3	33:L:48:VAL:HG11	1.96	0.48
42:U:73:LYS:HB2	42:U:106:VAL:HB	1.96	0.48
1:a:138:G:H2'	1:a:139:A:C8	2.49	0.47
1:a:356:A:N3	1:a:368:U:O2'	2.38	0.47
1:a:950:U:H2'	1:a:951:G:H8	1.79	0.47
1:a:1088:G:H21	1:a:1167:A:N6	2.12	0.47
1:a:1457:G:N3	1:a:1458:G:H1'	2.28	0.47
4:d:62:ARG:HH21	4:d:69:GLU:N	2.12	0.47
4:d:125:VAL:HG11	4:d:135:TYR:HE2	1.79	0.47
25:A:594:U:H2'	25:A:595:C:C6	2.49	0.47
25:A:667:U:H2'	25:A:668:A:O4'	2.14	0.47
25:A:1292:G:H2'	25:A:1293:C:C6	2.49	0.47
25:A:1478:G:H1	25:A:1513:U:H3	1.60	0.47
25:A:1733:G:H2'	25:A:1734:G:H8	1.78	0.47
34:M:68:GLY:HA3	34:M:77:ILE:O	2.14	0.47
36:O:35:ALA:HA	36:O:128:THR:HG22	1.96	0.47
41:T:16:GLU:OE2	41:T:101:ILE:N	2.45	0.47
1:a:929:G:O2'	1:a:930:C:OP1	2.27	0.47
1:a:981:U:OP1	14:n:6:MET:HE1	2.14	0.47
20:t:27:MET:O	20:t:30:THR:HG22	2.14	0.47
22:w:75:C:H2'	22:w:76:A:C8	2.49	0.47
25:A:81:G:H2'	25:A:82:U:O4'	2.14	0.47
25:A:543:G:H2'	25:A:544:C:O4'	2.13	0.47
25:A:2739:U:C2'	25:A:2740:A:H5'	2.44	0.47
1:a:131:A:H2'	1:a:132:C:H6	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:264:C:O2'	17:q:66:PRO:O	2.28	0.47
1:a:322:C:H2'	1:a:323:U:C6	2.50	0.47
1:a:691:G:H1'	1:a:696:A:N6	2.30	0.47
1:a:925:G:C2	1:a:927:G:C8	3.01	0.47
1:a:1002:G:H2'	1:a:1003:G:O4'	2.15	0.47
22:w:15:G:H22	22:w:48:C:N4	2.12	0.47
25:A:1417:C:HO2'	25:A:1587:G:HO2'	1.48	0.47
26:B:42:C:O2'	26:B:43:C:OP1	2.32	0.47
27:C:21:ASN:HB3	27:C:24:LEU:HG	1.95	0.47
28:D:25:THR:HG21	28:D:193:VAL:HG22	1.96	0.47
31:G:17:VAL:O	31:G:17:VAL:HG12	2.14	0.47
36:O:30:SER:HA	36:O:133:LYS:HG3	1.94	0.47
41:T:21:ARG:HG3	41:T:93:PHE:HB2	1.97	0.47
43:V:38:ALA:O	43:V:81:LYS:NZ	2.42	0.47
1:a:376:G:H5''	16:p:5:ARG:HB2	1.96	0.47
1:a:1040:U:H2'	1:a:1041:G:C8	2.49	0.47
15:o:58:ARG:NH1	15:o:62:GLN:OE1	2.47	0.47
19:s:36:ARG:HB3	19:s:72:GLY:HA3	1.95	0.47
20:t:31:PHE:O	20:t:35:VAL:HG23	2.14	0.47
25:A:52:A:H2'	25:A:53:A:C8	2.49	0.47
25:A:414:C:H2'	25:A:415:A:H8	1.79	0.47
25:A:1365:A:O5'	47:Z:28:ARG:NH2	2.47	0.47
25:A:1654:A:O2'	28:D:118:PHE:O	2.27	0.47
25:A:2014:A:H2'	25:A:2015:A:C8	2.49	0.47
25:A:2107:G:C6	25:A:2108:A:N1	2.83	0.47
25:A:2191:A:O2'	25:A:2192:U:OP1	2.31	0.47
25:A:2305:U:H5''	30:F:131:GLY:HA3	1.96	0.47
25:A:2783:U:H2'	25:A:2784:U:C6	2.49	0.47
25:A:2804:U:H2'	25:A:2805:C:H6	1.79	0.47
31:G:8:PRO:HB3	31:G:51:THR:HG22	1.94	0.47
38:Q:62:LEU:HD22	38:Q:70:ALA:HA	1.97	0.47
45:X:38:LEU:HD21	45:X:65:VAL:HG11	1.96	0.47
1:a:362:G:N2	1:a:365:U:OP2	2.47	0.47
1:a:692:U:O2'	1:a:694:A:N7	2.39	0.47
1:a:1074:G:O2'	1:a:1101:A:N1	2.43	0.47
9:i:46:MET:O	9:i:50:GLN:HB3	2.14	0.47
10:j:67:ILE:HG13	14:n:96:LEU:HD13	1.96	0.47
25:A:1263:U:O2'	51:4:8:PRO:HD2	2.15	0.47
25:A:1563:U:H2'	25:A:1564:C:C6	2.49	0.47
25:A:1653:G:H3'	37:P:2:ARG:HG3	1.96	0.47
1:a:269:C:H2'	1:a:270:A:C8	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:455:G:H2'	1:a:456:A:C8	2.48	0.47
5:e:148:ASN:HA	5:e:152:MET:HE3	1.97	0.47
12:l:25:GLU:OE1	12:l:59:ASN:ND2	2.37	0.47
22:w:64:A:H2'	22:w:65:G:C8	2.48	0.47
25:A:27:G:N2	25:A:512:G:H1'	2.29	0.47
25:A:78:U:H2'	25:A:79:C:C6	2.50	0.47
25:A:1410:G:H2'	25:A:1411:U:C6	2.49	0.47
25:A:1545:A:H2'	25:A:1546:G:O4'	2.14	0.47
29:E:126:VAL:HG11	29:E:134:LEU:HB3	1.96	0.47
1:a:41:G:H2'	1:a:42:G:H8	1.80	0.47
1:a:246:A:C2	1:a:282:A:C5	3.02	0.47
1:a:505:G:H2'	1:a:506:G:C8	2.50	0.47
1:a:737:C:H2'	1:a:738:C:H6	1.79	0.47
1:a:1326:U:H2'	1:a:1327:C:C6	2.50	0.47
6:f:5:GLU:OE2	18:r:23:TYR:OH	2.25	0.47
6:f:29:ILE:HD11	6:f:66:ALA:HB2	1.96	0.47
17:q:8:LEU:O	17:q:60:GLU:HG2	2.15	0.47
21:u:4:ILE:HD11	21:u:19:PHE:HB2	1.97	0.47
22:w:34:G:H2'	22:w:35:A:C8	2.50	0.47
22:w:51:U:H2'	22:w:52:G:H8	1.80	0.47
25:A:126:A:OP1	53:6:45:SER:OG	2.33	0.47
25:A:582:A:H2'	25:A:583:G:H8	1.80	0.47
25:A:922:C:O2'	46:Y:29:GLU:OE2	2.33	0.47
25:A:1645:G:H5''	25:A:1646:C:H5'	1.95	0.47
25:A:2031:A:C6	25:A:2498:OMC:H1'	2.50	0.47
25:A:2705:A:O2'	25:A:2852:G:OP1	2.26	0.47
26:B:61:G:H2'	26:B:62:C:C6	2.50	0.47
31:G:30:ASN:HB3	31:G:79:VAL:O	2.14	0.47
31:G:88:GLN:O	31:G:162:VAL:HA	2.15	0.47
37:P:32:GLU:OE2	37:P:86:ARG:NH2	2.26	0.47
46:Y:50:ASN:HB2	46:Y:82:ILE:HB	1.96	0.47
1:a:35:G:H2'	1:a:36:C:C6	2.49	0.47
1:a:600:A:H2'	1:a:601:G:C8	2.49	0.47
1:a:1273:C:H2'	1:a:1274:A:O4'	2.14	0.47
4:d:23:SER:O	4:d:161:LEU:HD21	2.15	0.47
4:d:174:ASP:O	4:d:178:MET:CA	2.62	0.47
13:m:27:LYS:O	13:m:31:LYS:HG2	2.15	0.47
22:w:63:G:O2'	25:A:2482:A:H4'	2.15	0.47
25:A:964:C:O2'	25:A:2273:A:N3	2.41	0.47
25:A:1182:G:H2'	25:A:1183:U:O4'	2.15	0.47
25:A:1198:U:H2'	25:A:1199:U:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:1441:G:H2'	25:A:1442:U:C6	2.49	0.47
25:A:2532:G:O2'	25:A:2657:A:N1	2.44	0.47
25:A:2836:U:H2'	25:A:2837:A:C8	2.50	0.47
30:F:113:ASP:OD1	30:F:113:ASP:N	2.47	0.47
43:V:30:ILE:HG21	43:V:93:LEU:HD21	1.97	0.47
1:a:68:G:H22	1:a:101:A:H2	1.63	0.47
1:a:73:C:H2'	1:a:74:A:C8	2.50	0.47
1:a:1125:U:O2'	1:a:1126:U:O5'	2.29	0.47
1:a:1130:A:C8	1:a:1146:A:C2	3.03	0.47
1:a:1321:U:O2'	19:s:78:ARG:NH1	2.47	0.47
3:c:150:LYS:HG3	3:c:169:ARG:HB2	1.96	0.47
15:o:12:VAL:HG11	15:o:22:THR:HG22	1.96	0.47
19:s:50:ALA:HB1	19:s:57:HIS:HB3	1.97	0.47
19:s:55:ARG:HH21	19:s:79:THR:HG21	1.79	0.47
25:A:251:A:OP1	35:N:58:TYR:OH	2.31	0.47
25:A:1046:A:H5''	25:A:1047:G:H5''	1.95	0.47
25:A:1715:G:O2'	25:A:1743:G:O6	2.30	0.47
25:A:2081:U:H2'	25:A:2082:A:H8	1.79	0.47
26:B:66:A:H61	26:B:107:G:H2'	1.80	0.47
28:D:152:PRO:HG3	28:D:156:PHE:CZ	2.50	0.47
31:G:47:ASP:N	31:G:47:ASP:OD1	2.46	0.47
16:p:75:ILE:HA	16:p:78:VAL:HG12	1.95	0.47
25:A:659:G:O2'	29:E:95:LYS:O	2.31	0.47
25:A:858:G:N3	25:A:2268:A:H2'	2.30	0.47
25:A:1225:G:H2'	25:A:1226:A:C8	2.49	0.47
1:a:1410:A:H2'	1:a:1411:C:C6	2.51	0.46
1:a:1513:A:H2'	1:a:1514:G:H8	1.81	0.46
2:b:151:ILE:HA	2:b:154:MET:HB2	1.97	0.46
3:c:19:ASN:C	3:c:56:VAL:HG23	2.40	0.46
5:e:107:ALA:HB2	5:e:125:ALA:HB3	1.97	0.46
8:h:3:MET:HE1	8:h:9:ASP:OD2	2.15	0.46
16:p:4:ILE:HB	16:p:67:ILE:HD13	1.98	0.46
25:A:117:G:OP2	25:A:119:A:O2'	2.27	0.46
25:A:1275:A:N1	25:A:1295:C:O2'	2.45	0.46
25:A:1567:G:OP2	27:C:83:TYR:OH	2.30	0.46
28:D:101:PHE:HD1	28:D:104:VAL:HG11	1.80	0.46
30:F:110:ARG:NH1	30:F:139:PRO:HB3	2.29	0.46
31:G:17:VAL:O	31:G:19:ILE:HG13	2.15	0.46
1:a:460:A:H2'	1:a:461:A:H8	1.79	0.46
1:a:555:U:H2'	1:a:556:C:H6	1.77	0.46
1:a:635:A:H2'	1:a:636:U:H6	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1118:U:H2'	1:a:1119:C:H6	1.80	0.46
1:a:1330:U:H4'	13:m:23:TYR:CE2	2.50	0.46
5:e:41:ASP:HB2	5:e:45:ARG:HB3	1.96	0.46
25:A:538:A:H4'	33:L:7:LYS:HG2	1.97	0.46
25:A:1443:U:H2'	25:A:1444:G:C8	2.50	0.46
25:A:2233:U:H2'	25:A:2234:G:C8	2.49	0.46
25:A:2292:U:H2'	25:A:2293:G:H8	1.81	0.46
27:C:78:VAL:HG21	27:C:110:LEU:HD11	1.96	0.46
28:D:38:LYS:HE3	28:D:81:GLU:OE2	2.15	0.46
30:F:116:GLY:HA3	30:F:178:ARG:HB2	1.97	0.46
38:Q:53:THR:HB	38:Q:65:THR:HB	1.96	0.46
1:a:981:U:O2'	14:n:61:ARG:NH1	2.48	0.46
25:A:1709:U:H2'	25:A:1710:G:H8	1.80	0.46
25:A:2111:U:H5	25:A:2145:C:C2	2.34	0.46
25:A:2484:G:O2'	36:O:123:LYS:O	2.30	0.46
25:A:2845:U:H5''	39:R:52:ASN:O	2.15	0.46
42:U:20:VAL:HG11	42:U:44:ALA:HA	1.98	0.46
1:a:652:U:O4	1:a:752:G:O2'	2.27	0.46
1:a:1139:G:H4'	1:a:1140:C:H5'	1.97	0.46
1:a:1158:C:C4	1:a:1160:G:C8	3.04	0.46
11:k:82:LEU:HD21	11:k:100:LEU:HD13	1.98	0.46
25:A:111:A:O2'	48:1:58:ASN:ND2	2.46	0.46
25:A:598:U:H2'	25:A:599:A:C8	2.50	0.46
25:A:631:A:N3	25:A:2415:G:O2'	2.46	0.46
27:C:24:LEU:HD13	27:C:83:TYR:HB2	1.97	0.46
51:4:38:HIS:ND1	51:4:39:LEU:O	2.47	0.46
1:a:745:G:O2'	1:a:746:A:H5'	2.15	0.46
1:a:939:G:N3	1:a:1375:A:H2	2.14	0.46
6:f:32:ALA:O	6:f:33:GLU:HG3	2.15	0.46
23:x:24:U:O2'	25:A:1923:U:OP1	2.33	0.46
25:A:499:U:H2'	25:A:500:G:O4'	2.15	0.46
25:A:581:C:H2'	25:A:582:A:H8	1.79	0.46
25:A:1590:A:H2'	25:A:1591:A:H8	1.80	0.46
28:D:55:LYS:HD3	28:D:60:VAL:HG12	1.97	0.46
37:P:28:LEU:HD23	37:P:48:VAL:HG11	1.97	0.46
45:X:10:LYS:HD2	45:X:10:LYS:HA	1.74	0.46
48:1:9:LYS:HD2	48:1:14:LEU:HB3	1.98	0.46
1:a:552:U:H2'	1:a:553:A:H8	1.80	0.46
1:a:563:A:H2'	1:a:567:G:C8	2.51	0.46
4:d:140:ASN:N	4:d:182:PHE:O	2.48	0.46
5:e:80:THR:HG23	5:e:122:ASN:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:x:66:C:H2'	23:x:67:C:C6	2.51	0.46
25:A:64:A:H2'	25:A:65:U:H6	1.80	0.46
25:A:634:C:H2'	25:A:635:C:C6	2.50	0.46
25:A:920:A:OP1	49:2:19:LYS:NZ	2.47	0.46
25:A:1418:G:N2	25:A:1579:A:N7	2.64	0.46
25:A:2515:C:H2'	25:A:2516:A:H8	1.80	0.46
26:B:2:G:H2'	26:B:3:C:H6	1.80	0.46
28:D:178:VAL:HB	28:D:188:LEU:HD12	1.98	0.46
29:E:134:LEU:HD21	29:E:161:ALA:HB2	1.98	0.46
1:a:270:A:H2'	1:a:271:C:C6	2.51	0.46
1:a:649:A:H2'	1:a:650:G:O4'	2.16	0.46
1:a:1009:U:O2	1:a:1020:G:N2	2.31	0.46
25:A:793:A:OP2	25:A:2071:A:O2'	2.30	0.46
25:A:2247:A:H2'	25:A:2248:C:H6	1.81	0.46
36:O:63:ILE:HD13	36:O:105:MET:HG2	1.98	0.46
52:5:38:LYS:HB2	52:5:49:TYR:CD2	2.51	0.46
1:a:77:A:H2'	1:a:78:A:C8	2.51	0.46
1:a:539:A:H2'	1:a:540:G:H8	1.79	0.46
1:a:966:2MG:HM23	1:a:967:5MC:H1'	1.97	0.46
1:a:1477:U:H2'	1:a:1478:U:C6	2.50	0.46
2:b:114:LEU:HB2	2:b:144:LEU:CD2	2.45	0.46
3:c:6:HIS:CE1	3:c:8:ASN:HB3	2.51	0.46
11:k:29:ASN:OD1	11:k:30:THR:N	2.49	0.46
25:A:544:C:H4'	25:A:545:U:C5	2.51	0.46
25:A:1168:G:H2'	25:A:1169:A:C8	2.50	0.46
26:B:42:C:C6	30:F:66:LEU:HB2	2.51	0.46
36:O:42:THR:HG22	36:O:93:VAL:HG12	1.97	0.46
45:X:80:HIS:ND1	45:X:83:LYS:HB2	2.30	0.46
1:a:728:A:H2'	1:a:729:A:C8	2.50	0.46
1:a:744:C:H2'	1:a:745:G:C8	2.50	0.46
25:A:438:G:H2'	25:A:439:A:H8	1.80	0.46
25:A:2285:C:OP2	52:5:6:ARG:NH1	2.40	0.46
25:A:2494:G:O2'	36:O:79:ALA:HA	2.16	0.46
25:A:2579:C:O2'	28:D:136:ASN:OD1	2.34	0.46
1:a:21:G:H2'	1:a:22:G:C8	2.51	0.46
1:a:134:G:H2'	1:a:135:C:O4'	2.17	0.46
22:w:27:G:H2'	22:w:28:G:H8	1.81	0.46
25:A:532:A:H4'	25:A:533:G:C8	2.50	0.46
25:A:729:G:C6	27:C:207:LYS:HB2	2.51	0.46
25:A:807:U:OP2	35:N:41:ARG:NH2	2.48	0.46
25:A:1668:A:O2'	25:A:1674:G:N7	2.36	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:2112:G:H5'	25:A:2113:U:H5	1.80	0.46
25:A:2834:G:H2'	25:A:2879:A:H61	1.81	0.46
1:a:257:G:H2'	1:a:258:G:H8	1.81	0.45
1:a:1181:G:H1'	1:a:1182:G:C4	2.52	0.45
1:a:1193:G:O6	3:c:2:GLY:N	2.49	0.45
1:a:1302:C:C5	13:m:17:ILE:HG13	2.51	0.45
11:k:23:ILE:HG12	11:k:32:VAL:HG23	1.98	0.45
11:k:89:PRO:HG3	21:u:32:VAL:HG11	1.97	0.45
15:o:45:GLU:HG3	15:o:46:HIS:ND1	2.26	0.45
19:s:15:LEU:HD12	19:s:18:LYS:HD2	1.99	0.45
25:A:1667:G:O2'	25:A:1991:U:O4	2.28	0.45
31:G:95:ARG:HH21	31:G:128:GLN:NE2	2.13	0.45
51:4:46:ASP:N	51:4:46:ASP:OD1	2.49	0.45
1:a:334:C:H2'	1:a:335:C:H6	1.82	0.45
1:a:1352:C:H2'	1:a:1353:G:C8	2.51	0.45
18:r:50:LYS:HA	18:r:53:ARG:HD3	1.98	0.45
22:y:43:C:H2'	22:y:44:G:C8	2.51	0.45
25:A:354:A:H2'	25:A:355:U:O4'	2.16	0.45
25:A:2143:C:H2'	25:A:2144:G:H8	1.81	0.45
25:A:2273:A:H2'	25:A:2274:A:C8	2.51	0.45
25:A:2290:G:H2'	25:A:2291:U:C6	2.51	0.45
25:A:2314:A:H2'	25:A:2315:G:H8	1.81	0.45
25:A:2680:U:O2'	25:A:2681:C:H5'	2.16	0.45
30:F:8:TYR:HB2	30:F:173:PHE:HZ	1.81	0.45
35:N:64:PHE:HB3	54:7:25:LYS:HD2	1.99	0.45
1:a:82:G:H2'	1:a:83:C:C6	2.51	0.45
1:a:154:U:H2'	1:a:155:A:H8	1.80	0.45
1:a:476:U:H2'	1:a:477:C:C6	2.52	0.45
1:a:500:G:H2'	1:a:501:C:C6	2.51	0.45
1:a:592:G:H2'	1:a:593:U:C6	2.51	0.45
1:a:1249:C:O2'	9:i:75:GLN:NE2	2.50	0.45
15:o:33:THR:HA	15:o:36:ILE:HG22	1.98	0.45
25:A:353:C:H2'	25:A:354:A:C8	2.52	0.45
25:A:1219:U:H2'	25:A:1220:G:C8	2.52	0.45
25:A:1531:C:H2'	25:A:1532:A:C8	2.51	0.45
25:A:1842:G:H2'	25:A:1843:C:C6	2.52	0.45
25:A:2230:G:H2'	25:A:2231:U:C6	2.51	0.45
25:A:2567:G:H2'	25:A:2568:U:C6	2.52	0.45
25:A:2728:U:O2'	25:A:2729:G:H8	1.99	0.45
29:E:181:ILE:HG23	35:N:1:MET:HG2	1.97	0.45
1:a:680:C:H5'	1:a:681:A:OP2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1401:G:H2'	1:a:1402:4OC:O4'	2.17	0.45
17:q:12:VAL:HG22	17:q:21:ILE:HD12	1.98	0.45
21:u:40:LYS:HG2	21:u:42:THR:HG22	1.99	0.45
25:A:832:U:H2'	25:A:833:A:H8	1.81	0.45
25:A:1341:G:OP2	25:A:1394:U:O2'	2.28	0.45
25:A:1484:U:H2'	25:A:1485:U:C6	2.51	0.45
25:A:2245:U:H5''	25:A:2246:G:H5'	1.97	0.45
25:A:2847:U:H2'	25:A:2848:G:O4'	2.16	0.45
38:Q:79:ALA:HB3	38:Q:113:ALA:HB3	1.97	0.45
44:W:86:ARG:HH12	44:W:100:SER:HG	1.57	0.45
45:X:63:ILE:HG22	45:X:65:VAL:HG23	1.97	0.45
47:Z:7:VAL:HG21	47:Z:59:ILE:HD11	1.99	0.45
52:5:17:THR:HG21	52:5:43:VAL:HG13	1.97	0.45
1:a:524:G:H2'	1:a:525:C:C6	2.50	0.45
1:a:558:G:OP2	1:a:559:A:O2'	2.33	0.45
1:a:1250:A:N3	1:a:1370:G:O2'	2.40	0.45
4:d:49:SER:O	4:d:53:VAL:HG23	2.16	0.45
4:d:118:VAL:HG22	4:d:123:ILE:HG13	1.97	0.45
6:f:64:VAL:HG12	6:f:66:ALA:N	2.31	0.45
16:p:5:ARG:HG2	16:p:5:ARG:HH11	1.80	0.45
25:A:30:G:H2'	25:A:31:C:C6	2.51	0.45
25:A:587:C:C2	35:N:19:LEU:HD23	2.52	0.45
25:A:829:A:N7	25:A:2247:A:O2'	2.47	0.45
25:A:2052:A:H4'	28:D:148:GLN:O	2.16	0.45
25:A:2108:A:H2'	25:A:2109:U:C6	2.51	0.45
25:A:2339:C:O3'	26:B:41:G:N2	2.50	0.45
25:A:2479:U:O3'	25:A:2537:U:H5''	2.17	0.45
25:A:2740:A:H2'	25:A:2741:A:C8	2.52	0.45
28:D:149:ASN:OD1	28:D:150:MEQ:N	2.50	0.45
46:Y:38:VAL:HG22	46:Y:59:LEU:HB2	1.98	0.45
1:a:356:A:H2'	1:a:357:G:O4'	2.17	0.45
1:a:1506:U:O2'	1:a:1507:A:H5'	2.17	0.45
2:b:15:HIS:HB3	2:b:43:LEU:HD11	1.99	0.45
9:i:47:VAL:HG13	9:i:80:ARG:HD3	1.98	0.45
9:i:114:LYS:NZ	9:i:118:LEU:O	2.48	0.45
12:l:54:ARG:NH2	12:l:62:GLU:OE1	2.46	0.45
25:A:851:C:H2'	25:A:852:U:C6	2.51	0.45
25:A:1928:A:H2'	25:A:1929:G:O4'	2.16	0.45
25:A:2700:A:H2'	25:A:2701:U:C6	2.52	0.45
27:C:107:PRO:HB3	27:C:142:HIS:CE1	2.51	0.45
30:F:69:LYS:HG2	30:F:84:PRO:HA	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:G:105:LEU:HB2	31:G:113:VAL:HB	1.97	0.45
37:P:54:LEU:HD11	37:P:65:LEU:HD23	1.97	0.45
1:a:8:A:C6	4:d:206:LYS:HB2	2.51	0.45
1:a:312:C:H2'	1:a:313:A:C8	2.52	0.45
1:a:689:C:H5'	11:k:31:ILE:HD11	1.98	0.45
15:o:7:ALA:O	15:o:11:ILE:HG12	2.17	0.45
23:x:47:U:H5'	23:x:48:C:H5'	1.98	0.45
25:A:57:C:H2'	25:A:58:G:O4'	2.16	0.45
25:A:671:C:H2'	25:A:672:C:C6	2.51	0.45
25:A:813:U:O2'	25:A:1225:G:H1'	2.16	0.45
25:A:936:A:H2'	25:A:937:C:C6	2.52	0.45
25:A:1111:A:N3	25:A:1112:G:H1'	2.32	0.45
25:A:1239:G:H2'	25:A:1240:U:O4'	2.17	0.45
25:A:1319:C:O2'	25:A:1320:C:H5'	2.17	0.45
25:A:1790:C:H2'	25:A:1791:A:C5	2.51	0.45
25:A:1902:C:H4'	27:C:242:LYS:O	2.16	0.45
26:B:2:G:H2'	26:B:3:C:C6	2.52	0.45
26:B:5:U:H2'	26:B:6:G:H8	1.81	0.45
42:U:29:VAL:HB	42:U:55:ILE:HD11	1.97	0.45
1:a:408:A:O3'	4:d:23:SER:OG	2.31	0.45
1:a:455:G:H2'	1:a:456:A:H8	1.82	0.45
3:c:7:PRO:HG3	3:c:201:TRP:HE1	1.82	0.45
4:d:141:ASP:OD1	4:d:142:VAL:N	2.50	0.45
9:i:27:LYS:N	9:i:62:ASP:OD1	2.40	0.45
9:i:48:VAL:HG13	9:i:79:ILE:HG21	1.98	0.45
22:y:19:G:OP1	22:y:60:U:N3	2.48	0.45
22:y:51:U:H3	22:y:63:G:H1	1.64	0.45
30:F:170:LEU:O	30:F:175:PHE:HB2	2.17	0.45
35:N:90:VAL:HG13	35:N:95:LEU:HD13	1.98	0.45
44:W:4:LYS:HE3	44:W:83:VAL:O	2.17	0.45
1:a:36:C:OP1	12:l:120:LYS:HE2	2.17	0.45
1:a:335:C:H2'	1:a:336:A:C8	2.48	0.45
1:a:393:A:OP2	16:p:12:LYS:NZ	2.49	0.45
1:a:1122:U:H2'	1:a:1123:U:C6	2.52	0.45
1:a:1387:G:O2'	1:a:1388:C:OP1	2.30	0.45
25:A:1989:G:H2'	25:A:1990:C:O4'	2.17	0.45
25:A:2538:C:O2'	25:A:2539:C:OP1	2.33	0.45
28:D:39:ASP:N	28:D:39:ASP:OD1	2.49	0.45
31:G:49:THR:O	31:G:51:THR:HG23	2.16	0.45
1:a:76:G:N1	1:a:93:U:C2	2.85	0.45
1:a:1062:U:H2'	1:a:1063:C:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1437:A:H5'	20:t:29:ARG:NH1	2.31	0.45
6:f:72:ASP:O	6:f:75:GLU:HG3	2.17	0.45
25:A:698:C:O2'	25:A:734:A:N6	2.48	0.45
25:A:1880:U:H2'	25:A:1881:C:C6	2.51	0.45
25:A:2386:A:H4'	46:Y:56:ASP:HA	1.97	0.45
25:A:2389:G:H5''	25:A:2390:U:O4'	2.16	0.45
25:A:2637:U:H2'	25:A:2638:G:O4'	2.16	0.45
26:B:78:A:H2'	26:B:79:G:O4'	2.17	0.45
33:L:1:MET:HE3	33:L:2:LYS:H	1.82	0.45
36:O:75:GLU:HB2	36:O:90:GLU:HG3	1.99	0.45
1:a:350:G:H2'	1:a:351:G:C8	2.52	0.44
1:a:376:G:H5''	16:p:5:ARG:HD2	1.99	0.44
1:a:1261:A:N6	1:a:1274:A:O2'	2.50	0.44
6:f:18:VAL:HG11	6:f:58:HIS:CD2	2.53	0.44
9:i:50:GLN:HG2	9:i:51:PRO:HD3	1.99	0.44
25:A:576:U:H2'	25:A:577:G:C8	2.52	0.44
25:A:1188:U:H4'	41:T:81:LYS:O	2.17	0.44
25:A:2039:U:H2'	25:A:2040:G:C8	2.52	0.44
30:F:13:VAL:HG23	30:F:28:VAL:HG11	2.00	0.44
31:G:103:ILE:HG22	31:G:105:LEU:HD22	1.99	0.44
36:O:57:VAL:HG12	36:O:112:LEU:HG	1.98	0.44
1:a:918:A:H2'	1:a:919:A:C8	2.52	0.44
22:y:58:A:O2'	22:y:59:U:OP1	2.35	0.44
25:A:682:G:H5'	53:6:26:ASN:CG	2.41	0.44
25:A:1037:G:HO2'	25:A:1038:G:P	2.39	0.44
25:A:1486:U:H2'	25:A:1487:U:H6	1.81	0.44
25:A:2313:C:H5''	30:F:88:LYS:HD3	1.99	0.44
33:L:44:TYR:HA	33:L:50:THR:HG21	1.99	0.44
1:a:193:C:H2'	1:a:194:C:C6	2.52	0.44
1:a:505:G:H2'	1:a:506:G:H8	1.80	0.44
1:a:1018:G:H2'	1:a:1019:A:C8	2.53	0.44
2:b:56:GLU:HA	2:b:59:LYS:HG2	1.99	0.44
11:k:57:LYS:HB3	11:k:57:LYS:HE3	1.57	0.44
14:n:9:ARG:HB3	14:n:13:ARG:NH1	2.33	0.44
23:x:63:G:H5'	46:Y:11:ARG:HH12	1.83	0.44
22:y:20:U:H2'	22:y:20:U:OP2	2.18	0.44
25:A:372:G:O2'	25:A:400:G:O6	2.31	0.44
25:A:544:C:O3'	25:A:545:U:H2'	2.17	0.44
25:A:593:U:H2'	25:A:594:U:H6	1.82	0.44
25:A:828:U:H4'	25:A:831:G:N1	2.32	0.44
25:A:863:A:H2'	25:A:864:G:H8	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:1036:G:C6	25:A:1120:G:C6	3.05	0.44
25:A:1178:C:H2'	25:A:1179:G:H8	1.82	0.44
25:A:1775:U:O4	25:A:1789:A:H2	2.00	0.44
25:A:2241:A:H2'	25:A:2242:G:C8	2.52	0.44
25:A:2820:A:N3	25:A:2820:A:H2'	2.32	0.44
1:a:126:G:OP1	1:a:605:U:O2'	2.28	0.44
2:b:83:ALA:O	2:b:87:CYS:CB	2.65	0.44
11:k:117:PRO:HG2	21:u:35:ARG:HD3	2.00	0.44
13:m:87:ARG:HG3	13:m:97:VAL:HB	1.98	0.44
15:o:63:ARG:O	15:o:67:LEU:HD23	2.17	0.44
17:q:60:GLU:OE1	17:q:77:ARG:NH1	2.50	0.44
22:w:58:A:O2'	22:w:60:U:OP2	2.31	0.44
25:A:544:C:H4'	25:A:545:U:C4	2.52	0.44
25:A:710:U:H2'	25:A:711:G:O4'	2.17	0.44
25:A:1003:G:O2'	25:A:1010:A:N1	2.47	0.44
25:A:1484:U:H2'	25:A:1485:U:H6	1.83	0.44
25:A:1703:G:H2'	25:A:1704:C:C6	2.52	0.44
25:A:1880:U:H2'	25:A:1881:C:H6	1.83	0.44
25:A:2116:G:O6	25:A:2165:C:N4	2.31	0.44
25:A:2676:C:P	34:M:31:ARG:HH22	2.40	0.44
25:A:2836:U:H2'	25:A:2837:A:H8	1.83	0.44
51:4:31:ASP:OD2	51:4:44:THR:HG21	2.17	0.44
1:a:89:U:H2'	1:a:90:C:C6	2.53	0.44
1:a:244:U:O4	1:a:906:A:H1'	2.18	0.44
1:a:996:A:H2'	1:a:997:U:C6	2.53	0.44
1:a:1458:G:H2'	1:a:1458:G:N3	2.32	0.44
11:k:87:LYS:HG3	11:k:114:THR:HA	1.98	0.44
22:w:37:MIA:H2'	22:w:38:A:O4'	2.18	0.44
25:A:471:A:H2'	25:A:472:A:O4'	2.18	0.44
25:A:1114:C:H2'	25:A:1115:G:C8	2.52	0.44
25:A:2489:U:H2'	25:A:2490:G:O4'	2.17	0.44
25:A:2700:A:H2'	25:A:2701:U:H6	1.82	0.44
1:a:399:G:H2'	1:a:400:C:C6	2.53	0.44
1:a:475:C:H2'	1:a:476:U:C6	2.53	0.44
1:a:514:C:H2'	1:a:515:G:H8	1.83	0.44
1:a:1121:U:C2	1:a:1122:U:C5	3.06	0.44
6:f:22:ILE:O	6:f:26:THR:HG23	2.17	0.44
6:f:57:ALA:HB3	6:f:59:TYR:CE1	2.53	0.44
7:g:68:ASN:HD22	7:g:130:ASN:CG	2.24	0.44
25:A:40:U:H2'	25:A:41:C:C6	2.53	0.44
25:A:1442:U:H2'	25:A:1443:U:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:2380:C:O2'	25:A:2381:A:H8	1.98	0.44
26:B:5:U:OP1	26:B:61:G:O2'	2.25	0.44
27:C:67:PHE:HB3	27:C:152:GLY:H	1.81	0.44
31:G:140:VAL:O	31:G:144:VAL:HG23	2.18	0.44
33:L:69:ARG:HD3	33:L:89:PHE:HD2	1.81	0.44
1:a:590:U:OP1	8:h:31:LYS:HG2	2.17	0.44
1:a:591:U:OP1	8:h:31:LYS:NZ	2.51	0.44
1:a:618:C:H5'	1:a:619:U:H5''	1.98	0.44
1:a:687:A:C8	1:a:701:U:C4	3.06	0.44
1:a:1070:U:H2'	1:a:1071:C:C6	2.52	0.44
3:c:55:ILE:HG23	3:c:68:ILE:HG22	2.00	0.44
4:d:125:VAL:HG11	4:d:135:TYR:CE2	2.52	0.44
22:y:31:A:H2'	22:y:32:PSU:H6	1.83	0.44
25:A:154:U:H2'	25:A:155:A:H8	1.83	0.44
25:A:360:U:H2'	25:A:361:G:O4'	2.17	0.44
25:A:2092:U:OP1	25:A:2199:A:O2'	2.27	0.44
25:A:2271:G:OP1	46:Y:18:ALA:HB1	2.18	0.44
25:A:2364:C:H2'	25:A:2365:G:O4'	2.17	0.44
25:A:2467:C:H2'	25:A:2468:A:O4'	2.18	0.44
25:A:2577:A:H2'	25:A:2614:A:N6	2.33	0.44
25:A:2639:A:H2'	25:A:2640:G:O4'	2.17	0.44
25:A:2774:C:H2'	25:A:2775:G:O4'	2.18	0.44
30:F:106:ILE:HG23	50:3:34:LEU:HD22	1.99	0.44
34:M:1:MET:HA	34:M:32:TYR:HB3	2.00	0.44
36:O:50:ARG:HD3	36:O:65:ILE:HD11	1.99	0.44
45:X:83:LYS:HD3	45:X:85:LYS:HE2	2.00	0.44
1:a:312:C:H2'	1:a:313:A:H8	1.83	0.44
1:a:456:A:H2'	1:a:457:G:C8	2.53	0.44
1:a:1071:C:OP1	5:e:54:ARG:NH2	2.50	0.44
1:a:1118:U:H2'	1:a:1119:C:C6	2.52	0.44
3:c:43:LEU:O	3:c:47:LEU:HB2	2.18	0.44
4:d:57:GLU:OE1	4:d:200:ILE:HG12	2.17	0.44
16:p:18:GLN:OE1	16:p:35:ARG:NE	2.29	0.44
25:A:363:G:H2'	25:A:364:C:C6	2.53	0.44
25:A:1149:G:H2'	25:A:1150:C:C6	2.52	0.44
25:A:1179:G:H2'	25:A:1180:U:C6	2.52	0.44
25:A:1438:U:H2'	25:A:1439:A:H8	1.83	0.44
25:A:1754:A:O3'	39:R:103:ARG:NH2	2.50	0.44
25:A:2155:U:H2'	25:A:2156:G:O4'	2.18	0.44
25:A:2547:A:H2'	25:A:2548:U:H6	1.81	0.44
25:A:2783:U:H2'	25:A:2784:U:H6	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:27:ARG:NH2	47:Z:60:ASP:OD2	2.47	0.44
1:a:280:C:N3	17:q:41:THR:HG23	2.32	0.44
1:a:470:C:H2'	1:a:471:U:C6	2.53	0.44
1:a:697:U:H2'	1:a:698:G:H5'	2.00	0.44
1:a:1147:C:H4'	9:i:7:TYR:CZ	2.53	0.44
4:d:174:ASP:O	4:d:178:MET:N	2.50	0.44
25:A:244:A:OP2	54:7:8:ARG:NH2	2.39	0.44
49:2:10:THR:OG1	49:2:54:MET:O	2.34	0.44
1:a:197:A:N1	1:a:220:G:O2'	2.44	0.43
1:a:859:G:H2'	1:a:860:A:H8	1.82	0.43
1:a:1023:U:C2	1:a:1024:G:C8	3.06	0.43
1:a:1486:G:H2'	1:a:1487:G:O4'	2.18	0.43
1:a:1512:U:H2'	1:a:1513:A:C8	2.53	0.43
8:h:10:MET:O	8:h:14:ILE:HG13	2.17	0.43
11:k:98:ARG:HH22	21:u:16:LEU:HD11	1.82	0.43
25:A:493:G:H2'	25:A:494:G:O4'	2.18	0.43
25:A:570:G:H2'	25:A:2030:6MZ:N7	2.33	0.43
25:A:671:C:H2'	25:A:672:C:H6	1.83	0.43
25:A:1278:C:H2'	25:A:1279:G:H8	1.82	0.43
25:A:1394:U:H2'	25:A:1395:A:O4'	2.17	0.43
25:A:2266:A:H4'	25:A:2267:A:N3	2.33	0.43
25:A:2455:G:H2'	25:A:2456:C:C6	2.53	0.43
29:E:133:LEU:HD23	29:E:133:LEU:HA	1.85	0.43
44:W:5:ILE:HD11	44:W:67:VAL:HG23	1.99	0.43
1:a:855:U:OP2	1:a:871:U:N3	2.44	0.43
1:a:1077:G:N2	1:a:1080:A:OP2	2.45	0.43
1:a:1121:U:H2'	1:a:1122:U:C6	2.54	0.43
9:i:21:ILE:HD12	9:i:61:LEU:HD21	1.99	0.43
19:s:55:ARG:NH2	19:s:79:THR:HG21	2.33	0.43
25:A:150:U:H2'	25:A:151:C:C6	2.53	0.43
25:A:592:A:C2	54:7:4:ILE:HD11	2.53	0.43
25:A:1360:G:N7	25:A:1361:G:C8	2.85	0.43
25:A:1494:A:H2'	25:A:1495:A:C8	2.52	0.43
25:A:2636:C:O2'	28:D:45:TYR:OH	2.22	0.43
28:D:35:THR:HG22	28:D:73:VAL:HG21	1.99	0.43
38:Q:4:LYS:O	38:Q:8:ILE:HG12	2.18	0.43
45:X:42:LEU:HD12	45:X:47:VAL:HG21	2.00	0.43
55:8:30:GLU:OE2	55:8:32:LYS:HD3	2.19	0.43
1:a:750:C:H2'	1:a:751:U:H6	1.83	0.43
1:a:859:G:H2'	1:a:860:A:C8	2.52	0.43
1:a:868:C:H2'	1:a:869:G:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:978:A:C4	1:a:1319:A:C2	3.07	0.43
1:a:1414:U:H2'	1:a:1415:G:H8	1.83	0.43
2:b:101:LEU:HB3	2:b:179:LEU:HD12	2.00	0.43
3:c:110:GLU:OE1	3:c:140:ASN:HB3	2.18	0.43
6:f:38:ARG:NH2	6:f:63:ASN:HD21	2.17	0.43
6:f:61:LEU:HD11	18:r:24:LYS:HE2	2.00	0.43
15:o:29:VAL:HG11	15:o:81:LEU:HD21	2.00	0.43
25:A:586:A:N1	25:A:809:G:O2'	2.38	0.43
25:A:633:A:O2'	25:A:2404:U:OP1	2.34	0.43
25:A:753:A:H2'	25:A:754:U:H6	1.83	0.43
25:A:1183:U:H2'	25:A:1184:U:C6	2.52	0.43
25:A:1495:A:H2'	25:A:1496:A:C8	2.53	0.43
25:A:1753:G:H5''	39:R:93:ARG:HD3	2.01	0.43
25:A:2199:A:OP1	47:Z:37:ARG:NH2	2.51	0.43
26:B:61:G:H2'	26:B:62:C:H6	1.84	0.43
38:Q:31:THR:HB	38:Q:32:PRO:HD2	2.01	0.43
1:a:891:U:H2'	1:a:892:A:H8	1.84	0.43
1:a:1107:C:C4	1:a:1108:G:C8	3.06	0.43
1:a:1162:C:H2'	1:a:1163:A:H8	1.83	0.43
1:a:1219:A:H2'	1:a:1220:G:C8	2.53	0.43
1:a:1233:G:H2'	1:a:1234:C:C6	2.53	0.43
3:c:62:LYS:HD3	3:c:62:LYS:HA	1.81	0.43
4:d:13:ARG:HB2	4:d:36:GLN:O	2.18	0.43
4:d:50:ASP:O	4:d:54:GLN:OE1	2.36	0.43
4:d:58:LYS:HA	4:d:200:ILE:HD11	2.00	0.43
25:A:81:G:O2'	25:A:295:G:O2'	2.24	0.43
25:A:948:C:H1'	25:A:984:A:C8	2.54	0.43
25:A:1028:A:N6	25:A:1125:G:H2'	2.33	0.43
25:A:1440:U:H2'	25:A:1441:G:C8	2.54	0.43
38:Q:45:SER:O	38:Q:45:SER:OG	2.28	0.43
43:V:29:THR:OG1	43:V:86:THR:HG22	2.18	0.43
1:a:138:G:H2'	1:a:139:A:H8	1.84	0.43
1:a:691:G:O2'	1:a:797:C:H4'	2.18	0.43
1:a:721:G:H4'	1:a:722:G:O4'	2.18	0.43
1:a:765:G:H1	1:a:812:G:HO2'	1.61	0.43
1:a:936:C:C2	1:a:937:A:C8	3.07	0.43
1:a:1253:G:H2'	1:a:1254:A:H8	1.83	0.43
1:a:1457:G:H2'	1:a:1458:G:O4'	2.18	0.43
3:c:65:ARG:HA	3:c:100:GLN:O	2.18	0.43
25:A:541:A:H2'	25:A:542:C:O4'	2.19	0.43
25:A:1709:U:H2'	25:A:1710:G:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:1734:G:H2'	25:A:1735:A:C8	2.53	0.43
25:A:2898:U:H2'	25:A:2899:A:C8	2.52	0.43
35:N:78:ARG:HG2	35:N:113:ALA:HB3	2.00	0.43
37:P:51:LEU:HD21	37:P:70:THR:HG22	2.01	0.43
46:Y:23:VAL:HA	46:Y:38:VAL:HG12	2.00	0.43
1:a:601:G:H2'	1:a:602:A:H8	1.84	0.43
1:a:707:U:H2'	1:a:708:C:C6	2.54	0.43
1:a:1343:G:O2'	9:i:123:ARG:HD2	2.18	0.43
2:b:188:ASP:OD1	2:b:189:THR:N	2.49	0.43
8:h:45:PHE:HE2	8:h:101:ILE:HG12	1.83	0.43
11:k:97:ILE:HG22	21:u:12:PHE:CZ	2.53	0.43
15:o:35:GLN:OE1	15:o:39:LEU:HG	2.19	0.43
25:A:225:C:H2'	25:A:226:A:O4'	2.19	0.43
25:A:594:U:H2'	25:A:595:C:H6	1.83	0.43
25:A:851:C:H2'	25:A:852:U:H6	1.83	0.43
25:A:871:U:H2'	25:A:872:U:H6	1.82	0.43
25:A:1130:U:C2	25:A:2025:C:H5''	2.54	0.43
25:A:1178:C:H2'	25:A:1179:G:C8	2.53	0.43
25:A:1771:C:H2'	25:A:1772:A:C8	2.53	0.43
25:A:2795:C:H2'	25:A:2796:U:C6	2.54	0.43
31:G:95:ARG:HH21	31:G:128:GLN:HE22	1.66	0.43
1:a:26:A:H61	1:a:558:G:H1'	1.84	0.43
1:a:333:U:C2	1:a:334:C:C5	3.06	0.43
1:a:737:C:H2'	1:a:738:C:C6	2.52	0.43
1:a:1255:G:O2'	1:a:1258:G:N3	2.38	0.43
1:a:1457:G:OP1	20:t:34:LYS:NZ	2.47	0.43
5:e:77:ASN:OD1	5:e:82:GLN:NE2	2.51	0.43
25:A:284:U:H2'	25:A:285:G:C8	2.52	0.43
25:A:636:G:N7	35:N:109:LYS:HD3	2.34	0.43
25:A:788:A:OP1	25:A:791:C:N4	2.41	0.43
25:A:978:G:O4'	25:A:1001:A:H2	2.01	0.43
25:A:987:C:O2'	25:A:1000:A:N3	2.40	0.43
25:A:2590:A:H2'	25:A:2591:C:H6	1.83	0.43
49:2:53:PHE:CD2	49:2:54:MET:HG3	2.53	0.43
1:a:154:U:H2'	1:a:155:A:C8	2.54	0.43
1:a:1288:A:N1	1:a:1371:G:H1'	2.34	0.43
1:a:1315:U:H2'	1:a:1316:G:O4'	2.19	0.43
7:g:26:PHE:HE1	7:g:120:LEU:HD21	1.83	0.43
19:s:17:LYS:O	19:s:20:GLU:HG3	2.18	0.43
25:A:608:A:H2'	25:A:609:A:C8	2.53	0.43
25:A:891:G:C2	25:A:892:A:C5	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:1572:A:H2'	25:A:1573:G:H8	1.84	0.43
25:A:1677:A:H2'	25:A:1678:A:C8	2.53	0.43
25:A:1733:G:H2'	25:A:1734:G:C8	2.54	0.43
25:A:1809:A:H2'	25:A:1810:A:C8	2.54	0.43
25:A:2114:A:C6	25:A:2115:G:H1'	2.54	0.43
26:B:45:A:C4	26:B:46:A:C8	3.07	0.43
34:M:114:LYS:HE2	34:M:118:LEU:HD11	1.99	0.43
37:P:2:ARG:O	37:P:3:HIS:C	2.60	0.43
43:V:28:ASN:ND2	43:V:87:LEU:HB2	2.34	0.43
51:4:38:HIS:HB3	51:4:44:THR:HG22	2.01	0.43
1:a:113:G:H1'	1:a:354:G:H5'	2.01	0.43
1:a:158:G:C6	1:a:159:G:C6	3.07	0.43
1:a:636:U:H2'	1:a:637:C:H6	1.83	0.43
1:a:1180:A:OP2	9:i:99:ARG:NH2	2.51	0.43
1:a:1216:A:H2'	1:a:1217:C:H6	1.83	0.43
12:l:21:VAL:HB	12:l:24:LEU:HD13	2.00	0.43
22:y:1:G:H2'	22:y:2:C:H6	1.84	0.43
25:A:296:U:H2'	25:A:297:G:C8	2.54	0.43
25:A:819:A:H5''	25:A:973:A:N1	2.34	0.43
25:A:918:A:H5''	26:B:97:C:O2'	2.18	0.43
25:A:998:C:OP1	40:S:84:LYS:NZ	2.40	0.43
25:A:2301:C:H2'	25:A:2302:U:C6	2.54	0.43
25:A:2302:U:N3	25:A:2303:G:N7	2.67	0.43
25:A:2687:U:H2'	25:A:2688:G:O4'	2.19	0.43
26:B:43:C:OP1	50:3:6:HIS:NE2	2.52	0.43
33:L:23:LYS:HD3	33:L:28:LEU:HD13	2.01	0.43
38:Q:51:ALA:HB3	38:Q:78:VAL:HB	2.00	0.43
48:1:6:LEU:HA	48:1:9:LYS:HE3	2.00	0.43
49:2:56:LYS:HE3	49:2:56:LYS:HB3	1.75	0.43
1:a:256:U:H2'	1:a:257:G:C8	2.54	0.43
1:a:1008:U:H2'	1:a:1009:U:O4'	2.18	0.43
1:a:1026:G:H4'	1:a:1027:C:OP1	2.19	0.43
1:a:1326:U:H2'	1:a:1327:C:H6	1.82	0.43
2:b:9:MET:HE3	2:b:47:VAL:HG12	2.01	0.43
2:b:56:GLU:HG2	2:b:198:PHE:CE2	2.53	0.43
7:g:75:VAL:HG11	7:g:144:MET:HE1	2.01	0.43
19:s:32:ARG:HD2	19:s:57:HIS:CE1	2.53	0.43
25:A:29:U:H2'	25:A:30:G:C8	2.54	0.43
25:A:44:A:H2'	25:A:45:G:O4'	2.19	0.43
25:A:589:U:H2'	25:A:590:A:C8	2.54	0.43
25:A:613:A:H2'	25:A:614:A:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:639:U:H2'	25:A:640:C:H6	1.80	0.43
25:A:1506:U:H2'	25:A:1507:C:C6	2.54	0.43
25:A:2076:U:OP2	25:A:2238:G:N2	2.39	0.43
25:A:2849:U:H4'	25:A:2868:A:C2	2.54	0.43
30:F:5:HIS:HB2	30:F:97:TRP:CD1	2.54	0.43
45:X:30:ILE:HD11	45:X:40:ILE:HD13	2.01	0.43
1:a:34:C:H2'	1:a:35:G:C8	2.54	0.42
1:a:429:U:H3'	4:d:9:LEU:HD12	2.00	0.42
1:a:1147:C:H2'	1:a:1148:U:H6	1.85	0.42
1:a:1163:A:H2'	1:a:1164:G:H8	1.84	0.42
1:a:1238:A:H2	1:a:1241:G:N3	2.17	0.42
3:c:114:LYS:N	3:c:185:ASN:HD22	2.17	0.42
25:A:222:A:C2	25:A:233:A:H5''	2.54	0.42
25:A:902:C:H2'	25:A:903:C:C6	2.54	0.42
25:A:1416:G:H2'	25:A:1417:C:H6	1.84	0.42
25:A:1534:U:O2'	25:A:1537:G:N1	2.52	0.42
25:A:1734:G:H2'	25:A:1735:A:H8	1.83	0.42
25:A:2070:A:H2'	25:A:2071:A:C8	2.53	0.42
30:F:111:ILE:HG22	30:F:112:ARG:N	2.34	0.42
35:N:121:THR:HG22	35:N:141:LYS:HG2	2.00	0.42
47:Z:38:PHE:HZ	47:Z:56:MET:HG2	1.84	0.42
1:a:264:C:H2'	1:a:265:G:O4'	2.20	0.42
1:a:303:A:H2'	1:a:304:U:O4'	2.19	0.42
1:a:456:A:H2'	1:a:457:G:H8	1.84	0.42
1:a:509:A:H5'	4:d:52:GLY:HA2	2.00	0.42
1:a:1335:U:H5''	1:a:1336:C:H5'	2.01	0.42
2:b:171:ILE:O	2:b:175:GLU:HG3	2.19	0.42
22:y:31:A:H2'	22:y:32:PSU:C6	2.54	0.42
25:A:479:A:N3	25:A:481:G:H5''	2.34	0.42
25:A:781:A:OP1	27:C:217:ARG:NH2	2.37	0.42
25:A:2368:C:H5'	25:A:2369:A:OP2	2.19	0.42
31:G:101:ASN:O	31:G:117:LEU:HB2	2.20	0.42
36:O:20:LEU:HD22	45:X:81:PRO:HG2	2.00	0.42
1:a:343:U:H2'	1:a:345:C:C4	2.54	0.42
1:a:587:G:OP1	8:h:84:ARG:NH2	2.52	0.42
1:a:720:C:H5''	18:r:41:PRO:HA	2.00	0.42
15:o:74:ASP:OD2	15:o:77:ARG:HD3	2.18	0.42
16:p:70:ARG:HD2	16:p:70:ARG:HA	1.63	0.42
25:A:84:A:H4'	25:A:85:G:O5'	2.19	0.42
25:A:568:U:OP1	35:N:36:LYS:HD2	2.20	0.42
25:A:1680:U:H2'	25:A:1681:G:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:2291:U:H2'	25:A:2292:U:H6	1.81	0.42
25:A:2322:A:N6	25:A:2333:A:H62	2.17	0.42
25:A:2445:2MG:P	29:E:69:ARG:HH12	2.43	0.42
27:C:160:THR:HB	27:C:177:ARG:HG3	2.01	0.42
30:F:140:GLU:OE1	30:F:140:GLU:N	2.52	0.42
36:O:38:ARG:HB2	36:O:98:PRO:HD3	2.01	0.42
3:c:184:TYR:HA	3:c:200:VAL:O	2.19	0.42
4:d:98:LEU:HD12	4:d:98:LEU:HA	1.91	0.42
16:p:5:ARG:NH2	16:p:22:ALA:HB3	2.32	0.42
25:A:935:C:H2'	25:A:936:A:H8	1.84	0.42
25:A:1282:U:H2'	25:A:1283:G:O4'	2.19	0.42
25:A:1842:G:H2'	25:A:1843:C:H6	1.84	0.42
25:A:2262:U:H2'	25:A:2263:C:H6	1.83	0.42
25:A:2720:U:OP1	39:R:53:ARG:NH2	2.53	0.42
25:A:2898:U:C2	25:A:2899:A:C8	3.07	0.42
27:C:71:LYS:NZ	27:C:100:GLU:OE1	2.28	0.42
37:P:24:MET:HE1	37:P:40:LYS:HB3	2.02	0.42
1:a:824:G:H2'	1:a:825:A:H8	1.84	0.42
2:b:100:MET:HE2	2:b:100:MET:HB2	1.94	0.42
8:h:14:ILE:HG23	8:h:63:LEU:HD21	2.00	0.42
25:A:61:C:OP1	48:1:44:LYS:HD3	2.19	0.42
25:A:578:G:OP1	25:A:1255:U:O2'	2.30	0.42
25:A:657:U:H2'	25:A:658:U:C6	2.53	0.42
25:A:997:G:OP1	40:S:92:ARG:HD3	2.18	0.42
25:A:2282:G:H4'	25:A:2389:G:O2'	2.20	0.42
26:B:31:C:O2'	26:B:53:A:N1	2.47	0.42
41:T:73:LYS:HB3	41:T:73:LYS:HE2	1.79	0.42
1:a:408:A:OP1	4:d:112:ALA:HB3	2.19	0.42
1:a:608:A:H2'	1:a:609:A:O4'	2.20	0.42
1:a:1070:U:H2'	1:a:1071:C:H6	1.84	0.42
3:c:134:MET:CE	3:c:153:VAL:HG12	2.49	0.42
7:g:113:ASP:HB2	7:g:119:ARG:HG2	2.02	0.42
12:l:30:LYS:HG2	12:l:57:LEU:HD13	2.01	0.42
17:q:46:VAL:HG12	17:q:73:TRP:CB	2.45	0.42
25:A:340:A:H2'	25:A:341:C:O4'	2.20	0.42
25:A:1790:C:H2'	25:A:1791:A:C8	2.55	0.42
27:C:142:HIS:CD2	27:C:195:VAL:HG22	2.54	0.42
1:a:1:A:N6	1:a:614:C:O2'	2.52	0.42
1:a:215:C:H2'	1:a:216:U:C6	2.54	0.42
4:d:124:MET:HE2	4:d:146:ARG:CD	2.50	0.42
12:l:86:ARG:HA	12:l:94:ARG:HA	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:x:13:C:O2'	25:A:1924:C:H4'	2.19	0.42
22:y:63:G:H2'	22:y:64:A:H8	1.84	0.42
25:A:146:A:H2'	25:A:147:C:C6	2.55	0.42
25:A:1716:U:H2'	25:A:1717:A:H8	1.85	0.42
25:A:1853:A:H2'	25:A:1854:A:C8	2.55	0.42
25:A:2627:G:O2'	25:A:2781:A:N1	2.44	0.42
30:F:63:GLN:NE2	30:F:89:VAL:HB	2.33	0.42
33:L:95:ARG:CD	33:L:96:ARG:HG2	2.37	0.42
1:a:254:G:H5''	17:q:71:LYS:HD3	2.02	0.42
1:a:715:A:H2'	1:a:716:A:C8	2.54	0.42
1:a:947:G:H2'	1:a:948:C:H6	1.85	0.42
1:a:966:2MG:N2	23:x:34:C:H5'	2.35	0.42
1:a:1063:C:OP2	1:a:1064:G:O2'	2.33	0.42
15:o:48:LYS:HA	15:o:48:LYS:HD3	1.73	0.42
21:u:16:LEU:O	21:u:20:LYS:HG3	2.20	0.42
22:w:63:G:H2'	22:w:64:A:C8	2.53	0.42
25:A:2525:G:O2'	25:A:2742:G:O2'	2.24	0.42
46:Y:71:VAL:HA	46:Y:77:ARG:O	2.19	0.42
1:a:137:U:H2'	1:a:138:G:H5'	2.02	0.42
1:a:237:G:H5''	17:q:27:ARG:CZ	2.49	0.42
1:a:451:A:N6	1:a:481:G:O5'	2.42	0.42
1:a:1120:C:C2	1:a:1121:U:C5	3.07	0.42
1:a:1272:G:H2'	1:a:1273:C:C6	2.54	0.42
4:d:168:PRO:HG2	4:d:171:LEU:HD21	2.02	0.42
6:f:42:TRP:CH2	6:f:102:MET:HG3	2.54	0.42
6:f:49:TYR:CE1	18:r:66:SER:HA	2.55	0.42
8:h:96:MET:SD	8:h:130:ALA:HB1	2.60	0.42
18:r:65:LEU:HD23	18:r:65:LEU:HA	1.90	0.42
22:y:2:C:H2'	22:y:3:C:C6	2.54	0.42
25:A:154:U:H2'	25:A:155:A:C8	2.55	0.42
25:A:708:G:H2'	25:A:709:U:C6	2.55	0.42
25:A:1426:G:O2'	25:A:1572:A:N6	2.45	0.42
25:A:1433:A:H2'	25:A:1434:A:H8	1.80	0.42
29:E:106:LYS:HG3	29:E:200:LEU:HD23	2.02	0.42
42:U:18:ARG:HG3	42:U:76:VAL:HG12	2.01	0.42
1:a:601:G:H2'	1:a:602:A:C8	2.55	0.42
1:a:982:U:H4'	1:a:983:A:O4'	2.20	0.42
1:a:1459:G:H2'	1:a:1460:C:O4'	2.20	0.42
1:a:1522:U:H2'	1:a:1523:G:H8	1.84	0.42
2:b:24:ASN:HD22	2:b:192:ASP:HA	1.85	0.42
9:i:14:SER:O	9:i:14:SER:OG	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:k:83:GLU:HB2	11:k:109:ASN:O	2.20	0.42
17:q:10:GLY:HA3	17:q:25:ILE:HD13	2.02	0.42
19:s:14:HIS:O	19:s:18:LYS:HG2	2.20	0.42
23:x:23:C:H2'	23:x:24:U:C6	2.55	0.42
25:A:244:A:H5''	35:N:67:THR:HG21	2.02	0.42
25:A:1209:U:O2'	25:A:1237:A:N1	2.49	0.42
25:A:2064:C:H2'	25:A:2065:C:H6	1.81	0.42
25:A:2229:U:O2	47:Z:34:HIS:HE1	2.03	0.42
25:A:2370:G:H4'	52:5:44:ARG:NH2	2.35	0.42
25:A:2873:A:O2'	25:A:2874:C:H5'	2.18	0.42
27:C:123:ALA:O	27:C:128:ASN:ND2	2.41	0.42
27:C:145:GLU:HB2	27:C:188:CYS:HB3	2.01	0.42
30:F:36:LEU:HD12	30:F:61:SER:HB2	2.02	0.42
38:Q:92:PHE:CZ	38:Q:107:ALA:HB2	2.54	0.42
50:3:35:ASP:OD1	50:3:35:ASP:N	2.48	0.42
1:a:110:C:O2'	16:p:25:ARG:O	2.29	0.41
1:a:938:A:N3	1:a:1376:U:O2'	2.36	0.41
1:a:1033:G:H2'	1:a:1034:G:C5	2.55	0.41
6:f:39:LEU:HD13	6:f:62:MET:HG2	2.01	0.41
10:j:59:LYS:HZ1	10:j:62:ARG:HH21	1.68	0.41
13:m:24:GLY:HA3	13:m:65:VAL:HG12	2.02	0.41
13:m:81:MET:O	13:m:92:ARG:NH2	2.52	0.41
18:r:26:ILE:HD11	18:r:67:LEU:HB3	2.02	0.41
25:A:3:U:O2'	25:A:4:U:OP1	2.33	0.41
25:A:248:G:H5'	25:A:250:G:N7	2.35	0.41
25:A:1564:C:H2'	25:A:1565:C:C6	2.55	0.41
25:A:1771:C:H2'	25:A:1772:A:H8	1.84	0.41
25:A:2142:A:H2'	25:A:2143:C:C6	2.55	0.41
26:B:103:U:H4'	45:X:75:GLN:HE22	1.84	0.41
28:D:122:VAL:HG21	28:D:129:THR:HG22	2.02	0.41
34:M:121:GLU:OE2	39:R:65:SER:OG	2.31	0.41
39:R:18:PRO:HG3	39:R:84:ILE:O	2.20	0.41
1:a:704:A:C4	1:a:705:G:C8	3.08	0.41
1:a:1014:A:N3	1:a:1219:A:H1'	2.35	0.41
1:a:1161:C:H2'	1:a:1162:C:H6	1.85	0.41
4:d:105:MET:SD	4:d:180:GLY:HA3	2.60	0.41
7:g:97:ASN:O	7:g:101:MET:HG3	2.19	0.41
10:j:50:THR:HG22	10:j:62:ARG:HH11	1.85	0.41
15:o:30:ALA:HA	15:o:85:LEU:HD11	2.02	0.41
21:u:28:VAL:O	21:u:32:VAL:HG23	2.20	0.41
25:A:947:A:H2'	25:A:948:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:1316:U:H2'	25:A:1317:G:H8	1.84	0.41
25:A:1614:A:C2	42:U:93:ALA:HB2	2.55	0.41
25:A:1677:A:H2'	25:A:1678:A:H8	1.85	0.41
25:A:2615:U:H2'	25:A:2616:C:H6	1.85	0.41
30:F:130:MET:N	30:F:154:ILE:O	2.39	0.41
45:X:28:ALA:HB3	45:X:40:ILE:HG13	2.02	0.41
49:2:53:PHE:CE2	49:2:54:MET:HG3	2.55	0.41
1:a:62:U:H5'	1:a:385:C:H1'	2.02	0.41
1:a:180:U:H2'	1:a:181:A:H8	1.85	0.41
1:a:215:C:H2'	1:a:216:U:H6	1.84	0.41
5:e:81:LEU:HB2	5:e:98:PRO:HG3	2.02	0.41
5:e:134:ILE:O	5:e:138:ARG:HG3	2.20	0.41
5:e:148:ASN:HD22	8:h:96:MET:HE1	1.84	0.41
22:w:23:A:H2'	22:w:24:G:H8	1.84	0.41
22:w:64:A:O2'	22:w:65:G:OP1	2.33	0.41
25:A:143:C:H2'	25:A:144:A:C8	2.55	0.41
25:A:503:A:H4'	25:A:504:A:H3'	2.02	0.41
25:A:1292:G:H2'	25:A:1293:C:H6	1.84	0.41
25:A:2118:U:H5''	25:A:2148:G:O2'	2.19	0.41
25:A:2514:U:H2'	25:A:2515:C:H6	1.84	0.41
25:A:2607:G:H2'	25:A:2608:G:O4'	2.20	0.41
25:A:2723:C:H2'	25:A:2724:U:O4'	2.20	0.41
26:B:16:G:N2	26:B:69:G:H1'	2.35	0.41
34:M:23:LYS:HE2	34:M:23:LYS:HB2	1.87	0.41
40:S:17:ILE:HD12	40:S:36:PHE:HA	2.02	0.41
42:U:48:LYS:O	42:U:52:GLU:HG3	2.20	0.41
48:1:49:ASP:HA	48:1:52:ARG:HG2	2.02	0.41
1:a:465:A:H2'	1:a:466:A:C8	2.55	0.41
3:c:110:GLU:HB2	3:c:144:LEU:HD22	2.02	0.41
4:d:58:LYS:HD3	4:d:203:LEU:HD21	2.03	0.41
4:d:170:TRP:CD2	4:d:186:PRO:HB3	2.56	0.41
20:t:4:ILE:C	20:t:6:SER:H	2.29	0.41
22:w:4:C:C2	22:w:5:G:C8	3.08	0.41
25:A:17:G:H2'	25:A:18:U:C6	2.55	0.41
25:A:457:A:N1	25:A:470:A:H5''	2.36	0.41
25:A:935:C:H2'	25:A:936:A:C8	2.56	0.41
25:A:1321:A:C4	25:A:1322:A:C8	3.08	0.41
25:A:1432:G:O2'	25:A:1433:A:H5'	2.20	0.41
25:A:1869:G:N2	25:A:1872:A:OP2	2.53	0.41
25:A:2100:G:O6	25:A:2189:U:O2	2.38	0.41
31:G:137:ASP:OD2	31:G:139:GLN:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:O:53:MET:HE1	36:O:103:TYR:CG	2.54	0.41
40:S:52:GLN:HE21	40:S:56:GLN:NE2	2.17	0.41
43:V:80:TRP:CZ3	43:V:82:LYS:HB3	2.55	0.41
1:a:86:G:H5'	1:a:87:C:C6	2.53	0.41
1:a:867:G:O2'	1:a:873:A:N1	2.53	0.41
1:a:883:C:O2'	1:a:884:U:H5'	2.21	0.41
1:a:958:A:H1'	1:a:985:C:O2'	2.20	0.41
1:a:1130:A:H5'	9:i:20:PHE:CZ	2.55	0.41
1:a:1160:G:C2	1:a:1161:C:C6	3.08	0.41
1:a:1435:G:H2'	1:a:1436:U:C6	2.56	0.41
3:c:90:VAL:O	3:c:94:ILE:HG12	2.21	0.41
4:d:185:LYS:NZ	4:d:187:GLU:OE1	2.50	0.41
7:g:72:THR:HA	7:g:96:ARG:HH21	1.85	0.41
17:q:8:LEU:HD13	17:q:73:TRP:CH2	2.56	0.41
22:y:58:A:H2'	22:y:60:U:OP2	2.20	0.41
25:A:52:A:H2'	25:A:53:A:H8	1.83	0.41
25:A:75:G:H4'	48:1:48:ARG:CZ	2.51	0.41
25:A:364:C:H2'	25:A:365:U:C6	2.56	0.41
25:A:1107:G:H2'	25:A:1108:U:C6	2.54	0.41
25:A:1203:U:H1'	35:N:4:ASN:HB3	2.03	0.41
25:A:1585:C:H2'	25:A:1586:A:O4'	2.20	0.41
25:A:1802:A:H2'	25:A:1803:A:H8	1.80	0.41
25:A:2134:A:N6	25:A:2156:G:N3	2.68	0.41
25:A:2839:G:N2	37:P:91:ALA:O	2.41	0.41
30:F:38:MET:SD	30:F:53:ALA:HB1	2.59	0.41
43:V:11:LEU:HD21	43:V:47:VAL:HG22	2.01	0.41
51:4:52:ARG:NH1	51:4:54:VAL:HG12	2.36	0.41
1:a:59:A:H3'	1:a:331:G:H22	1.85	0.41
1:a:884:U:H4'	1:a:885:G:H5''	2.01	0.41
1:a:1410:A:H2'	1:a:1411:C:H6	1.85	0.41
3:c:56:VAL:HG13	3:c:67:THR:HG23	2.03	0.41
4:d:89:ASN:O	4:d:93:LEU:HG	2.20	0.41
9:i:84:THR:CG2	9:i:98:LEU:HD21	2.46	0.41
25:A:222:A:N1	25:A:233:A:H5''	2.35	0.41
25:A:382:A:H2'	25:A:383:C:O4'	2.20	0.41
25:A:1364:G:P	47:Z:50:ARG:HH12	2.42	0.41
25:A:1490:A:H2'	25:A:1490:A:N3	2.34	0.41
25:A:1509:A:O2'	25:A:1510:G:H8	2.03	0.41
25:A:2138:G:H2'	25:A:2139:U:O4'	2.21	0.41
25:A:2532:G:N2	25:A:2663:G:O2'	2.53	0.41
27:C:43:ARG:HA	27:C:48:ARG:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:E:161:ALA:HA	29:E:164:LEU:HD13	2.03	0.41
36:O:17:ASN:O	36:O:38:ARG:HD3	2.21	0.41
44:W:35:ILE:HD13	44:W:64:ALA:HA	2.02	0.41
49:2:9:GLN:HB2	49:2:29:LEU:HD22	2.02	0.41
1:a:8:A:N6	4:d:205:SER:OG	2.43	0.41
1:a:705:G:C5	1:a:706:A:C8	3.08	0.41
1:a:837:U:H2'	1:a:838:G:C8	2.55	0.41
2:b:47:VAL:HG23	2:b:48:PRO:HD3	2.03	0.41
3:c:23:PHE:CZ	10:j:11:LYS:HG2	2.56	0.41
4:d:9:LEU:O	4:d:13:ARG:HG2	2.21	0.41
4:d:152:GLN:HB2	4:d:155:VAL:HG23	2.03	0.41
25:A:592:A:H2'	25:A:593:U:C6	2.56	0.41
25:A:648:G:O2'	25:A:2351:G:OP1	2.25	0.41
25:A:1429:G:H2'	25:A:1430:G:C8	2.55	0.41
25:A:2683:C:H4'	28:D:13:ARG:HH21	1.85	0.41
25:A:2703:C:C2	25:A:2704:C:C5	3.09	0.41
25:A:2820:A:O2'	25:A:2821:A:OP1	2.38	0.41
1:a:236:A:H2'	1:a:237:G:H8	1.85	0.41
1:a:635:A:H2'	1:a:636:U:C6	2.56	0.41
1:a:1121:U:H2'	1:a:1122:U:H6	1.85	0.41
4:d:110:THR:O	4:d:113:GLU:HB2	2.21	0.41
6:f:10:VAL:HG23	6:f:83:ALA:C	2.45	0.41
6:f:74:LEU:HB3	6:f:78:PHE:HE1	1.85	0.41
15:o:36:ILE:O	15:o:40:GLN:HG2	2.20	0.41
22:w:9:A:H1'	22:w:45:U:O2'	2.21	0.41
22:w:37:MIA:H162	22:w:37:MIA:H121	1.87	0.41
23:x:38:A:H2'	23:x:39:C:O4'	2.21	0.41
22:y:62:C:H2'	22:y:63:G:H8	1.85	0.41
25:A:94:A:H2'	25:A:95:A:C8	2.55	0.41
25:A:296:U:H2'	25:A:297:G:H8	1.85	0.41
25:A:697:G:H2'	25:A:698:C:C6	2.56	0.41
25:A:741:U:H2'	25:A:742:A:C8	2.55	0.41
25:A:1278:C:H2'	25:A:1279:G:C8	2.56	0.41
25:A:1365:A:OP1	47:Z:3:ARG:HD3	2.21	0.41
25:A:2110:G:H5'	25:A:2111:U:O5'	2.20	0.41
26:B:3:C:H2'	26:B:4:C:H6	1.85	0.41
31:G:11:VAL:N	31:G:48:ASN:OD1	2.52	0.41
37:P:71:ARG:HA	37:P:71:ARG:HD2	1.89	0.41
48:1:11:VAL:O	48:1:15:ASN:HB2	2.21	0.41
1:a:263:A:H2'	1:a:264:C:C5	2.55	0.41
1:a:333:U:H2'	1:a:334:C:H6	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:392:C:H2'	1:a:393:A:C8	2.56	0.41
1:a:1318:A:O2'	19:s:37:ARG:HD2	2.20	0.41
1:a:1530:G:H2'	1:a:1531:A:C8	2.55	0.41
4:d:188:ARG:NH2	4:d:195:ILE:O	2.54	0.41
19:s:47:LEU:HD23	19:s:47:LEU:H	1.86	0.41
20:t:6:SER:O	20:t:10:ARG:HG2	2.21	0.41
25:A:782:A:N7	27:C:220:VAL:HG21	2.35	0.41
25:A:1047:G:O2'	25:A:1110:G:N1	2.28	0.41
25:A:1127:A:N7	25:A:2488:G:O2'	2.52	0.41
25:A:1289:C:H2'	25:A:1290:C:C6	2.56	0.41
25:A:1360:G:C8	25:A:1361:G:C8	3.09	0.41
25:A:1641:A:H2'	25:A:1642:G:O4'	2.21	0.41
25:A:1747:U:H2'	25:A:1748:C:C6	2.56	0.41
25:A:2104:C:N4	25:A:2105:U:O4	2.53	0.41
25:A:2107:G:C2	25:A:2183:A:C6	3.09	0.41
25:A:2155:U:H3'	25:A:2156:G:H8	1.85	0.41
25:A:2215:C:H2'	25:A:2216:G:C8	2.56	0.41
28:D:125:TRP:CD1	28:D:160:LYS:HB2	2.56	0.41
30:F:98:GLU:HG3	50:3:24:ILE:HD11	2.02	0.41
31:G:159:GLY:HA3	31:G:163:ARG:NH2	2.33	0.41
33:L:88:THR:OG1	33:L:91:GLU:HG3	2.21	0.41
38:Q:29:HIS:O	38:Q:29:HIS:CG	2.74	0.41
45:X:21:ARG:HA	45:X:25:LYS:O	2.21	0.41
45:X:51:GLN:HG2	45:X:86:LEU:HD11	2.02	0.41
53:6:1:MET:HE2	53:6:1:MET:HB3	1.85	0.41
1:a:203:G:O2'	1:a:204:G:H8	2.03	0.41
1:a:545:C:H5'	4:d:69:GLU:CB	2.51	0.41
1:a:985:C:H2'	1:a:986:U:H6	1.85	0.41
1:a:1319:A:C8	1:a:1323:G:C6	3.09	0.41
2:b:72:THR:HA	2:b:93:ASN:O	2.21	0.41
8:h:18:GLN:HE21	8:h:72:VAL:HG23	1.86	0.41
9:i:12:ARG:HA	9:i:106:ARG:HH12	1.86	0.41
23:x:2:G:H2'	23:x:3:C:C6	2.56	0.41
23:x:43:A:H2'	23:x:44:A:H8	1.84	0.41
25:A:599:A:O2'	25:A:600:G:H5'	2.20	0.41
25:A:1126:A:H4'	25:A:1127:A:H5''	2.02	0.41
25:A:1526:C:H2'	25:A:1527:G:O4'	2.21	0.41
25:A:1668:A:H4'	25:A:1669:A:O5'	2.21	0.41
25:A:2303:G:O2'	30:F:121:SER:O	2.39	0.41
25:A:2379:G:C6	25:A:2380:C:N4	2.89	0.41
26:B:8:C:O2'	38:Q:25:ARG:NH2	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:B:30:C:H2'	26:B:31:C:H5'	2.03	0.41
27:C:145:GLU:HG2	27:C:151:GLY:C	2.45	0.41
28:D:25:THR:OG1	28:D:191:GLY:O	2.36	0.41
29:E:100:MET:O	29:E:104:ALA:N	2.49	0.41
29:E:149:ILE:HG21	29:E:175:ILE:HD11	2.03	0.41
44:W:86:ARG:NH1	44:W:100:SER:HG	2.17	0.41
45:X:6:ALA:HB1	45:X:40:ILE:HB	2.03	0.41
1:a:5:U:H6	1:a:5:U:OP1	2.04	0.40
1:a:177:G:H5'	20:t:60:ARG:NH1	2.35	0.40
1:a:545:C:OP1	4:d:58:LYS:NZ	2.33	0.40
1:a:979:C:O2	14:n:59:ARG:NH1	2.54	0.40
3:c:114:LYS:HB2	3:c:185:ASN:ND2	2.36	0.40
5:e:76:LEU:HD13	5:e:79:GLY:HA2	2.03	0.40
7:g:31:MET:SD	7:g:34:GLY:HA2	2.61	0.40
11:k:74:VAL:HG23	11:k:74:VAL:O	2.21	0.40
12:l:102:LEU:H	12:l:102:LEU:HG	1.63	0.40
19:s:44:MET:HB2	19:s:47:LEU:HD21	2.02	0.40
25:A:152:A:H2'	25:A:153:U:C6	2.56	0.40
25:A:675:A:N3	25:A:2443:C:O2'	2.50	0.40
25:A:817:C:O2'	25:A:839:U:H5''	2.22	0.40
25:A:1328:A:H2'	25:A:1330:C:C5	2.57	0.40
25:A:2131:U:O5'	25:A:2133:G:H4'	2.21	0.40
25:A:2193:G:H2'	25:A:2194:U:C6	2.57	0.40
25:A:2298:A:H3'	25:A:2299:U:H6	1.86	0.40
25:A:2683:C:H5''	39:R:56:HIS:HB3	2.03	0.40
25:A:2756:U:H1'	25:A:2757:A:H5''	2.02	0.40
1:a:180:U:H2'	1:a:181:A:C8	2.57	0.40
1:a:730:G:C5	1:a:731:G:H1'	2.57	0.40
1:a:1014:A:H2'	1:a:1015:G:C8	2.56	0.40
1:a:1015:G:N2	1:a:1218:C:O2	2.53	0.40
19:s:10:PHE:O	19:s:39:THR:HG22	2.21	0.40
25:A:272:A:H2'	25:A:273:G:H8	1.84	0.40
25:A:305:C:H2'	25:A:306:U:C6	2.56	0.40
25:A:359:G:H2'	25:A:360:U:H6	1.86	0.40
25:A:608:A:H2'	25:A:609:A:H8	1.86	0.40
25:A:709:U:H2'	25:A:710:U:C6	2.55	0.40
25:A:843:G:H2'	25:A:844:A:C8	2.56	0.40
25:A:1316:U:H2'	25:A:1317:G:C8	2.57	0.40
25:A:1993:U:H4'	28:D:133:THR:OG1	2.21	0.40
25:A:2030:6MZ:C2	25:A:2499:C:H5''	2.51	0.40
25:A:2065:C:H2'	25:A:2066:C:H6	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:2215:C:H2'	25:A:2216:G:H8	1.86	0.40
25:A:2480:C:H2'	25:A:2481:G:H5'	2.03	0.40
25:A:2538:C:HO2'	25:A:2539:C:P	2.44	0.40
34:M:76:VAL:HG12	39:R:73:VAL:HB	2.03	0.40
1:a:166:U:C2	1:a:167:A:N7	2.90	0.40
1:a:214:C:H2'	1:a:215:C:H6	1.86	0.40
1:a:763:G:H2'	1:a:764:C:C6	2.56	0.40
1:a:779:C:H2'	1:a:780:A:O4'	2.20	0.40
1:a:1277:C:H2'	1:a:1279:G:H21	1.86	0.40
3:c:73:PRO:O	3:c:77:ILE:HG12	2.20	0.40
4:d:105:MET:HE1	4:d:171:LEU:HB2	2.03	0.40
4:d:170:TRP:NE1	4:d:171:LEU:HD23	2.36	0.40
9:i:36:GLU:HA	9:i:45:ARG:HH11	1.87	0.40
17:q:19:LYS:C	17:q:20:SER:HG	2.29	0.40
19:s:11:ILE:HG23	19:s:16:LEU:HD21	2.02	0.40
25:A:61:C:H5''	48:1:43:LEU:HD11	2.04	0.40
25:A:182:A:H2'	25:A:183:C:H6	1.87	0.40
25:A:469:G:O6	53:6:37:LYS:HE2	2.21	0.40
25:A:1409:U:H2'	25:A:1410:G:H8	1.86	0.40
25:A:1440:U:H2'	25:A:1441:G:H8	1.85	0.40
25:A:2483:C:N3	36:O:123:LYS:HE3	2.36	0.40
25:A:2543:G:H2'	25:A:2544:G:C8	2.57	0.40
27:C:53:HIS:CD2	27:C:219:THR:HA	2.55	0.40
27:C:79:GLU:OE2	27:C:95:LEU:HB2	2.21	0.40
27:C:205:LEU:HB3	27:C:210:ALA:HB3	2.04	0.40
40:S:17:ILE:HD13	40:S:36:PHE:HD1	1.85	0.40
43:V:5:GLU:HG3	48:1:22:LEU:HD13	2.04	0.40
1:a:648:A:H2'	1:a:649:A:C8	2.56	0.40
1:a:701:U:OP1	1:a:702:A:O2'	2.30	0.40
1:a:1014:A:C2	1:a:1219:A:H1'	2.56	0.40
1:a:1020:G:H2'	1:a:1021:A:H8	1.86	0.40
1:a:1332:A:H2'	1:a:1333:A:C8	2.56	0.40
4:d:21:LEU:H	4:d:21:LEU:HD23	1.86	0.40
5:e:149:SER:H	5:e:152:MET:HE2	1.86	0.40
16:p:5:ARG:HG2	16:p:5:ARG:NH1	2.36	0.40
22:w:20:U:N3	22:w:59:U:OP1	2.41	0.40
25:A:271:G:C2	25:A:272:A:C5	3.10	0.40
25:A:468:G:H5''	29:E:55:SER:HB3	2.04	0.40
25:A:995:C:O2	33:L:3:THR:OG1	2.30	0.40
25:A:1213:A:H2'	25:A:1214:A:C8	2.57	0.40
25:A:1421:G:O2'	25:A:1494:A:N6	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:1531:C:H2'	25:A:1532:A:H8	1.85	0.40
25:A:1689:A:H2'	25:A:1690:A:H8	1.87	0.40
25:A:2105:U:H2'	25:A:2106:U:C6	2.56	0.40
25:A:2229:U:H2'	25:A:2230:G:C8	2.57	0.40
35:N:29:LYS:HG3	35:N:30:THR:N	2.36	0.40
9:i:17:ALA:HB2	9:i:67:VAL:HG12	2.04	0.40
12:l:44:LYS:HE2	24:v:20:U:O3'	2.22	0.40
25:A:396:G:OP2	47:Z:10:LYS:NZ	2.44	0.40
26:B:5:U:H2'	26:B:6:G:C8	2.56	0.40
30:F:119:ALA:HB1	30:F:167:ARG:HH11	1.87	0.40
37:P:51:LEU:HD21	37:P:70:THR:CG2	2.51	0.40
47:Z:74:ARG:NH2	47:Z:76:GLU:OE1	2.54	0.40
54:7:15:LYS:HB2	54:7:23:LYS:HE2	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	b	222/241 (92%)	206 (93%)	16 (7%)	0	100	100
3	c	204/233 (88%)	197 (97%)	7 (3%)	0	100	100
4	d	203/206 (98%)	200 (98%)	3 (2%)	0	100	100
5	e	154/167 (92%)	149 (97%)	5 (3%)	0	100	100
6	f	100/131 (76%)	83 (83%)	14 (14%)	3 (3%)	3	14
7	g	150/156 (96%)	143 (95%)	7 (5%)	0	100	100
8	h	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
9	i	124/130 (95%)	118 (95%)	6 (5%)	0	100	100
10	j	95/103 (92%)	90 (95%)	4 (4%)	1 (1%)	11	36
11	k	113/129 (88%)	106 (94%)	7 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	l	118/124 (95%)	111 (94%)	7 (6%)	0	100	100
13	m	111/118 (94%)	107 (96%)	4 (4%)	0	100	100
14	n	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
15	o	86/89 (97%)	86 (100%)	0	0	100	100
16	p	78/82 (95%)	75 (96%)	3 (4%)	0	100	100
17	q	77/84 (92%)	75 (97%)	2 (3%)	0	100	100
18	r	52/75 (69%)	51 (98%)	1 (2%)	0	100	100
19	s	80/92 (87%)	76 (95%)	4 (5%)	0	100	100
20	t	83/87 (95%)	80 (96%)	3 (4%)	0	100	100
21	u	53/71 (75%)	53 (100%)	0	0	100	100
27	C	269/273 (98%)	261 (97%)	8 (3%)	0	100	100
28	D	206/209 (99%)	200 (97%)	5 (2%)	1 (0%)	24	54
29	E	199/201 (99%)	195 (98%)	4 (2%)	0	100	100
30	F	175/179 (98%)	163 (93%)	12 (7%)	0	100	100
31	G	173/177 (98%)	152 (88%)	21 (12%)	0	100	100
32	H	39/149 (26%)	36 (92%)	2 (5%)	1 (3%)	4	17
33	L	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
34	M	121/123 (98%)	120 (99%)	1 (1%)	0	100	100
35	N	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
36	O	132/136 (97%)	129 (98%)	3 (2%)	0	100	100
37	P	116/127 (91%)	112 (97%)	4 (3%)	0	100	100
38	Q	114/117 (97%)	102 (90%)	11 (10%)	1 (1%)	14	41
39	R	112/115 (97%)	108 (96%)	4 (4%)	0	100	100
40	S	115/118 (98%)	115 (100%)	0	0	100	100
41	T	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
42	U	108/110 (98%)	107 (99%)	1 (1%)	0	100	100
43	V	91/100 (91%)	83 (91%)	8 (9%)	0	100	100
44	W	100/104 (96%)	94 (94%)	6 (6%)	0	100	100
45	X	92/94 (98%)	86 (94%)	6 (6%)	0	100	100
46	Y	82/85 (96%)	78 (95%)	3 (4%)	1 (1%)	10	34
47	Z	75/78 (96%)	73 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	1	59/63 (94%)	57 (97%)	2 (3%)	0	100	100
49	2	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
50	3	56/70 (80%)	52 (93%)	4 (7%)	0	100	100
51	4	53/57 (93%)	53 (100%)	0	0	100	100
52	5	49/55 (89%)	49 (100%)	0	0	100	100
53	6	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
54	7	62/65 (95%)	59 (95%)	2 (3%)	1 (2%)	7	27
55	8	36/38 (95%)	36 (100%)	0	0	100	100
All	All	5445/5886 (92%)	5219 (96%)	217 (4%)	9 (0%)	44	72

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	f	37	HIS
6	f	68	GLN
38	Q	90	VAL
10	j	57	VAL
28	D	149	ASN
32	H	30	LEU
6	f	48	ALA
46	Y	71	VAL
54	7	32	ILE

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	115/199 (58%)	115 (100%)	0	100	100
3	c	167/190 (88%)	167 (100%)	0	100	100
4	d	172/173 (99%)	172 (100%)	0	100	100
5	e	110/126 (87%)	110 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	f	77/112 (69%)	77 (100%)	0	100	100
7	g	89/129 (69%)	89 (100%)	0	100	100
8	h	102/105 (97%)	102 (100%)	0	100	100
9	i	87/107 (81%)	87 (100%)	0	100	100
10	j	55/90 (61%)	55 (100%)	0	100	100
11	k	85/98 (87%)	82 (96%)	3 (4%)	32	66
12	l	97/103 (94%)	97 (100%)	0	100	100
13	m	78/96 (81%)	78 (100%)	0	100	100
14	n	78/84 (93%)	78 (100%)	0	100	100
15	o	74/77 (96%)	74 (100%)	0	100	100
16	p	58/65 (89%)	58 (100%)	0	100	100
17	q	70/78 (90%)	70 (100%)	0	100	100
18	r	46/65 (71%)	46 (100%)	0	100	100
19	s	68/79 (86%)	68 (100%)	0	100	100
20	t	61/66 (92%)	61 (100%)	0	100	100
21	u	28/61 (46%)	28 (100%)	0	100	100
27	C	213/218 (98%)	213 (100%)	0	100	100
28	D	161/163 (99%)	161 (100%)	0	100	100
29	E	161/165 (98%)	161 (100%)	0	100	100
30	F	146/150 (97%)	146 (100%)	0	100	100
31	G	133/138 (96%)	133 (100%)	0	100	100
32	H	32/114 (28%)	32 (100%)	0	100	100
33	L	116/116 (100%)	116 (100%)	0	100	100
34	M	104/104 (100%)	104 (100%)	0	100	100
35	N	102/103 (99%)	102 (100%)	0	100	100
36	O	107/107 (100%)	107 (100%)	0	100	100
37	P	98/103 (95%)	98 (100%)	0	100	100
38	Q	82/87 (94%)	82 (100%)	0	100	100
39	R	98/100 (98%)	98 (100%)	0	100	100
40	S	89/90 (99%)	89 (100%)	0	100	100
41	T	84/84 (100%)	84 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	U	92/93 (99%)	92 (100%)	0	100	100
43	V	80/84 (95%)	80 (100%)	0	100	100
44	W	80/85 (94%)	80 (100%)	0	100	100
45	X	77/78 (99%)	77 (100%)	0	100	100
46	Y	62/63 (98%)	62 (100%)	0	100	100
47	Z	67/68 (98%)	67 (100%)	0	100	100
48	1	54/55 (98%)	54 (100%)	0	100	100
49	2	48/49 (98%)	48 (100%)	0	100	100
50	3	53/62 (86%)	53 (100%)	0	100	100
51	4	46/48 (96%)	46 (100%)	0	100	100
52	5	46/49 (94%)	46 (100%)	0	100	100
53	6	38/38 (100%)	38 (100%)	0	100	100
54	7	51/52 (98%)	51 (100%)	0	100	100
55	8	34/34 (100%)	34 (100%)	0	100	100
All	All	4271/4803 (89%)	4268 (100%)	3 (0%)	87	97

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	k	56	ARG
11	k	57	LYS
11	k	59	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (83) such sidechains are listed below:

Mol	Chain	Res	Type
2	b	39	HIS
3	c	69	HIS
3	c	100	GLN
3	c	140	ASN
3	c	185	ASN
4	d	59	GLN
4	d	131	ASN
4	d	198	HIS
5	e	19	ASN
5	e	82	GLN

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Mol	Chain	Res	Type
5	e	89	HIS
5	e	97	GLN
5	e	135	ASN
5	e	146	ASN
6	f	63	ASN
8	h	4	GLN
8	h	16	ASN
9	i	31	ASN
9	i	50	GLN
9	i	75	GLN
9	i	126	GLN
10	j	56	HIS
10	j	58	ASN
11	k	28	ASN
12	l	96	HIS
13	m	8	ASN
13	m	14	HIS
13	m	105	ASN
15	o	40	GLN
15	o	51	HIS
16	p	63	GLN
16	p	79	ASN
17	q	47	HIS
18	r	31	ASN
18	r	52	GLN
19	s	83	HIS
20	t	20	HIS
20	t	68	HIS
27	C	46	ASN
27	C	90	ASN
27	C	153	GLN
27	C	239	ASN
27	C	260	ASN
28	D	32	ASN
28	D	67	HIS
28	D	130	GLN
28	D	164	GLN
28	D	185	ASN
29	E	97	ASN
29	E	156	ASN
29	E	163	ASN
30	F	5	HIS

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Mol	Chain	Res	Type
31	G	38	ASN
31	G	143	GLN
33	L	40	HIS
33	L	58	ASN
33	L	80	HIS
33	L	131	ASN
34	M	9	ASN
34	M	89	ASN
34	M	93	GLN
36	O	22	GLN
36	O	45	GLN
36	O	60	GLN
37	P	23	ASN
38	Q	38	GLN
39	R	41	GLN
39	R	77	HIS
40	S	52	GLN
40	S	81	ASN
41	T	6	GLN
41	T	89	HIS
44	W	66	GLN
46	Y	3	HIS
46	Y	12	ASN
46	Y	57	HIS
46	Y	76	ASN
47	Z	6	GLN
47	Z	23	ASN
48	1	58	ASN
51	4	6	ASN
54	7	28	ASN
55	8	35	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1526/1542 (98%)	207 (13%)	0
22	w	72/76 (94%)	12 (16%)	0
22	y	72/76 (94%)	17 (23%)	0
23	x	75/77 (97%)	8 (10%)	0
24	v	11/24 (45%)	3 (27%)	0
25	A	2842/2904 (97%)	399 (14%)	11 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
26	B	119/120 (99%)	12 (10%)	3 (2%)
All	All	4717/4819 (97%)	658 (13%)	14 (0%)

All (658) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	4	U
1	a	5	U
1	a	6	G
1	a	9	G
1	a	22	G
1	a	32	A
1	a	39	G
1	a	47	C
1	a	48	C
1	a	51	A
1	a	71	A
1	a	79	G
1	a	82	G
1	a	84	U
1	a	85	U
1	a	86	G
1	a	95	C
1	a	121	U
1	a	130	A
1	a	131	A
1	a	136	C
1	a	138	G
1	a	144	G
1	a	146	G
1	a	163	C
1	a	164	G
1	a	169	C
1	a	173	U
1	a	174	A
1	a	183	C
1	a	184	G
1	a	197	A
1	a	199	A
1	a	208	U
1	a	209	U
1	a	210	C

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Mol	Chain	Res	Type
1	a	211	G
1	a	212	G
1	a	226	G
1	a	240	G
1	a	245	U
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	306	A
1	a	321	A
1	a	328	C
1	a	341	C
1	a	344	A
1	a	345	C
1	a	346	G
1	a	351	G
1	a	352	C
1	a	354	G
1	a	367	U
1	a	372	C
1	a	373	A
1	a	398	U
1	a	406	G
1	a	412	A
1	a	413	G
1	a	414	A
1	a	421	U
1	a	422	C
1	a	429	U
1	a	462	G
1	a	465	A
1	a	467	U
1	a	468	A
1	a	478	A
1	a	484	G
1	a	486	U
1	a	495	A
1	a	496	A

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Mol	Chain	Res	Type
1	a	497	G
1	a	509	A
1	a	511	C
1	a	518	C
1	a	521	G
1	a	526	C
1	a	527	G7M
1	a	531	U
1	a	547	A
1	a	564	C
1	a	572	A
1	a	573	A
1	a	576	C
1	a	577	G
1	a	596	A
1	a	642	A
1	a	650	G
1	a	653	U
1	a	665	A
1	a	679	C
1	a	680	C
1	a	681	A
1	a	686	U
1	a	687	A
1	a	688	G
1	a	689	C
1	a	703	G
1	a	721	G
1	a	723	U
1	a	734	G
1	a	746	A
1	a	748	G
1	a	755	G
1	a	777	A
1	a	793	U
1	a	794	A
1	a	815	A
1	a	817	C
1	a	821	G
1	a	829	G
1	a	836	G
1	a	838	G

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Mol	Chain	Res	Type
1	a	851	G
1	a	890	G
1	a	902	G
1	a	914	A
1	a	926	G
1	a	929	G
1	a	930	C
1	a	934	C
1	a	935	A
1	a	960	U
1	a	966	2MG
1	a	969	A
1	a	975	A
1	a	976	G
1	a	977	A
1	a	992	U
1	a	993	G
1	a	994	A
1	a	1003	G
1	a	1004	A
1	a	1009	U
1	a	1027	C
1	a	1030	U
1	a	1032	G
1	a	1033	G
1	a	1036	A
1	a	1053	G
1	a	1065	U
1	a	1094	G
1	a	1095	U
1	a	1101	A
1	a	1132	C
1	a	1134	G
1	a	1137	C
1	a	1139	G
1	a	1159	U
1	a	1167	A
1	a	1184	G
1	a	1196	A
1	a	1197	A
1	a	1213	A
1	a	1214	C

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Mol	Chain	Res	Type
1	a	1227	A
1	a	1228	C
1	a	1238	A
1	a	1241	G
1	a	1258	G
1	a	1260	G
1	a	1275	A
1	a	1280	A
1	a	1285	A
1	a	1286	U
1	a	1287	A
1	a	1300	G
1	a	1302	C
1	a	1305	G
1	a	1317	C
1	a	1320	C
1	a	1346	A
1	a	1363	A
1	a	1370	G
1	a	1378	C
1	a	1379	G
1	a	1387	G
1	a	1388	C
1	a	1419	G
1	a	1432	G
1	a	1438	G
1	a	1441	A
1	a	1443	C
1	a	1446	A
1	a	1448	C
1	a	1452	C
1	a	1454	G
1	a	1455	G
1	a	1458	G
1	a	1459	G
1	a	1461	G
1	a	1487	G
1	a	1492	A
1	a	1497	G
1	a	1499	A
1	a	1506	U
1	a	1517	G

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Mol	Chain	Res	Type
1	a	1519	MA6
1	a	1529	G
1	a	1530	G
22	w	19	G
22	w	20	U
22	w	24	G
22	w	40	C
22	w	41	C
22	w	45	U
22	w	46	7MG
22	w	48	C
22	w	58	A
22	w	65	G
22	w	67	C
22	w	74	C
23	x	9	G
23	x	21	A
23	x	35	A
23	x	47	U
23	x	48	C
23	x	58	A
23	x	70	G
23	x	76	A
22	y	6	G
22	y	7	A
22	y	8	4SU
22	y	13	C
22	y	19	G
22	y	20	U
22	y	21	A
22	y	35	A
22	y	37	MIA
22	y	44	G
22	y	45	U
22	y	46	7MG
22	y	48	C
22	y	55	PSU
22	y	57	G
22	y	59	U
22	y	76	A
24	v	15	A
24	v	16	A

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Mol	Chain	Res	Type
24	v	24	A
25	A	3	U
25	A	4	U
25	A	6	A
25	A	10	A
25	A	15	G
25	A	34	U
25	A	35	G
25	A	42	A
25	A	45	G
25	A	51	G
25	A	71	A
25	A	74	A
25	A	75	G
25	A	95	A
25	A	96	C
25	A	100	U
25	A	101	A
25	A	118	A
25	A	119	A
25	A	120	U
25	A	125	A
25	A	131	A
25	A	136	G
25	A	139	U
25	A	140	C
25	A	141	G
25	A	142	A
25	A	160	A
25	A	163	C
25	A	181	A
25	A	196	A
25	A	199	A
25	A	215	G
25	A	216	A
25	A	222	A
25	A	223	A
25	A	228	C
25	A	233	A
25	A	248	G
25	A	267	C
25	A	269	C

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Mol	Chain	Res	Type
25	A	270	A
25	A	271	G
25	A	273	G
25	A	274	C
25	A	276	U
25	A	277	G
25	A	279	A
25	A	281	C
25	A	288	U
25	A	291	G
25	A	311	A
25	A	329	G
25	A	330	A
25	A	356	G
25	A	362	A
25	A	386	G
25	A	396	G
25	A	398	C
25	A	399	U
25	A	400	G
25	A	403	U
25	A	406	G
25	A	411	G
25	A	412	A
25	A	481	G
25	A	491	G
25	A	505	A
25	A	509	C
25	A	532	A
25	A	545	U
25	A	546	U
25	A	547	A
25	A	548	G
25	A	549	G
25	A	563	A
25	A	573	U
25	A	575	A
25	A	596	U
25	A	603	A
25	A	614	A
25	A	615	U
25	A	627	A

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Mol	Chain	Res	Type
25	A	637	A
25	A	642	U
25	A	645	C
25	A	646	U
25	A	647	G
25	A	654	A
25	A	655	A
25	A	686	U
25	A	711	G
25	A	712	G
25	A	717	C
25	A	720	U
25	A	721	A
25	A	726	G
25	A	730	A
25	A	740	C
25	A	747	5MU
25	A	764	A
25	A	775	G
25	A	776	G
25	A	782	A
25	A	784	G
25	A	785	G
25	A	805	G
25	A	812	C
25	A	827	U
25	A	828	U
25	A	845	A
25	A	846	U
25	A	847	U
25	A	859	G
25	A	869	G
25	A	874	G
25	A	876	C
25	A	877	A
25	A	883	G
25	A	888	C
25	A	890	C
25	A	891	G
25	A	895	U
25	A	896	A
25	A	900	A

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Mol	Chain	Res	Type
25	A	901	C
25	A	907	G
25	A	910	A
25	A	915	C
25	A	927	A
25	A	945	A
25	A	946	C
25	A	961	C
25	A	973	A
25	A	974	G
25	A	983	A
25	A	989	G
25	A	996	A
25	A	1012	U
25	A	1013	C
25	A	1026	G
25	A	1033	U
25	A	1038	G
25	A	1040	A
25	A	1047	G
25	A	1108	U
25	A	1111	A
25	A	1112	G
25	A	1115	G
25	A	1119	U
25	A	1132	U
25	A	1133	A
25	A	1135	C
25	A	1142	A
25	A	1169	A
25	A	1170	C
25	A	1172	C
25	A	1212	G
25	A	1236	G
25	A	1250	G
25	A	1253	A
25	A	1256	G
25	A	1271	G
25	A	1272	A
25	A	1273	U
25	A	1300	G
25	A	1301	A

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Mol	Chain	Res	Type
25	A	1352	U
25	A	1365	A
25	A	1378	A
25	A	1379	U
25	A	1383	A
25	A	1395	A
25	A	1416	G
25	A	1419	A
25	A	1427	A
25	A	1428	C
25	A	1433	A
25	A	1452	G
25	A	1453	A
25	A	1460	U
25	A	1482	G
25	A	1493	C
25	A	1497	U
25	A	1508	A
25	A	1509	A
25	A	1510	G
25	A	1515	A
25	A	1521	G
25	A	1522	A
25	A	1524	G
25	A	1535	A
25	A	1536	C
25	A	1537	G
25	A	1566	A
25	A	1569	A
25	A	1578	U
25	A	1581	G
25	A	1584	U
25	A	1598	A
25	A	1607	C
25	A	1626	A
25	A	1647	U
25	A	1648	U
25	A	1649	G
25	A	1667	G
25	A	1674	G
25	A	1675	C
25	A	1715	G

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Mol	Chain	Res	Type
25	A	1729	U
25	A	1730	C
25	A	1742	U
25	A	1764	C
25	A	1773	A
25	A	1782	U
25	A	1786	A
25	A	1800	C
25	A	1801	A
25	A	1808	A
25	A	1816	C
25	A	1829	A
25	A	1847	A
25	A	1858	A
25	A	1871	A
25	A	1872	A
25	A	1873	G
25	A	1875	G
25	A	1879	C
25	A	1906	G
25	A	1912	A
25	A	1929	G
25	A	1930	G
25	A	1937	A
25	A	1955	U
25	A	1967	C
25	A	1970	A
25	A	1971	U
25	A	1972	G
25	A	1991	U
25	A	1993	U
25	A	2021	C
25	A	2023	C
25	A	2030	6MZ
25	A	2031	A
25	A	2033	A
25	A	2036	C
25	A	2043	C
25	A	2055	C
25	A	2056	G
25	A	2060	A
25	A	2061	G

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Mol	Chain	Res	Type
25	A	2062	A
25	A	2069	G7M
25	A	2093	G
25	A	2098	U
25	A	2100	G
25	A	2108	A
25	A	2110	G
25	A	2111	U
25	A	2112	G
25	A	2113	U
25	A	2118	U
25	A	2119	A
25	A	2131	U
25	A	2132	U
25	A	2133	G
25	A	2136	G
25	A	2145	C
25	A	2151	U
25	A	2152	G
25	A	2157	G
25	A	2162	G
25	A	2164	C
25	A	2170	A
25	A	2171	A
25	A	2172	U
25	A	2173	A
25	A	2179	C
25	A	2182	U
25	A	2187	U
25	A	2189	U
25	A	2190	G
25	A	2192	U
25	A	2193	G
25	A	2194	U
25	A	2198	A
25	A	2203	U
25	A	2204	G
25	A	2225	A
25	A	2227	A
25	A	2238	G
25	A	2239	G
25	A	2278	A

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Mol	Chain	Res	Type
25	A	2283	C
25	A	2287	A
25	A	2288	A
25	A	2305	U
25	A	2308	G
25	A	2319	G
25	A	2322	A
25	A	2325	G
25	A	2328	A
25	A	2330	G
25	A	2331	G
25	A	2333	A
25	A	2335	A
25	A	2336	A
25	A	2340	A
25	A	2345	G
25	A	2347	C
25	A	2350	C
25	A	2351	G
25	A	2354	C
25	A	2356	U
25	A	2357	G
25	A	2368	C
25	A	2369	A
25	A	2378	A
25	A	2380	C
25	A	2381	A
25	A	2382	G
25	A	2383	G
25	A	2385	C
25	A	2396	G
25	A	2406	A
25	A	2425	A
25	A	2429	G
25	A	2435	A
25	A	2441	U
25	A	2448	A
25	A	2469	A
25	A	2470	G
25	A	2475	C
25	A	2484	G
25	A	2494	G

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Mol	Chain	Res	Type
25	A	2498	OMC
25	A	2502	G
25	A	2505	G
25	A	2518	A
25	A	2520	C
25	A	2527	C
25	A	2529	G
25	A	2537	U
25	A	2539	C
25	A	2547	A
25	A	2566	A
25	A	2567	G
25	A	2602	A
25	A	2609	U
25	A	2613	U
25	A	2615	U
25	A	2629	U
25	A	2630	G
25	A	2636	C
25	A	2646	C
25	A	2649	C
25	A	2652	C
25	A	2654	A
25	A	2663	G
25	A	2669	G
25	A	2673	G
25	A	2689	U
25	A	2690	U
25	A	2714	G
25	A	2716	C
25	A	2726	A
25	A	2732	G
25	A	2733	A
25	A	2740	A
25	A	2741	A
25	A	2743	U
25	A	2744	G
25	A	2748	A
25	A	2749	A
25	A	2750	A
25	A	2752	C
25	A	2757	A

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Mol	Chain	Res	Type
25	A	2765	A
25	A	2778	A
25	A	2798	U
25	A	2800	A
25	A	2818	U
25	A	2820	A
25	A	2821	A
25	A	2832	U
25	A	2833	U
25	A	2835	A
25	A	2849	U
25	A	2850	A
25	A	2861	U
25	A	2873	A
25	A	2880	C
25	A	2883	A
25	A	2884	U
25	A	2891	U
25	A	2896	C
25	A	2897	U
25	A	2898	U
25	A	2900	A
26	B	4	C
26	B	9	G
26	B	24	G
26	B	35	C
26	B	43	C
26	B	53	A
26	B	56	G
26	B	62	C
26	B	89	U
26	B	99	A
26	B	109	A
26	B	119	A

All (14) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	A	3	U
25	A	784	G
25	A	1026	G
25	A	1037	G

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Mol	Chain	Res	Type
25	A	2189	U
25	A	2191	A
25	A	2193	G
25	A	2538	C
25	A	2756	U
25	A	2895	G
25	A	2897	U
26	B	3	C
26	B	42	C
26	B	61	G

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

58 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$
1	PSU	a	516	1	18,21,22	1.37	2 (11%)	21,30,33	2.05	4 (19%)
25	PSU	A	746	25,56	18,21,22	1.40	3 (16%)	21,30,33	2.02	4 (19%)
1	UR3	a	1498	1	19,22,23	0.95	0	26,32,35	1.72	2 (7%)
25	5MC	A	1962	25	19,22,23	1.41	3 (15%)	26,32,35	1.09	2 (7%)
22	5MU	w	54	22	19,22,23	1.40	5 (26%)	27,32,35	1.94	5 (18%)
12	D2T	l	89	12	8,9,10	1.98	1 (12%)	6,11,13	2.56	2 (33%)
36	MS6	O	82	36	5,7,8	0.56	0	2,7,9	1.24	0
22	PSU	y	55	22	18,21,22	1.37	2 (11%)	21,30,33	2.04	3 (14%)
25	H2U	A	2449	25	18,21,22	1.11	3 (16%)	19,30,33	1.11	2 (10%)
1	MA6	a	1519	1	23,26,27	1.47	5 (21%)	33,38,41	2.43	13 (39%)
23	5MC	x	32	23	19,22,23	1.46	3 (15%)	26,32,35	1.23	3 (11%)
25	PSU	A	1911	25	18,21,22	1.40	3 (16%)	21,30,33	2.06	3 (14%)
25	PSU	A	2504	25	18,21,22	1.41	4 (22%)	21,30,33	2.04	3 (14%)
25	3TD	A	1915	25	19,22,23	4.22	7 (36%)	23,32,35	1.83	4 (17%)
25	PSU	A	2457	25	18,21,22	1.42	4 (22%)	21,30,33	2.10	5 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
25	PSU	A	2604	25	18,21,22	1.41	3 (16%)	21,30,33	2.08	4 (19%)
1	2MG	a	966	1	23,26,27	1.29	4 (17%)	33,38,41	2.21	7 (21%)
22	PSU	y	39	22	18,21,22	1.36	2 (11%)	21,30,33	2.00	3 (14%)
25	1MG	A	745	25	23,26,27	1.17	3 (13%)	33,39,42	1.77	5 (15%)
28	MEQ	D	150	28	8,9,10	0.51	0	5,10,12	0.34	0
1	5MC	a	967	1	19,22,23	1.52	3 (15%)	26,32,35	1.11	2 (7%)
1	4OC	a	1402	1	20,23,24	0.75	0	25,32,35	0.95	1 (4%)
22	4SU	w	8	22	18,21,22	1.90	4 (22%)	25,30,33	2.10	4 (16%)
25	6MZ	A	1618	25	22,25,26	1.44	5 (22%)	29,36,39	2.21	10 (34%)
23	PSU	x	55	23	18,21,22	1.37	2 (11%)	21,30,33	2.06	4 (19%)
22	PSU	w	55	22	18,21,22	1.36	2 (11%)	21,30,33	2.02	3 (14%)
22	MIA	w	37	22	28,31,32	2.33	6 (21%)	38,44,47	2.83	14 (36%)
1	2MG	a	1516	1	23,26,27	1.23	4 (17%)	33,38,41	2.26	9 (27%)
23	4SU	x	8	23	18,21,22	1.86	4 (22%)	25,30,33	2.29	5 (20%)
25	2MG	A	1835	25	23,26,27	1.25	3 (13%)	33,38,41	2.27	9 (27%)
22	4SU	y	8	22	18,21,22	1.83	4 (22%)	25,30,33	2.34	5 (20%)
23	5MU	x	54	23	19,22,23	1.36	5 (26%)	27,32,35	2.13	6 (22%)
25	PSU	A	2605	25	18,21,22	1.40	3 (16%)	21,30,33	2.09	4 (19%)
25	PSU	A	2580	25	18,21,22	1.44	5 (27%)	21,30,33	2.17	4 (19%)
25	2MG	A	2445	25	23,26,27	1.27	3 (13%)	33,38,41	2.23	9 (27%)
1	5MC	a	1407	1	19,22,23	1.47	3 (15%)	26,32,35	1.13	3 (11%)
25	OMC	A	2498	25,56	19,22,23	0.82	0	25,31,34	0.95	1 (4%)
22	MIA	y	37	22	21,24,32	1.56	4 (19%)	30,35,47	2.02	7 (23%)
25	2MA	A	2503	25,56	22,25,26	1.46	5 (22%)	32,37,40	2.28	9 (28%)
36	4D4	O	81	36	9,11,12	2.72	3 (33%)	7,13,15	0.81	0
22	7MG	w	46	22	23,26,27	1.31	3 (13%)	27,39,42	2.62	6 (22%)
25	PSU	A	955	25	18,21,22	1.42	4 (22%)	21,30,33	2.08	3 (14%)
25	G7M	A	2069	25	23,26,27	1.56	4 (17%)	34,39,42	1.68	5 (14%)
1	2MG	a	1207	1	23,26,27	1.27	4 (17%)	33,38,41	2.20	7 (21%)
1	MA6	a	1518	1	23,26,27	1.48	5 (21%)	33,38,41	2.39	13 (39%)
22	PSU	w	39	22	18,21,22	1.29	2 (11%)	21,30,33	2.26	3 (14%)
22	5MU	y	54	22	19,22,23	1.38	6 (31%)	27,32,35	2.07	6 (22%)
11	IAS	k	119	11	6,7,8	0.97	0	3,8,10	1.45	1 (33%)
25	5MU	A	747	25	19,22,23	1.38	4 (21%)	27,32,35	2.20	6 (22%)
22	PSU	w	32	22	18,21,22	1.37	2 (11%)	21,30,33	2.03	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	G7M	a	527	1	23,26,27	1.59	3 (13%)	34,39,42	1.78	5 (14%)
25	5MU	A	1939	25	19,22,23	1.39	4 (21%)	27,32,35	2.15	6 (22%)
25	PSU	A	1917	25	18,21,22	1.42	3 (16%)	21,30,33	2.01	3 (14%)
25	OMG	A	2251	25,23	23,26,27	1.22	3 (13%)	32,38,41	1.97	6 (18%)
25	6MZ	A	2030	25	22,25,26	1.45	5 (22%)	29,36,39	2.32	11 (37%)
22	7MG	y	46	22	23,26,27	1.31	3 (13%)	27,39,42	2.59	6 (22%)
22	PSU	y	32	22	18,21,22	1.36	2 (11%)	21,30,33	2.00	3 (14%)
25	OMU	A	2552	25	19,22,23	1.26	3 (15%)	25,31,34	1.82	5 (20%)

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
1	PSU	a	516	1	-	0/7/25/26	0/2/2/2
25	PSU	A	746	25,56	-	2/7/25/26	0/2/2/2
1	UR3	a	1498	1	-	0/7/25/26	0/2/2/2
25	5MC	A	1962	25	-	0/7/25/26	0/2/2/2
22	5MU	w	54	22	-	0/7/25/26	0/2/2/2
12	D2T	l	89	12	-	1/7/12/14	-
36	MS6	O	82	36	-	4/4/6/8	-
22	PSU	y	55	22	-	3/7/25/26	0/2/2/2
25	H2U	A	2449	25	-	0/7/38/39	0/2/2/2
1	MA6	a	1519	1	-	4/11/29/30	0/3/3/3
23	5MC	x	32	23	-	0/7/25/26	0/2/2/2
25	PSU	A	1911	25	-	0/7/25/26	0/2/2/2
25	PSU	A	2504	25	-	1/7/25/26	0/2/2/2
25	3TD	A	1915	25	-	0/7/25/26	0/2/2/2
25	PSU	A	2457	25	-	0/7/25/26	0/2/2/2
25	PSU	A	2604	25	-	0/7/25/26	0/2/2/2
1	2MG	a	966	1	-	0/9/27/28	0/3/3/3
22	PSU	y	39	22	-	0/7/25/26	0/2/2/2
25	1MG	A	745	25	-	0/7/25/26	0/3/3/3
28	MEQ	D	150	28	-	2/8/9/11	-
1	5MC	a	967	1	-	0/7/25/26	0/2/2/2
1	4OC	a	1402	1	-	1/9/29/30	0/2/2/2
22	4SU	w	8	22	-	0/7/25/26	0/2/2/2
25	6MZ	A	1618	25	-	0/9/27/28	0/3/3/3
23	PSU	x	55	23	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	PSU	w	55	22	-	0/7/25/26	0/2/2/2
22	MIA	w	37	22	-	2/15/33/34	0/3/3/3
1	2MG	a	1516	1	-	0/9/27/28	0/3/3/3
23	4SU	x	8	23	-	0/7/25/26	0/2/2/2
25	2MG	A	1835	25	-	0/9/27/28	0/3/3/3
22	4SU	y	8	22	-	2/7/25/26	0/2/2/2
23	5MU	x	54	23	-	0/7/25/26	0/2/2/2
25	PSU	A	2605	25	-	0/7/25/26	0/2/2/2
25	PSU	A	2580	25	-	0/7/25/26	0/2/2/2
25	2MG	A	2445	25	-	0/9/27/28	0/3/3/3
1	5MC	a	1407	1	-	0/7/25/26	0/2/2/2
25	OMC	A	2498	25,56	-	1/9/27/28	0/2/2/2
22	MIA	y	37	22	-	2/7/25/34	0/3/3/3
25	2MA	A	2503	25,56	-	0/7/25/26	0/3/3/3
36	4D4	O	81	36	-	2/11/12/14	-
22	7MG	w	46	22	-	2/7/37/38	0/3/3/3
25	PSU	A	955	25	-	0/7/25/26	0/2/2/2
25	G7M	A	2069	25	-	0/7/25/26	0/3/3/3
1	2MG	a	1207	1	-	0/9/27/28	0/3/3/3
1	MA6	a	1518	1	-	2/11/29/30	0/3/3/3
22	PSU	w	39	22	-	0/7/25/26	0/2/2/2
22	5MU	y	54	22	-	0/7/25/26	0/2/2/2
11	IAS	k	119	11	-	3/7/7/8	-
25	5MU	A	747	25	-	0/7/25/26	0/2/2/2
22	PSU	w	32	22	-	0/7/25/26	0/2/2/2
1	G7M	a	527	1	-	2/7/25/26	0/3/3/3
25	5MU	A	1939	25	-	0/7/25/26	0/2/2/2
25	PSU	A	1917	25	-	2/7/25/26	0/2/2/2
25	OMG	A	2251	25,23	-	0/9/27/28	0/3/3/3
25	6MZ	A	2030	25	-	2/9/27/28	0/3/3/3
22	7MG	y	46	22	-	6/7/37/38	0/3/3/3
22	PSU	y	32	22	-	0/7/25/26	0/2/2/2
25	OMU	A	2552	25	-	0/9/27/28	0/2/2/2

All (185) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	A	1915	3TD	C6-C5	12.56	1.49	1.35
25	A	1915	3TD	C2-N1	9.74	1.49	1.37
22	w	37	MIA	C2-S10	-7.36	1.69	1.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	w	37	MIA	C13-C14	6.73	1.52	1.32
36	O	81	4D4	CZ-NE	6.33	1.45	1.33
25	A	1915	3TD	C6-N1	5.78	1.45	1.36
1	a	967	5MC	C5-C4	5.33	1.48	1.44
1	a	527	G7M	C5-N7	-5.29	1.33	1.39
25	A	2069	G7M	C5-N7	-5.16	1.33	1.39
23	x	8	4SU	C4-S4	-5.11	1.59	1.68
1	a	1407	5MC	C5-C4	5.08	1.48	1.44
22	y	8	4SU	C4-S4	-5.07	1.59	1.68
25	A	1915	3TD	C2-N3	5.02	1.49	1.38
22	w	8	4SU	C4-S4	-5.00	1.59	1.68
23	x	32	5MC	C5-C4	4.95	1.47	1.44
22	y	37	MIA	C5-C4	4.86	1.47	1.39
12	l	89	D2T	CB-CA	-4.79	1.53	1.54
25	A	1962	5MC	C5-C4	4.76	1.47	1.44
22	w	37	MIA	C5-C4	4.51	1.47	1.39
1	a	1518	MA6	C5-C4	4.48	1.47	1.39
1	a	1519	MA6	C5-C4	4.45	1.47	1.39
25	A	1618	6MZ	C5-C4	4.37	1.46	1.39
25	A	2503	2MA	C5-C4	4.28	1.46	1.39
25	A	2030	6MZ	C5-C4	4.28	1.46	1.39
36	O	81	4D4	CZ-NH2	3.77	1.45	1.32
22	w	8	4SU	C4-N3	-3.71	1.33	1.37
22	y	55	PSU	C6-C5	3.58	1.39	1.35
22	y	39	PSU	C6-C5	3.47	1.39	1.35
23	x	8	4SU	C4-N3	-3.41	1.34	1.37
22	y	8	4SU	C4-N3	-3.39	1.34	1.37
23	x	55	PSU	C6-C5	3.31	1.39	1.35
22	y	32	PSU	C6-C5	3.29	1.38	1.35
22	y	46	7MG	C5-C4	3.24	1.47	1.37
22	w	46	7MG	C5-C4	3.23	1.47	1.37
22	w	32	PSU	C6-C5	3.16	1.38	1.35
25	A	1911	PSU	C6-C5	3.15	1.38	1.35
1	a	527	G7M	C5-C4	3.13	1.46	1.38
25	A	1917	PSU	C6-C5	3.11	1.38	1.35
1	a	966	2MG	C5-C4	3.08	1.47	1.38
1	a	1207	2MG	C5-C4	3.07	1.47	1.38
25	A	745	1MG	C5-C4	3.07	1.47	1.38
22	w	55	PSU	C6-C5	3.05	1.38	1.35
25	A	746	PSU	C6-C5	3.01	1.38	1.35
1	a	516	PSU	C6-C5	3.00	1.38	1.35
25	A	2605	PSU	C6-C5	2.99	1.38	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	A	2605	PSU	C4-N3	-2.97	1.33	1.38
25	A	2251	OMG	C5-C4	2.96	1.46	1.38
22	w	46	7MG	C4-N9	-2.96	1.34	1.37
25	A	2604	PSU	C4-N3	-2.95	1.33	1.38
25	A	2069	G7M	C5-C4	2.94	1.45	1.38
25	A	2604	PSU	C6-C5	2.94	1.38	1.35
25	A	2457	PSU	C4-N3	-2.94	1.33	1.38
25	A	746	PSU	C4-N3	-2.93	1.33	1.38
25	A	747	5MU	C4-N3	-2.93	1.33	1.38
25	A	2552	OMU	C4-N3	-2.93	1.33	1.38
25	A	1835	2MG	C5-C4	2.91	1.46	1.38
25	A	955	PSU	C4-N3	-2.91	1.33	1.38
25	A	2504	PSU	C4-N3	-2.91	1.33	1.38
25	A	955	PSU	C6-C5	2.90	1.38	1.35
25	A	1939	5MU	C4-N3	-2.89	1.33	1.38
22	w	8	4SU	C5-C4	-2.89	1.39	1.42
23	x	8	4SU	C5-C4	-2.89	1.39	1.42
1	a	1516	2MG	C5-C4	2.88	1.46	1.38
22	w	39	PSU	C6-C5	2.87	1.38	1.35
25	A	1911	PSU	C4-N3	-2.85	1.33	1.38
22	w	54	5MU	C4-N3	-2.82	1.33	1.38
25	A	2445	2MG	C5-C4	2.81	1.46	1.38
22	y	46	7MG	C4-N9	-2.80	1.34	1.37
25	A	2580	PSU	C4-N3	-2.80	1.33	1.38
25	A	2504	PSU	C6-C5	2.78	1.38	1.35
25	A	2580	PSU	C6-C5	2.76	1.38	1.35
25	A	2449	H2U	C2-N3	-2.76	1.33	1.38
25	A	2445	2MG	C6-N1	-2.76	1.33	1.38
22	y	54	5MU	C6-C5	2.76	1.39	1.34
25	A	1917	PSU	C4-N3	-2.76	1.33	1.38
1	a	966	2MG	C6-N1	-2.75	1.33	1.38
25	A	2251	OMG	C6-N1	-2.74	1.33	1.38
25	A	1915	3TD	C4-N3	2.74	1.46	1.40
1	a	516	PSU	C4-N3	-2.74	1.33	1.38
22	w	55	PSU	C4-N3	-2.73	1.33	1.38
1	a	1519	MA6	C5-C6	2.73	1.48	1.41
22	y	37	MIA	C5-C6	2.70	1.48	1.41
22	y	8	4SU	C5-C4	-2.67	1.39	1.42
25	A	2449	H2U	C4-N3	-2.66	1.33	1.37
25	A	1835	2MG	C6-N1	-2.66	1.33	1.38
23	x	54	5MU	C4-N3	-2.65	1.33	1.38
23	x	55	PSU	C4-N3	-2.64	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	a	1207	2MG	C6-N1	-2.63	1.33	1.38
25	A	2030	6MZ	C5-C6	2.63	1.48	1.41
22	w	32	PSU	C4-N3	-2.63	1.33	1.38
25	A	1915	3TD	O2-C2	-2.63	1.18	1.23
25	A	1939	5MU	C6-C5	2.63	1.38	1.34
25	A	1618	6MZ	C5-C6	2.62	1.48	1.41
25	A	2069	G7M	C6-N1	-2.61	1.34	1.38
1	a	1518	MA6	C5-C6	2.59	1.48	1.41
22	y	32	PSU	C4-N3	-2.59	1.34	1.38
22	w	37	MIA	C5-C6	2.59	1.48	1.41
1	a	967	5MC	C6-C5	2.58	1.38	1.34
23	x	54	5MU	C6-C5	2.58	1.38	1.34
1	a	527	G7M	C6-N1	-2.57	1.34	1.38
23	x	32	5MC	C6-C5	2.57	1.38	1.34
25	A	2503	2MA	C5-C6	2.56	1.48	1.41
22	y	54	5MU	C4-N3	-2.56	1.34	1.38
25	A	747	5MU	C6-N1	-2.55	1.33	1.38
25	A	2457	PSU	C6-C5	2.55	1.38	1.35
1	a	1518	MA6	C5-N7	-2.54	1.34	1.39
22	w	54	5MU	C6-C5	2.54	1.38	1.34
1	a	1516	2MG	C6-N1	-2.53	1.34	1.38
23	x	32	5MC	C6-N1	-2.53	1.33	1.38
25	A	1939	5MU	C6-N1	-2.52	1.33	1.38
25	A	1962	5MC	C6-N1	-2.51	1.33	1.38
1	a	1407	5MC	C6-C5	2.51	1.38	1.34
25	A	2552	OMU	C2-N3	-2.51	1.33	1.38
25	A	747	5MU	C6-C5	2.51	1.38	1.34
22	y	55	PSU	C4-N3	-2.49	1.34	1.38
22	y	39	PSU	C4-N3	-2.48	1.34	1.38
25	A	2503	2MA	C5-N7	-2.45	1.34	1.39
25	A	2030	6MZ	C5-N7	-2.44	1.34	1.39
1	a	967	5MC	C6-N1	-2.43	1.33	1.38
25	A	1962	5MC	C6-C5	2.43	1.38	1.34
22	w	8	4SU	C2-N3	-2.42	1.33	1.38
1	a	1407	5MC	C6-N1	-2.41	1.33	1.38
22	w	37	MIA	C5-N7	-2.41	1.34	1.39
25	A	1939	5MU	C2-N3	-2.41	1.33	1.38
25	A	1618	6MZ	C5-N7	-2.41	1.34	1.39
22	w	54	5MU	C2-N3	-2.40	1.33	1.38
36	O	81	4D4	CZ-NH1	-2.39	1.25	1.34
1	a	1519	MA6	C5-N7	-2.39	1.34	1.39
23	x	54	5MU	C6-N1	-2.36	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	A	2445	2MG	C5-N7	-2.36	1.34	1.39
22	w	54	5MU	C6-N1	-2.35	1.34	1.38
25	A	2251	OMG	C5-N7	-2.34	1.34	1.39
22	w	46	7MG	C6-N1	-2.33	1.34	1.38
25	A	2030	6MZ	C4-N9	-2.33	1.32	1.37
22	y	46	7MG	C6-N1	-2.32	1.34	1.38
25	A	2580	PSU	O4'-C1'	-2.29	1.40	1.43
1	a	966	2MG	C5-N7	-2.29	1.34	1.39
22	y	54	5MU	C4-C5	2.29	1.48	1.44
22	y	37	MIA	C5-N7	-2.29	1.34	1.39
25	A	2457	PSU	C2-N3	-2.29	1.33	1.37
25	A	2503	2MA	C8-N7	2.29	1.36	1.31
25	A	1835	2MG	C5-N7	-2.28	1.34	1.39
25	A	2504	PSU	C2-N3	-2.27	1.33	1.37
22	w	39	PSU	C4-N3	-2.27	1.34	1.38
25	A	745	1MG	C5-N7	-2.26	1.34	1.39
25	A	747	5MU	C2-N3	-2.26	1.34	1.38
22	y	37	MIA	C8-N7	2.25	1.36	1.31
1	a	966	2MG	C2-N3	2.25	1.36	1.32
1	a	1519	MA6	C8-N7	2.25	1.36	1.31
25	A	1915	3TD	O4-C4	-2.23	1.18	1.23
22	w	37	MIA	C8-N7	2.21	1.35	1.31
23	x	8	4SU	C2-N3	-2.21	1.34	1.38
1	a	1207	2MG	C2-N3	2.21	1.36	1.32
25	A	2552	OMU	C5-C4	-2.20	1.38	1.43
22	y	54	5MU	C6-N1	-2.19	1.34	1.38
25	A	955	PSU	C2-N3	-2.19	1.33	1.37
25	A	2580	PSU	C2-N1	-2.18	1.33	1.36
22	y	8	4SU	C2-N3	-2.18	1.34	1.38
25	A	1618	6MZ	C8-N7	2.18	1.35	1.31
25	A	2030	6MZ	C8-N7	2.17	1.35	1.31
25	A	2449	H2U	C2-N1	-2.16	1.32	1.35
1	a	1207	2MG	C5-N7	-2.16	1.34	1.39
1	a	1518	MA6	C4-N9	-2.16	1.33	1.37
25	A	2605	PSU	C2-N3	-2.15	1.33	1.37
25	A	745	1MG	C2-N1	2.14	1.41	1.37
25	A	2604	PSU	C2-N3	-2.14	1.33	1.37
25	A	746	PSU	C2-N3	-2.14	1.34	1.37
25	A	2580	PSU	C2-N3	-2.13	1.34	1.37
25	A	2457	PSU	C2-N1	-2.13	1.33	1.36
22	y	54	5MU	C2-N1	2.11	1.41	1.38
1	a	1516	2MG	C5-N7	-2.10	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	A	1618	6MZ	C4-N9	-2.10	1.33	1.37
25	A	2503	2MA	C4-N9	-2.09	1.33	1.37
25	A	1917	PSU	C2-N1	-2.09	1.33	1.36
25	A	955	PSU	C2-N1	-2.09	1.33	1.36
23	x	54	5MU	C4-C5	2.08	1.48	1.44
25	A	2504	PSU	C2-N1	-2.07	1.34	1.36
23	x	54	5MU	C2-N3	-2.07	1.34	1.38
25	A	2069	G7M	C4-N9	-2.06	1.32	1.38
22	w	54	5MU	C4-C5	2.03	1.48	1.44
1	a	1516	2MG	C4-N9	-2.03	1.32	1.38
1	a	1518	MA6	C8-N7	2.03	1.35	1.31
1	a	1519	MA6	C4-N9	-2.01	1.33	1.37
25	A	1911	PSU	C2-N3	-2.01	1.34	1.37
22	y	54	5MU	C2-N3	-2.00	1.34	1.38

All (282) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	w	37	MIA	C12-C13-C14	-9.20	110.50	127.01
22	w	46	7MG	N9-C4-N3	8.88	138.48	125.46
22	y	46	7MG	N9-C4-N3	8.75	138.28	125.46
25	A	2503	2MA	C5-C4-N3	-8.00	118.75	127.18
22	w	37	MIA	C5-C4-N3	-7.93	118.83	127.18
25	A	1835	2MG	C2-N3-C4	7.35	121.19	112.00
22	y	8	4SU	C4-N3-C2	-7.21	120.40	127.31
1	a	1207	2MG	C2-N3-C4	7.20	121.00	112.00
1	a	1516	2MG	C2-N3-C4	7.16	120.96	112.00
25	A	2445	2MG	C2-N3-C4	7.12	120.90	112.00
1	a	966	2MG	C2-N3-C4	7.09	120.87	112.00
23	x	8	4SU	C4-N3-C2	-6.95	120.66	127.31
22	w	39	PSU	N1-C2-N3	6.81	122.35	115.17
1	a	1498	UR3	C4-N3-C2	-6.80	119.11	124.58
25	A	2580	PSU	N1-C2-N3	6.66	122.19	115.17
25	A	2457	PSU	N1-C2-N3	6.58	122.11	115.17
25	A	1911	PSU	N1-C2-N3	6.53	122.05	115.17
1	a	966	2MG	C5-C4-N3	-6.49	118.07	128.39
25	A	955	PSU	N1-C2-N3	6.48	122.01	115.17
25	A	2604	PSU	N1-C2-N3	6.47	122.00	115.17
25	A	2605	PSU	N1-C2-N3	6.44	121.96	115.17
25	A	2504	PSU	N1-C2-N3	6.41	121.93	115.17
23	x	55	PSU	N1-C2-N3	6.38	121.90	115.17
25	A	746	PSU	N1-C2-N3	6.37	121.89	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	a	1207	2MG	C5-C4-N3	-6.37	118.25	128.39
1	a	516	PSU	N1-C2-N3	6.36	121.88	115.17
22	w	32	PSU	N1-C2-N3	6.35	121.87	115.17
25	A	1917	PSU	N1-C2-N3	6.33	121.85	115.17
22	y	55	PSU	N1-C2-N3	6.29	121.80	115.17
22	y	39	PSU	N1-C2-N3	6.27	121.78	115.17
25	A	1835	2MG	C5-C4-N3	-6.24	118.46	128.39
22	y	32	PSU	N1-C2-N3	6.24	121.75	115.17
22	w	55	PSU	N1-C2-N3	6.22	121.73	115.17
22	w	37	MIA	N3-C4-N9	6.21	134.87	126.99
25	A	2251	OMG	C5-C4-N3	-6.20	118.52	128.39
22	w	8	4SU	C4-N3-C2	-6.11	121.45	127.31
25	A	2503	2MA	N3-C4-N9	6.02	134.63	126.99
25	A	2445	2MG	C5-C4-N3	-6.00	118.84	128.39
22	y	37	MIA	C5-C4-N3	-5.97	118.49	126.72
22	y	8	4SU	C5-C4-N3	5.97	120.30	114.75
23	x	8	4SU	C5-C4-N3	5.86	120.20	114.75
1	a	1516	2MG	C5-C4-N3	-5.86	119.07	128.39
25	A	1915	3TD	N1-C2-N3	5.78	120.34	116.13
25	A	1618	6MZ	C5-C4-N3	-5.74	118.81	126.72
1	a	1519	MA6	C5-C4-N3	-5.74	118.81	126.72
1	a	527	G7M	N9-C4-N3	5.70	137.35	125.95
22	w	8	4SU	C5-C4-N3	5.69	120.04	114.75
1	a	1518	MA6	C5-C4-N3	-5.65	118.94	126.72
1	a	527	G7M	C5-C4-N3	-5.60	117.57	128.15
22	w	46	7MG	C5-C4-N3	-5.54	117.73	128.13
25	A	745	1MG	C5-C4-N3	-5.53	119.59	128.39
22	y	46	7MG	C5-C4-N3	-5.50	117.81	128.13
25	A	2030	6MZ	C5-C4-N3	-5.39	119.30	126.72
25	A	1939	5MU	N3-C2-N1	5.34	121.85	114.89
25	A	747	5MU	C4-N3-C2	-5.32	120.36	127.34
25	A	1939	5MU	C4-N3-C2	-5.30	120.39	127.34
25	A	747	5MU	N3-C2-N1	5.30	121.79	114.89
22	w	46	7MG	N9-C8-N7	-5.25	95.94	103.37
25	A	2069	G7M	N9-C4-N3	5.19	136.33	125.95
23	x	54	5MU	C4-N3-C2	-5.17	120.56	127.34
22	y	46	7MG	N9-C8-N7	-5.14	96.10	103.37
25	A	2069	G7M	C5-C4-N3	-5.10	118.52	128.15
22	y	54	5MU	C4-N3-C2	-5.08	120.68	127.34
25	A	2251	OMG	C2-N3-C4	5.00	120.92	112.30
1	a	966	2MG	N9-C4-N3	4.97	135.89	125.95
22	y	54	5MU	N3-C2-N1	4.96	121.35	114.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	A	2030	6MZ	C9-N6-C6	-4.96	118.25	122.85
25	A	2552	OMU	C4-N3-C2	-4.89	120.54	126.61
22	w	39	PSU	C4-N3-C2	-4.89	119.64	126.37
1	a	527	G7M	C2-N3-C4	4.85	120.65	112.30
23	x	54	5MU	N3-C2-N1	4.81	121.16	114.89
22	y	37	MIA	N3-C4-N9	4.81	135.34	127.17
1	a	1207	2MG	N9-C4-N3	4.78	135.52	125.95
1	a	1519	MA6	C10-N6-C6	-4.68	108.61	120.52
23	x	54	5MU	C5-C4-N3	4.62	119.34	115.32
1	a	1518	MA6	C10-N6-C6	-4.61	108.80	120.52
22	w	54	5MU	N3-C2-N1	4.59	120.87	114.89
25	A	1835	2MG	N9-C4-N3	4.58	135.11	125.95
25	A	2251	OMG	N9-C4-N3	4.58	135.11	125.95
25	A	2069	G7M	C2-N3-C4	4.57	120.18	112.30
22	w	54	5MU	C4-N3-C2	-4.57	121.35	127.34
1	a	1518	MA6	N3-C4-N9	4.54	134.88	127.17
25	A	1618	6MZ	N3-C4-N9	4.53	134.87	127.17
1	a	1519	MA6	C9-N6-C6	-4.51	109.05	120.52
23	x	54	5MU	O4-C4-C5	-4.50	119.77	124.92
22	y	46	7MG	C2-N3-C4	4.44	119.95	112.30
22	w	46	7MG	C2-N3-C4	4.43	119.94	112.30
25	A	745	1MG	C2-N3-C4	4.42	121.92	111.98
22	w	39	PSU	O2-C2-N1	-4.41	118.24	122.79
22	y	8	4SU	N3-C2-N1	4.41	120.63	114.89
25	A	2445	2MG	N9-C4-N3	4.40	134.75	125.95
22	y	54	5MU	C5-C4-N3	4.37	119.12	115.32
25	A	1939	5MU	C5-C4-N3	4.35	119.10	115.32
25	A	2552	OMU	N3-C2-N1	4.34	120.54	114.89
25	A	746	PSU	C4-N3-C2	-4.33	120.41	126.37
1	a	1519	MA6	N3-C4-N9	4.32	134.52	127.17
25	A	1915	3TD	C4-N3-C2	-4.32	120.04	124.61
25	A	747	5MU	O4-C4-C5	-4.32	119.98	124.92
25	A	747	5MU	C5-C4-N3	4.31	119.07	115.32
25	A	2605	PSU	C4-N3-C2	-4.28	120.47	126.37
12	l	89	D2T	CB1-SB-CB	4.28	110.06	102.36
25	A	2457	PSU	C4-N3-C2	-4.26	120.51	126.37
25	A	745	1MG	N9-C4-N3	4.26	134.46	125.95
23	x	8	4SU	C5-C4-S4	-4.18	119.53	124.31
25	A	2030	6MZ	C6-C5-N7	4.18	136.99	132.43
23	x	55	PSU	C4-N3-C2	-4.17	120.62	126.37
25	A	2604	PSU	C4-N3-C2	-4.17	120.62	126.37
25	A	2580	PSU	C4-N3-C2	-4.16	120.64	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	A	955	PSU	C4-N3-C2	-4.16	120.64	126.37
22	w	55	PSU	C4-N3-C2	-4.16	120.65	126.37
22	w	54	5MU	C5-C4-N3	4.15	118.93	115.32
1	a	1518	MA6	C2-N1-C6	4.11	121.88	111.83
23	x	8	4SU	N3-C2-N1	4.11	120.24	114.89
22	y	55	PSU	C4-N3-C2	-4.11	120.71	126.37
1	a	1519	MA6	C2-N1-C6	4.11	121.87	111.83
25	A	2030	6MZ	N3-C4-N9	4.11	134.16	127.17
1	a	1516	2MG	N9-C4-N3	4.09	134.13	125.95
25	A	1911	PSU	C4-N3-C2	-4.09	120.74	126.37
25	A	2504	PSU	C4-N3-C2	-4.07	120.77	126.37
25	A	2580	PSU	O2-C2-N1	-4.06	118.60	122.79
1	a	516	PSU	C4-N3-C2	-4.04	120.81	126.37
22	y	54	5MU	O4-C4-C5	-4.03	120.30	124.92
22	w	32	PSU	C4-N3-C2	-4.03	120.82	126.37
22	w	37	MIA	C16-C14-C13	-3.99	110.67	122.66
25	A	1939	5MU	O4-C4-C5	-3.97	120.38	124.92
22	y	39	PSU	C4-N3-C2	-3.93	120.95	126.37
1	a	1518	MA6	C9-N6-C6	-3.93	110.52	120.52
22	y	32	PSU	C4-N3-C2	-3.93	120.96	126.37
22	w	37	MIA	C15-C14-C13	-3.92	110.89	122.66
25	A	2552	OMU	C5-C4-N3	3.91	120.28	114.80
22	y	8	4SU	C5-C4-S4	-3.91	119.84	124.31
1	a	516	PSU	O2-C2-N1	-3.82	118.84	122.79
25	A	1917	PSU	O2-C2-N1	-3.82	118.85	122.79
22	w	54	5MU	O4-C4-C5	-3.81	120.56	124.92
1	a	1518	MA6	N1-C6-N6	3.81	121.50	116.86
25	A	1917	PSU	C4-N3-C2	-3.81	121.13	126.37
25	A	2030	6MZ	C4-C5-N7	-3.80	106.24	110.58
22	w	8	4SU	N3-C2-N1	3.79	119.83	114.89
25	A	1939	5MU	C5-C6-N1	-3.79	119.20	123.31
25	A	747	5MU	C5-C6-N1	-3.75	119.24	123.31
22	y	37	MIA	C2-N3-C4	3.73	120.93	111.83
1	a	1519	MA6	C4-C5-N7	-3.72	106.32	110.58
25	A	1618	6MZ	C2-N3-C4	3.72	120.91	111.83
23	x	55	PSU	O2-C2-N1	-3.71	118.96	122.79
22	y	55	PSU	O2-C2-N1	-3.69	118.98	122.79
25	A	955	PSU	O2-C2-N1	-3.67	119.00	122.79
1	a	1519	MA6	C2-N3-C4	3.67	120.80	111.83
22	w	32	PSU	O2-C2-N1	-3.67	119.00	122.79
25	A	2457	PSU	O2-C2-N1	-3.66	119.01	122.79
22	y	39	PSU	O2-C2-N1	-3.65	119.03	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	A	2503	2MA	C4-C5-N7	-3.64	106.42	110.58
22	y	32	PSU	O2-C2-N1	-3.62	119.06	122.79
1	a	1516	2MG	C6-C5-N7	3.61	136.86	130.29
25	A	1618	6MZ	C9-N6-C6	-3.60	119.51	122.85
1	a	1518	MA6	C2-N3-C4	3.60	120.61	111.83
25	A	2604	PSU	O2-C2-N1	-3.59	119.09	122.79
22	w	55	PSU	O2-C2-N1	-3.59	119.09	122.79
25	A	2030	6MZ	C2-N3-C4	3.58	120.58	111.83
23	x	54	5MU	C5-C6-N1	-3.56	119.44	123.31
22	w	37	MIA	C11-S10-C2	-3.55	99.59	102.25
25	A	1911	PSU	O2-C2-N1	-3.54	119.14	122.79
25	A	2605	PSU	O2-C2-N1	-3.53	119.15	122.79
25	A	2504	PSU	O2-C2-N1	-3.50	119.18	122.79
22	w	8	4SU	C5-C4-S4	-3.50	120.31	124.31
22	w	37	MIA	C4-C5-N7	-3.48	106.61	110.58
25	A	1618	6MZ	C6-C5-N7	3.48	136.22	132.43
22	y	54	5MU	C5-C6-N1	-3.46	119.56	123.31
25	A	746	PSU	O2-C2-N1	-3.46	119.22	122.79
25	A	1618	6MZ	C4-C5-N7	-3.45	106.63	110.58
22	y	37	MIA	N3-C2-N1	-3.42	123.40	128.58
23	x	32	5MC	C5-C6-N1	-3.42	119.60	123.31
12	l	89	D2T	OD2-CG-CB	3.42	120.54	113.15
1	a	1498	UR3	C5-C4-N3	3.39	119.50	115.04
1	a	967	5MC	C5-C6-N1	-3.38	119.64	123.31
22	w	37	MIA	C2-N3-C4	3.37	121.12	112.29
25	A	2445	2MG	C6-C5-N7	3.36	136.40	130.29
22	y	37	MIA	C4-C5-N7	-3.33	106.78	110.58
25	A	1618	6MZ	N1-C2-N3	-3.31	123.57	128.58
1	a	1518	MA6	C4-C5-N7	-3.28	106.83	110.58
22	w	54	5MU	C5-C6-N1	-3.24	119.79	123.31
22	w	37	MIA	C6-C5-N7	3.20	135.92	132.43
1	a	1518	MA6	N1-C2-N3	-3.19	123.75	128.58
25	A	1835	2MG	C6-C5-N7	3.19	136.10	130.29
25	A	2030	6MZ	N1-C2-N3	-3.18	123.76	128.58
1	a	1519	MA6	N1-C2-N3	-3.18	123.77	128.58
1	a	1407	5MC	C5-C6-N1	-3.16	119.89	123.31
25	A	2251	OMG	C6-C5-N7	3.14	136.01	130.29
1	a	1516	2MG	N1-C2-N2	3.06	119.68	116.56
1	a	1207	2MG	C6-C5-N7	3.04	135.83	130.29
25	A	1962	5MC	C5-C6-N1	-3.04	120.01	123.31
25	A	2030	6MZ	C4-N9-C8	2.96	108.84	105.74
25	A	2552	OMU	O4-C4-C5	-2.94	120.10	125.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	A	1939	5MU	O2-C2-N1	-2.93	118.98	122.80
1	a	1519	MA6	N1-C6-N6	2.83	120.30	116.86
1	a	1519	MA6	C10-N6-C9	-2.81	107.14	116.18
23	x	32	5MC	C5-C4-N3	-2.81	118.87	121.75
22	w	46	7MG	C5-C6-N1	2.79	115.85	110.94
1	a	966	2MG	C6-C5-N7	2.77	135.33	130.29
25	A	2503	2MA	C2-N1-C6	2.77	122.35	118.10
1	a	1516	2MG	C4-C5-N7	-2.76	106.30	110.67
25	A	1618	6MZ	C4-N9-C8	2.74	108.61	105.74
25	A	2030	6MZ	C5-N7-C8	2.72	107.73	103.45
1	a	1518	MA6	C5-C6-N6	-2.72	121.03	125.33
22	y	46	7MG	C5-C6-N1	2.71	115.72	110.94
25	A	2503	2MA	N6-C6-N1	2.69	120.66	117.03
25	A	1962	5MC	C5-C4-N3	-2.68	119.00	121.75
22	y	54	5MU	O2-C2-N1	-2.67	119.32	122.80
25	A	1835	2MG	N1-C2-N2	2.65	119.27	116.56
1	a	1407	5MC	C5-C4-N3	-2.64	119.05	121.75
25	A	745	1MG	C6-C5-N7	2.63	135.20	129.36
1	a	967	5MC	C5-C4-N3	-2.62	119.07	121.75
22	w	37	MIA	C4-N9-C8	2.61	108.48	105.74
25	A	2503	2MA	C4-N9-C8	2.61	108.48	105.74
25	A	2503	2MA	C5-N7-C8	2.61	107.55	103.45
25	A	2445	2MG	N1-C2-N2	2.59	119.21	116.56
1	a	1518	MA6	C4-N9-C8	2.59	108.46	105.74
25	A	745	1MG	C4-C5-N7	-2.59	106.57	110.67
25	A	2445	2MG	C4-C5-N7	-2.58	106.58	110.67
1	a	1519	MA6	C5-N7-C8	2.57	107.49	103.45
23	x	54	5MU	O2-C2-N1	-2.56	119.46	122.80
22	w	37	MIA	C5-N7-C8	2.55	107.46	103.45
25	A	1835	2MG	C4-C5-N7	-2.53	106.65	110.67
25	A	747	5MU	O2-C2-N1	-2.52	119.52	122.80
1	a	1207	2MG	C4-C5-N7	-2.51	106.69	110.67
25	A	2251	OMG	C4-C5-N7	-2.50	106.71	110.67
25	A	1618	6MZ	C5-N7-C8	2.48	107.34	103.45
25	A	2449	H2U	C5-C6-N1	-2.47	104.03	111.52
22	y	37	MIA	C4-N9-C8	2.47	108.33	105.74
25	A	2580	PSU	O4'-C1'-C2'	2.46	108.56	105.15
23	x	32	5MC	O2-C2-N3	-2.45	118.47	122.33
1	a	1519	MA6	C4-N9-C8	2.44	108.31	105.74
22	y	37	MIA	C5-N7-C8	2.43	107.27	103.45
22	y	8	4SU	O2-C2-N1	-2.43	119.64	122.80
1	a	527	G7M	O6-C6-C5	-2.42	122.61	128.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	k	119	IAS	OD1-CG-CB	-2.41	118.36	125.38
25	A	2503	2MA	C6-C5-N7	2.41	136.73	132.09
25	A	1835	2MG	CM2-N2-C2	-2.39	118.51	123.65
25	A	2449	H2U	O2-C2-N1	-2.38	120.24	123.10
25	A	2069	G7M	O6-C6-C5	-2.38	122.70	128.01
1	a	966	2MG	C4-C5-N7	-2.37	106.91	110.67
1	a	1516	2MG	N2-C2-N3	-2.35	117.52	120.51
25	A	2445	2MG	CM2-N2-C2	-2.34	118.61	123.65
22	w	37	MIA	N3-C2-N1	-2.34	122.73	127.00
1	a	1518	MA6	C5-N7-C8	2.33	107.11	103.45
22	w	37	MIA	C2-N1-C6	2.33	121.96	117.54
25	A	2030	6MZ	N9-C8-N7	-2.32	110.64	113.94
1	a	1402	4OC	C6-C5-C4	2.32	119.79	117.00
25	A	2604	PSU	C5-C6-N1	-2.30	118.95	122.14
25	A	2498	OMC	O2-C2-N3	-2.28	118.74	122.33
25	A	1915	3TD	C6-C5-C4	2.23	119.69	118.19
1	a	527	G7M	C5-C6-N1	2.23	116.45	111.84
25	A	746	PSU	C5-C6-N1	-2.23	119.05	122.14
25	A	2552	OMU	O2-C2-N1	-2.21	119.93	122.80
25	A	2457	PSU	C5-C6-N1	-2.18	119.12	122.14
1	a	1516	2MG	CM2-N2-C2	-2.17	118.98	123.65
1	a	1518	MA6	C10-N6-C9	-2.17	109.22	116.18
1	a	1516	2MG	O6-C6-C5	-2.16	120.84	126.53
25	A	1835	2MG	O6-C6-C5	-2.15	120.85	126.53
1	a	516	PSU	O4'-C1'-C2'	2.15	108.12	105.15
22	w	46	7MG	O6-C6-C5	-2.14	122.37	127.62
25	A	2445	2MG	O6-C6-C5	-2.14	120.89	126.53
1	a	1207	2MG	O6-C6-C5	-2.12	120.94	126.53
25	A	2503	2MA	N9-C8-N7	-2.12	110.93	113.94
1	a	966	2MG	O6-C6-C5	-2.10	120.98	126.53
1	a	1407	5MC	O2-C2-N3	-2.10	119.02	122.33
22	y	46	7MG	O6-C6-C5	-2.10	122.47	127.62
23	x	55	PSU	C5-C6-N1	-2.10	119.23	122.14
22	w	37	MIA	N6-C6-N1	2.09	121.14	118.33
25	A	1835	2MG	N2-C2-N3	-2.07	117.87	120.51
1	a	966	2MG	C2-N1-C6	-2.07	122.05	124.55
25	A	2069	G7M	C5-C6-N1	2.07	116.11	111.84
25	A	1915	3TD	C1'-C5-C4	2.07	120.74	117.61
1	a	1519	MA6	C5-C6-N6	-2.06	122.07	125.33
23	x	8	4SU	O2-C2-N1	-2.05	120.13	122.80
25	A	2251	OMG	O6-C6-C5	-2.03	121.16	126.53
25	A	2445	2MG	N2-C2-N3	-2.03	117.92	120.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	w	32	PSU	O4'-C1'-C2'	2.02	107.94	105.15
25	A	2605	PSU	C5-C6-N1	-2.02	119.34	122.14
1	a	1207	2MG	C2-N1-C6	-2.01	122.12	124.55
25	A	2457	PSU	O4'-C1'-C2'	2.01	107.94	105.15
25	A	1618	6MZ	N9-C8-N7	-2.01	111.09	113.94
25	A	2030	6MZ	C2-N1-C6	2.00	121.87	115.24

There are no chirality outliers.

All (46) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	a	1519	MA6	O4'-C4'-C5'-O5'
1	a	1519	MA6	C5-C6-N6-C9
22	w	37	MIA	C12-C13-C14-C16
22	y	55	PSU	C2'-C1'-C5-C4
36	O	82	MS6	CA-CB-CG-SD
1	a	527	G7M	C3'-C4'-C5'-O5'
22	y	37	MIA	O4'-C4'-C5'-O5'
1	a	1519	MA6	N1-C6-N6-C9
22	w	46	7MG	C2'-C1'-N9-C8
28	D	150	MEQ	NE2-CD-CG-CB
1	a	1519	MA6	C3'-C4'-C5'-O5'
28	D	150	MEQ	OE1-CD-CG-CB
1	a	527	G7M	O4'-C4'-C5'-O5'
22	y	8	4SU	O4'-C4'-C5'-O5'
22	y	37	MIA	C3'-C4'-C5'-O5'
25	A	2030	6MZ	O4'-C4'-C5'-O5'
25	A	1917	PSU	C3'-C4'-C5'-O5'
25	A	2030	6MZ	C3'-C4'-C5'-O5'
1	a	1518	MA6	C5-C6-N6-C9
36	O	82	MS6	CB-CG-SD-CE
22	y	46	7MG	C3'-C4'-C5'-O5'
11	k	119	IAS	O-C-CA-CB
11	k	119	IAS	OXT-C-CA-CB
22	y	46	7MG	C2'-C1'-N9-C8
36	O	81	4D4	OB-CB-CG-CD
22	y	46	7MG	O4'-C4'-C5'-O5'
36	O	82	MS6	N-CA-CB-CG
12	l	89	D2T	CG-CB-SB-CB1
36	O	81	4D4	CA-CB-CG-CD
25	A	1917	PSU	O4'-C4'-C5'-O5'
25	A	2504	PSU	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
22	y	46	7MG	C4'-C5'-O5'-P
22	y	55	PSU	C4'-C5'-O5'-P
1	a	1518	MA6	N1-C6-N6-C9
22	y	55	PSU	O4'-C1'-C5-C4
22	w	37	MIA	N6-C12-C13-C14
25	A	2498	OMC	O4'-C4'-C5'-O5'
22	y	46	7MG	O4'-C1'-N9-C4
25	A	746	PSU	O4'-C1'-C5-C6
1	a	1402	4OC	O4'-C4'-C5'-O5'
25	A	746	PSU	C2'-C1'-C5-C6
36	O	82	MS6	C-CA-CB-CG
11	k	119	IAS	OXT-C-CA-N
22	y	8	4SU	C4'-C5'-O5'-P
22	w	46	7MG	O4'-C1'-N9-C8
22	y	46	7MG	O4'-C1'-N9-C8

There are no ring outliers.

14 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	a	1519	MA6	2	0
1	a	966	2MG	2	0
28	D	150	MEQ	1	0
1	a	967	5MC	1	0
1	a	1402	4OC	2	0
22	w	37	MIA	2	0
22	y	8	4SU	2	0
25	A	2445	2MG	1	0
25	A	2498	OMC	2	0
25	A	2503	2MA	1	0
1	a	1518	MA6	3	0
25	A	2030	6MZ	3	0
22	y	46	7MG	1	0
22	y	32	PSU	2	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 479 ligands modelled in this entry, 476 are monoatomic - leaving 3 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
58	PHE	w	101	22	10,11,12	1.70	1 (10%)	8,13,15	0.58	0
57	AKN	a	3099	-	41,42,42	2.02	10 (24%)	55,61,61	1.22	6 (10%)
57	AKN	A	3360	-	41,42,42	1.96	11 (26%)	55,61,61	1.09	3 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	PHE	w	101	22	-	3/5/6/8	0/1/1/1
57	AKN	a	3099	-	-	3/23/83/83	0/3/3/3
57	AKN	A	3360	-	-	6/23/83/83	0/3/3/3

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	A	3360	AKN	C35-N12	5.87	1.46	1.34
57	a	3099	AKN	C35-N12	5.72	1.46	1.34
57	a	3099	AKN	C22-C24	-5.40	1.46	1.53
58	w	101	PHE	CB-CG	-5.21	1.39	1.51
57	A	3360	AKN	C22-C24	-5.06	1.47	1.53
57	a	3099	AKN	C26-C24	-4.65	1.47	1.53
57	A	3360	AKN	C24-N25	4.53	1.54	1.47
57	a	3099	AKN	C24-N25	4.42	1.54	1.47
57	A	3360	AKN	C26-C24	-3.92	1.48	1.53
57	A	3360	AKN	C38-C39	3.08	1.62	1.52
57	a	3099	AKN	C38-C39	2.97	1.61	1.52
57	a	3099	AKN	O29-C21	2.77	1.49	1.41
57	a	3099	AKN	O40-C37	-2.68	1.37	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	A	3360	AKN	O29-C21	2.66	1.48	1.41
57	a	3099	AKN	O36-C35	-2.60	1.18	1.23
57	a	3099	AKN	C5-C4	-2.55	1.45	1.52
57	A	3360	AKN	O40-C37	-2.52	1.37	1.42
57	A	3360	AKN	O36-C35	-2.37	1.18	1.23
57	A	3360	AKN	C5-C4	-2.23	1.46	1.52
57	A	3360	AKN	O8-C7	2.21	1.49	1.44
57	a	3099	AKN	O8-C7	2.20	1.49	1.44
57	A	3360	AKN	O33-C4	2.01	1.47	1.43

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	a	3099	AKN	C13-C11-N12	-3.36	105.65	110.78
57	a	3099	AKN	C21-O20-C19	-3.00	110.86	117.98
57	A	3360	AKN	C21-O20-C19	-2.73	111.52	117.98
57	a	3099	AKN	C11-N12-C35	-2.69	118.57	123.25
57	a	3099	AKN	C19-C17-C16	2.59	114.35	109.11
57	A	3360	AKN	C1-O2-C16	-2.35	112.41	117.98
57	a	3099	AKN	C1-O2-C16	-2.22	112.72	117.98
57	A	3360	AKN	O29-C28-C26	2.07	113.42	109.70
57	a	3099	AKN	C9-C7-C5	-2.05	108.00	112.80

There are no chirality outliers.

All (12) torsion outliers are listed below:

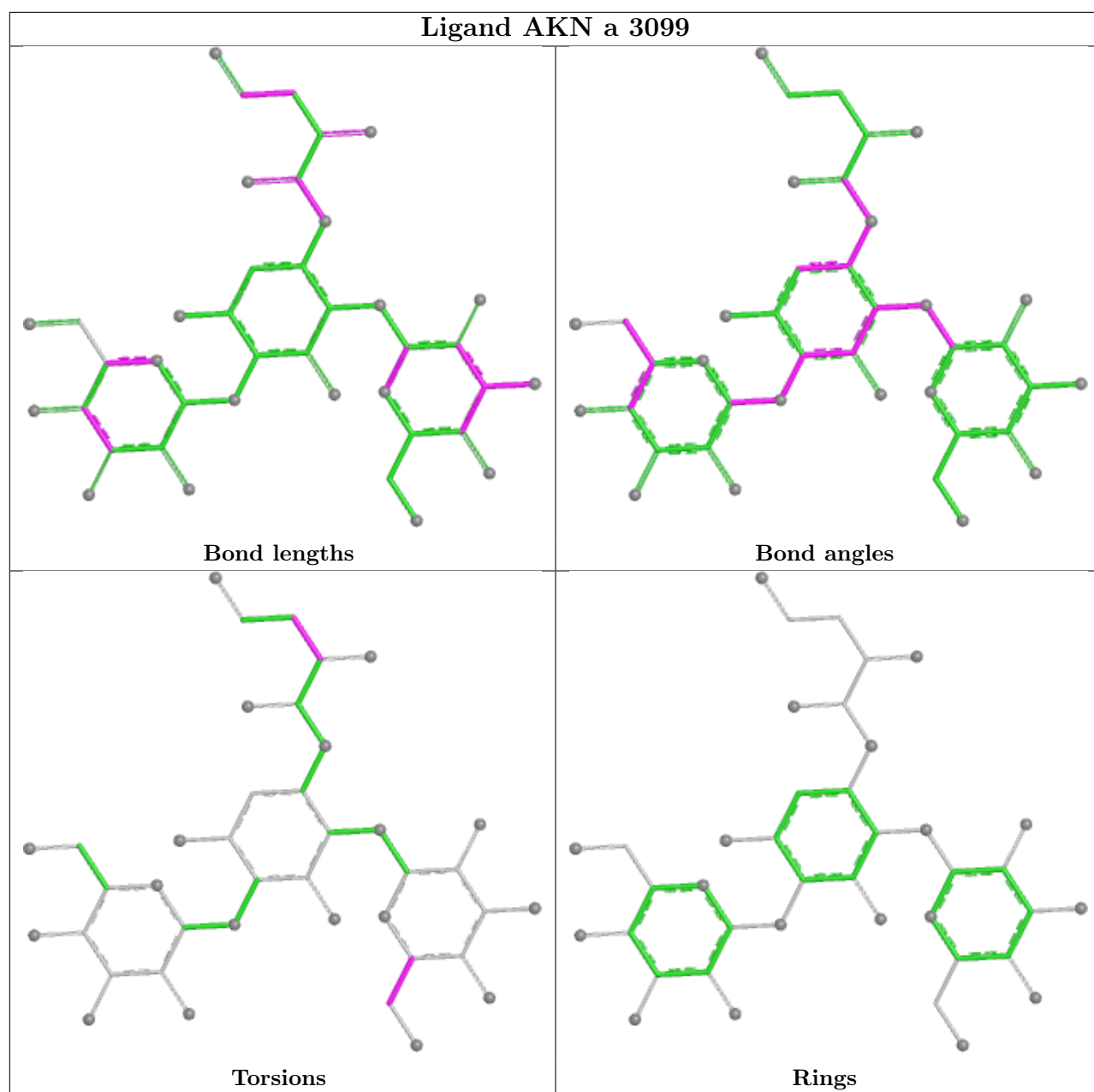
Mol	Chain	Res	Type	Atoms
57	A	3360	AKN	C14-C16-O2-C1
57	A	3360	AKN	C35-C37-C38-C39
57	A	3360	AKN	O40-C37-C38-C39
58	w	101	PHE	O-C-CA-CB
58	w	101	PHE	C-CA-CB-CG
57	A	3360	AKN	O29-C28-C30-O31
57	A	3360	AKN	C26-C28-C30-O31
57	A	3360	AKN	C17-C16-O2-C1
58	w	101	PHE	N-CA-CB-CG
57	a	3099	AKN	C26-C28-C30-O31
57	a	3099	AKN	O29-C28-C30-O31
57	a	3099	AKN	O40-C37-C38-C39

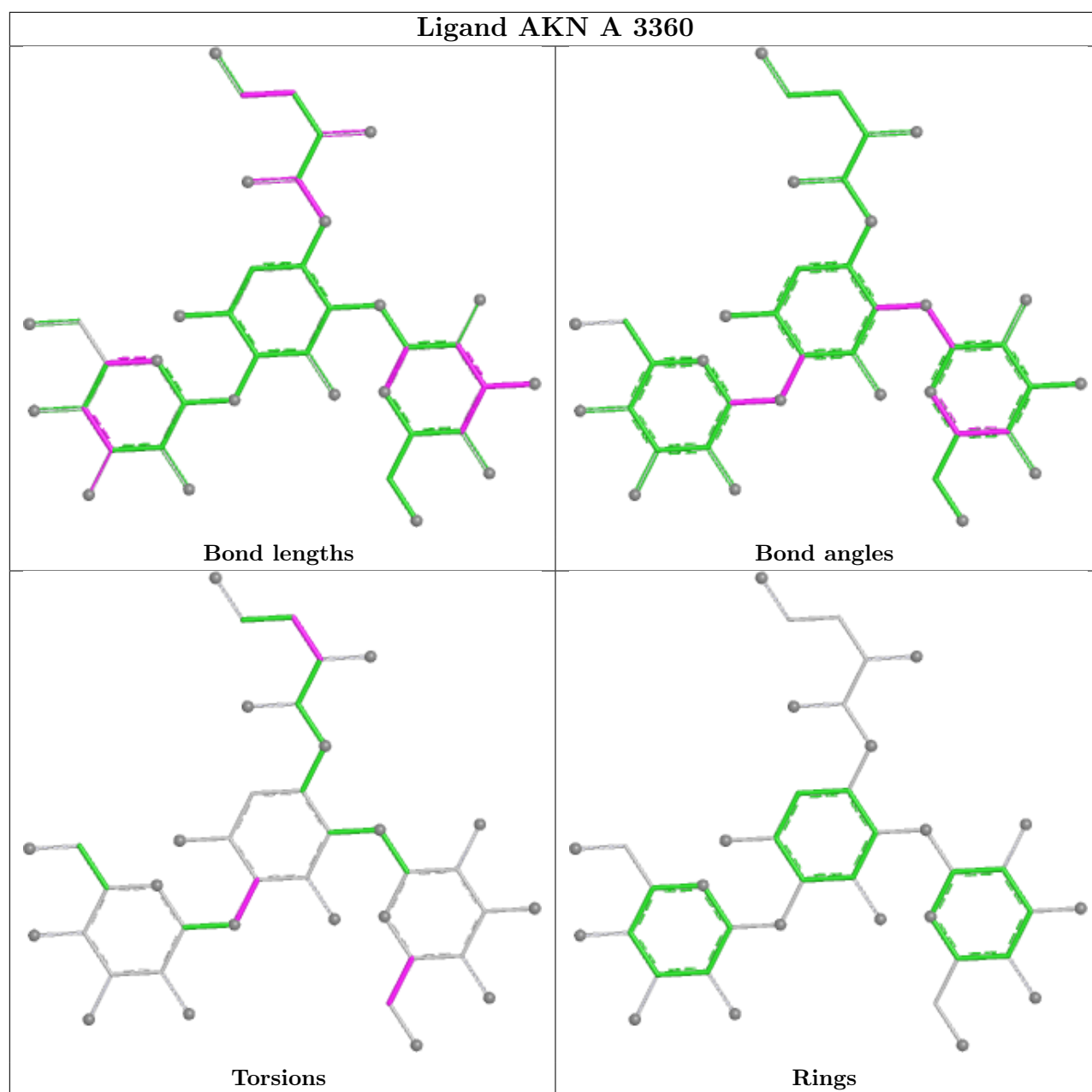
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	w	101	PHE	1	0
57	a	3099	AKN	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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.

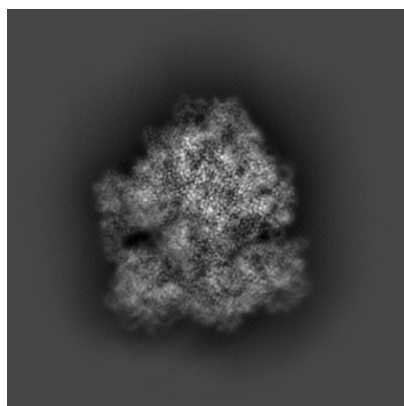
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-40882. These allow visual inspection of the internal detail of the map and identification of artifacts.

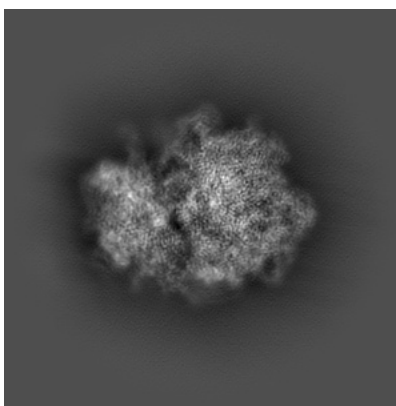
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

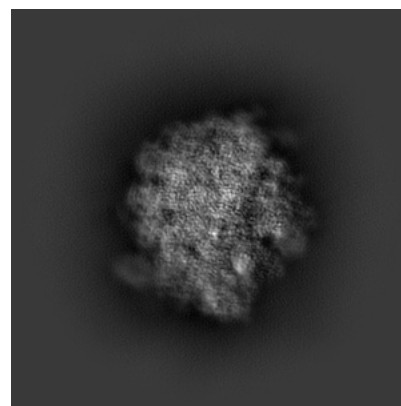
6.1.1 Primary map



X

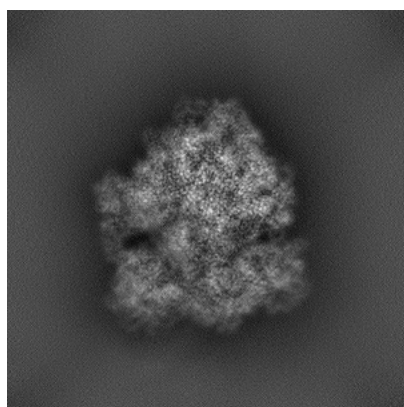


Y

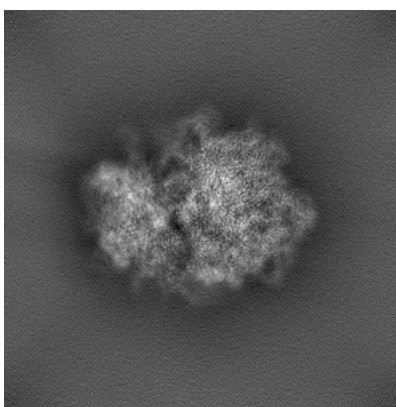


Z

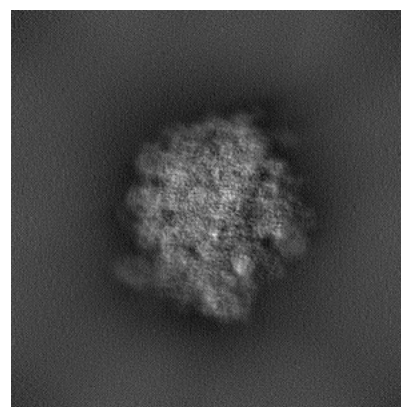
6.1.2 Raw map



X



Y

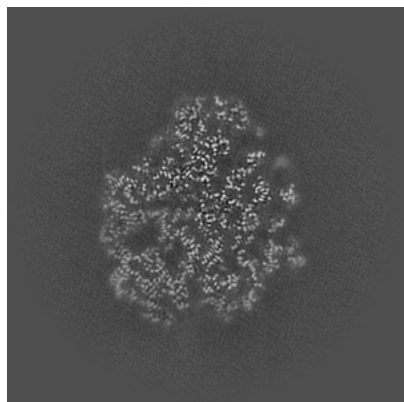


Z

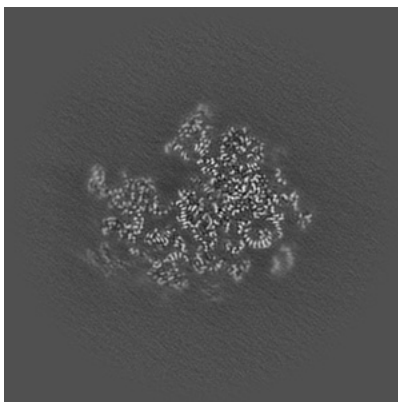
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

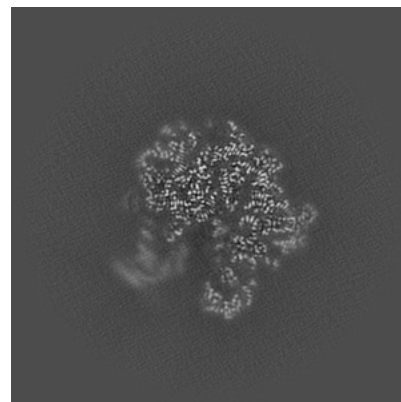
6.2.1 Primary map



X Index: 256

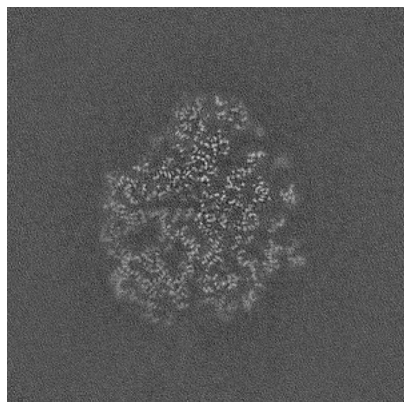


Y Index: 256

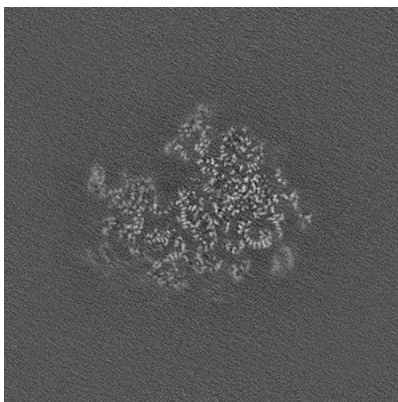


Z Index: 256

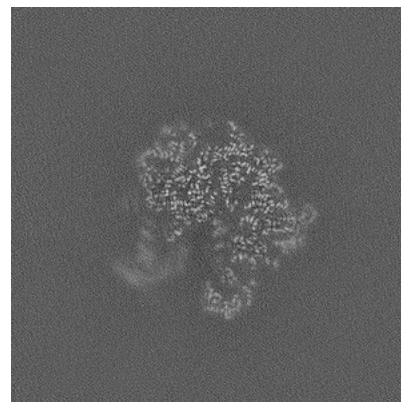
6.2.2 Raw map



X Index: 256



Y Index: 256

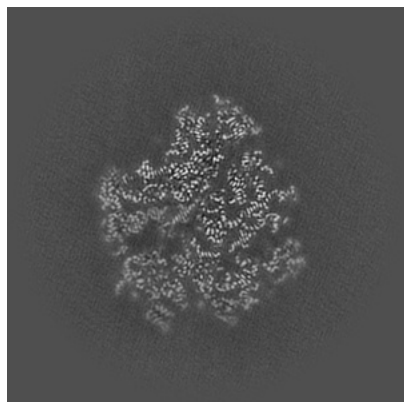


Z Index: 256

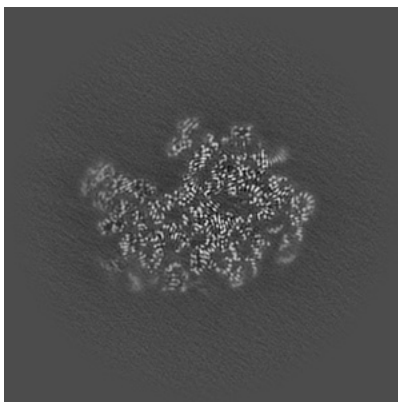
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

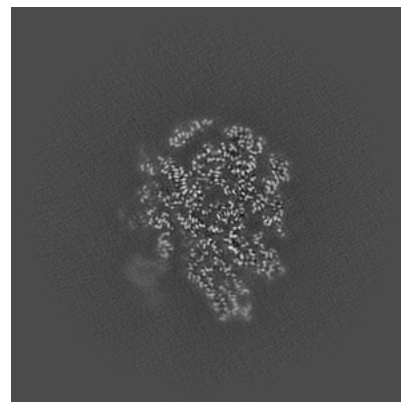
6.3.1 Primary map



X Index: 262

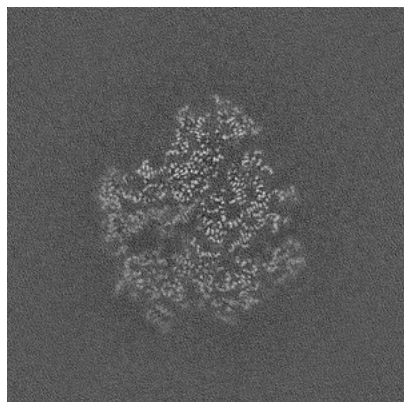


Y Index: 270

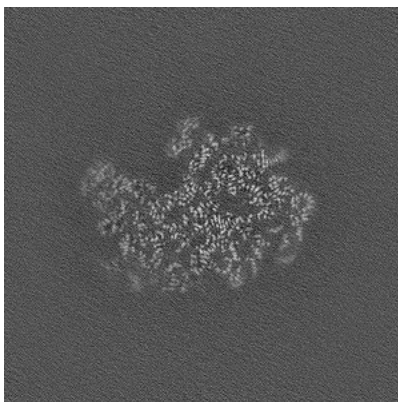


Z Index: 284

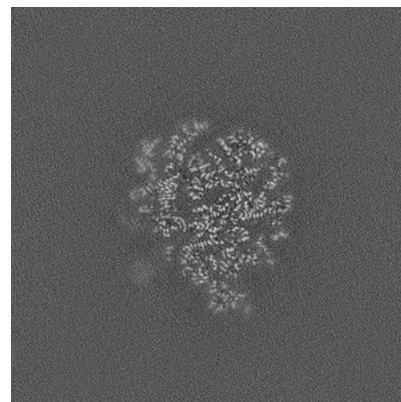
6.3.2 Raw map



X Index: 262



Y Index: 270

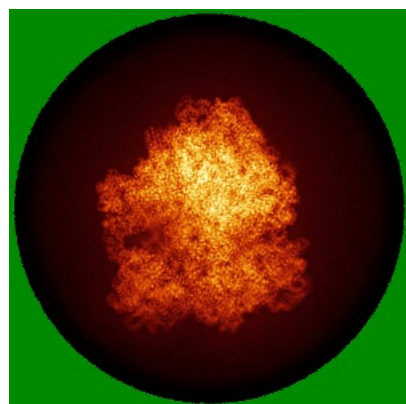


Z Index: 293

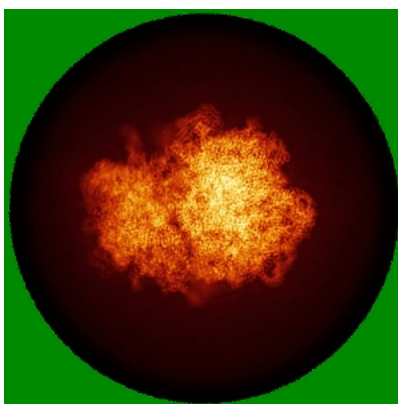
The images above show the largest variance slices of the map in three orthogonal directions.

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

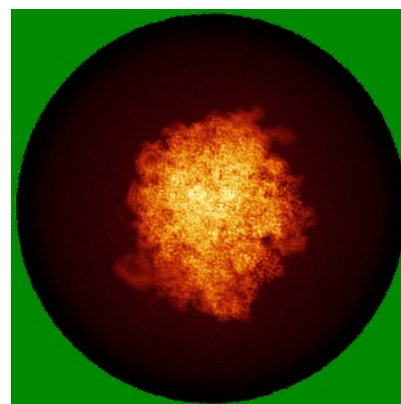
6.4.1 Primary map



X

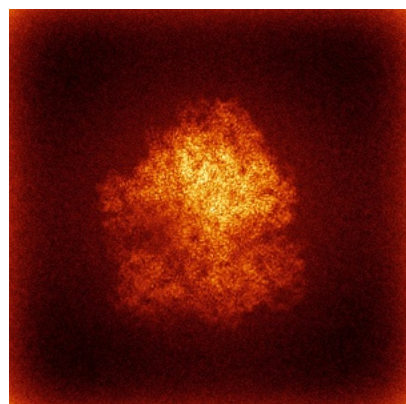


Y

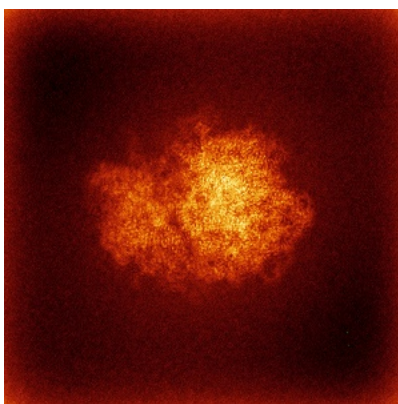


Z

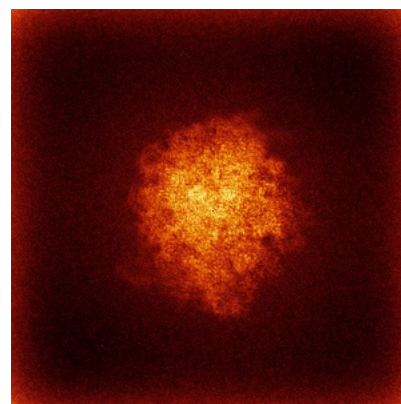
6.4.2 Raw map



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



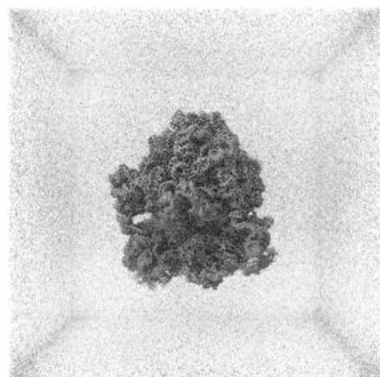
Y



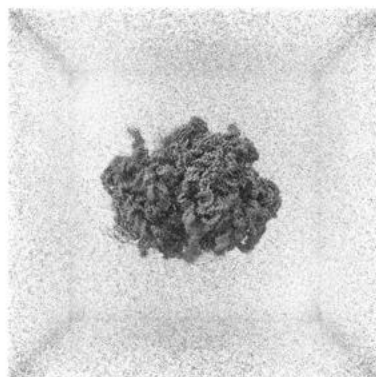
Z

The images above show the 3D surface view of the map at the recommended contour level 0.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

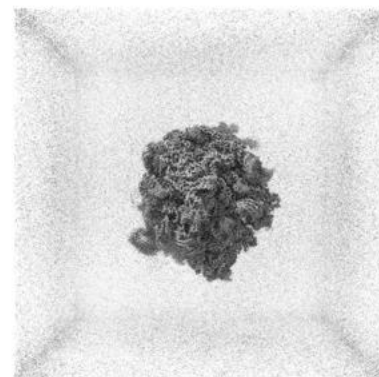
6.5.2 Raw map



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.

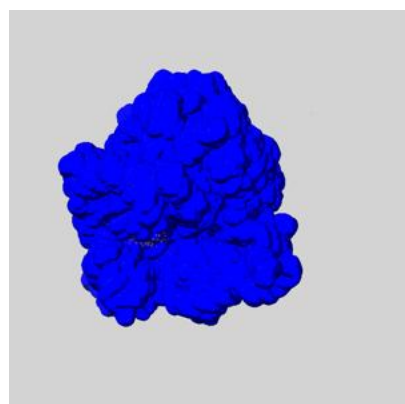
6.6 Mask visualisation [i](#)

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

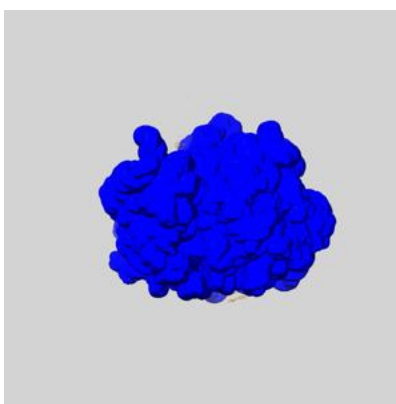
A mask typically either:

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

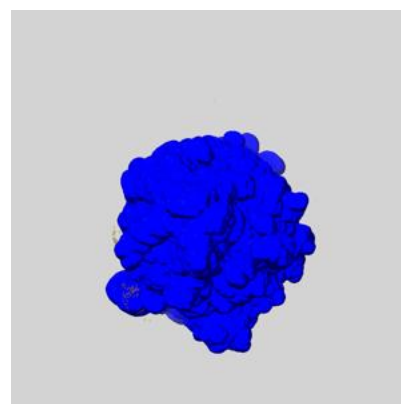
6.6.1 emd_40882_msk_1.map [i](#)



X



Y

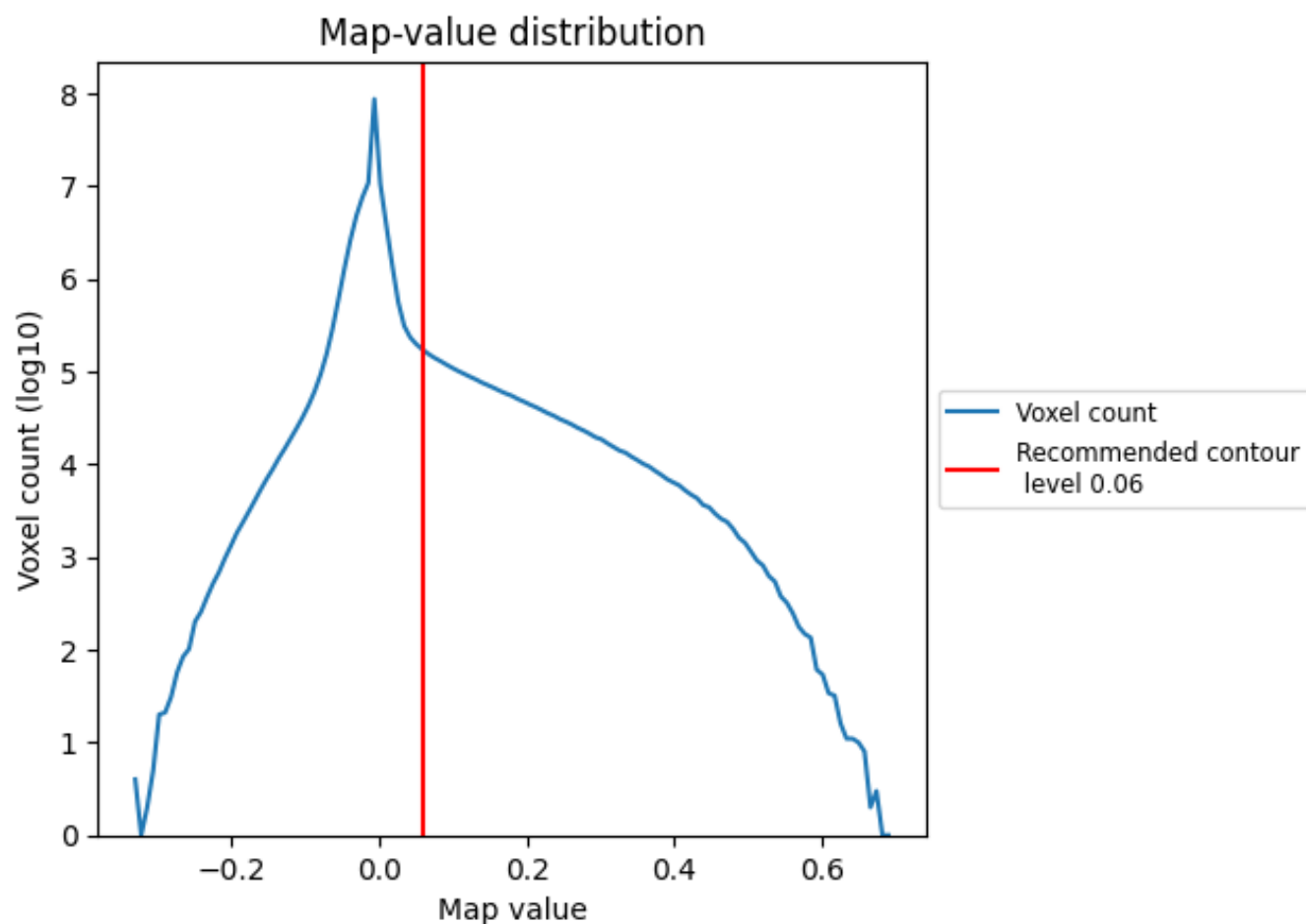


Z

7 Map analysis [i](#)

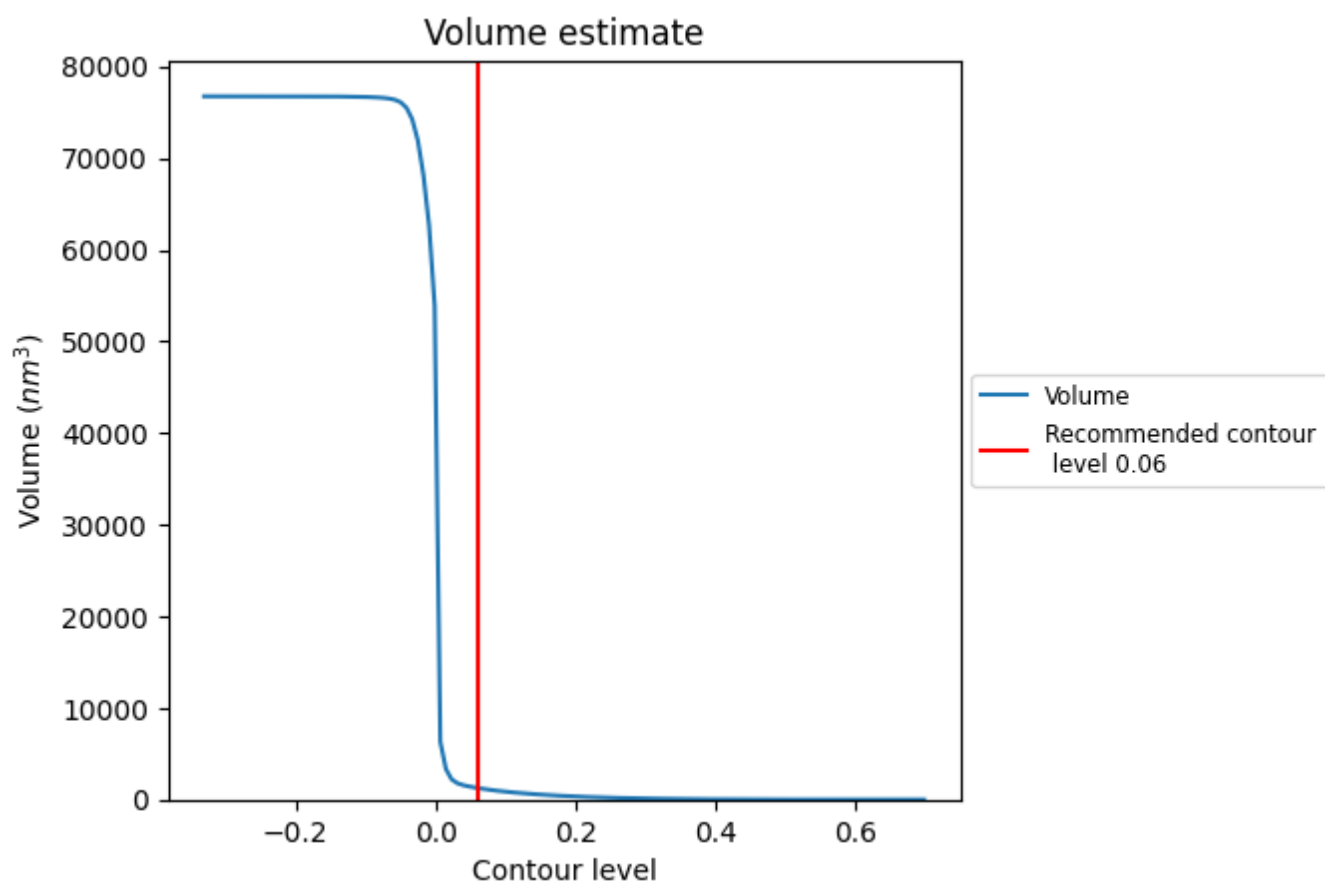
This section contains the results of statistical analysis of the map.

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.

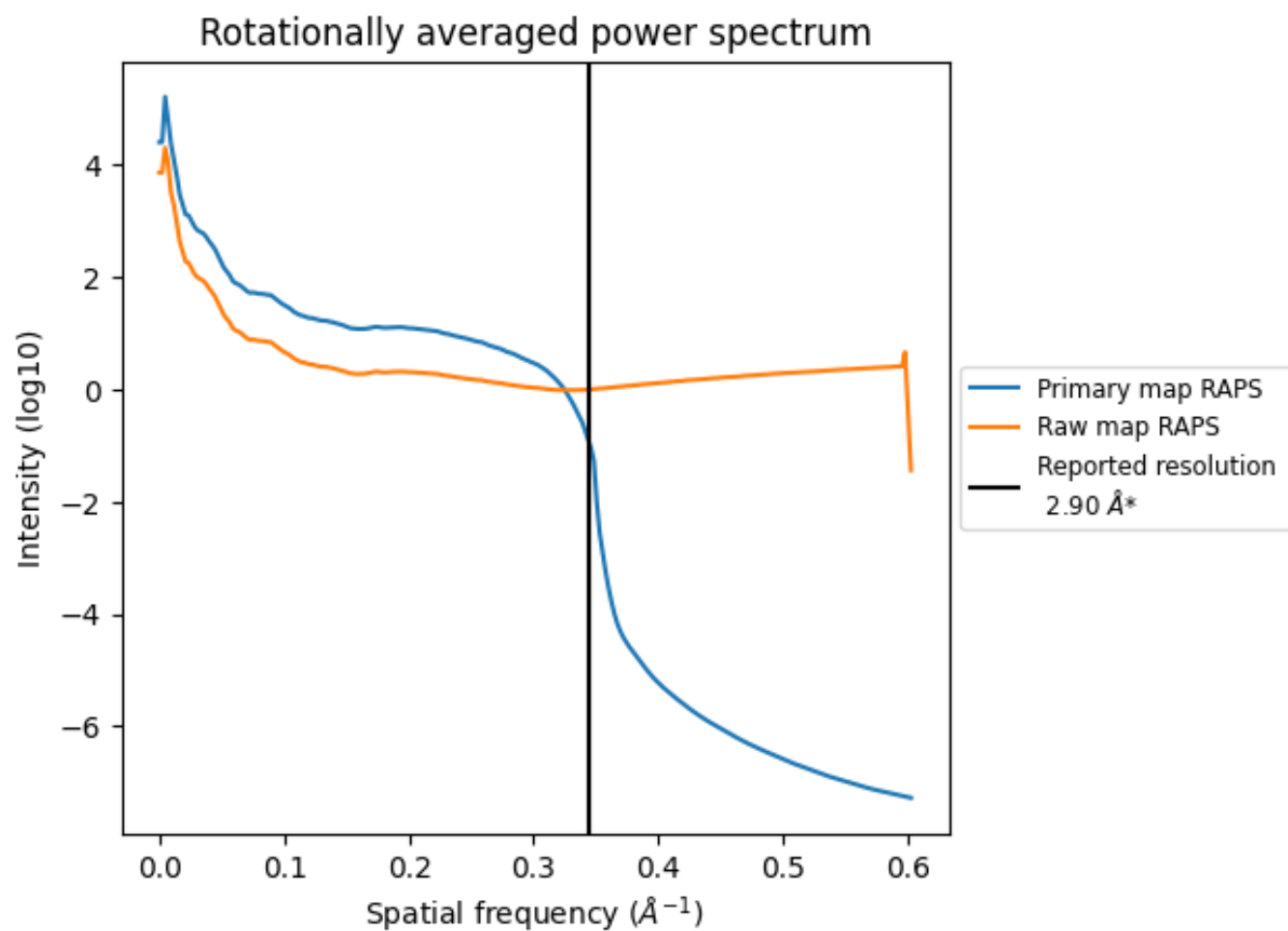
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1266 nm^3 ; this corresponds to an approximate mass of 1144 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 ⓘ

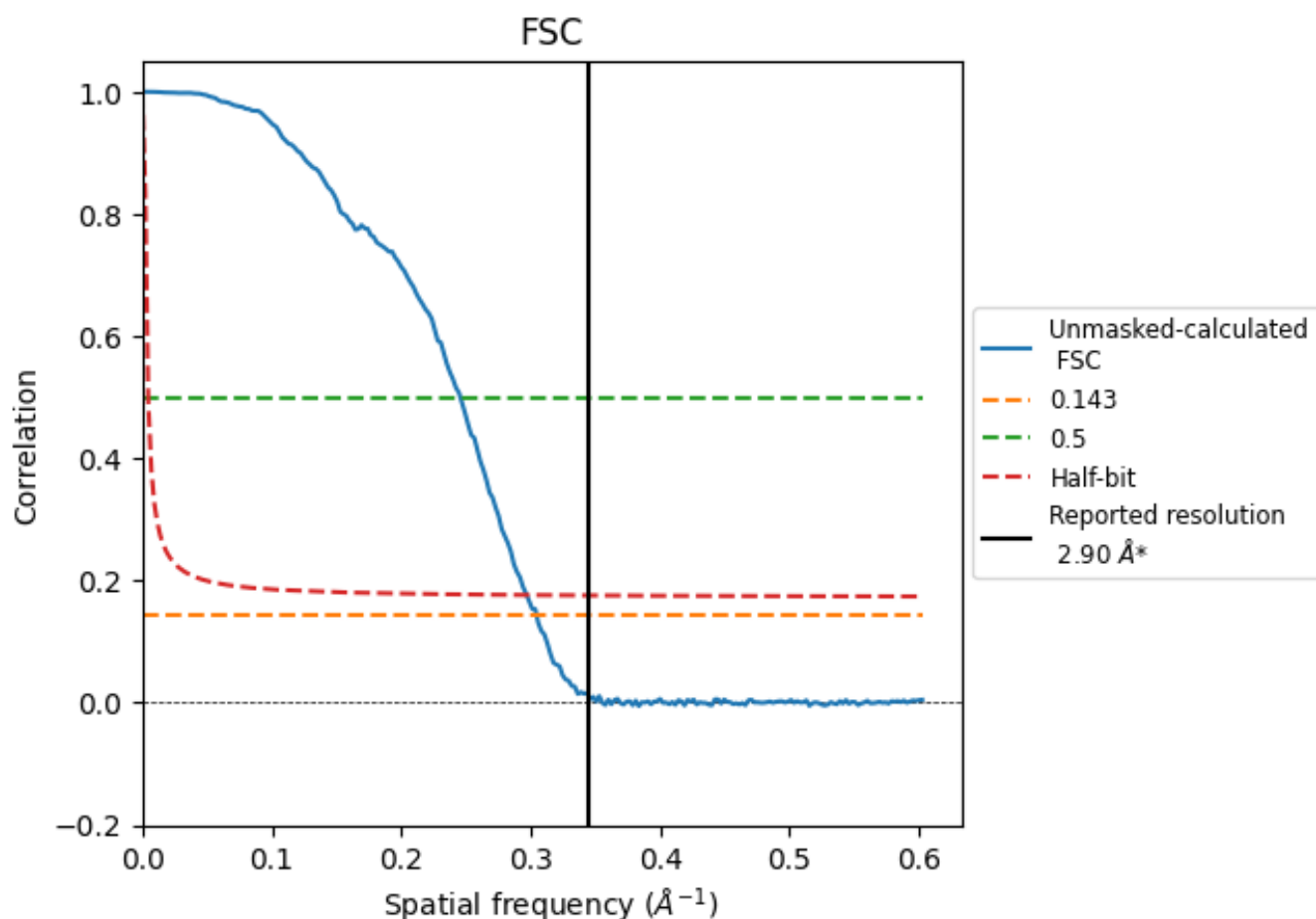


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.345 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

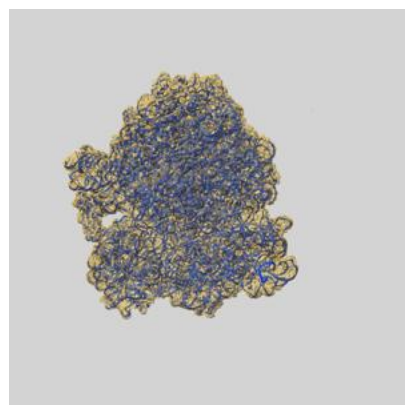
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.28	4.07	3.37

*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 3.28 differs from the reported value 2.9 by more than 10 %

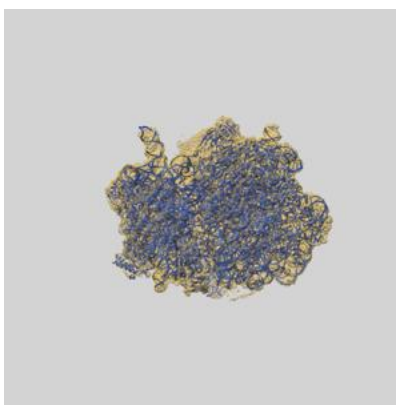
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-40882 and PDB model 8SYL. Per-residue inclusion information can be found in section 3 on page 17.

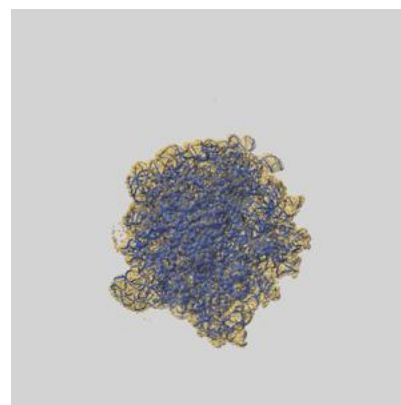
9.1 Map-model overlay [i](#)



X



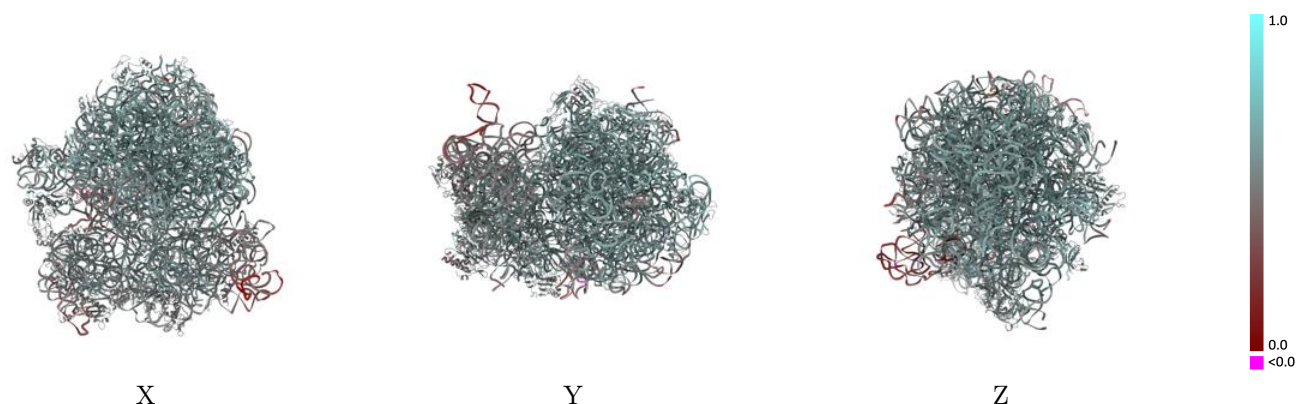
Y



Z

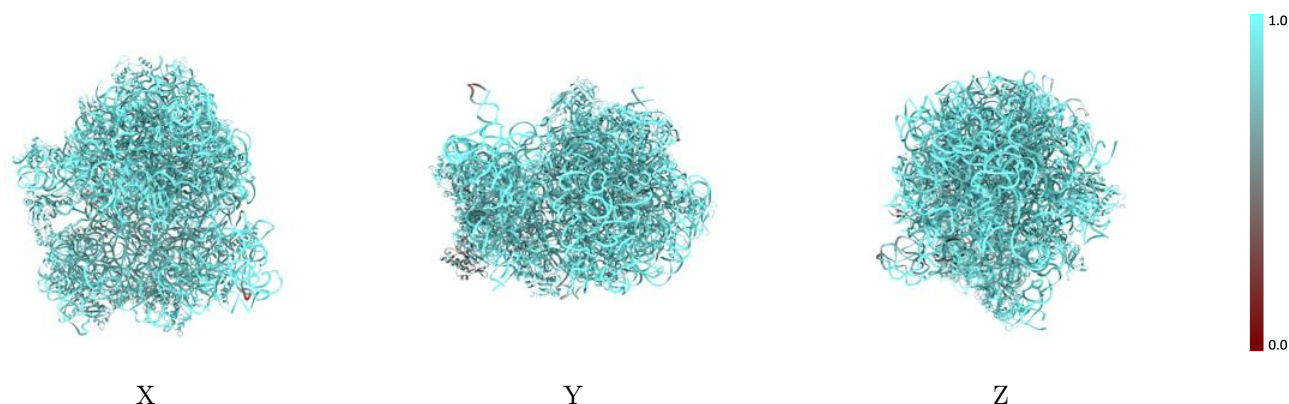
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



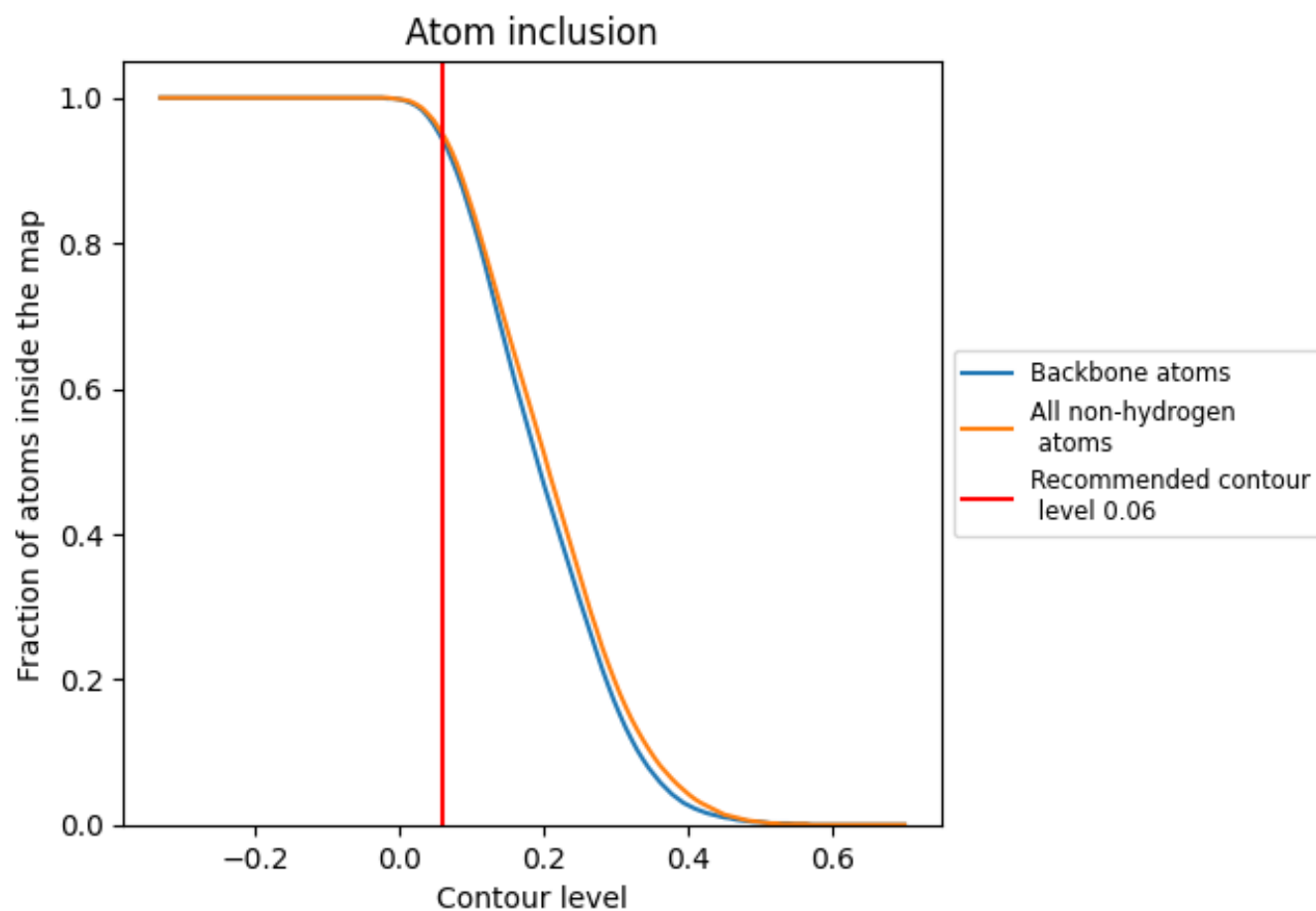
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.06).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 95% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9500	 0.5440
1	 0.9380	 0.5210
2	 0.9450	 0.5780
3	 0.8250	 0.4950
4	 0.9620	 0.5920
5	 0.8730	 0.5670
6	 0.9610	 0.6030
7	 0.9630	 0.6060
8	 0.9420	 0.5770
A	 0.9850	 0.5650
B	 0.9890	 0.5450
C	 0.9520	 0.5930
D	 0.9570	 0.5890
E	 0.9460	 0.5760
F	 0.8870	 0.5130
G	 0.9170	 0.5230
H	 0.5530	 0.5060
L	 0.9540	 0.5890
M	 0.9380	 0.5900
N	 0.9530	 0.5790
O	 0.9440	 0.5880
P	 0.9780	 0.5990
Q	 0.9540	 0.5430
R	 0.9230	 0.5840
S	 0.9780	 0.5990
T	 0.9520	 0.5820
U	 0.9510	 0.5910
V	 0.9150	 0.5580
W	 0.9430	 0.5520
X	 0.9240	 0.5600
Y	 0.9210	 0.5870
Z	 0.9580	 0.5880
a	 0.9780	 0.5190
b	 0.5300	 0.4590
c	 0.8340	 0.5230



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Chain	Atom inclusion	Q-score
d	 0.8450	 0.4770
e	 0.9170	 0.5530
f	 0.8910	 0.5000
g	 0.9020	 0.5020
h	 0.9050	 0.5360
i	 0.9070	 0.5050
j	 0.8500	 0.5110
k	 0.8940	 0.5350
l	 0.9210	 0.5660
m	 0.9100	 0.5190
n	 0.8630	 0.5180
o	 0.9130	 0.5340
p	 0.9200	 0.5050
q	 0.8980	 0.5270
r	 0.9030	 0.5300
s	 0.8790	 0.5050
t	 0.8990	 0.5000
u	 0.7310	 0.5210
v	 0.9610	 0.5640
w	 0.8730	 0.4950
x	 0.9410	 0.5370
y	 0.5170	 0.2430