



Full wwPDB EM Validation Report ⓘ

Mar 29, 2026 – 11:44 PM UTC

PDB ID : 8Y5M / pdb_00008y5m
EMDB ID : EMD-38942
Title : E.coli transcription translation coupling complex in TTC-B state 2 containing mRNA with 27-mer spacer, NusG, NusA, fMet-tRNA(iMet), Phe-tRNA(Phe), and viomycin
Authors : Zhang, J.; Lu, G.; Wang, C.; Lin, J.
Deposited on : 2024-01-31
Resolution : 4.50 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

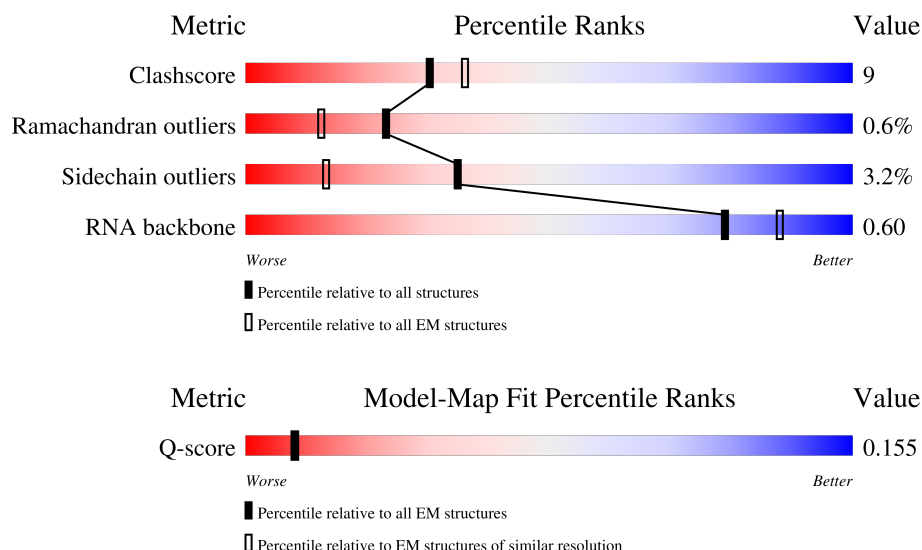
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

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

The reported resolution of this entry is 4.50 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.



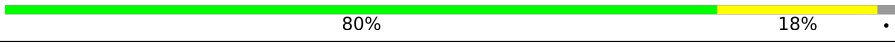
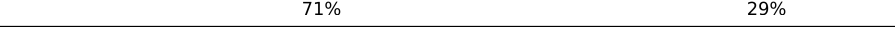
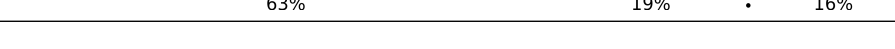
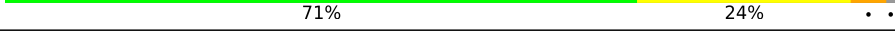
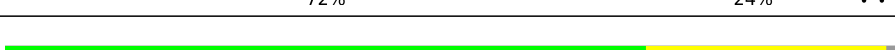
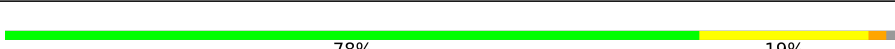
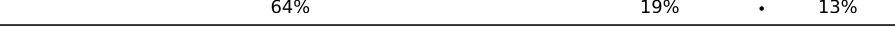
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	2937 (4.00 - 5.00)

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	70	
2	B	57	
3	C	55	

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Mol	Chain	Length	Quality of chain
4	D	46	
5	E	65	
6	F	38	
7	G	241	
8	H	233	
9	I	206	
10	J	167	
11	K	135	
12	L	179	
13	M	130	
14	N	130	
15	O	103	
16	P	129	
17	Q	124	
18	R	118	
19	S	101	
20	T	89	
21	U	82	
22	V	84	
23	W	75	
24	X	92	
25	Y	87	
26	Z	71	
27	b	273	
28	c	209	

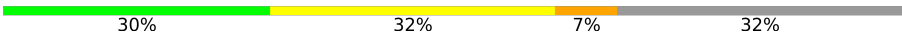
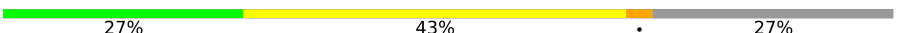
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Mol	Chain	Length	Quality of chain
29	d	201	 83% 17%
30	e	179	 76% 22% ..
31	f	177	 85% 14% ...
32	g	149	 6% 80% 18% .
33	i	142	 54% 38% 6% ..
34	j	142	 84% 15% .
35	k	123	 77% 20% ..
36	l	144	 72% 26% ..
37	m	136	 81% 18% .
38	n	127	 74% 20% . 6%
39	o	117	 75% 22% ..
40	p	115	 78% 21% .
41	q	118	 77% 19% ..
42	r	103	 75% 23% .
43	s	110	 79% 21%
44	t	100	 73% 20% 7%
45	u	104	 84% 13% ..
46	v	94	 74% 26%
47	w	85	 69% 18% . 12%
48	x	78	 79% 17% ..
49	y	63	 81% 17% .
50	z	59	 78% 19% ..
51	1	2904	 56% 38% 7%
52	2	120	 53% 44% ..
53	3	1542	 55% 39% 6%

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Mol	Chain	Length	Quality of chain
54	4	44	
55	8	37	
56	9	37	
57	A1	329	
57	A2	329	
58	B1	1407	
59	B2	1342	
60	W0	91	
61	NA	495	
62	NG	181	
63	5	76	
64	6	77	
65	a	234	
66	0	716	
67	h	6	

2 Entry composition

There are 70 unique types of molecules in this entry. The entry contains 183546 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L31.

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

- Molecule 2 is a protein called 50S ribosomal protein L32.

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

- Molecule 3 is a protein called 50S ribosomal protein L33.

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

- Molecule 4 is a protein called 50S ribosomal protein L34.

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

- Molecule 5 is a protein called 50S ribosomal protein L35.

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

- Molecule 6 is a protein called 50S ribosomal protein L36.

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

- Molecule 7 is a protein called 30S ribosomal protein S2.

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

- Molecule 8 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	206	Total	C	N	O	S	0	0
			1620	1025	304	288	3		

- Molecule 9 is a protein called 30S ribosomal protein S4.

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

- Molecule 10 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	157	Total	C	N	O	S	0	0
			1152	717	218	211	6		

- Molecule 11 is a protein called 30S ribosomal protein S6, fully modified isoform.

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

- Molecule 12 is a protein called 30S ribosomal protein S7.

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

- Molecule 13 is a protein called 30S ribosomal protein S8.

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

- Molecule 14 is a protein called 30S ribosomal protein S9.

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

- Molecule 15 is a protein called 30S ribosomal protein S10.

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

- Molecule 16 is a protein called 30S ribosomal protein S11.

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

- Molecule 17 is a protein called 30S ribosomal protein S12.

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

- Molecule 18 is a protein called 30S ribosomal protein S13.

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

- Molecule 19 is a protein called 30S ribosomal protein S14.

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

- Molecule 20 is a protein called 30S ribosomal protein S15.

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

- Molecule 21 is a protein called 30S ribosomal protein S16.

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

- Molecule 22 is a protein called 30S ribosomal protein S17.

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

- Molecule 23 is a protein called 30S ribosomal protein S18.

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

- Molecule 24 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 25 is a protein called 30S ribosomal protein S20.

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

- Molecule 26 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	65	Total	C	N	O	S	0	0
			544	335	117	91	1		

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 33 is a protein called 50S ribosomal protein L11.

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

- Molecule 34 is a protein called 50S ribosomal protein L13.

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

- Molecule 35 is a protein called 50S ribosomal protein L14.

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

- Molecule 36 is a protein called 50S ribosomal protein L15.

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

- Molecule 37 is a protein called 50S ribosomal protein L16.

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

- Molecule 38 is a protein called 50S ribosomal protein L17.

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

- Molecule 39 is a protein called 50S ribosomal protein L18.

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

- Molecule 40 is a protein called 50S ribosomal protein L19.

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

- Molecule 41 is a protein called 50S ribosomal protein L20.

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

- Molecule 42 is a protein called 50S ribosomal protein L21.

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

- Molecule 43 is a protein called 50S ribosomal protein L22.

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

- Molecule 44 is a protein called 50S ribosomal protein L23.

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

- Molecule 45 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	u	102	Total	C	N	O	0	0
			776	489	146	141		

- Molecule 46 is a protein called 50S ribosomal protein L25.

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

- Molecule 47 is a protein called 50S ribosomal protein L27.

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

- Molecule 48 is a protein called 50S ribosomal protein L28.

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

- Molecule 49 is a protein called 50S ribosomal protein L29.

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

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

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

- Molecule 51 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	1	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 1929590828

- Molecule 52 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	2	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	120	A	U	conflict	GB NR_103249

- Molecule 53 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 54 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	4	30	Total	C	N	O	P	0	0
			627	280	92	225	30		

- Molecule 55 is a DNA chain called templete DNA strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	8	27	Total	C	N	O	P	0	0
			539	257	88	167	27		

- Molecule 56 is a DNA chain called non-templete DNA strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	9	20	Total	C	N	O	P	0	0
			417	195	84	118	20		

- Molecule 57 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	A1	301	Total	C	N	O	S	0	0
			2088	1293	380	409	6		
57	A2	288	Total	C	N	O	S	0	0
			2029	1257	366	400	6		

- Molecule 58 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	B1	1335	Total	C	N	O	S	0	0
			10353	6509	1842	1955	47		

- Molecule 59 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	B2	1340	Total	C	N	O	S	0	0
			10546	6616	1839	2048	43		

- Molecule 60 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	W0	82	Total	C	N	O	S	0	0
			650	396	122	131	1		

- Molecule 61 is a protein called Transcription termination/antitermination protein NusA.

Mol	Chain	Residues	Atoms				AltConf	Trace
61	NA	492	Total	C	N	O	0	0
			2432	1448	492	492		

- Molecule 62 is a protein called Transcription termination/antitermination protein NusG.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	NG	154	Total	C	N	O	0	0
			758	450	154	154		

- Molecule 63 is a RNA chain called tRNA(Phe).

Mol	Chain	Residues	Atoms					AltConf	Trace
63	5	76	Total	C	N	O	P	0	0
			1622	723	290	533	76		

- Molecule 64 is a RNA chain called tRNA(fMet).

Mol	Chain	Residues	Atoms					AltConf	Trace
64	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 65 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	a	134	Total	C	N	O	S	0	0
			1026	645	186	193	2		

- Molecule 66 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	0	697	Total	C	N	O	S	0	0
			5399	3403	929	1042	25		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	705	GLY	-	expression tag	UNP P0A6M8
0	706	SER	-	expression tag	UNP P0A6M8
0	707	SER	-	expression tag	UNP P0A6M8
0	708	GLY	-	expression tag	UNP P0A6M8
0	709	HIS	-	expression tag	UNP P0A6M8
0	710	HIS	-	expression tag	UNP P0A6M8
0	711	HIS	-	expression tag	UNP P0A6M8
0	712	HIS	-	expression tag	UNP P0A6M8
0	713	HIS	-	expression tag	UNP P0A6M8
0	714	HIS	-	expression tag	UNP P0A6M8

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Chain	Residue	Modelled	Actual	Comment	Reference
0	715	HIS	-	expression tag	UNP P0A6M8
0	716	HIS	-	expression tag	UNP P0A6M8

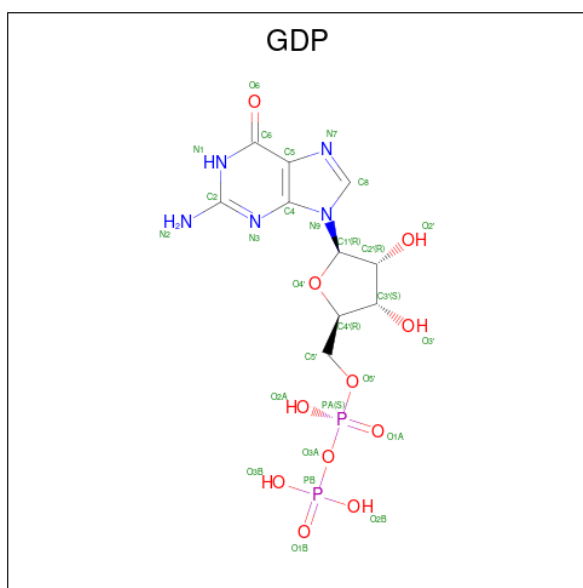
- Molecule 67 is a protein (with D amino acids) called Viomycin.

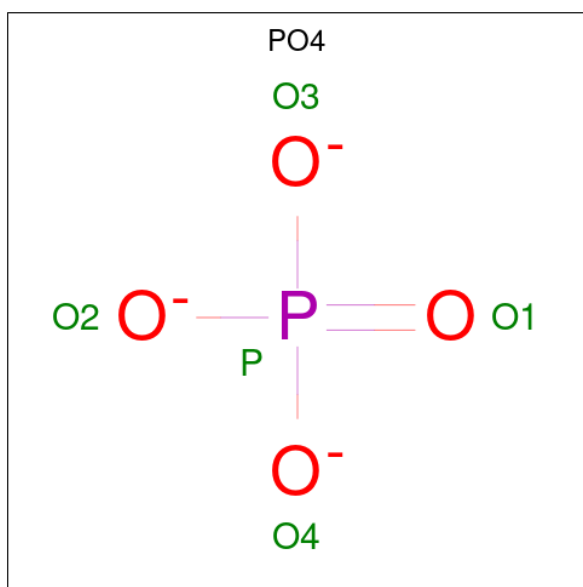
Mol	Chain	Residues	Atoms				AltConf	Trace
67	h	6	Total	C	N	O	0	0
			48	25	13	10		

- Molecule 68 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
68	B1	1	Total	Mg	0
			1	1	

- Molecule 69 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



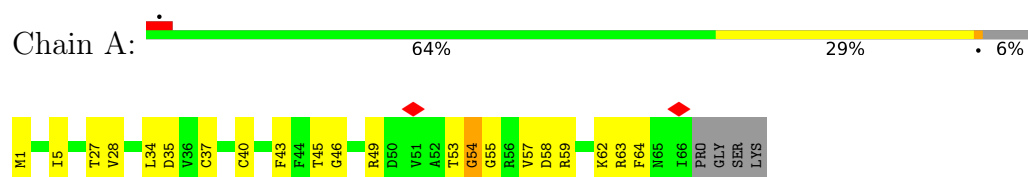


Mol	Chain	Residues	Atoms			AltConf
			Total	O	P	
70	0	1	5	4	1	0

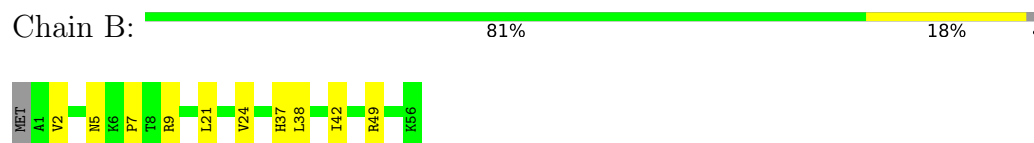
3 Residue-property plots [i](#)

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

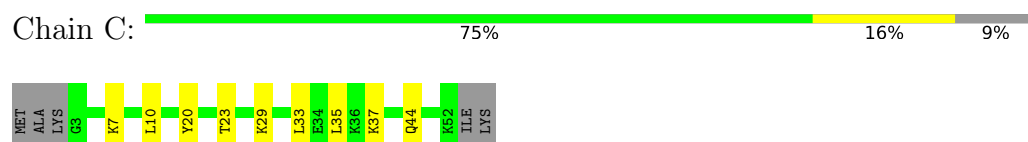
- Molecule 1: 50S ribosomal protein L31



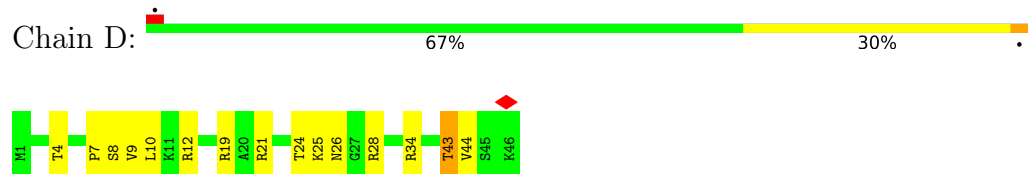
- Molecule 2: 50S ribosomal protein L32



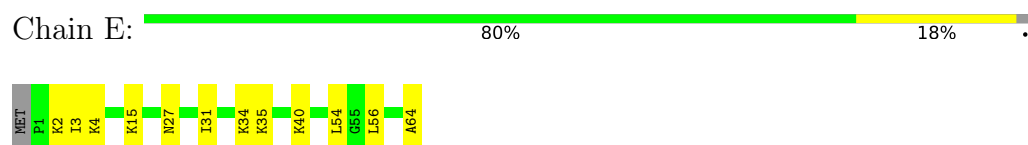
- Molecule 3: 50S ribosomal protein L33



- Molecule 4: 50S ribosomal protein L34



- Molecule 5: 50S ribosomal protein L35



- Molecule 6: 50S ribosomal protein L36

Chain F:  71% 29%



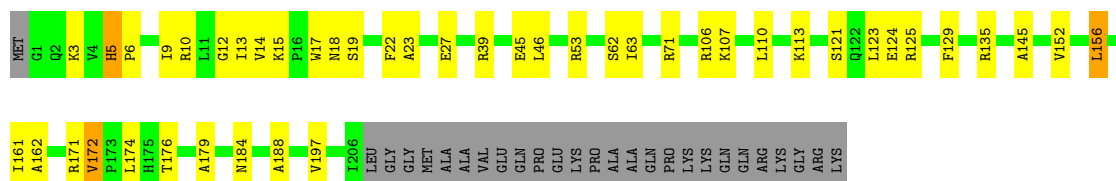
- Molecule 7: 30S ribosomal protein S2

Chain G:  70% 18% 10%



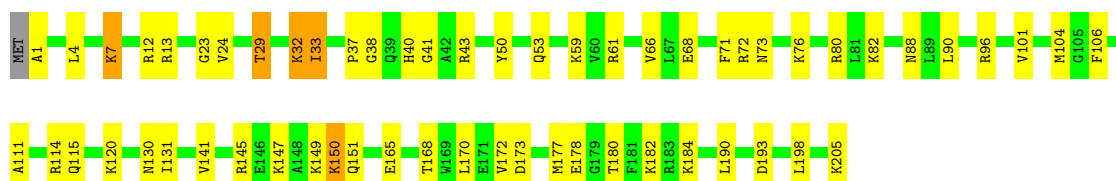
- Molecule 8: 30S ribosomal protein S3

Chain H:  69% 18% 12%



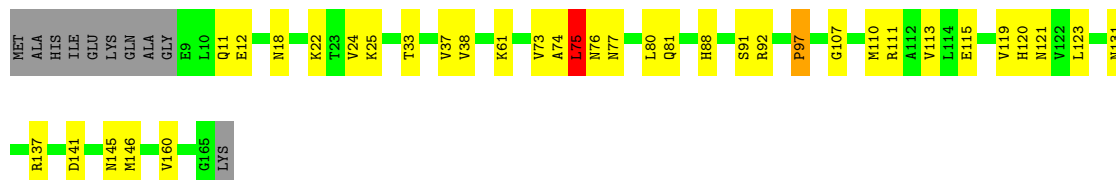
- Molecule 9: 30S ribosomal protein S4

Chain I:  71% 26%



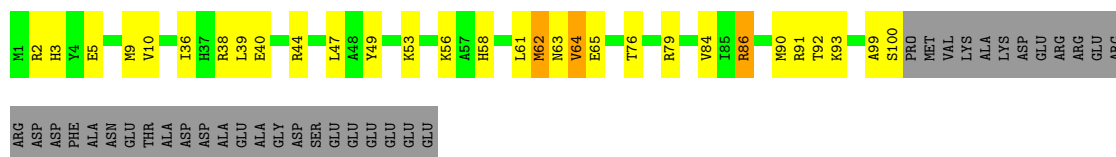
- Molecule 10: 30S ribosomal protein S5

Chain J:  72% 20% 6%



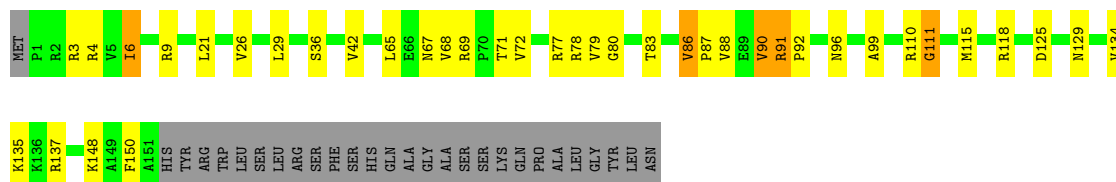
- Molecule 11: 30S ribosomal protein S6, fully modified isoform

Chain K:  52% 20% 26%



• Molecule 12: 30S ribosomal protein S7

Chain L: 63% 19% 16%



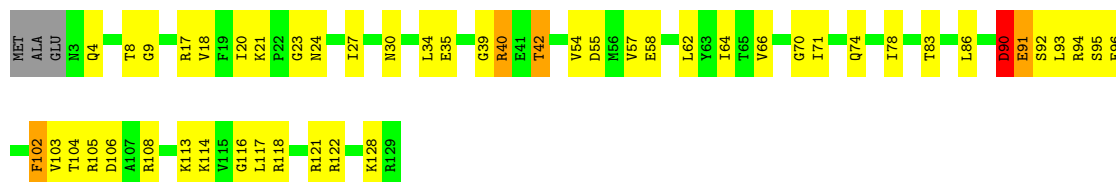
• Molecule 13: 30S ribosomal protein S8

Chain M: 84% 15%



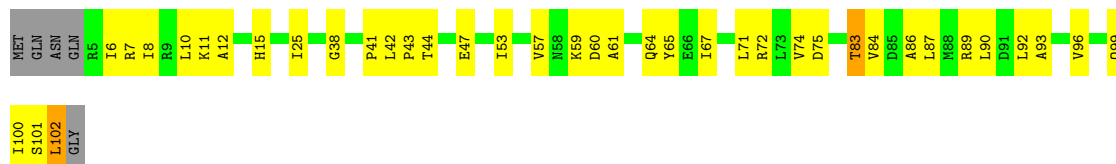
• Molecule 14: 30S ribosomal protein S9

Chain N: 59% 35%



• Molecule 15: 30S ribosomal protein S10

Chain O: 57% 36% 5%



• Molecule 16: 30S ribosomal protein S11

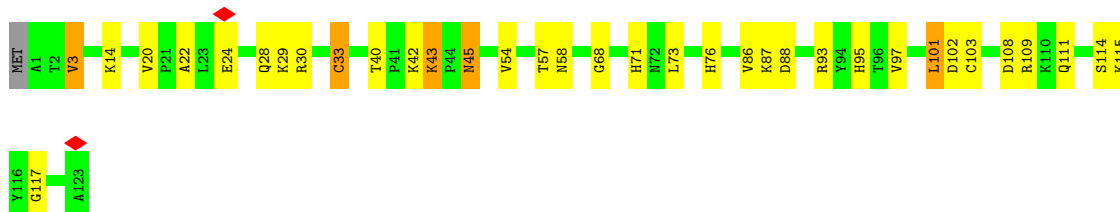
Chain P: 65% 23% 10%





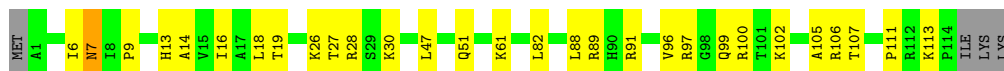
- Molecule 17: 30S ribosomal protein S12

Chain Q: 71% 24% . .



- Molecule 18: 30S ribosomal protein S13

Chain R: 72% 24% . .



- Molecule 19: 30S ribosomal protein S14

Chain S: 72% 27% .



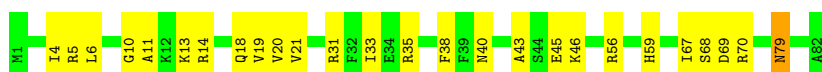
- Molecule 20: 30S ribosomal protein S15

Chain T: 78% 19% . .



- Molecule 21: 30S ribosomal protein S16

Chain U: 68% 30% .



- Molecule 22: 30S ribosomal protein S17

Chain V: 63% 32% 5%



- Molecule 23: 30S ribosomal protein S18

Chain W:  64% 19% 13%



- Molecule 24: 30S ribosomal protein S19

Chain X:  60% 25% 14%



- Molecule 25: 30S ribosomal protein S20

Chain Y:  72% 25% 3%



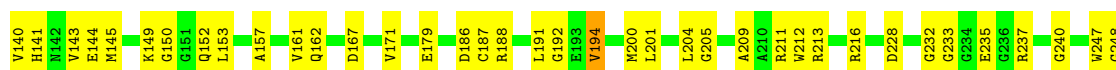
- Molecule 26: 30S ribosomal protein S21

Chain Z:  70% 18% 8%



- Molecule 27: 50S ribosomal protein L2

Chain b:  72% 26% 2%



- Molecule 28: 50S ribosomal protein L3

Chain c:  78% 21% 1%





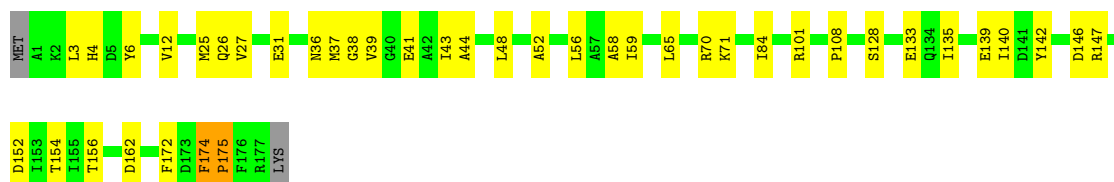
- Molecule 29: 50S ribosomal protein L4

Chain d: 83% 17%



- Molecule 30: 50S ribosomal protein L5

Chain e: 76% 22% ..



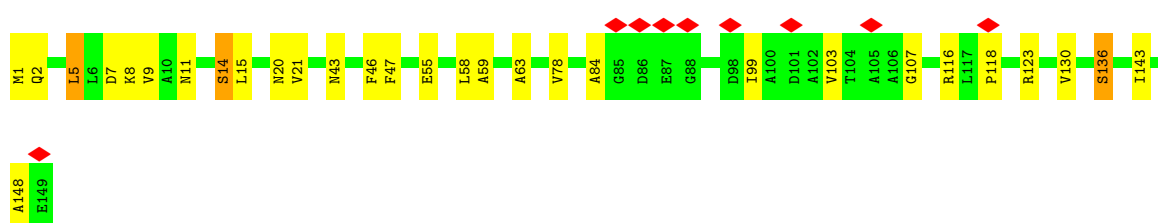
- Molecule 31: 50S ribosomal protein L6

Chain f: 85% 14% ...



- Molecule 32: 50S ribosomal protein L9

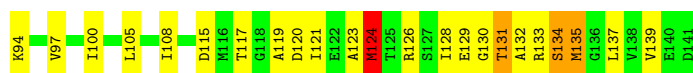
Chain g: 6% 80% 18% .



- Molecule 33: 50S ribosomal protein L11

Chain i: 54% 38% 6% ..





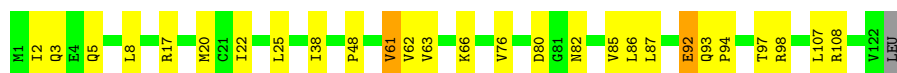
- Molecule 34: 50S ribosomal protein L13

Chain j: 84% 15% .



- Molecule 35: 50S ribosomal protein L14

Chain k: 77% 20% ..



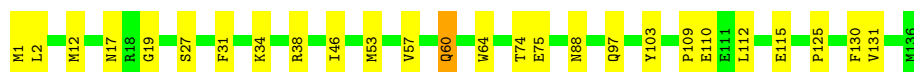
- Molecule 36: 50S ribosomal protein L15

Chain l: 72% 26% ..



- Molecule 37: 50S ribosomal protein L16

Chain m: 81% 18% .



- Molecule 38: 50S ribosomal protein L17

Chain n: 74% 20% 6%



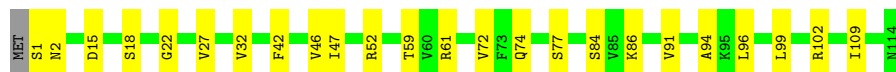
- Molecule 39: 50S ribosomal protein L18

Chain o: 75% 22% ..



- Molecule 40: 50S ribosomal protein L19

Chain p:  78% 21%



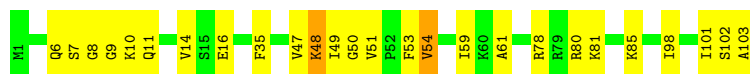
- Molecule 41: 50S ribosomal protein L20

Chain q:  77% 19%



- Molecule 42: 50S ribosomal protein L21

Chain r:  75% 23%



- Molecule 43: 50S ribosomal protein L22

Chain s:  79% 21%



- Molecule 44: 50S ribosomal protein L23

Chain t:  73% 20% 7%



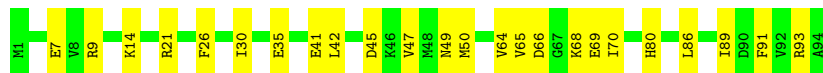
- Molecule 45: 50S ribosomal protein L24

Chain u:  84% 13%



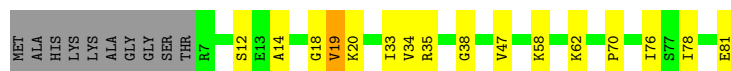
- Molecule 46: 50S ribosomal protein L25

Chain v:  74% 26%



- Molecule 47: 50S ribosomal protein L27

Chain w:  69% 18% 12%



- Molecule 48: 50S ribosomal protein L28

Chain x:  79% 17% ..



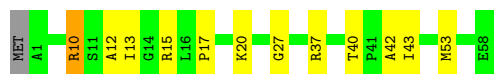
- Molecule 49: 50S ribosomal protein L29

Chain y:  81% 17% .



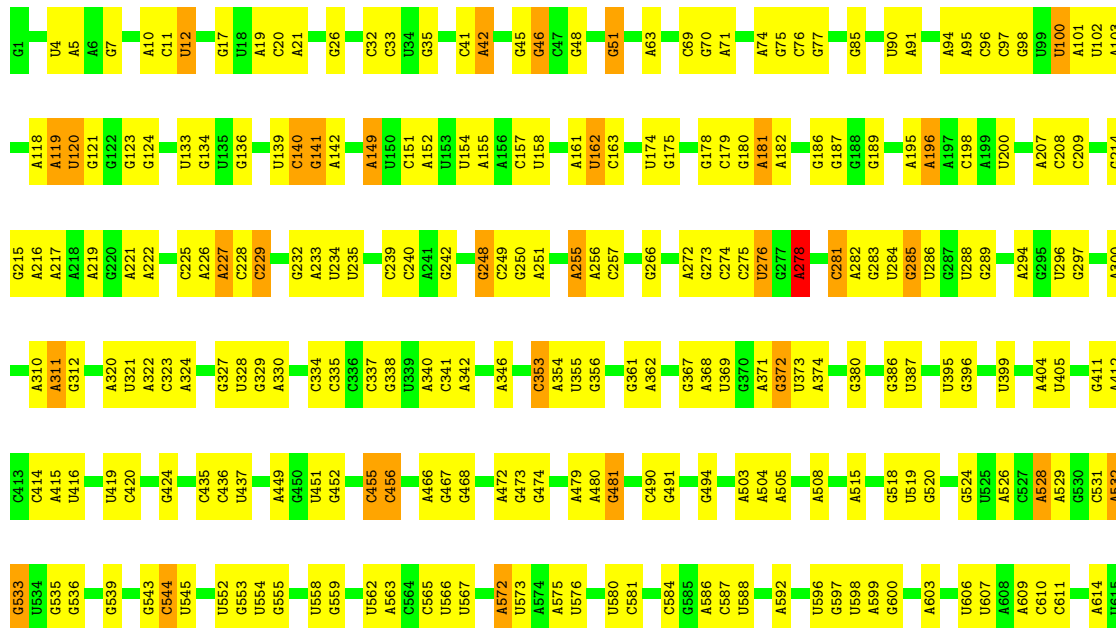
- Molecule 50: 50S ribosomal protein L30

Chain z:  78% 19% ..

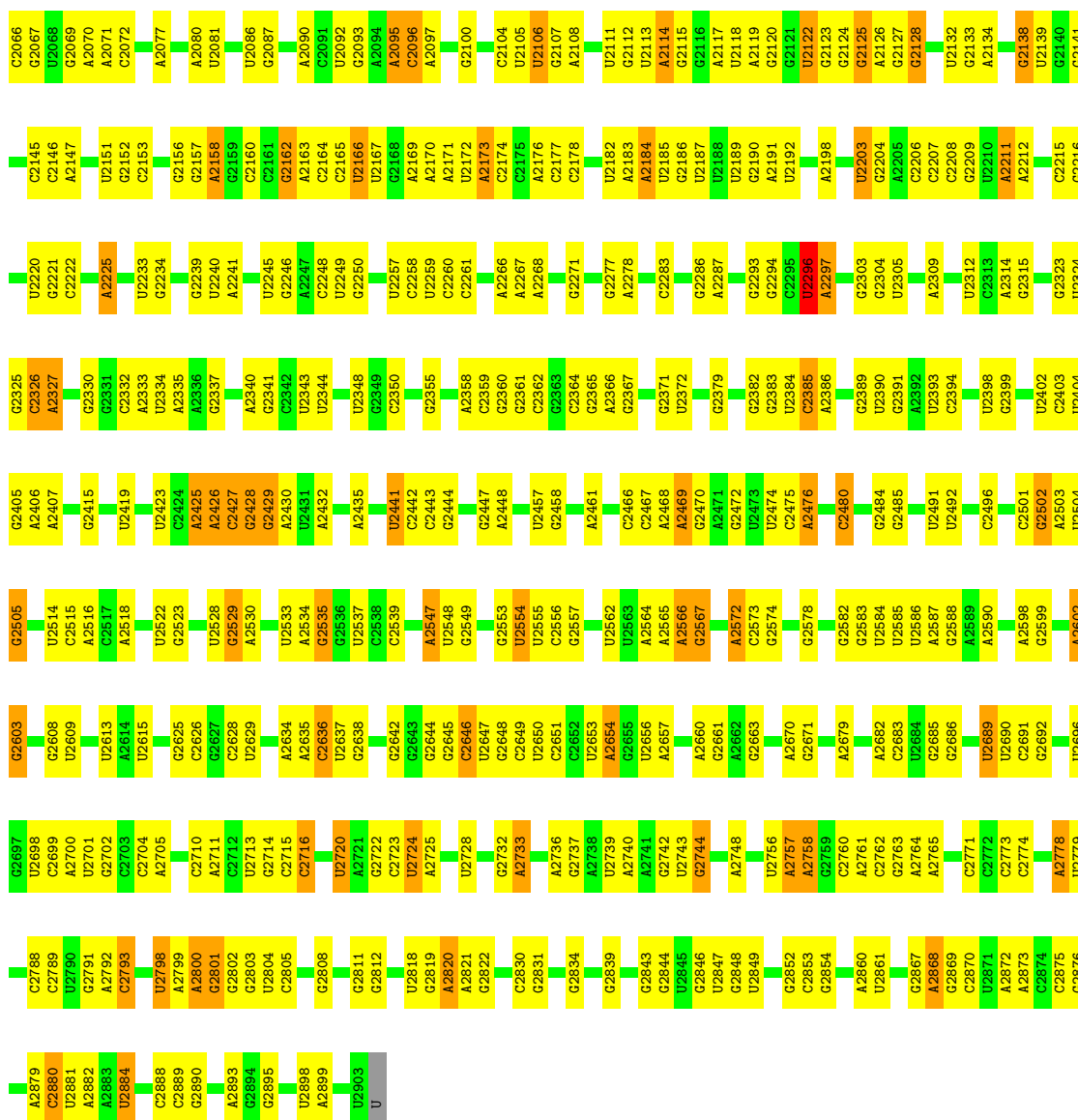


- Molecule 51: 23S rRNA

Chain 1:  56% 38% 7%

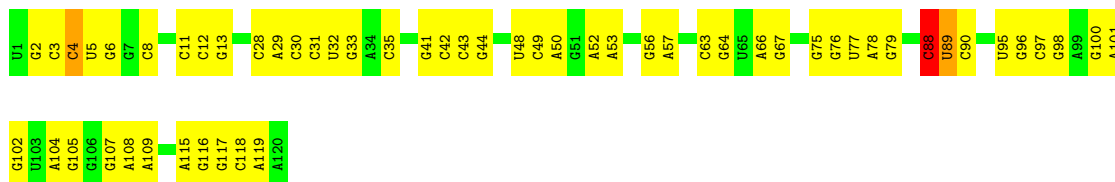


C1967	G1873	U1775	G1555	U1458	G1357	G1252	G1122	G1056	A975	A878	A792	U694	A616
A1970	A1877	G1776	C1556	G1459	G1358	G1253	C1123	A1057	A979	G879	A793	G695	G617
U1971	A1878	A1780	C1557	U1460	A1254	A1254	G1124	U1058		C885	G797	G700	A621
G1972	G1673	U1781	U1559	C1461	U1255	U1256	G1125	G1059		A886	G798	G701	G622
C1974	U1882	U1782	G1560	U1468	C1363	G1257	U1130	U1060		U887	G799	U702	A826
	U1883	A1783	C1564	A1469	A1365	G1258	G1131	G1062		A892	A800	U703	A827
U1991	C1893	A1784	C1565	A1470	U1375	U1259	U1132	G1063		C893	G801	G704	G628
G1992	C1894	U1785	G1568	G1471	G1376	G1259	A1133	U1064		C894	A802	A716	G629
U1993	C1895	A1786	G1569	G1472	G1377	U1263	A1134	U1065		U895	A803	A717	G630
	A1899	C1790	A1569	G1473	G1378	U1263	C1135	U1066		A896	A804	A718	A631
C1996	A1900	A1791	U1578	U1474	U1379	G1271	G1136	A1067		C897	C806	C719	
C1997	A1901	G1697	U1579	G1475	G1380	A1272	G1137	G1068		G907	U807		C634
A1998	C1795	A1698	U1584	G1478	A1383	A1273	G1138	A1069		G908	G808	G726	C635
C1999	G1907	U1796	U1585	G1482	A1384	U1274	C1139	A1070		G909	G809	G727	G636
G2004	C1908	G1797	G1587	A1490	C1386	A1275	U1141	G1071		G910	U810	A730	A637
A2005	G1909	U1798	G1588	A1491	A1387	G1276	A1142	A1072		G911	U811	A731	G638
	G1910	G1799	C1589	G1492	U1394	C1277	A1143	G1074		A908	C908	C732	U639
G2010	U1911	C1800	A1596	G1493	U1395	C1278	A1155	C1075		A909	U812	C733	C640
U2011	A1912	A1801	A1597	C1494	U1396	G1279	A1156	C1076		G914	C814	G734	
G2012	A1913	U1716	A1598	A1495	U1397	A1287	G1157	A1077		G915	C815	C740	A644
	C1914	A1805	G1601	A1496	C1398	G1288	G1158	C1078		G916	C816	U646	U646
A2020	U1915	C1806	U1602	A1504	U1409	G1289	U1159	A1080		A917	G818	A743	C650
C2021	A1916	G1807	A1603	A1505	G1410	G1290	G1160	U1081		U918	A819	U744	
U2022	U1917	A1808	U1604	A1506	C1411	C1291	G1161	U1082		U919	U827	C747	A654
C2023	C1908	A1810	A1605	C1507	G1412	G1292	G1162	U1083		A920	U828	G748	A655
G2024	G1909	G1797	A1606	A1508	C1413	G1293	U1172	A1084		A921	A829	A749	
C2025	U1911	C1811	G1611	A1509	G1414	C1294	C1172	A1085		U922	G830	A750	U658
U2026	U1912	U1728	C1612	A1510	A1415	C1295	U1173	A1086		U923	U831	A751	G659
G2027	C1924	U1729	A1616	C1510	U1416	G1300	U1174	C1087		U924	U832	U752	C660
U2028	U1925	C1730	A1617	A1511	A1417	A1301	A1175	A1088		U925	A833	A753	A661
G2029	U1926	G1731	A1618	A1512	G1424	G1302	G1176	G1091		U926	U834	G757	G662
A2030	A1927	C1732	A1619	A1513	G1425	G1303	G1177	C1092		U927	U835	G758	G663
A2031	A1928	A1821	G1625	A1514	G1426	G1304	G1178	C1093		U928	U836	G759	G664
G2032	G1929	C1822	A1626	G1524	A1427	U1318	U1180	A1095		U929	A845	A761	A688
C2033	C1930	G1823	G1627	G1525	C1428	C1319	U1181	A1096		U930	U846	U762	G689
U2034	U1931	U1827	G1628	A1528	G1429	C1320	G1182	U1097		U931	G855	G763	A670
G2035	G1932	G1828	U1636	G1529	G1430	A1321	U1183	A1098		U932	U856	A764	C671
C2036	C1933	G1829	U1637	G1530	A1431	A1322	G1184	A1099		U933	G857	G770	C672
	C1934	A1829	C1638	U1534	A1432	U1326	G1185	C1102		U934	G858	U773	A676
U2039	A1937	C1748	G1645	A1535	G1435	A1327	U1186	A1103		U935	U859	G774	A677
A2041	A1938	A1749	U1646	A1536	G1436	C1330	A1189	C1104		U936	U860	G775	
A2042	U1944	G1945	U1647	G1537	C1437	C1331	G1190	U1105		U937	U861	G776	G681
G2048	C1945	G1842	U1648	G1538	U1438	C1332	U1201	U1033		U938	U862	G777	G682
G2049	A1952	C1843	G1649	U1539	A1439	C1333	G1202	U1034		U939	A863	G778	U683
C2050	U1955	G1844	A1650	G1540	U1440	A1336	G1203	U1035		U940	G864	U779	G684
A2051	U1956	G1845	G1651	G1541	G1441	U1337	U1204	G1036		U941	C865	G780	A685
	U1957	A1847	A1652	U1542	U1442	G1339	C1211	A1111		U942	G866	G781	U686
C2055	A1960	U1758	A1653	G1543	U1443	U1340	G1212	G1112		U943	U867	A782	C968
G2056	C1961	A1759	A1654	A1544	G1444	A1341	U1113	U1113		U944	U868	G783	U689
	U1962	C1760	A1655	A1545	C1445	G1342	C1221	G1114		U945	U869	G784	A690
A2060	U1963	G1764	C1658	U1546	C1446	U1343	G1222	C1115		U946	U870	G785	C690
G2061	G1964	A1773	A1665	C1550	G1447	U1344	G1223	U1116		U947	U871	A786	C691
A2062	C1965	C1774	G1666	A1551	G1448	C1345	G1224	G1117		U948	U872	G787	C692
	A1966				G1449	U1346	G1225	C1118		U949	C873	G788	A693
					G1450	U1352	U1249	G1120		U950	C874	A789	
								G1121		U951	C875	A790	
								C1122		U952	C876	A791	
								U1119		U953	C877	A792	
								G1120		U954	C878	A793	
								C1121		U955	C879	A794	



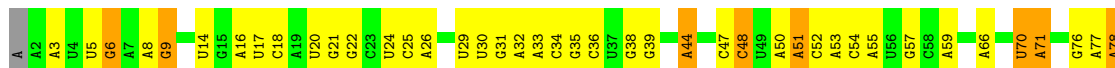
• Molecule 52: 5S rRNA

Chain 2: 53% 44% ..



• Molecule 53: 16S rRNA

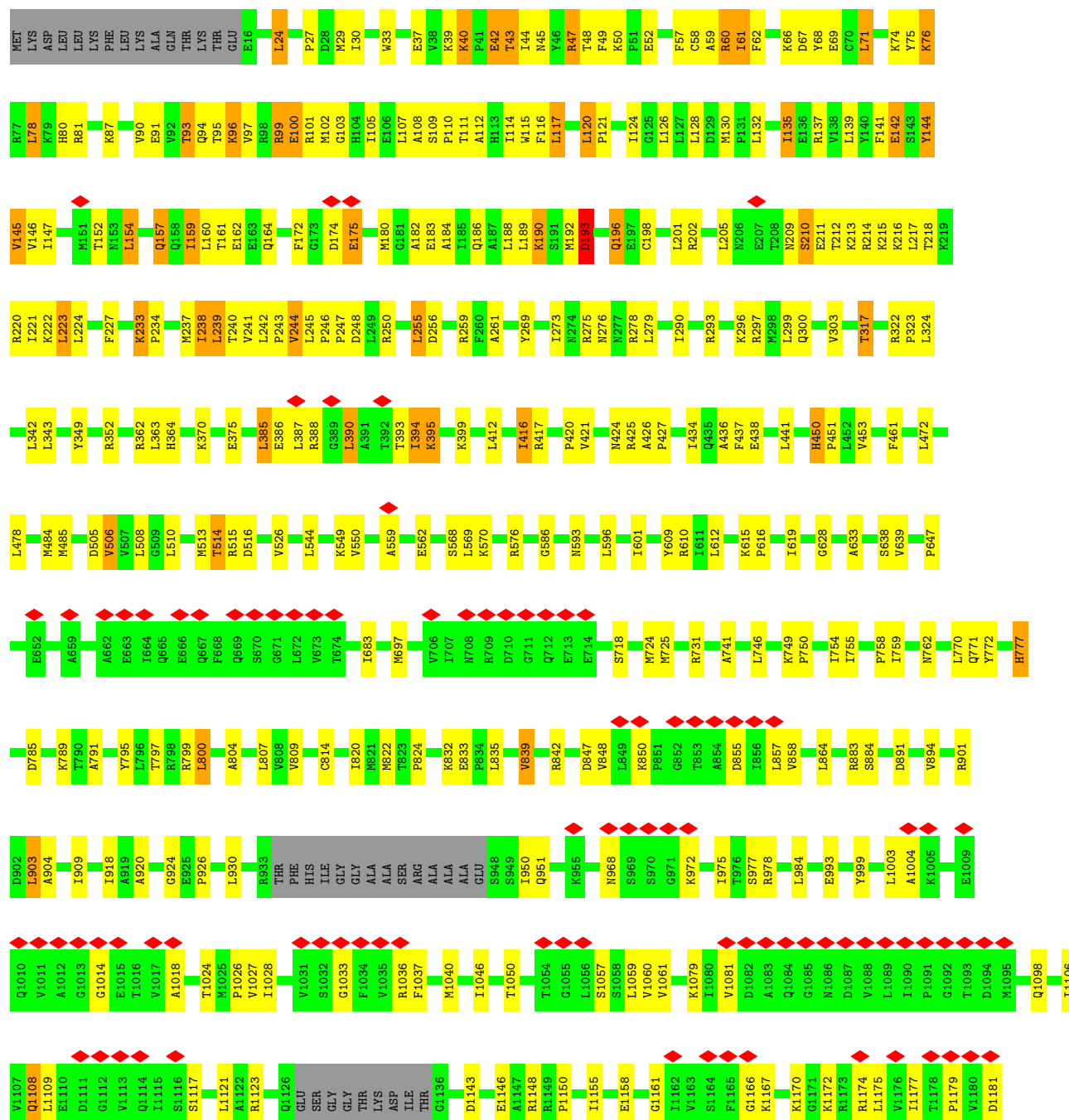
Chain 3: 55% 39% 6%

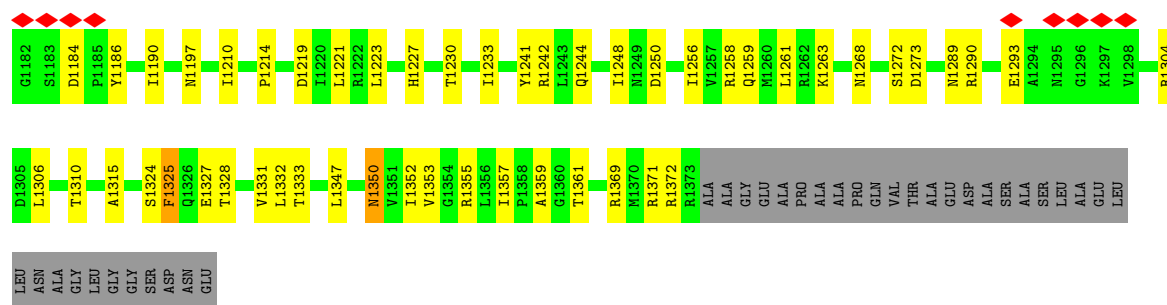




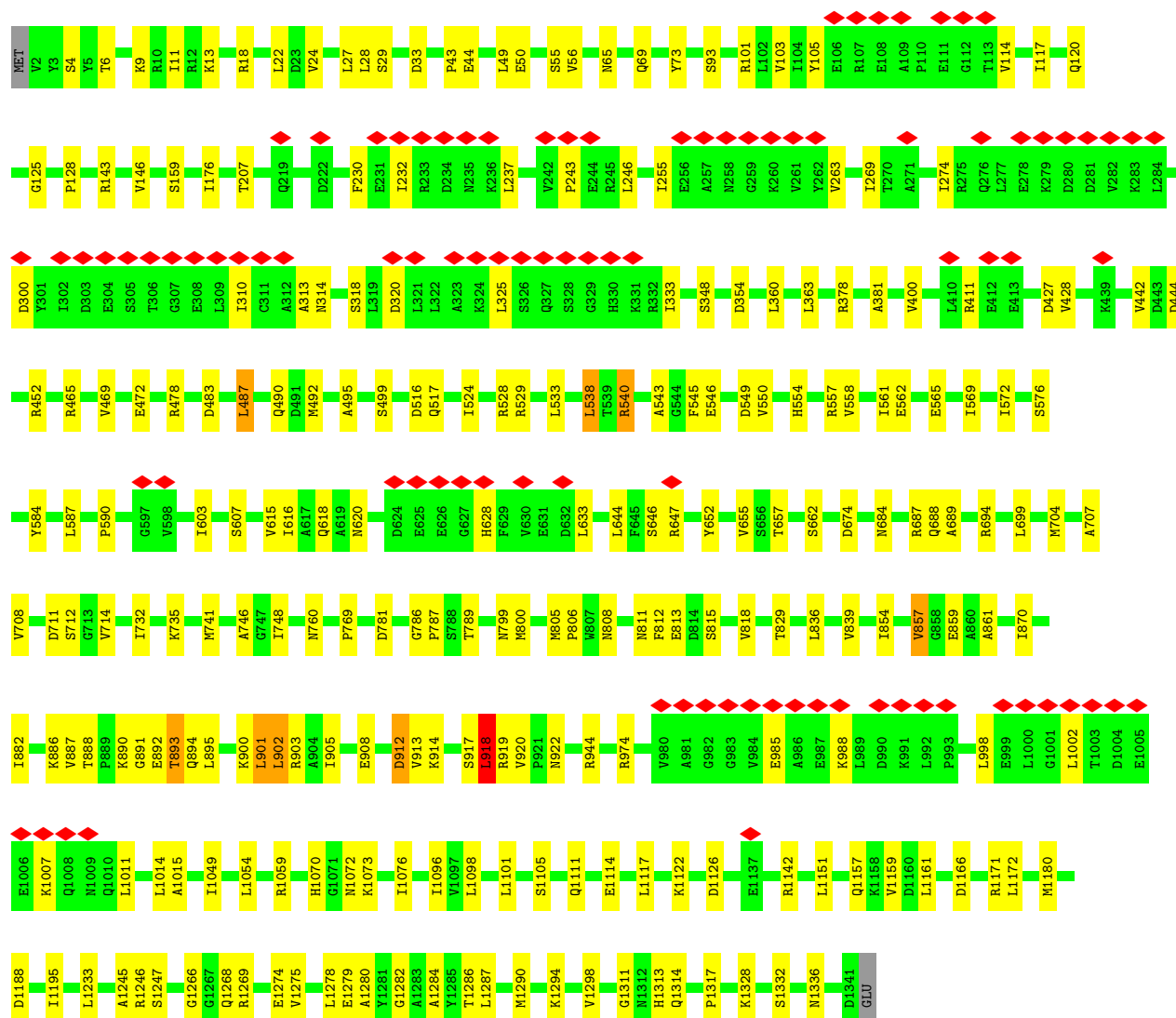
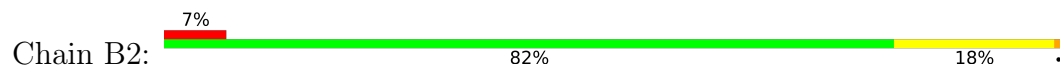


• Molecule 58: DNA-directed RNA polymerase subunit beta'

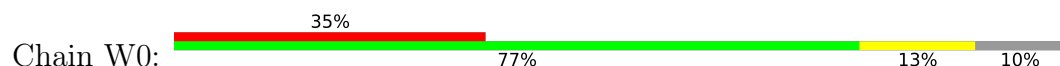


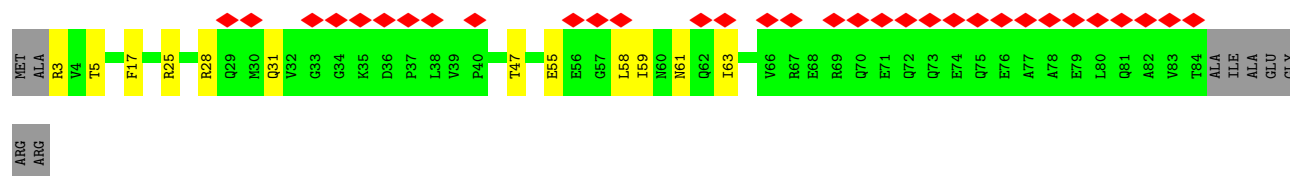


• Molecule 59: DNA-directed RNA polymerase subunit beta

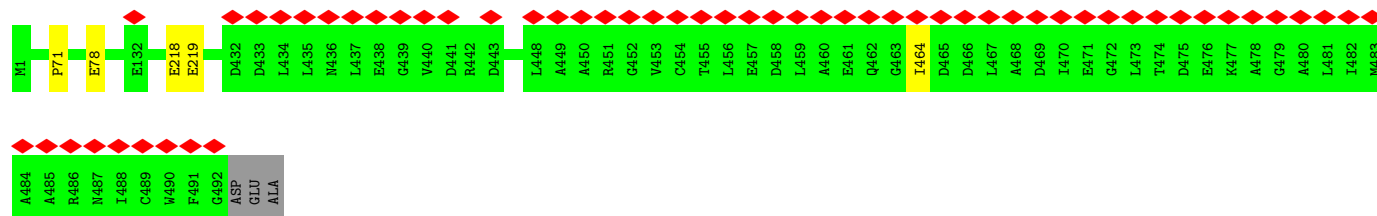


• Molecule 60: DNA-directed RNA polymerase subunit omega

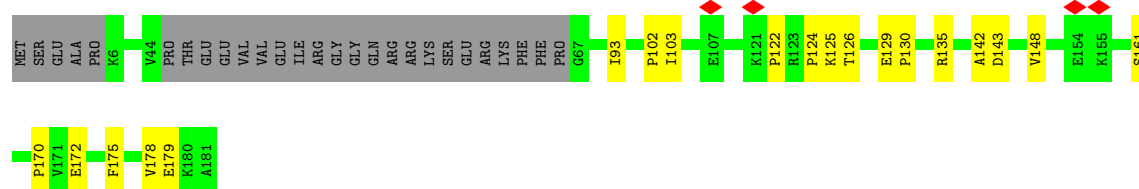
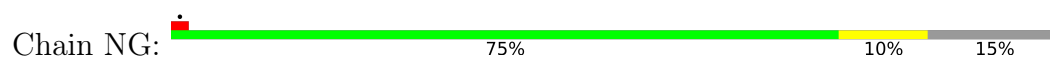




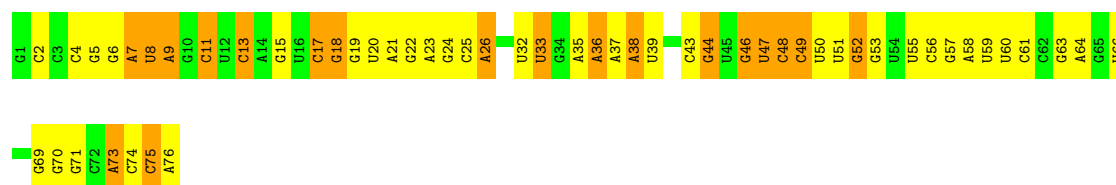
- Molecule 61: Transcription termination/antitermination protein NusA



- Molecule 62: Transcription termination/antitermination protein NusG



- Molecule 63: tRNA(Phe)

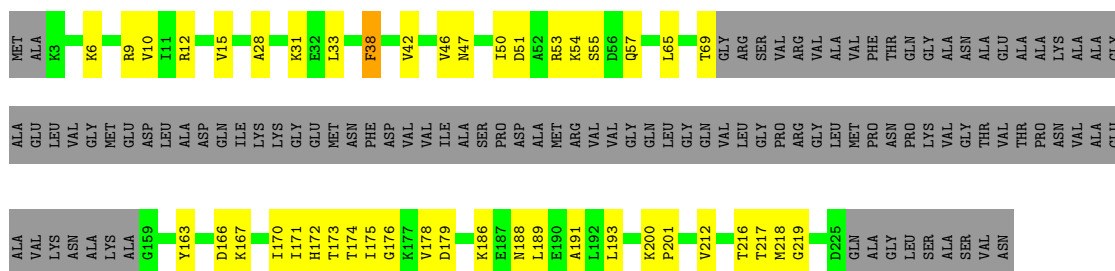


- Molecule 64: tRNA(fMet)

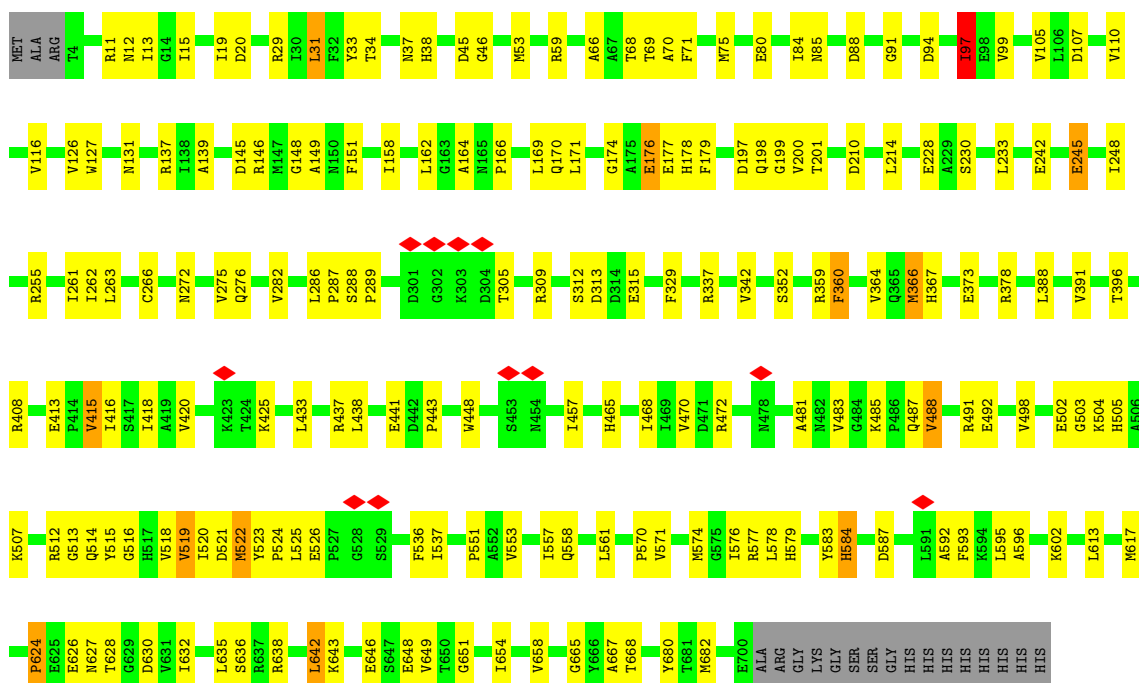


- Molecule 65: Large ribosomal subunit protein uL1

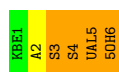




• Molecule 66: Elongation factor G



• Molecule 67: Viomycin



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	31000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	47	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.091	Depositor
Minimum map value	-0.035	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.0075	Depositor
Map size ($\text{\AA}$)	753.60004, 753.60004, 753.60004	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.57, 1.57, 1.57	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 5OH, DPP, UAL, KBE, PO4, GDP

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	0.47	0/531	0.99	4/709 (0.6%)
2	B	0.50	0/450	0.84	0/599
3	C	0.35	0/416	0.73	0/554
4	D	0.41	0/380	0.89	1/498 (0.2%)
5	E	0.40	0/513	0.86	0/676
6	F	0.35	0/303	0.77	0/397
7	G	0.48	0/1735	0.95	7/2338 (0.3%)
8	H	0.45	0/1647	0.88	3/2221 (0.1%)
9	I	0.45	0/1665	0.98	8/2227 (0.4%)
10	J	0.45	0/1165	0.95	7/1568 (0.4%)
11	K	0.58	0/835	1.02	5/1128 (0.4%)
12	L	0.44	0/1195	1.02	8/1602 (0.5%)
13	M	0.38	0/989	0.80	0/1326
14	N	0.48	0/1034	1.06	6/1375 (0.4%)
15	O	0.54	0/796	1.01	3/1077 (0.3%)
16	P	0.41	0/885	0.98	5/1195 (0.4%)
17	Q	0.51	1/969 (0.1%)	1.06	5/1300 (0.4%)
18	R	0.39	0/892	0.87	1/1193 (0.1%)
19	S	0.39	0/817	0.90	2/1088 (0.2%)
20	T	0.34	0/722	0.85	1/964 (0.1%)
21	U	0.40	0/659	0.91	2/884 (0.2%)
22	V	0.41	0/657	0.85	2/881 (0.2%)
23	W	0.47	0/544	0.95	2/731 (0.3%)
24	X	0.40	0/652	0.95	1/877 (0.1%)
25	Y	0.38	0/671	0.90	2/888 (0.2%)
26	Z	0.59	0/550	1.12	2/728 (0.3%)
27	b	0.45	0/2121	0.93	6/2852 (0.2%)
28	c	0.39	0/1586	0.84	3/2134 (0.1%)
29	d	0.43	0/1571	0.78	0/2113
30	e	0.44	1/1434 (0.1%)	0.91	5/1926 (0.3%)
31	f	0.41	0/1343	0.82	2/1816 (0.1%)
32	g	0.47	0/1122	0.93	3/1515 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	i	0.70	1/1046 (0.1%)	1.16	6/1410 (0.4%)
34	j	0.39	0/1152	0.86	4/1551 (0.3%)
35	k	0.49	0/947	0.95	2/1268 (0.2%)
36	l	0.40	0/1054	0.95	5/1403 (0.4%)
37	m	0.39	0/1093	0.85	3/1460 (0.2%)
38	n	0.39	0/973	0.92	3/1301 (0.2%)
39	o	0.39	0/902	0.92	3/1209 (0.2%)
40	p	0.40	0/929	0.85	1/1242 (0.1%)
41	q	0.46	0/960	0.90	3/1278 (0.2%)
42	r	0.45	0/829	0.96	4/1107 (0.4%)
43	s	0.38	0/864	0.84	2/1156 (0.2%)
44	t	0.39	0/744	0.78	0/994
45	u	0.41	0/784	0.92	3/1047 (0.3%)
46	v	0.39	0/766	0.78	0/1025
47	w	0.33	0/582	0.72	0/769
48	x	0.36	0/635	0.85	2/848 (0.2%)
49	y	0.34	0/510	0.87	1/677 (0.1%)
50	z	0.50	0/453	0.75	0/605
51	1	0.44	0/69796	0.54	8/108888 (0.0%)
52	2	0.45	0/2872	0.53	1/4479 (0.0%)
53	3	0.45	0/36963	0.53	3/57662 (0.0%)
54	4	0.56	0/695	0.72	0/1076
55	8	0.56	0/599	0.70	1/919 (0.1%)
56	9	0.48	0/468	0.53	0/719
57	A1	0.55	0/2106	0.82	0/2868
57	A2	0.48	0/2048	0.75	0/2786
58	B1	0.55	5/10510 (0.0%)	0.74	8/14196 (0.1%)
59	B2	0.45	0/10714	0.67	1/14459 (0.0%)
60	W0	0.29	0/652	0.61	0/879
61	NA	0.71	0/2431	1.20	0/3385
62	NG	1.12	0/756	1.03	2/1048 (0.2%)
63	5	0.56	0/1812	0.88	2/2823 (0.1%)
64	6	0.43	0/1832	0.56	0/2855
65	a	0.46	0/1033	0.98	5/1387 (0.4%)
66	0	0.51	0/5501	0.96	19/7446 (0.3%)
67	h	3.18	2/11 (18.2%)	0.75	0/13
All	All	0.46	10/196871 (0.0%)	0.69	188/289618 (0.1%)

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
67	h	3	SER	CA-C	-6.72	1.38	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
67	h	4	SER	CA-C	-6.20	1.40	1.52
30	e	174	PHE	N-CA	5.74	1.54	1.46
58	B1	1350	ASN	CG-ND2	-5.27	1.22	1.33
58	B1	424	ASN	CG-ND2	-5.16	1.22	1.33
33	i	2	LYS	N-CA	5.13	1.49	1.46
58	B1	777	HIS	ND1-CE1	5.13	1.37	1.32
58	B1	1108	GLN	CD-OE1	5.11	1.33	1.23
17	Q	43	LYS	N-CA	5.07	1.50	1.46
58	B1	1268	ASN	CG-OD1	5.01	1.33	1.23

All (188) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
66	0	174	GLY	N-CA-C	10.08	123.45	111.35
11	K	99	ALA	N-CA-C	9.93	123.44	111.02
65	a	179	ASP	N-CA-C	-9.71	99.88	114.64
16	P	73	VAL	N-CA-C	-9.11	104.46	113.20
66	0	45	ASP	N-CA-C	-8.82	103.64	114.75
8	H	9	ILE	N-CA-C	8.69	115.51	106.21
12	L	111	GLY	N-CA-C	8.59	121.41	111.36
15	O	60	ASP	N-CA-C	-8.56	104.86	114.62
9	I	7	LYS	N-CA-C	8.47	121.73	111.40
39	o	22	GLY	N-CA-C	-8.43	101.23	111.35
43	s	24	ILE	N-CA-C	8.39	115.19	106.21
37	m	60	GLN	N-CA-C	8.24	122.37	110.10
1	A	45	THR	N-CA-C	-8.22	102.70	112.89
51	1	876	C	C2'-C3'-O3'	-8.11	101.54	113.70
66	0	38	HIS	N-CA-C	-7.89	97.55	109.94
66	0	413	GLU	N-CA-C	7.71	119.49	109.93
33	i	90	GLY	N-CA-C	-7.67	105.35	114.48
7	G	88	GLN	N-CA-C	7.66	121.74	110.17
31	f	46	ASP	N-CA-C	-7.53	103.01	111.14
51	1	1020	A	C2'-C3'-O3'	7.34	120.52	109.50
17	Q	22	ALA	N-CA-C	-7.30	102.93	111.03
9	I	168	THR	N-CA-C	7.29	122.24	111.96
34	j	105	VAL	N-CA-C	-7.11	106.14	111.90
4	D	7	PRO	N-CA-C	7.07	122.45	111.21
65	a	10	VAL	N-CA-C	-7.06	103.59	110.72
27	b	87	SER	N-CA-C	-6.97	105.30	113.88
19	S	39	ASP	N-CA-C	-6.92	103.84	112.90
16	P	126	ARG	N-CA-C	6.89	118.97	110.91
26	Z	66	ARG	N-CA-C	6.87	119.61	111.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	L	91	ARG	CA-C-N	6.85	126.09	118.97
12	L	91	ARG	C-N-CA	6.85	126.09	118.97
33	i	119	ALA	N-CA-C	6.83	120.39	110.42
66	0	366	MET	N-CA-C	6.82	118.89	110.91
39	o	10	ARG	N-CA-C	-6.80	105.13	113.50
1	A	54	GLY	N-CA-C	6.76	123.26	112.58
65	a	178	VAL	N-CA-C	6.75	113.43	106.21
21	U	46	LYS	N-CA-C	-6.63	99.02	109.50
34	j	81	ILE	N-CA-C	6.63	117.32	110.36
48	x	17	ARG	N-CA-C	6.54	119.20	111.02
27	b	30	ALA	N-CA-C	6.52	121.62	112.75
58	B1	450	HIS	CB-CG-CD2	-6.51	122.74	131.20
41	q	6	GLY	N-CA-C	6.48	116.11	110.21
27	b	121	ALA	N-CA-C	6.48	118.66	110.24
27	b	248	GLY	N-CA-C	6.47	122.93	113.48
21	U	79	ASN	N-CA-C	6.45	118.65	110.33
28	c	59	ARG	N-CA-C	-6.42	107.30	114.62
24	X	48	ILE	N-CA-C	6.41	118.03	109.37
58	B1	61	ILE	CA-C-N	-6.36	114.01	121.64
58	B1	61	ILE	C-N-CA	-6.36	114.01	121.64
30	e	147	ARG	N-CA-C	6.35	118.06	110.19
58	B1	777	HIS	CB-CG-CD2	-6.33	122.97	131.20
30	e	43	ILE	N-CA-C	-6.32	103.19	111.09
15	O	83	THR	CB-CA-C	-6.28	101.30	110.96
38	n	104	ALA	N-CA-C	6.26	118.91	111.71
25	Y	6	ALA	N-CA-C	-6.24	103.33	113.19
16	P	90	PRO	N-CA-C	-6.23	105.52	114.18
33	i	21	PRO	N-CA-C	6.23	118.30	110.70
36	l	95	LEU	N-CA-C	-6.20	105.55	113.23
12	L	86	VAL	N-CA-C	6.19	114.78	109.02
16	P	125	LYS	N-CA-C	6.13	123.86	110.80
10	J	11	GLN	N-CA-C	6.13	119.70	111.24
45	u	6	ARG	N-CA-C	6.11	123.82	110.80
23	W	68	PRO	N-CA-C	6.11	120.57	111.41
18	R	14	ALA	N-CA-C	6.07	118.69	111.71
38	n	14	SER	N-CA-C	6.07	117.56	111.07
10	J	110	MET	N-CA-C	-6.05	105.81	113.43
12	L	135	LYS	N-CA-C	-6.04	105.95	113.38
7	G	212	TYR	N-CA-C	6.04	117.73	111.03
66	0	408	ARG	N-CA-C	6.03	118.56	108.73
10	J	77	ASN	N-CA-C	6.02	119.54	111.24
34	j	31	GLU	N-CA-C	-6.01	104.84	111.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	I	177	MET	N-CA-C	6.00	117.93	110.91
37	m	110	GLU	N-CA-C	6.00	117.49	111.07
11	K	86	ARG	N-CA-C	5.99	117.92	110.91
10	J	74	ALA	N-CA-C	5.95	123.47	110.80
27	b	145	MET	N-CA-C	-5.93	106.69	114.04
42	r	54	VAL	N-CA-C	5.93	121.67	109.34
1	A	43	PHE	N-CA-C	-5.92	106.18	113.41
25	Y	43	LYS	N-CA-C	5.92	117.53	111.14
14	N	42	THR	N-CA-C	5.91	119.79	111.52
48	x	60	LYS	N-CA-C	-5.90	104.48	111.03
14	N	90	ASP	N-CA-C	5.89	123.35	110.80
30	e	4	HIS	N-CA-C	-5.86	104.49	111.69
36	l	115	GLU	N-CA-C	5.85	117.75	110.91
7	G	13	VAL	N-CA-C	5.84	121.48	109.34
8	H	10	ARG	N-CA-C	-5.80	105.57	114.16
52	2	88	C	C2'-C3'-O3'	-5.80	105.00	113.70
51	1	1085	A	C2'-C3'-O3'	-5.80	105.00	113.70
12	L	90	VAL	N-CA-C	5.79	117.66	108.87
45	u	89	GLY	N-CA-C	-5.78	107.17	114.16
28	c	86	GLU	N-CA-C	5.77	119.21	111.24
8	H	5	HIS	N-CA-C	5.77	116.67	109.57
17	Q	33	CYS	N-CA-C	5.74	117.62	110.91
7	G	123	GLY	N-CA-C	5.72	117.34	111.56
34	j	119	PHE	N-CA-C	-5.71	106.44	113.41
20	T	43	ALA	N-CA-C	-5.69	105.00	111.14
14	N	58	GLU	N-CA-C	-5.66	103.88	112.99
35	k	94	PRO	N-CA-C	5.66	124.13	112.47
16	P	89	GLY	N-CA-C	5.65	123.86	112.34
51	1	2296	U	C2'-C3'-O3'	-5.64	105.24	113.70
14	N	71	ILE	N-CA-C	5.63	116.08	110.23
30	e	172	PHE	N-CA-C	-5.62	106.42	113.28
33	i	53	PRO	N-CA-C	5.62	119.91	111.14
58	B1	450	HIS	CB-CG-ND1	5.62	131.13	122.70
41	q	75	TYR	N-CA-C	5.62	117.08	111.07
66	0	359	ARG	N-CA-C	5.62	117.16	110.19
22	V	58	VAL	N-CA-C	5.61	116.66	107.24
39	o	21	LEU	N-CA-C	-5.60	105.04	113.89
43	s	62	ASP	N-CA-C	5.60	118.46	111.24
66	0	635	LEU	N-CA-C	-5.59	104.88	110.97
33	i	124	MET	N-CA-C	-5.59	104.81	111.69
35	k	108	ARG	N-CA-C	5.55	118.69	108.58
7	G	151	LYS	N-CA-C	5.53	117.75	111.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	Q	115	LYS	N-CA-C	-5.53	101.53	110.32
17	Q	117	GLY	N-CA-C	5.52	122.44	114.10
30	e	175	PRO	N-CA-C	5.52	123.84	112.47
11	K	62	MET	N-CA-C	5.51	119.68	112.13
66	0	242	GLU	N-CA-C	-5.50	100.15	108.67
45	u	31	GLY	N-CA-C	-5.50	107.20	114.95
66	0	37	ASN	N-CA-C	5.49	118.35	109.40
66	0	31	LEU	N-CA-C	-5.49	105.71	112.90
11	K	39	LEU	N-CA-C	-5.48	104.46	113.50
63	5	73	A	C3'-C2'-O2'	5.48	118.92	110.70
41	q	6	GLY	O-C-N	5.47	124.91	121.85
26	Z	34	ARG	N-CA-C	5.46	122.43	110.80
66	0	287	PRO	N-CA-C	5.43	119.71	111.19
17	Q	3	VAL	N-CA-C	5.42	120.62	109.34
51	1	278	A	N9-C1'-C2'	5.42	120.13	112.00
58	B1	777	HIS	CB-CG-ND1	5.42	130.84	122.70
55	8	7	DC	C2'-C3'-O3'	-5.42	103.37	111.50
9	I	13	ARG	N-CA-C	-5.41	106.69	113.28
11	K	64	VAL	N-CA-C	5.40	115.72	108.17
23	W	51	GLN	N-CA-C	-5.39	106.38	113.12
22	V	79	GLU	N-CA-C	5.39	117.22	110.91
63	5	75	C	C4'-C3'-O3'	5.39	117.48	109.40
9	I	29	THR	N-CA-C	5.38	122.27	110.80
66	0	245	GLU	N-CA-C	5.38	118.64	111.75
49	y	24	GLU	N-CA-C	5.38	122.25	110.80
62	NG	103	ILE	CA-C-N	-5.36	114.02	122.76
62	NG	103	ILE	C-N-CA	-5.36	114.02	122.76
51	1	1104	C	C4'-C3'-O3'	5.36	121.03	113.00
42	r	50	GLY	N-CA-C	-5.36	105.92	112.77
28	c	174	SER	N-CA-C	5.35	117.17	110.91
12	L	6	ILE	N-CA-C	5.33	120.43	109.34
7	G	46	VAL	N-CA-CB	5.33	113.86	110.50
53	3	754	C	N1-C1'-C2'	5.32	119.98	112.00
42	r	53	PHE	CB-CA-C	5.32	121.00	110.42
33	i	72	THR	N-CA-C	-5.30	98.09	109.81
59	B2	891	GLY	O-C-N	5.30	124.82	121.85
9	I	150	LYS	N-CA-C	5.29	117.10	110.91
31	f	174	LYS	N-CA-C	5.27	122.02	110.80
66	0	46	GLY	N-CA-C	-5.26	108.06	115.32
58	B1	27	PRO	N-CA-C	-5.23	106.23	113.81
66	0	80	GLU	N-CA-C	-5.22	102.88	110.08
66	0	97	ILE	N-CA-C	-5.22	105.45	110.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	J	160	VAL	N-CA-C	5.21	115.93	110.62
66	0	441	GLU	N-CA-C	5.20	117.95	111.24
9	I	182	LYS	N-CA-C	5.20	119.26	112.13
12	L	129	ASN	N-CA-C	5.19	118.36	111.30
14	N	40	ARG	N-CA-C	-5.18	106.06	114.09
32	g	136	SER	N-CA-C	5.18	121.83	110.80
38	n	50	PRO	N-CA-C	-5.16	107.41	113.86
32	g	63	ALA	N-CA-C	-5.16	106.94	113.18
66	0	13	ILE	N-CA-C	5.15	116.72	108.89
66	0	624	PRO	N-CA-C	5.15	120.30	113.40
19	S	13	VAL	N-CA-C	-5.14	105.40	111.00
10	J	92	ARG	N-CA-CB	-5.13	104.46	111.65
51	1	100	U	N1-C1'-C2'	5.13	119.70	112.00
15	O	38	GLY	N-CA-C	5.12	122.80	112.34
65	a	38	PHE	N-CA-C	-5.12	100.83	109.07
58	B1	61	ILE	CA-C-O	-5.10	115.65	120.95
65	a	191	ALA	N-CA-C	-5.10	106.91	113.02
40	p	18	SER	N-CA-C	5.09	117.93	110.30
36	l	29	LYS	CA-C-N	5.08	131.24	121.54
36	l	29	LYS	C-N-CA	5.08	131.24	121.54
9	I	165	GLU	N-CA-C	5.08	121.61	110.80
51	1	1111	A	N9-C1'-C2'	5.07	119.61	112.00
7	G	56	LEU	N-CA-C	-5.07	105.84	111.36
14	N	103	VAL	N-CA-C	-5.06	107.87	112.12
1	A	5	ILE	N-CA-C	-5.06	107.87	112.12
27	b	157	ALA	N-CA-C	5.06	117.68	110.24
36	l	96	LYS	N-CA-C	-5.04	106.64	112.89
10	J	75	LEU	N-CA-C	5.04	121.54	110.80
37	m	27	SER	N-CA-C	5.04	119.43	113.28
32	g	14	SER	N-CA-C	5.03	117.26	110.06
53	3	368	U	N1-C1'-C2'	5.03	119.55	112.00
42	r	47	VAL	CA-C-O	-5.02	118.26	122.63
53	3	1301	U	C4'-C3'-O3'	5.01	116.92	109.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	522	0	524	18	0
2	B	444	0	461	8	0
3	C	409	0	440	7	0
4	D	377	0	418	14	0
5	E	504	0	574	9	0
6	F	302	0	341	10	0
7	G	1704	0	1732	27	0
8	H	1620	0	1688	28	0
9	I	1643	0	1710	43	0
10	J	1152	0	1195	19	0
11	K	817	0	808	15	0
12	L	1181	0	1240	26	0
13	M	979	0	1034	13	0
14	N	1022	0	1070	38	0
15	O	786	0	828	26	0
16	P	869	0	878	21	0
17	Q	955	0	1019	20	0
18	R	883	0	944	22	0
19	S	805	0	847	21	0
20	T	714	0	737	13	0
21	U	649	0	666	21	0
22	V	648	0	691	19	0
23	W	535	0	552	14	0
24	X	637	0	665	23	0
25	Y	665	0	714	20	0
26	Z	544	0	579	10	0
27	b	2082	0	2157	51	0
28	c	1565	0	1616	37	0
29	d	1552	0	1619	26	0
30	e	1410	0	1447	26	0
31	f	1323	0	1374	19	0
32	g	1111	0	1148	19	0
33	i	1032	0	1088	61	0
34	j	1129	0	1162	19	0
35	k	938	0	1012	17	0
36	l	1045	0	1117	29	0
37	m	1074	0	1157	17	0
38	n	960	0	1000	21	0
39	o	892	0	923	21	0
40	p	917	0	965	21	0
41	q	947	0	1022	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	r	816	0	839	16	0
43	s	857	0	922	16	0
44	t	738	0	807	12	0
45	u	776	0	825	7	0
46	v	753	0	780	17	0
47	w	575	0	592	16	0
48	x	625	0	655	15	0
49	y	509	0	543	8	0
50	z	449	0	491	9	0
51	1	62317	0	31346	968	0
52	2	2568	0	1303	58	0
53	3	33012	0	16618	568	0
54	4	627	0	313	8	0
55	8	539	0	305	29	0
56	9	417	0	224	1	0
57	A1	2088	0	1895	26	0
57	A2	2029	0	1864	14	0
58	B1	10353	0	10548	314	0
59	B2	10546	0	10550	161	0
60	W0	650	0	658	10	0
61	NA	2432	0	1171	8	0
62	NG	758	0	334	16	0
63	5	1622	0	821	23	0
64	6	1640	0	837	19	0
65	a	1026	0	1092	32	0
66	0	5399	0	5363	108	0
67	h	48	0	40	7	0
68	B1	1	0	0	0	0
69	0	28	0	12	2	0
70	0	5	0	0	1	0
All	All	183546	0	132910	2831	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 9.

All (2831) 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)
23:W:42:ARG:NH2	53:3:721:G:H5''	1.59	1.18
35:k:48:PRO:HB3	53:3:1423:G:H5''	1.23	1.14
51:1:2682:A:H61	51:1:2728:U:H1'	1.18	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:42:ARG:HH21	53:3:721:G:H5''	0.97	1.08
33:i:93:ASN:HB2	51:1:1077:A:H5'	1.12	1.08
51:1:1064:C:H3'	51:1:1065:U:H5''	1.37	1.07
51:1:1019:U:OP1	51:1:1036:G:H5'	1.54	1.04
64:6:26:G:H2'	64:6:27:U:H5''	1.39	1.04
22:V:5:ARG:HH22	53:3:128:G:H5'	1.20	1.04
51:1:814:C:H1'	51:1:1225:G:H21	1.20	1.04
57:A1:287:VAL:CB	61:NA:78:GLU:CB	2.38	1.02
33:i:7:TYR:HE2	33:i:57:VAL:HB	1.24	1.02
51:1:1645:G:H5''	51:1:1646:C:H5'	1.42	1.01
58:B1:750:PRO:HB3	59:B2:549:ASP:OD2	1.60	1.01
33:i:123:ALA:HB1	51:1:1081:U:H4'	1.44	1.00
51:1:1557:C:H3'	51:1:1558:C:H5''	1.42	1.00
58:B1:111:THR:HG23	58:B1:300:GLN:CD	1.86	1.00
33:i:92:PRO:HB2	51:1:1077:A:O4'	1.62	0.99
53:3:1421:G:H3'	53:3:1422:G:H4'	1.44	0.99
15:O:41:PRO:HB3	53:3:1151:A:H1'	1.40	0.99
1:A:64:PHE:HD1	53:3:1011:C:H4'	1.26	0.98
33:i:93:ASN:HB2	51:1:1077:A:C5'	1.93	0.98
51:1:2382:G:H5''	51:1:2383:G:H5'	1.44	0.97
58:B1:352:ARG:HD2	59:B2:1268:GLN:NE2	1.79	0.97
34:j:27:ARG:HH22	51:1:1142:A:H4'	1.29	0.96
6:F:3:VAL:HG21	51:1:2539:C:H5'	1.47	0.96
22:V:5:ARG:NH2	53:3:128:G:H5'	1.83	0.94
58:B1:68:TYR:O	58:B1:75:TYR:CE2	2.20	0.94
51:1:562:U:H2'	51:1:572:A:H1'	1.50	0.94
51:1:1394:U:H4'	51:1:1603:A:H4'	1.49	0.94
66:0:524:PRO:HA	66:0:574:MET:HA	1.47	0.94
51:1:1098:A:H2'	51:1:1099:G:H5'	1.48	0.93
51:1:663:G:H2'	51:1:664:G:H5''	1.51	0.90
33:i:93:ASN:CB	51:1:1077:A:H5'	2.02	0.90
58:B1:68:TYR:C	58:B1:75:TYR:HE2	1.80	0.90
59:B2:854:ILE:HG21	59:B2:917:SER:HB3	1.54	0.90
21:U:31:ARG:HB2	53:3:310:G:H5''	1.53	0.89
58:B1:317:THR:HA	58:B1:323:PRO:HA	1.55	0.89
51:1:1697:G:H3'	51:1:1698:A:H5''	1.52	0.89
58:B1:202:ARG:HG2	58:B1:202:ARG:HH11	1.35	0.89
51:1:1045:C:H5'	51:1:1046:A:C8	2.09	0.88
51:1:45:G:H5''	51:1:46:G:H5'	1.51	0.88
54:4:44:G:H21	58:B1:427:PRO:HD3	1.38	0.88
63:5:9:A:H2'	63:5:11:C:H41	1.38	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:6:69:C:H2'	64:6:70:G:H5''	1.56	0.88
53:3:1421:G:N7	53:3:1422:G:H1'	1.88	0.87
53:3:813:U:H2'	53:3:814:A:H5''	1.58	0.85
51:1:2653:U:H3'	51:1:2654:A:H5''	1.58	0.85
51:1:1075:C:H3'	51:1:1076:C:H5''	1.58	0.85
51:1:876:C:H3'	51:1:877:A:C4'	2.06	0.84
17:Q:57:THR:HG21	53:3:362:G:H5''	1.57	0.84
46:v:49:ASN:HD21	51:1:1040:A:H4'	1.40	0.84
58:B1:68:TYR:HB3	58:B1:75:TYR:OH	1.76	0.84
51:1:2656:U:H5''	66:0:146:ARG:HE	1.40	0.83
15:O:43:PRO:HA	53:3:1151:A:H5'	1.59	0.83
58:B1:633:ALA:HB2	59:B2:808:ASN:H	1.41	0.83
2:B:5:ASN:HD22	51:1:2020:A:H62	1.23	0.83
21:U:5:ARG:HB2	53:3:376:G:H5''	1.59	0.83
21:U:14:ARG:HH12	53:3:618:C:H1'	1.43	0.83
51:1:740:C:H6	51:1:740:C:H5'	1.44	0.83
27:b:38:LYS:HB2	51:1:692:C:H5''	1.59	0.82
51:1:814:C:H1'	51:1:1225:G:N2	1.93	0.82
53:3:335:C:H2'	53:3:336:A:H8	1.44	0.82
52:2:3:C:H2'	52:2:4:C:H5''	1.62	0.82
58:B1:68:TYR:O	58:B1:75:TYR:HE2	1.58	0.82
58:B1:770:LEU:HD13	59:B2:618:GLN:HG3	1.61	0.82
51:1:161:A:H3'	51:1:162:U:H5''	1.62	0.82
55:8:1:DC:H5''	58:B1:210:SER:OG	1.80	0.82
53:3:405:U:H3'	53:3:406:G:H5'	1.61	0.81
51:1:2107:G:H2'	51:1:2108:A:H8	1.44	0.81
58:B1:144:TYR:HE1	58:B1:162:GLU:OE2	1.64	0.81
51:1:2553:G:H3'	51:1:2554:U:H5''	1.63	0.81
53:3:1422:G:H2'	53:3:1423:G:C8	2.15	0.81
58:B1:141:PHE:CE2	58:B1:296:LYS:HB2	2.15	0.80
51:1:2156:G:H2'	51:1:2157:G:H5'	1.63	0.80
58:B1:141:PHE:HE2	58:B1:296:LYS:HB2	1.44	0.80
58:B1:37:GLU:O	58:B1:61:ILE:HD11	1.81	0.80
58:B1:111:THR:HG23	58:B1:300:GLN:OE1	1.81	0.80
21:U:10:GLY:HA2	53:3:624:C:H4'	1.64	0.79
51:1:740:C:H42	51:1:757:G:H1	1.27	0.79
53:3:1088:G:H21	53:3:1167:A:H61	1.30	0.79
64:6:47:U:H2'	64:6:50:U:OP1	1.82	0.79
36:l:17:LYS:HD2	51:1:663:G:H5''	1.62	0.79
15:O:7:ARG:HB2	15:O:101:SER:HB2	1.62	0.79
62:NG:126:THR:CB	62:NG:175:PHE:O	2.31	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:186:GLN:HG3	58:B1:238:ILE:HG13	1.65	0.78
52:2:88:C:H5''	52:2:89:U:OP1	1.82	0.78
12:L:68:VAL:HG13	12:L:99:ALA:HB1	1.65	0.78
52:2:30:C:H2'	52:2:31:C:H5'	1.66	0.78
51:1:1064:C:H3'	51:1:1065:U:C5'	2.14	0.78
53:3:112:G:H21	53:3:354:G:H5'	1.47	0.77
33:i:7:TYR:CE2	33:i:57:VAL:HB	2.16	0.77
38:n:4:ARG:HB2	51:1:2722:G:H4'	1.64	0.77
51:1:2128:G:H1	51:1:2160:C:N4	1.82	0.77
51:1:2799:A:H2'	51:1:2800:A:H5'	1.65	0.77
58:B1:202:ARG:HG2	58:B1:202:ARG:NH1	1.99	0.77
66:0:632:ILE:HD11	66:0:654:ILE:HG12	1.66	0.77
2:B:49:ARG:HG3	51:1:2884:U:H6	1.48	0.76
51:1:1020:A:H1'	51:1:1021:A:OP2	1.86	0.76
53:3:1012:A:H5'	53:3:1012:A:H8	1.48	0.76
51:1:974:G:H1'	51:1:975:A:C8	2.20	0.76
51:1:2656:U:H5''	66:0:146:ARG:NE	2.01	0.76
39:o:33:ARG:HB2	52:2:52:A:N6	2.00	0.76
64:6:26:G:C2'	64:6:27:U:H5''	2.16	0.76
58:B1:110:PRO:HG2	58:B1:183:GLU:HG3	1.68	0.75
53:3:769:G:H4'	53:3:1513:A:H4'	1.67	0.75
55:8:13:DT:H72	58:B1:791:ALA:HB2	1.67	0.75
39:o:15:ARG:NH2	52:2:8:C:H5''	2.02	0.75
15:O:41:PRO:HB3	53:3:1151:A:C1'	2.16	0.75
43:s:6:LYS:HG3	51:1:494:G:H4'	1.68	0.75
51:1:855:G:H2'	51:1:856:G:H5''	1.67	0.75
55:8:15:DC:H1'	58:B1:426:ALA:HB1	1.67	0.75
14:N:30:ASN:HD21	14:N:66:VAL:H	1.35	0.75
51:1:1326:U:H2'	51:1:1327:A:H8	1.51	0.75
25:Y:55:PRO:HD3	53:3:193:C:H4'	1.69	0.75
55:8:3:DC:H2'	55:8:4:DT:H72	1.69	0.74
51:1:694:U:OP1	51:1:1569:A:H1'	1.86	0.74
51:1:572:A:H61	51:1:2029:G:H21	1.35	0.74
51:1:760:G:H5'	51:1:760:G:H8	1.50	0.74
9:I:38:GLY:HA3	53:3:542:G:H5'	1.69	0.74
51:1:940:G:H2'	51:1:941:A:H5''	1.68	0.74
31:f:174:LYS:HD2	51:1:2529:G:H5'	1.68	0.74
18:R:105:ALA:HA	53:3:948:C:OP1	1.88	0.74
53:3:1028:C:H3'	53:3:1029:U:H5''	1.68	0.74
66:0:448:TRP:HB2	66:0:457:ILE:HB	1.70	0.74
53:3:1421:G:H3'	53:3:1422:G:C4'	2.18	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:107:LEU:HD11	58:B1:242:LEU:HB2	1.70	0.73
58:B1:211:GLU:HG2	58:B1:215:LYS:HE3	1.70	0.73
51:1:1062:G:OP1	51:1:1063:G:OP2	2.06	0.73
58:B1:210:SER:HB3	58:B1:213:LYS:HB2	1.71	0.73
12:L:72:VAL:HG23	12:L:88:VAL:O	1.89	0.73
51:1:2163:A:H2'	51:1:2164:C:H5'	1.71	0.73
1:A:64:PHE:CD1	53:3:1011:C:H4'	2.17	0.73
58:B1:105:ILE:HD12	58:B1:242:LEU:HD22	1.71	0.73
58:B1:142:GLU:HG3	58:B1:142:GLU:O	1.89	0.73
58:B1:68:TYR:C	58:B1:75:TYR:CE2	2.65	0.73
64:6:44:A:H2'	64:6:45:G:C8	2.24	0.72
9:I:12:ARG:HG2	9:I:33:ILE:HA	1.71	0.72
51:1:2502:G:H5'	51:1:2503:A:H5''	1.70	0.72
53:3:352:C:H4'	53:3:354:G:OP1	1.89	0.72
55:8:3:DC:C2'	55:8:4:DT:H72	2.19	0.72
53:3:1088:G:N2	53:3:1167:A:H61	1.86	0.72
33:i:10:LEU:CD1	51:1:1061:U:H1'	2.20	0.72
58:B1:157:GLN:OE1	58:B1:157:GLN:HA	1.88	0.72
46:v:49:ASN:ND2	51:1:1040:A:H4'	2.05	0.72
51:1:1252:G:O2'	51:1:1253:A:H5''	1.90	0.72
58:B1:1143:ASP:OD1	58:B1:1148:ARG:NH1	2.21	0.72
47:w:38:GLY:HA2	51:1:2330:G:H21	1.53	0.72
8:H:71:ARG:HH12	54:4:17:U:H4'	1.54	0.72
31:f:70:LEU:HD11	51:1:2758:A:C2	2.25	0.72
33:i:79:LEU:HD21	33:i:132:ALA:HB2	1.71	0.71
51:1:663:G:C2'	51:1:664:G:H5''	2.20	0.71
33:i:130:GLY:HA3	51:1:1079:C:H1'	1.71	0.71
27:b:201:LEU:HD22	53:3:773:G:H5''	1.72	0.71
37:m:12:MET:HA	51:1:910:A:H62	1.55	0.71
51:1:414:C:H2'	51:1:415:A:H8	1.54	0.71
51:1:2743:U:H2'	51:1:2744:G:H5''	1.72	0.71
62:NG:125:LYS:O	62:NG:179:GLU:HA	1.89	0.71
14:N:70:GLY:HA3	53:3:1371:G:O3'	1.90	0.71
19:S:52:ARG:HH11	53:3:1317:C:H42	1.38	0.71
39:o:55:GLU:HG2	52:2:116:G:H5'	1.72	0.71
58:B1:93:THR:HB	58:B1:97:VAL:HG21	1.73	0.71
51:1:703:U:H2'	51:1:704:G:H5'	1.72	0.71
51:1:718:A:H2'	51:1:719:C:O4'	1.91	0.71
53:3:560:A:H5'	53:3:566:G:N2	2.05	0.71
35:k:87:LEU:HD12	35:k:92:GLU:HB3	1.72	0.71
36:l:19:LEU:HD23	51:1:587:C:C2	2.25	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2792:A:H2'	51:1:2793:C:H5''	1.72	0.70
53:3:1316:G:H2'	53:3:1317:C:H5''	1.73	0.70
4:D:34:ARG:HD3	51:1:467:G:OP2	1.91	0.70
33:i:92:PRO:CB	51:1:1077:A:H1'	2.22	0.70
52:2:115:A:H2'	52:2:116:G:C8	2.26	0.70
10:J:61:LYS:NZ	53:3:1073:U:OP2	2.24	0.70
15:O:44:THR:HG23	53:3:1151:A:H5''	1.71	0.70
51:1:2691:C:H2'	51:1:2692:G:C8	2.26	0.70
58:B1:128:LEU:HD11	58:B1:189:LEU:HG	1.73	0.70
53:3:1218:C:H2'	53:3:1219:A:C8	2.27	0.70
58:B1:220:ARG:HG2	58:B1:220:ARG:HH11	1.55	0.70
38:n:20:MET:HE2	51:1:1277:G:H5'	1.74	0.70
51:1:807:U:H2'	51:1:808:G:H8	1.55	0.70
53:3:335:C:H2'	53:3:336:A:C8	2.26	0.70
53:3:1422:G:H2'	53:3:1423:G:H8	1.55	0.70
48:x:17:ARG:HG3	51:1:380:G:H5'	1.73	0.70
51:1:876:C:H3'	51:1:877:A:H4'	1.73	0.70
53:3:78:A:H2'	53:3:79:G:O4'	1.91	0.70
53:3:1421:G:C8	53:3:1422:G:H1'	2.26	0.69
51:1:2634:A:H2'	51:1:2635:A:O4'	1.91	0.69
67:h:6:5OH:N	67:h:6:5OH:HS	2.07	0.69
33:i:79:LEU:HD13	33:i:128:ILE:HG22	1.73	0.69
51:1:2123:G:N7	51:1:2170:A:H4'	2.07	0.69
33:i:92:PRO:CB	51:1:1077:A:C1'	2.70	0.69
51:1:760:G:H2'	51:1:761:A:H5'	1.73	0.69
51:1:2566:A:H4'	51:1:2567:G:H5''	1.74	0.69
53:3:483:C:H2'	53:3:484:G:C8	2.27	0.69
58:B1:352:ARG:HD2	59:B2:1268:GLN:HE22	1.55	0.69
53:3:358:U:H2'	53:3:359:G:C8	2.28	0.69
53:3:1293:C:H2'	53:3:1294:G:H8	1.58	0.69
40:p:1:SER:H1	51:1:2875:C:H4'	1.57	0.69
40:p:59:THR:HG22	40:p:72:VAL:HG12	1.75	0.69
59:B2:65:ASN:HB3	59:B2:105:TYR:HB2	1.73	0.69
53:3:837:U:H2'	53:3:838:G:H8	1.57	0.69
53:3:1513:A:H2'	53:3:1514:G:H8	1.58	0.69
58:B1:243:PRO:HG2	59:B2:1332:SER:O	1.93	0.69
58:B1:832:LYS:C	58:B1:1242:ARG:HH12	2.01	0.69
51:1:2296:U:H5''	51:1:2297:A:OP1	1.92	0.69
14:N:35:GLU:HA	14:N:39:GLY:HA3	1.75	0.68
51:1:1063:G:H5''	51:1:1064:C:C6	2.28	0.68
57:A2:294:ASN:HA	61:NA:464:ILE:H	1.57	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:39:LYS:O	58:B1:273:ILE:CG2	2.41	0.68
7:G:46:VAL:HG23	7:G:47:PRO:HD3	1.75	0.68
51:1:2691:C:H2'	51:1:2692:G:H8	1.58	0.68
52:2:3:C:C2'	52:2:4:C:H5''	2.23	0.68
28:c:13:ARG:HH11	51:1:2683:C:H4'	1.58	0.68
63:5:47:U:H4'	63:5:48:C:H5'	1.75	0.68
51:1:2638:G:H1'	51:1:2778:A:H61	1.58	0.68
9:I:111:ALA:HB1	53:3:407:U:H5''	1.75	0.68
53:3:207:C:H2'	53:3:208:U:H5''	1.74	0.68
39:o:12:THR:HB	51:1:2334:U:H5'	1.76	0.68
51:1:807:U:H2'	51:1:808:G:C8	2.28	0.68
67:h:4:SER:O	67:h:5:UAL:N1	2.26	0.68
32:g:8:LYS:HB2	32:g:15:LEU:HG	1.76	0.68
51:1:1869:G:H3'	51:1:1870:C:C5'	2.24	0.68
58:B1:141:PHE:CD2	58:B1:293:ARG:O	2.47	0.68
10:J:22:LYS:HG3	53:3:1081:A:H5'	1.75	0.68
58:B1:117:LEU:HD12	58:B1:117:LEU:O	1.94	0.68
66:0:515:TYR:HB3	66:0:584:HIS:CG	2.28	0.68
27:b:48:ILE:HG22	51:1:779:U:OP1	1.94	0.68
34:j:30:THR:HG21	51:1:1012:U:O4	1.94	0.67
51:1:1098:A:C2'	51:1:1099:G:H5'	2.22	0.67
35:k:48:PRO:HB3	53:3:1423:G:C5'	2.14	0.67
51:1:784:G:H5'	51:1:785:G:OP1	1.94	0.67
51:1:1550:C:H2'	51:1:1551:A:H8	1.60	0.67
53:3:603:U:H2'	53:3:604:G:H8	1.58	0.67
64:6:69:C:C2'	64:6:70:G:H5''	2.24	0.67
11:K:76:THR:HA	11:K:79:ARG:HG2	1.76	0.67
58:B1:1355:ARG:NH1	58:B1:1369:ARG:HH12	1.93	0.67
55:8:3:DC:C6	55:8:4:DT:H72	2.29	0.67
51:1:255:A:H2'	51:1:256:A:O4'	1.95	0.67
14:N:83:THR:HG21	14:N:102:PHE:HB3	1.77	0.67
51:1:1059:G:H3'	51:1:1060:U:H2'	1.77	0.67
53:3:76:G:H2'	53:3:77:A:H5'	1.76	0.67
58:B1:161:THR:HG22	58:B1:164:GLN:HB2	1.75	0.67
13:M:28:SER:HB2	13:M:56:PRO:HB2	1.78	0.66
51:1:729:G:H4'	51:1:763:G:H5'	1.78	0.66
55:8:23:DC:H2''	55:8:24:DC:C5	2.30	0.66
58:B1:1037:PHE:HB3	58:B1:1040:MET:HB2	1.78	0.66
66:0:66:ALA:HB3	66:0:88:ASP:HB3	1.76	0.66
51:1:635:C:H2'	51:1:636:G:C8	2.30	0.66
51:1:635:C:H2'	51:1:636:G:H8	1.58	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:8:13:DT:OP2	58:B1:791:ALA:HB1	1.95	0.66
14:N:4:GLN:HE22	53:3:1131:G:H5'	1.61	0.66
58:B1:108:ALA:HB3	58:B1:279:LEU:HD22	1.77	0.66
53:3:948:C:H5'	53:3:1306:A:O2'	1.95	0.66
53:3:1333:A:H2'	53:3:1334:G:O4'	1.95	0.66
58:B1:193:ASP:HB3	58:B1:196:GLN:HB2	1.78	0.66
58:B1:108:ALA:CB	58:B1:279:LEU:HD22	2.25	0.66
51:1:1378:A:H1'	51:1:1379:U:C5	2.30	0.66
4:D:26:ASN:CG	51:1:682:G:H5'	2.20	0.65
51:1:1297:C:OP1	51:1:2710:C:H4'	1.97	0.65
51:1:2383:G:O2'	51:1:2384:U:H5'	1.97	0.65
51:1:855:G:C2'	51:1:856:G:H5''	2.26	0.65
53:3:29:U:O2'	53:3:30:U:H5'	1.96	0.65
53:3:813:U:C2'	53:3:814:A:H5''	2.26	0.65
58:B1:141:PHE:HD2	58:B1:293:ARG:O	1.80	0.65
51:1:1752:C:H2'	51:1:1753:G:C8	2.31	0.65
17:Q:76:HIS:HB2	66:0:425:LYS:HD2	1.77	0.65
52:2:3:C:H42	52:2:117:G:H1	1.44	0.65
53:3:884:U:H4'	53:3:885:G:H5''	1.77	0.65
66:0:558:GLN:HA	66:0:561:LEU:HD12	1.78	0.65
53:3:663:A:H5'	53:3:836:G:OP1	1.96	0.65
58:B1:984:LEU:HB3	58:B1:993:GLU:HB2	1.77	0.65
51:1:310:A:C2'	51:1:311:A:H5''	2.27	0.65
51:1:2177:C:O2'	65:a:170:ILE:HG21	1.97	0.65
58:B1:975:ILE:HG22	58:B1:977:SER:H	1.62	0.65
58:B1:162:GLU:HA	58:B1:162:GLU:OE1	1.97	0.65
9:I:101:VAL:HG13	9:I:106:PHE:HB2	1.79	0.65
51:1:414:C:H2'	51:1:415:A:C8	2.32	0.65
51:1:2715:C:H3'	51:1:2716:C:H5''	1.79	0.65
36:l:20:GLY:HA2	36:l:28:GLY:HA2	1.79	0.65
58:B1:68:TYR:HB3	58:B1:75:TYR:CE2	2.32	0.65
51:1:1139:G:O2'	51:1:1140:C:H5'	1.97	0.65
52:2:95:U:H2'	52:2:96:G:H8	1.63	0.65
58:B1:395:LYS:HZ2	58:B1:399:LYS:CD	2.10	0.64
51:1:1906:G:C3'	51:1:1907:G:H5''	2.27	0.64
53:3:1260:G:H4'	53:3:1284:C:H5'	1.80	0.64
55:8:3:DC:C2'	55:8:4:DT:C7	2.75	0.64
51:1:855:G:C3'	51:1:856:G:H5''	2.28	0.64
53:3:664:G:H22	53:3:741:G:H1	1.45	0.64
43:s:42:LYS:HB2	51:1:2010:G:H5''	1.80	0.64
51:1:2808:G:H2'	51:1:2890:G:C6	2.32	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:461:PHE:HD2	59:B2:813:GLU:HB2	1.61	0.64
51:1:1752:C:H2'	51:1:1753:G:H8	1.62	0.64
51:1:1827:U:H2'	51:1:1828:G:H5'	1.80	0.64
53:3:1012:A:H5'	53:3:1012:A:C8	2.31	0.64
53:3:1293:C:H2'	53:3:1294:G:C8	2.33	0.64
2:B:49:ARG:HG3	51:1:2884:U:C6	2.32	0.64
51:1:151:C:H2'	51:1:152:A:H8	1.62	0.64
51:1:310:A:H2'	51:1:311:A:H5''	1.79	0.64
23:W:42:ARG:NH2	53:3:721:G:C5'	2.51	0.64
51:1:1186:G:H2'	51:1:1187:G:O4'	1.97	0.64
51:1:2682:A:N6	51:1:2728:U:H1'	2.02	0.64
52:2:3:C:C3'	52:2:4:C:H5''	2.28	0.64
53:3:971:G:H1'	53:3:1365:G:O2'	1.98	0.64
53:3:1274:A:O2'	53:3:1275:A:H5''	1.98	0.64
7:G:155:GLY:CA	61:NA:219:GLU:CB	2.76	0.63
7:G:155:GLY:HA2	61:NA:219:GLU:CB	2.28	0.63
14:N:118:ARG:NH2	53:3:1233:G:H5'	2.13	0.63
30:e:84:ILE:HG21	51:1:2312:U:H4'	1.80	0.63
58:B1:918:ILE:HG22	59:B2:1280:ALA:HB1	1.79	0.63
58:B1:978:ARG:HG2	58:B1:1197:ASN:HD21	1.60	0.63
7:G:8:MET:HE3	7:G:46:VAL:HG11	1.79	0.63
53:3:662:U:H2'	53:3:663:A:C8	2.33	0.63
59:B2:314:ASN:HD21	59:B2:348:SER:HA	1.62	0.63
33:i:27:LEU:HD21	33:i:34:ILE:HB	1.79	0.63
53:3:1513:A:H2'	53:3:1514:G:C8	2.33	0.63
33:i:92:PRO:HB2	51:1:1077:A:C1'	2.27	0.63
51:1:876:C:H3'	51:1:877:A:O4'	1.99	0.63
51:1:1960:A:H2'	51:1:1961:C:H5''	1.81	0.63
14:N:118:ARG:HH22	53:3:1233:G:H5'	1.62	0.63
15:O:12:ALA:HB2	15:O:96:VAL:HG13	1.81	0.63
33:i:123:ALA:HA	33:i:126:ARG:HD2	1.80	0.63
35:k:5:GLN:HA	35:k:20:MET:HE3	1.80	0.63
58:B1:245:LEU:HG	58:B1:246:PRO:HD2	1.80	0.63
66:O:632:ILE:HG23	66:O:642:LEU:HB3	1.80	0.63
27:b:144:GLU:HB2	27:b:187:CYS:HB3	1.81	0.63
39:o:100:HIS:NE2	52:2:48:U:H4'	2.14	0.63
43:s:11:ARG:HG3	51:1:1322:A:OP1	1.99	0.63
53:3:1349:A:H2'	53:3:1350:A:O4'	1.98	0.63
58:B1:1355:ARG:NH1	58:B1:1369:ARG:NH1	2.47	0.63
28:c:35:THR:HG22	28:c:73:VAL:HG21	1.79	0.63
51:1:2831:G:OP1	51:1:2834:G:H4'	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:0:228:GLU:HB2	66:0:255:ARG:HH12	1.63	0.63
59:B2:1282:GLY:HA3	60:W0:17:PHE:HE1	1.63	0.63
14:N:105:ARG:HG3	53:3:1118:U:H5'	1.79	0.62
33:i:10:LEU:HG	51:1:1061:U:H1'	1.81	0.62
58:B1:111:THR:CG2	58:B1:300:GLN:CD	2.66	0.62
59:B2:120:GLN:NE2	59:B2:490:GLN:OE1	2.32	0.62
28:c:170:VAL:HG21	51:1:2679:A:H5'	1.81	0.62
35:k:76:VAL:H	40:p:72:VAL:HG22	1.63	0.62
53:3:583:A:H2'	53:3:584:G:O4'	1.99	0.62
53:3:1304:G:H2'	53:3:1305:G:H1'	1.80	0.62
53:3:1421:G:C3'	53:3:1422:G:H4'	2.27	0.62
35:k:66:LYS:NZ	35:k:80:ASP:O	2.32	0.62
40:p:2:ASN:HD21	51:1:2876:G:H4'	1.63	0.62
51:1:1078:U:H5''	51:1:1079:C:H5'	1.81	0.62
53:3:79:G:O2'	53:3:80:A:H5'	1.98	0.62
53:3:1073:U:H2'	53:3:1074:G:H8	1.64	0.62
58:B1:128:LEU:HA	58:B1:192:MET:HE1	1.81	0.62
19:S:48:GLN:HE22	24:X:11:ASP:HA	1.64	0.62
10:J:107:GLY:HA3	53:3:9:G:H5'	1.80	0.62
31:f:70:LEU:HD11	51:1:2758:A:H2	1.64	0.62
39:o:33:ARG:HB2	52:2:52:A:H62	1.62	0.62
46:v:21:ARG:HH22	52:2:77:U:P	2.23	0.62
53:3:1421:G:H3'	53:3:1422:G:C5'	2.30	0.62
58:B1:144:TYR:CE1	58:B1:162:GLU:OE2	2.51	0.62
27:b:200:MET:HG3	51:1:1820:U:O2	2.00	0.62
33:i:9:LYS:NZ	51:1:1061:U:OP1	2.30	0.62
51:1:1701:A:H2'	51:1:1702:G:H5'	1.81	0.62
51:1:1837:C:H2'	51:1:1899:A:H61	1.65	0.62
51:1:2126:A:H2'	51:1:2162:G:H21	1.65	0.62
18:R:28:ARG:HH22	18:R:61:LYS:HB2	1.64	0.62
53:3:545:C:O2'	53:3:549:C:H5''	2.00	0.62
53:3:999:C:H2'	53:3:1000:A:H8	1.64	0.62
58:B1:201:LEU:HB2	58:B1:221:ILE:HD13	1.80	0.62
27:b:137:GLY:HA3	53:3:712:A:H5'	1.82	0.62
51:1:1655:A:C2	51:1:2049:G:H4'	2.35	0.62
51:1:2248:C:H2'	51:1:2249:U:H5'	1.81	0.62
53:3:950:U:H2'	53:3:951:G:H8	1.65	0.62
40:p:52:ARG:HH22	51:1:2720:U:P	2.23	0.62
51:1:1533:C:H3'	51:1:1534:U:H5''	1.82	0.62
52:2:63:C:H2'	52:2:64:G:H8	1.64	0.62
55:8:3:DC:H2'	55:8:4:DT:C7	2.30	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:67:LEU:HD12	7:G:160:LEU:HD22	1.81	0.61
58:B1:111:THR:CG2	58:B1:300:GLN:NE2	2.63	0.61
4:D:21:ARG:NH1	51:1:466:A:H5'	2.14	0.61
8:H:18:ASN:ND2	19:S:89:ARG:O	2.33	0.61
53:3:422:C:H4'	53:3:423:G:C2	2.35	0.61
53:3:999:C:H2'	53:3:1000:A:C8	2.35	0.61
55:8:1:DC:H2''	55:8:2:DC:C5	2.35	0.61
51:1:2185:U:H2'	51:1:2186:G:H8	1.65	0.61
53:3:1241:G:H2'	53:3:1242:G:H8	1.65	0.61
53:3:1479:C:H2'	53:3:1480:A:H8	1.66	0.61
58:B1:395:LYS:HZ2	58:B1:399:LYS:HD3	1.65	0.61
9:I:151:GLN:NE2	53:3:437:U:H5''	2.14	0.61
33:i:89:SER:HB3	51:1:1063:G:C8	2.36	0.61
53:3:768:A:OP1	53:3:804:U:H4'	2.01	0.61
58:B1:1357:ILE:HD11	59:B2:1287:LEU:HD13	1.81	0.61
66:0:29:ARG:HD2	66:0:272:ASN:HD22	1.66	0.61
14:N:116:GLY:N	53:3:1367:C:OP1	2.32	0.61
21:U:11:ALA:HA	53:3:44:A:OP1	2.01	0.61
53:3:622:A:H2'	53:3:623:C:H5'	1.83	0.61
57:A1:211:ILE:HG12	57:A1:219:ARG:HH12	1.65	0.61
53:3:91:U:C3'	53:3:92:U:H5''	2.31	0.61
53:3:1497:G:H2'	53:3:1498:U:H5'	1.82	0.61
53:3:219:U:H2'	53:3:220:G:H8	1.65	0.61
55:8:13:DT:C7	58:B1:791:ALA:HB2	2.29	0.61
17:Q:30:ARG:HB3	53:3:363:A:OP2	2.00	0.61
53:3:530:G:H3'	53:3:531:U:C5'	2.31	0.61
29:d:53:THR:HG21	51:1:452:G:H8	1.66	0.61
41:q:23:TYR:CD1	51:1:533:G:H5'	2.35	0.61
51:1:1180:U:H3'	51:1:1181:U:H6	1.64	0.61
51:1:1827:U:C2'	51:1:1828:G:H5'	2.30	0.61
58:B1:68:TYR:HB3	58:B1:75:TYR:CZ	2.35	0.61
58:B1:154:LEU:HD21	58:B1:160:LEU:HD21	1.83	0.61
31:f:123:GLU:HG3	31:f:125:PRO:HD3	1.82	0.60
51:1:1807:G:H2'	51:1:1808:A:H5'	1.82	0.60
58:B1:395:LYS:NZ	58:B1:399:LYS:HD3	2.15	0.60
19:S:7:ALA:HB1	53:3:995:C:H5'	1.84	0.60
26:Z:49:ALA:HA	53:3:723:U:O4	2.01	0.60
51:1:1097:U:H2'	51:1:1098:A:O4'	2.00	0.60
51:1:2128:G:P	65:a:38:PHE:HB3	2.41	0.60
51:1:2245:U:H5''	51:1:2246:G:H5'	1.83	0.60
58:B1:770:LEU:HD13	59:B2:618:GLN:CG	2.30	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:a:50:ILE:HB	65:a:57:GLN:HB3	1.82	0.60
32:g:43:ASN:HA	32:g:46:PHE:HB2	1.83	0.60
51:1:2128:G:H21	51:1:2173:A:H1'	1.66	0.60
53:3:130:A:H1'	53:3:264:C:H5'	1.82	0.60
58:B1:342:LEU:HD23	58:B1:1352:ILE:HG23	1.83	0.60
59:B2:528:ARG:NH2	59:B2:576:SER:O	2.30	0.60
34:j:27:ARG:HD2	51:1:1143:A:H62	1.67	0.60
38:n:39:PRO:HG3	51:1:1651:G:H5'	1.82	0.60
46:v:9:ARG:HB3	46:v:41:GLU:HB2	1.82	0.60
51:1:1417:C:H4'	51:1:1587:G:H21	1.66	0.60
51:1:2061:G:H2'	51:1:2501:C:O2'	2.01	0.60
51:1:2661:G:H5''	66:0:19:ILE:HD11	1.83	0.60
58:B1:100:GLU:HA	59:B2:1328:LYS:HE2	1.82	0.60
9:I:120:LYS:HB3	9:I:130:ASN:HB3	1.84	0.60
11:K:3:HIS:HA	11:K:65:GLU:HA	1.82	0.60
52:2:11:C:H2'	52:2:12:C:O4'	2.02	0.60
53:3:397:A:H3'	53:3:397:A:N3	2.16	0.60
53:3:651:C:H2'	53:3:652:U:C6	2.35	0.60
18:R:27:THR:HG21	53:3:1328:C:H5''	1.83	0.60
51:1:2220:U:H2'	51:1:2221:G:H8	1.66	0.60
51:1:2267:A:H5''	51:1:2268:A:H5'	1.84	0.60
53:3:1060:U:H3	53:3:1197:A:H61	1.48	0.60
55:8:11:DC:H2'	55:8:12:DG:C8	2.37	0.60
42:r:35:PHE:HB2	42:r:59:ILE:HB	1.83	0.60
50:z:12:ALA:HB1	50:z:20:LYS:HG2	1.83	0.60
51:1:41:C:H2'	51:1:42:A:H5''	1.84	0.60
53:3:1016:A:H4'	53:3:1218:C:H4'	1.83	0.60
53:3:1304:G:H2'	53:3:1305:G:C1'	2.32	0.60
58:B1:926:PRO:HG2	58:B1:1248:ILE:HD11	1.84	0.60
66:0:470:VAL:HG13	66:0:481:ALA:HB3	1.82	0.60
9:I:37:PRO:HD2	9:I:41:GLY:HA3	1.83	0.60
51:1:2107:G:H2'	51:1:2108:A:C8	2.32	0.60
51:1:2343:U:H2'	51:1:2344:U:C6	2.37	0.60
57:A1:38:THR:HB	57:A2:45:ARG:HD3	1.82	0.60
6:F:4:ARG:HG2	51:1:2466:C:OP1	2.02	0.60
51:1:2371:G:O2'	51:1:2372:U:H5'	2.02	0.60
53:3:91:U:H3'	53:3:92:U:H5''	1.84	0.60
51:1:1906:G:H3'	51:1:1907:G:H5''	1.84	0.59
51:1:2183:A:H2'	51:1:2184:A:H5'	1.83	0.59
57:A1:112:ALA:HB3	57:A1:126:PRO:HA	1.83	0.59
58:B1:370:LYS:HG2	58:B1:441:LEU:HD23	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:633:ALA:HA	59:B2:806:PRO:O	2.01	0.59
24:X:51:HIS:HA	24:X:56:HIS:HA	1.83	0.59
28:c:135:GLY:HA2	51:1:743:A:OP1	2.02	0.59
52:2:95:U:H2'	52:2:96:G:C8	2.37	0.59
59:B2:1072:ASN:ND2	59:B2:1111:GLN:OE1	2.34	0.59
2:B:5:ASN:ND2	51:1:2020:A:H62	1.96	0.59
6:F:2:LYS:NZ	6:F:32:LYS:O	2.36	0.59
40:p:102:ARG:NH2	51:1:1754:A:O3'	2.35	0.59
51:1:1068:G:N3	51:1:1096:A:H5'	2.16	0.59
53:3:1241:G:H2'	53:3:1242:G:C8	2.36	0.59
53:3:1530:G:H2'	53:3:1531:A:C8	2.36	0.59
58:B1:99:ARG:NH1	58:B1:99:ARG:HG3	2.17	0.59
58:B1:223:LEU:HG	58:B1:223:LEU:O	2.00	0.59
58:B1:725:MET:SD	59:B2:1101:LEU:HD23	2.42	0.59
59:B2:55:SER:OG	59:B2:465:ARG:NH1	2.33	0.59
52:2:104:A:H2'	52:2:105:G:O4'	2.02	0.59
55:8:9:DG:H4'	58:B1:120:LEU:HG	1.84	0.59
58:B1:1161:GLY:HA3	58:B1:1179:PRO:HA	1.83	0.59
59:B2:918:LEU:O	59:B2:918:LEU:HD23	2.02	0.59
65:a:28:ALA:HA	65:a:31:LYS:HD3	1.85	0.59
6:F:11:CYS:SG	6:F:14:CYS:N	2.75	0.59
9:I:149:LYS:HG2	9:I:150:LYS:HG3	1.83	0.59
28:c:56:LYS:HE3	51:1:2830:C:H5''	1.85	0.59
43:s:59:GLU:HB3	43:s:66:ILE:HD11	1.82	0.59
51:1:629:G:H5''	51:1:650:C:O2'	2.03	0.59
51:1:1095:A:C2	66:0:632:ILE:HD13	2.37	0.59
63:5:26:A:H61	63:5:44:G:H22	1.50	0.59
8:H:106:ARG:HG3	8:H:107:LYS:HG3	1.84	0.59
51:1:869:G:H1	51:1:908:C:H42	1.50	0.59
53:3:123:U:H5''	53:3:311:C:O2'	2.03	0.59
53:3:328:C:H4'	53:3:329:A:H5'	1.84	0.59
53:3:1275:A:H2'	53:3:1276:G:O4'	2.03	0.59
59:B2:1142:ARG:NH1	59:B2:1161:LEU:O	2.36	0.59
27:b:228:ASP:CG	51:1:780:G:H1	2.10	0.59
51:1:937:C:H2'	51:1:938:G:C8	2.38	0.59
51:1:1064:C:C3'	51:1:1065:U:H5''	2.24	0.59
53:3:381:C:H2'	53:3:382:A:O4'	2.02	0.59
20:T:22:GLY:O	20:T:27:GLN:NE2	2.36	0.59
33:i:75:ALA:HB3	51:1:1060:U:OP1	2.02	0.59
51:1:1095:A:N3	66:0:632:ILE:HG21	2.18	0.59
51:1:2663:G:OP1	66:0:59:ARG:HD3	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2715:C:C3'	51:1:2716:C:H5''	2.33	0.59
53:3:210:C:H5'	53:3:211:G:C2	2.37	0.59
53:3:358:U:H2'	53:3:359:G:H8	1.66	0.59
58:B1:161:THR:HG23	58:B1:164:GLN:H	1.68	0.59
32:g:55:GLU:HA	32:g:58:LEU:HB2	1.85	0.59
51:1:876:C:C3'	51:1:877:A:H4'	2.33	0.59
53:3:1352:C:H2'	53:3:1353:G:C8	2.37	0.59
58:B1:951:GLN:NE2	58:B1:1014:GLY:O	2.35	0.59
59:B2:69:GLN:HE21	59:B2:101:ARG:HD2	1.67	0.59
66:0:415:VAL:HB	66:0:416:ILE:HD12	1.84	0.59
9:I:1:ALA:HB2	53:3:499:A:N6	2.18	0.59
14:N:8:THR:OG1	14:N:9:GLY:N	2.36	0.59
51:1:1509:A:H2'	51:1:1510:G:C8	2.38	0.59
53:3:1326:U:H2'	53:3:1327:C:C6	2.37	0.59
58:B1:275:ARG:NH1	58:B1:278:ARG:NH1	2.51	0.59
58:B1:412:LEU:HD22	58:B1:441:LEU:HD21	1.84	0.59
59:B2:707:ALA:O	59:B2:711:ASP:HB2	2.03	0.59
20:T:23:SER:HA	53:3:751:U:H4'	1.85	0.58
26:Z:39:LYS:NZ	53:3:1530:G:O6	2.36	0.58
51:1:96:C:H2'	51:1:97:C:H6	1.68	0.58
51:1:1434:A:H2'	51:1:1435:G:C8	2.38	0.58
52:2:30:C:C2'	52:2:31:C:H5'	2.33	0.58
53:3:410:G:H2'	53:3:429:U:C4	2.38	0.58
53:3:936:C:H2'	53:3:937:A:O4'	2.02	0.58
55:8:7:DC:H2''	55:8:8:DT:H71	1.84	0.58
58:B1:97:VAL:HG11	58:B1:101:ARG:NH2	2.18	0.58
15:O:8:ILE:HB	15:O:74:VAL:HB	1.85	0.58
51:1:2138:G:H2'	51:1:2139:U:H5'	1.84	0.58
17:Q:111:GLN:HB2	53:3:538:G:OP2	2.03	0.58
20:T:68:TYR:HB2	53:3:754:C:H4'	1.84	0.58
40:p:91:VAL:HG11	40:p:96:LEU:HD21	1.85	0.58
51:1:1697:G:C3'	51:1:1698:A:H5''	2.31	0.58
51:1:1810:A:H2'	51:1:1811:G:O4'	2.04	0.58
53:3:132:C:H5'	53:3:262:A:O2'	2.03	0.58
53:3:1218:C:H2'	53:3:1219:A:H8	1.67	0.58
57:A1:304:LYS:CB	61:NA:71:PRO:CB	2.81	0.58
58:B1:514:THR:HG21	58:B1:596:LEU:HD12	1.84	0.58
58:B1:750:PRO:CB	59:B2:549:ASP:OD2	2.45	0.58
23:W:28:LEU:HD21	23:W:58:ILE:HG12	1.85	0.58
30:e:38:GLY:HA3	51:1:2312:U:O2	2.03	0.58
42:r:61:ALA:HB2	42:r:98:ILE:HD13	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1443:U:H2'	51:1:1444:G:C8	2.38	0.58
52:2:3:C:H3'	52:2:4:C:H5''	1.85	0.58
58:B1:615:LYS:HG2	60:W0:5:THR:HG21	1.85	0.58
58:B1:638:SER:OG	58:B1:639:VAL:N	2.36	0.58
33:i:126:ARG:HA	33:i:129:GLU:HG3	1.86	0.58
53:3:76:G:C2'	53:3:77:A:H5'	2.34	0.58
53:3:813:U:H2'	53:3:814:A:C5'	2.32	0.58
53:3:1395:C:C6	53:3:1395:C:H5'	2.38	0.58
33:i:10:LEU:CG	51:1:1061:U:H1'	2.34	0.58
33:i:92:PRO:CB	51:1:1077:A:O4'	2.47	0.58
36:l:126:ARG:NH1	51:1:635:C:OP2	2.37	0.58
37:m:125:PRO:HB3	51:1:2485:G:O3'	2.04	0.58
48:x:25:LYS:HE2	51:1:189:G:OP2	2.03	0.58
51:1:940:G:C2'	51:1:941:A:H5''	2.34	0.58
51:1:2650:U:H2'	51:1:2651:C:C6	2.38	0.58
53:3:670:G:H2'	53:3:671:G:H5''	1.86	0.58
22:V:63:CYS:HG	22:V:73:THR:HG1	1.52	0.58
33:i:120:ASP:HB3	33:i:123:ALA:HB3	1.83	0.58
47:w:20:LYS:HG3	51:1:2355:G:H4'	1.85	0.58
51:1:472:A:H2'	51:1:473:G:H5'	1.85	0.58
51:1:572:A:H61	51:1:2029:G:N2	2.00	0.58
51:1:748:G:O2'	51:1:749:A:H3'	2.03	0.58
66:0:515:TYR:HB3	66:0:584:HIS:HB2	1.86	0.58
16:P:23:HIS:HB3	16:P:30:ILE:HG23	1.85	0.58
17:Q:28:GLN:HE22	53:3:33:A:H2	1.51	0.58
51:1:703:U:C2'	51:1:704:G:H5'	2.33	0.58
51:1:1846:G:H2'	51:1:1847:A:O4'	2.04	0.58
4:D:9:VAL:HG12	51:1:1309:G:OP1	2.03	0.58
27:b:79:ARG:NH1	27:b:81:GLU:OE2	2.36	0.58
29:d:163:ASN:HD21	51:1:322:A:H2'	1.68	0.58
51:1:917:A:H5''	51:1:2268:A:H61	1.69	0.58
53:3:427:U:H2'	53:3:428:G:C8	2.39	0.58
57:A2:82:LEU:HD11	57:A2:171:LEU:HD23	1.86	0.58
3:C:44:GLN:OE1	51:1:2371:G:H4'	2.04	0.58
25:Y:55:PRO:HB3	53:3:193:C:O3'	2.04	0.58
39:o:10:ARG:HD2	51:1:2294:G:P	2.44	0.58
51:1:553:G:H2'	51:1:554:U:O4'	2.04	0.58
53:3:219:U:H2'	53:3:220:G:C8	2.38	0.58
58:B1:201:LEU:HD11	58:B1:220:ARG:HH11	1.67	0.58
58:B1:438:GLU:HG3	58:B1:485:MET:HE1	1.85	0.58
1:A:64:PHE:HA	53:3:1011:C:C5'	2.33	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:97:ARG:HH12	53:3:1308:U:H5	1.52	0.57
51:1:1783:A:H5'	51:1:2608:G:H4'	1.86	0.57
51:1:2469:A:H8	51:1:2469:A:H5'	1.69	0.57
53:3:837:U:H2'	53:3:838:G:C8	2.38	0.57
53:3:1395:C:H5'	53:3:1395:C:H6	1.69	0.57
58:B1:42:GLU:HB3	58:B1:52:GLU:HG3	1.86	0.57
53:3:1060:U:H2'	53:3:1061:G:H8	1.68	0.57
51:1:760:G:H2'	51:1:761:A:C5'	2.35	0.57
51:1:832:U:H2'	51:1:833:A:C8	2.39	0.57
51:1:1111:A:C2	51:1:1112:G:H1'	2.39	0.57
51:1:1386:C:H2'	51:1:1387:A:H8	1.69	0.57
51:1:1801:A:H5''	51:1:2203:U:H2'	1.87	0.57
51:1:2248:C:C2'	51:1:2249:U:H5'	2.35	0.57
52:2:118:C:H2'	52:2:119:A:H4'	1.86	0.57
53:3:70:U:H5''	53:3:71:A:OP1	2.03	0.57
58:B1:510:LEU:HD22	58:B1:601:ILE:HD12	1.86	0.57
8:H:162:ALA:HB2	53:3:1056:U:H5'	1.85	0.57
30:e:41:GLU:HG3	30:e:44:ALA:HB3	1.87	0.57
36:l:30:THR:HG22	51:1:810:U:O4	2.04	0.57
42:r:6:GLN:HG2	42:r:11:GLN:HG2	1.84	0.57
51:1:2151:U:H2'	51:1:2152:G:C8	2.39	0.57
51:1:2584:U:H2'	51:1:2585:U:H2'	1.86	0.57
51:1:2682:A:H61	51:1:2728:U:C1'	2.06	0.57
53:3:1404:C:H2'	53:3:1405:G:C8	2.40	0.57
58:B1:198:CYS:HA	58:B1:221:ILE:HD11	1.86	0.57
8:H:174:LEU:HB2	53:3:1108:G:OP1	2.04	0.57
30:e:3:LEU:HA	30:e:6:TYR:HB3	1.86	0.57
53:3:1014:A:C2	53:3:1219:A:H1'	2.40	0.57
7:G:107:ARG:HH22	61:NA:218:GLU:HA	1.69	0.57
38:n:64:ARG:HH22	51:1:2852:G:H5'	1.68	0.57
58:B1:102:MET:HG2	58:B1:246:PRO:HG3	1.87	0.57
9:I:131:ILE:HD13	53:3:620:C:N3	2.19	0.57
51:1:729:G:H4'	51:1:763:G:C5'	2.34	0.57
51:1:1058:U:H5	51:1:1080:A:H61	1.50	0.57
51:1:2124:G:H2'	51:1:2125:G:O4'	2.05	0.57
58:B1:1046:ILE:HD12	58:B1:1059:LEU:HB3	1.86	0.57
59:B2:1122:LYS:NZ	59:B2:1126:ASP:OD1	2.38	0.57
66:O:492:GLU:HB2	66:O:571:VAL:HG22	1.85	0.57
22:V:67:SER:OG	22:V:68:LYS:N	2.37	0.57
43:s:18:ARG:NH1	43:s:76:VAL:O	2.37	0.57
51:1:32:C:H2'	51:1:33:C:C6	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1458:U:H4'	51:1:1459:G:C4	2.40	0.57
51:1:2156:G:C2'	51:1:2157:G:H5'	2.34	0.57
51:1:2398:U:H2'	51:1:2399:G:C8	2.39	0.57
51:1:2514:U:H2'	51:1:2515:C:C6	2.39	0.57
51:1:2743:U:H2'	51:1:2744:G:C5'	2.35	0.57
58:B1:1361:THR:HB	59:B2:1284:ALA:HB3	1.85	0.57
14:N:86:LEU:HB3	14:N:93:LEU:HD13	1.86	0.57
28:c:156:PHE:HB3	34:j:81:ILE:HG22	1.85	0.57
47:w:38:GLY:HA2	51:1:2330:G:N2	2.19	0.57
51:1:1109:C:H2'	51:1:1110:G:O4'	2.05	0.57
51:1:2117:A:H61	51:1:2170:A:H61	1.53	0.57
51:1:2732:G:O2'	51:1:2733:A:H5'	2.05	0.57
6:F:23:ILE:HD13	51:1:1032:A:H1'	1.87	0.57
14:N:90:ASP:O	14:N:92:SER:N	2.38	0.57
16:P:51:PHE:HB3	16:P:55:ARG:HG3	1.85	0.57
33:i:4:VAL:HA	33:i:7:TYR:HB3	1.87	0.57
34:j:27:ARG:NE	51:1:1143:A:N7	2.46	0.57
53:3:57:G:H5'	66:0:373:GLU:OE2	2.05	0.57
58:B1:130:MET:HE2	58:B1:135:ILE:HG12	1.87	0.57
59:B2:839:VAL:HG12	59:B2:1049:ILE:HG12	1.87	0.57
9:I:7:LYS:HE2	53:3:408:A:OP2	2.04	0.56
21:U:40:ASN:HB3	21:U:43:ALA:HB2	1.87	0.56
25:Y:79:THR:HG21	53:3:187:G:H5'	1.86	0.56
28:c:146:ILE:HG12	51:1:2051:A:H4'	1.87	0.56
51:1:2757:A:H2'	51:1:2758:A:H5''	1.87	0.56
53:3:280:C:H5''	53:3:281:G:OP2	2.04	0.56
59:B2:818:VAL:HG22	59:B2:1096:ILE:HG12	1.87	0.56
19:S:52:ARG:HG3	53:3:1317:C:N3	2.20	0.56
36:l:2:ARG:NH1	36:l:5:THR:OG1	2.39	0.56
51:1:668:A:H2'	51:1:670:A:H62	1.70	0.56
51:1:1506:U:H2'	51:1:1507:C:C6	2.40	0.56
51:1:1775:U:H2'	51:1:1776:G:O4'	2.05	0.56
51:1:1893:C:H2'	51:1:1894:C:H5'	1.87	0.56
58:B1:247:PRO:HA	58:B1:250:ARG:HG3	1.87	0.56
12:L:115:MET:HA	12:L:118:ARG:HE	1.70	0.56
29:d:27:LEU:HD13	51:1:600:G:H5'	1.88	0.56
35:k:63:VAL:HG12	35:k:107:LEU:HD21	1.87	0.56
51:1:11:C:H2'	51:1:12:U:H5''	1.87	0.56
51:1:1287:A:C2	51:1:1649:G:H4'	2.40	0.56
51:1:1550:C:H2'	51:1:1551:A:C8	2.40	0.56
51:1:1557:C:C3'	51:1:1558:C:H5''	2.28	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1638:C:H4'	51:1:2710:C:O2	2.06	0.56
53:3:1201:A:H4'	53:3:1202:U:H5''	1.86	0.56
53:3:1305:G:H22	53:3:1331:G:H2'	1.69	0.56
58:B1:99:ARG:CG	58:B1:99:ARG:HH11	2.18	0.56
58:B1:241:VAL:O	58:B1:241:VAL:HG12	2.04	0.56
58:B1:741:ALA:O	58:B1:762:ASN:ND2	2.38	0.56
59:B2:13:LYS:HB2	59:B2:1180:MET:HE2	1.86	0.56
59:B2:892:GLU:HA	59:B2:913:VAL:HG22	1.87	0.56
14:N:27:ILE:HG23	14:N:62:LEU:HB2	1.87	0.56
40:p:47:ILE:HD11	40:p:61:ARG:HB3	1.88	0.56
51:1:1133:A:H4'	51:1:1134:A:H5''	1.87	0.56
51:1:2127:G:O3'	65:a:38:PHE:HB3	2.05	0.56
53:3:427:U:H5''	53:3:542:G:OP1	2.06	0.56
53:3:458:U:H2'	53:3:459:A:C8	2.40	0.56
58:B1:1166:GLY:HA3	58:B1:1174:ARG:HB2	1.88	0.56
25:Y:73:ARG:CZ	53:3:261:U:H5	2.18	0.56
51:1:151:C:H2'	51:1:152:A:C8	2.40	0.56
51:1:2167:U:H3	51:1:2170:A:N6	2.03	0.56
58:B1:160:LEU:HD22	58:B1:164:GLN:HB3	1.86	0.56
10:J:80:LEU:HB2	10:J:97:PRO:HB3	1.87	0.56
51:1:1318:U:H2'	51:1:1319:C:C6	2.40	0.56
51:1:2556:C:H2'	51:1:2557:G:O4'	2.05	0.56
58:B1:39:LYS:O	58:B1:273:ILE:HG21	2.06	0.56
58:B1:1167:LYS:HZ2	58:B1:1170:LYS:HB2	1.70	0.56
66:0:107:ASP:OD2	66:0:337:ARG:NH2	2.38	0.56
51:1:814:C:C1'	51:1:1225:G:H21	2.06	0.56
51:1:972:A:OP2	51:1:974:G:H5'	2.06	0.56
51:1:2403:C:O2'	51:1:2404:U:H5'	2.05	0.56
53:3:603:U:H2'	53:3:604:G:C8	2.40	0.56
22:V:15:LYS:HB2	53:3:275:G:H5'	1.87	0.56
33:i:10:LEU:HD12	51:1:1061:U:H1'	1.86	0.56
33:i:78:LEU:HG	33:i:108:ILE:HD12	1.87	0.56
51:1:760:G:H5'	51:1:760:G:C8	2.37	0.56
51:1:2183:A:C2'	51:1:2184:A:H5'	2.36	0.56
51:1:2660:A:H2'	51:1:2661:G:O4'	2.05	0.56
52:2:97:C:C2'	52:2:98:G:H5'	2.35	0.56
53:3:235:C:H2'	53:3:236:A:H8	1.69	0.56
58:B1:804:ALA:HA	58:B1:1259:GLN:HG3	1.88	0.56
11:K:38:ARG:HH21	11:K:61:LEU:HD23	1.70	0.56
51:1:967:U:H2'	51:1:968:C:C6	2.41	0.56
51:1:2792:A:C2'	51:1:2793:C:H5''	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1073:U:H2'	53:3:1074:G:C8	2.40	0.56
16:P:63:GLN:HG2	16:P:98:ALA:HB2	1.86	0.56
47:w:12:SER:HB3	51:1:2261:C:C5	2.41	0.56
58:B1:1175:LEU:HD22	58:B1:1190:ILE:HD11	1.88	0.56
50:z:37:ARG:NH2	51:1:929:U:H4'	2.21	0.55
51:1:296:U:H2'	51:1:297:G:C8	2.40	0.55
51:1:322:A:H5'	51:1:340:A:H1'	1.88	0.55
51:1:1062:G:O2'	51:1:1063:G:H4'	2.05	0.55
51:1:2113:U:H2'	51:1:2114:A:C8	2.41	0.55
53:3:1268:G:N2	53:3:1327:C:H1'	2.21	0.55
8:H:123:LEU:HD21	8:H:129:PHE:HB3	1.88	0.55
27:b:47:ARG:HD3	51:1:778:G:H5''	1.87	0.55
27:b:70:LYS:NZ	27:b:97:ASP:OD2	2.39	0.55
2:B:9:ARG:HG3	51:1:17:G:OP1	2.06	0.55
3:C:7:LYS:HA	3:C:23:THR:HA	1.88	0.55
7:G:45:THR:HG22	7:G:200:PRO:HB2	1.88	0.55
40:p:91:VAL:HG21	40:p:96:LEU:HD11	1.87	0.55
51:1:1386:C:H2'	51:1:1387:A:C8	2.42	0.55
52:2:97:C:H2'	52:2:98:G:H5'	1.87	0.55
53:3:211:G:H2'	53:3:212:G:H5'	1.88	0.55
53:3:570:G:H5'	53:3:820:U:O4'	2.07	0.55
59:B2:1142:ARG:NH2	59:B2:1166:ASP:OD1	2.38	0.55
12:L:36:SER:HB2	14:N:42:THR:HG22	1.87	0.55
22:V:67:SER:HB3	22:V:70:LYS:HB2	1.87	0.55
48:x:30:PRO:HG2	48:x:32:LEU:HD22	1.87	0.55
51:1:1258:U:H2'	51:1:1259:G:C8	2.42	0.55
51:1:1558:C:H4'	51:1:1559:U:H5'	1.88	0.55
51:1:1909:C:H2'	51:1:1910:G:C8	2.42	0.55
51:1:2169:A:H2'	51:1:2170:A:O4'	2.06	0.55
53:3:950:U:H2'	53:3:951:G:C8	2.41	0.55
53:3:994:A:H3'	53:3:994:A:OP2	2.06	0.55
8:H:161:ILE:HG22	53:3:1196:A:N1	2.22	0.55
13:M:52:GLY:HA3	13:M:56:PRO:HA	1.88	0.55
16:P:126:ARG:NH2	53:3:796:C:O3'	2.39	0.55
24:X:38:THR:HA	24:X:69:LYS:HA	1.89	0.55
26:Z:66:ARG:HH21	53:3:1099:G:H4'	1.71	0.55
51:1:1063:G:H5''	51:1:1064:C:H6	1.69	0.55
52:2:49:C:H2'	52:2:50:A:H8	1.70	0.55
53:3:82:G:H2'	53:3:83:C:H5'	1.88	0.55
14:N:4:GLN:NE2	53:3:1131:G:H5'	2.22	0.55
35:k:38:ILE:HG22	35:k:61:VAL:HB	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1790:C:H2'	51:1:1791:A:C5	2.42	0.55
53:3:169:C:H2'	53:3:170:U:C6	2.42	0.55
15:O:59:LYS:HD2	53:3:972:C:O3'	2.07	0.55
34:j:27:ARG:NH2	51:1:1142:A:H4'	2.11	0.55
51:1:572:A:N6	51:1:2029:G:H21	2.05	0.55
51:1:1159:U:H2'	51:1:1160:G:H8	1.71	0.55
51:1:1877:A:H2'	51:1:1878:G:O4'	2.07	0.55
58:B1:508:LEU:HD22	59:B2:1101:LEU:HD21	1.88	0.55
58:B1:799:ARG:HG2	58:B1:1325:PHE:HZ	1.72	0.55
18:R:89:ARG:HB2	18:R:96:VAL:HG12	1.88	0.55
25:Y:4:LYS:HE2	53:3:332:G:OP1	2.06	0.55
34:j:65:THR:OG1	51:1:1141:U:OP2	2.22	0.55
40:p:94:ALA:HB2	51:1:2848:G:C8	2.42	0.55
51:1:2800:A:H3'	51:1:2801:G:H5'	1.88	0.55
58:B1:833:GLU:HB2	58:B1:1242:ARG:NH1	2.22	0.55
58:B1:1155:ILE:HG13	58:B1:1210:ILE:HB	1.89	0.55
13:M:19:ALA:HB2	53:3:827:U:O2'	2.07	0.55
19:S:58:ARG:NH1	53:3:979:C:O2	2.39	0.55
25:Y:81:GLN:HA	25:Y:84:LYS:HE3	1.88	0.55
33:i:105:LEU:HA	33:i:108:ILE:HG12	1.89	0.55
36:l:25:SER:HA	51:1:813:U:O4	2.07	0.55
51:1:96:C:H2'	51:1:97:C:C6	2.41	0.55
51:1:1045:C:H5'	51:1:1046:A:N7	2.21	0.55
1:A:64:PHE:HB2	53:3:1012:A:OP1	2.07	0.55
35:k:48:PRO:CB	53:3:1423:G:H5''	2.16	0.55
51:1:760:G:C2'	51:1:761:A:H5'	2.36	0.55
51:1:1437:C:H2'	51:1:1438:U:C6	2.41	0.55
51:1:1794:A:H2'	51:1:1795:C:C6	2.41	0.55
51:1:2636:C:H2'	51:1:2637:U:C6	2.42	0.55
53:3:918:A:H2'	53:3:919:A:O4'	2.06	0.55
58:B1:58:CYS:SG	58:B1:59:ALA:N	2.80	0.55
58:B1:145:VAL:HG23	58:B1:159:ILE:HG22	1.89	0.55
59:B2:633:LEU:HD13	59:B2:644:LEU:HD23	1.89	0.55
30:e:25:MET:HG2	52:2:57:A:C6	2.42	0.54
51:1:644:A:H2'	51:1:645:C:H5''	1.89	0.54
51:1:2151:U:H2'	51:1:2152:G:H8	1.73	0.54
51:1:2389:G:H5''	51:1:2390:U:O4'	2.07	0.54
51:1:2398:U:H2'	51:1:2399:G:H8	1.71	0.54
52:2:63:C:H2'	52:2:64:G:C8	2.41	0.54
57:A2:100:LEU:HD23	57:A2:115:ILE:HG21	1.89	0.54
59:B2:360:LEU:HD13	59:B2:378:ARG:HH11	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:18:GLN:HA	21:U:38:PHE:HA	1.90	0.54
51:1:296:U:H2'	51:1:297:G:H8	1.71	0.54
51:1:1909:C:H2'	51:1:1910:G:H8	1.72	0.54
58:B1:37:GLU:O	58:B1:61:ILE:CD1	2.52	0.54
58:B1:144:TYR:HE1	58:B1:162:GLU:CD	2.14	0.54
59:B2:917:SER:O	59:B2:919:ARG:HG3	2.07	0.54
8:H:171:ARG:HG2	53:3:1106:G:H5''	1.90	0.54
24:X:49:ALA:HA	24:X:58:PRO:HA	1.90	0.54
42:r:14:VAL:HG21	42:r:98:ILE:HG13	1.88	0.54
51:1:2026:U:H2'	51:1:2027:G:O4'	2.06	0.54
51:1:2428:G:H5''	51:1:2429:G:O5'	2.08	0.54
51:1:2602:A:H4'	51:1:2603:G:H5'	1.90	0.54
53:3:5:U:H4'	53:3:6:G:N7	2.23	0.54
53:3:1280:A:O2'	53:3:1281:C:H5'	2.07	0.54
62:NG:126:THR:CB	62:NG:175:PHE:C	2.80	0.54
8:H:45:GLU:HB3	8:H:46:LEU:HD12	1.89	0.54
22:V:45:VAL:HG22	22:V:72:TRP:HB2	1.90	0.54
24:X:77:ARG:HH22	53:3:1322:C:P	2.30	0.54
27:b:137:GLY:O	27:b:162:GLN:NE2	2.39	0.54
32:g:1:MET:N	32:g:21:VAL:O	2.41	0.54
34:j:125:TYR:HH	34:j:132:HIS:HE2	1.55	0.54
44:t:15:HIS:HE1	51:1:1339:G:OP2	1.91	0.54
46:v:47:VAL:HA	46:v:50:MET:HG2	1.89	0.54
65:a:33:LEU:HD22	65:a:216:THR:HB	1.89	0.54
7:G:175:ALA:HB1	7:G:180:ILE:HB	1.90	0.54
10:J:141:ASP:O	10:J:145:ASN:ND2	2.40	0.54
14:N:17:ARG:HH12	53:3:1129:C:C5'	2.21	0.54
15:O:10:LEU:HB2	15:O:72:ARG:HB2	1.88	0.54
30:e:162:ASP:OD1	30:e:162:ASP:N	2.41	0.54
51:1:554:U:H2'	51:1:555:G:O4'	2.08	0.54
53:3:256:U:H2'	53:3:257:G:C8	2.43	0.54
57:A1:47:LEU:HD23	57:A1:51:MET:HG3	1.89	0.54
59:B2:29:SER:O	59:B2:33:ASP:HB2	2.08	0.54
59:B2:243:PRO:HB2	59:B2:274:ILE:HG23	1.90	0.54
4:D:4:THR:O	51:1:687:C:H5''	2.07	0.54
11:K:10:VAL:HG12	11:K:84:VAL:HG12	1.88	0.54
35:k:3:GLN:HE21	51:1:1666:G:H1'	1.73	0.54
45:u:11:ILE:HG13	45:u:21:ARG:HB3	1.90	0.54
48:x:16:ASN:ND2	51:1:2081:U:H5''	2.23	0.54
51:1:1095:A:H1'	66:0:632:ILE:HG22	1.89	0.54
51:1:2215:C:H2'	51:1:2216:G:C8	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:b:235:GLU:HG2	51:1:2599:G:C8	2.42	0.54
51:1:320:A:H4'	51:1:322:A:N7	2.23	0.54
51:1:740:C:H5'	51:1:740:C:C6	2.34	0.54
51:1:2122:U:H2'	51:1:2123:G:C4'	2.38	0.54
53:3:575:G:O2'	53:3:821:G:H5'	2.08	0.54
58:B1:746:LEU:HG	58:B1:758:PRO:HG3	1.90	0.54
58:B1:759:ILE:HG23	58:B1:771:GLN:HB3	1.89	0.54
59:B2:103:VAL:HB	59:B2:114:VAL:HG11	1.89	0.54
59:B2:811:ASN:HA	59:B2:815:SER:HB2	1.90	0.54
64:6:48:C:H5'	64:6:50:U:OP1	2.08	0.54
66:0:164:ALA:HB1	66:0:262:ILE:HD11	1.89	0.54
66:0:617:MET:HE2	66:0:682:MET:HE3	1.89	0.54
33:i:80:LYS:HD3	33:i:86:LYS:HD2	1.88	0.54
33:i:131:THR:HG22	33:i:135:MET:HE2	1.88	0.54
43:s:60:HIS:ND1	43:s:61:ASN:OD1	2.41	0.54
51:1:226:A:H5''	51:1:257:C:O2'	2.08	0.54
51:1:455:C:H3'	51:1:456:C:C5'	2.38	0.54
51:1:886:A:N3	51:1:886:A:H2'	2.23	0.54
51:1:1564:C:H2'	51:1:1565:C:O4'	2.08	0.54
53:3:1342:C:H2'	53:3:1343:G:H8	1.73	0.54
53:3:1379:G:O2'	53:3:1380:U:H5'	2.07	0.54
59:B2:684:ASN:OD1	59:B2:687:ARG:NH2	2.41	0.54
64:6:19:G:H1'	64:6:57:A:C2	2.42	0.54
13:M:95:MET:HE2	13:M:129:ALA:HB1	1.90	0.54
18:R:88:LEU:HD13	18:R:91:ARG:HD2	1.90	0.54
29:d:53:THR:HG21	51:1:452:G:C8	2.43	0.54
33:i:97:VAL:HG23	33:i:137:LEU:HD23	1.89	0.54
40:p:96:LEU:HB3	40:p:99:LEU:HD13	1.90	0.54
51:1:918:A:H5''	52:2:97:C:O2'	2.07	0.54
52:2:29:A:H2'	52:2:30:C:C6	2.43	0.54
52:2:115:A:H2'	52:2:116:G:H8	1.72	0.54
53:3:1002:G:H2'	53:3:1003:G:O4'	2.07	0.54
58:B1:39:LYS:O	58:B1:273:ILE:HG23	2.08	0.54
66:0:105:VAL:O	66:0:337:ARG:NH1	2.41	0.54
15:O:53:ILE:HG12	53:3:1060:U:H5''	1.90	0.54
30:e:37:MET:HB2	30:e:56:LEU:HD11	1.90	0.54
35:k:25:LEU:HD22	51:1:2562:U:H4'	1.89	0.54
51:1:1753:G:N2	51:1:1755:A:H3'	2.23	0.54
53:3:231:U:H2'	53:3:232:G:H8	1.73	0.54
53:3:1273:C:H2'	53:3:1274:A:O4'	2.07	0.54
58:B1:30:ILE:HG21	58:B1:241:VAL:O	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:814:CYS:SG	58:B1:883:ARG:NH2	2.81	0.54
24:X:5:LYS:HG2	53:3:1313:U:OP2	2.07	0.53
51:1:1028:A:N6	51:1:1125:G:H2'	2.24	0.53
51:1:1558:C:H4'	51:1:1559:U:C5'	2.39	0.53
57:A2:43:LEU:HD13	57:A2:217:ILE:HD11	1.90	0.53
59:B2:985:GLU:HB3	59:B2:988:LYS:HB2	1.88	0.53
13:M:101:ALA:HB3	13:M:112:ASP:HB3	1.89	0.53
51:1:1018:U:O2'	51:1:1120:G:N2	2.41	0.53
51:1:2029:G:O6	51:1:2032:G:H5''	2.08	0.53
53:3:166:U:H2'	53:3:167:A:C8	2.43	0.53
64:6:62:C:H5'	65:a:53:ARG:HE	1.73	0.53
1:A:55:GLY:O	24:X:20:LYS:NZ	2.41	0.53
51:1:995:C:H6	51:1:995:C:H5'	1.72	0.53
51:1:1965:C:H5''	51:1:1966:A:H2'	1.89	0.53
51:1:2572:A:H5'	51:1:2574:G:H4'	1.90	0.53
53:3:112:G:N2	53:3:354:G:H5'	2.22	0.53
53:3:346:G:H2'	53:3:347:G:O4'	2.08	0.53
53:3:1506:U:O2'	53:3:1507:A:H5'	2.08	0.53
59:B2:628:HIS:HB3	59:B2:647:ARG:HH21	1.74	0.53
59:B2:1117:LEU:HD12	59:B2:1195:ILE:HG12	1.90	0.53
6:F:1:MET:HE3	51:1:2742:G:H5''	1.91	0.53
8:H:3:LYS:HA	53:3:1190:G:OP1	2.08	0.53
28:c:77:ARG:NH2	28:c:200:ASP:OD2	2.40	0.53
51:1:1172:C:H2'	51:1:1173:U:C6	2.43	0.53
53:3:1005:A:H2'	53:3:1006:G:H5'	1.90	0.53
57:A1:205:MET:HE3	57:A1:213:PRO:HB3	1.91	0.53
9:I:59:LYS:NZ	9:I:193:ASP:OD2	2.42	0.53
26:Z:38:GLU:HB2	53:3:1526:G:OP2	2.08	0.53
27:b:20:ASN:HB3	27:b:23:LEU:HD23	1.89	0.53
30:e:59:ILE:O	30:e:101:ARG:NH1	2.41	0.53
37:m:46:ILE:O	37:m:103:TYR:OH	2.27	0.53
46:v:14:LYS:HB2	52:2:98:G:H1	1.74	0.53
51:1:161:A:C3'	51:1:162:U:H5''	2.36	0.53
51:1:575:A:O2'	51:1:576:U:H5'	2.08	0.53
51:1:1123:C:H2'	51:1:1124:G:H8	1.73	0.53
51:1:1611:C:H6	51:1:1611:C:H5'	1.72	0.53
51:1:2257:U:O2'	51:1:2258:C:H5'	2.09	0.53
53:3:231:U:H2'	53:3:232:G:C8	2.43	0.53
58:B1:800:LEU:HB3	58:B1:920:ALA:HB1	1.89	0.53
59:B2:786:GLY:N	59:B2:789:THR:OG1	2.41	0.53
66:0:583:TYR:HB2	66:0:593:PHE:HZ	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:18:ASN:O	8:H:39:ARG:NH2	2.41	0.53
22:V:63:CYS:SG	22:V:73:THR:OG1	2.65	0.53
45:u:14:THR:OG1	45:u:68:ASN:ND2	2.41	0.53
51:1:186:G:H2'	51:1:187:G:H8	1.74	0.53
51:1:644:A:H2'	51:1:645:C:C5'	2.39	0.53
51:1:1726:C:H2'	51:1:1727:C:C6	2.44	0.53
53:3:166:U:H2'	53:3:167:A:H8	1.74	0.53
58:B1:78:LEU:O	58:B1:78:LEU:HD13	2.08	0.53
58:B1:111:THR:HG22	58:B1:300:GLN:NE2	2.23	0.53
58:B1:832:LYS:HB3	58:B1:1242:ARG:NH1	2.24	0.53
65:a:163:TYR:HB2	65:a:171:ILE:HD12	1.89	0.53
31:f:103:ASN:ND2	31:f:113:ASP:OD1	2.41	0.53
51:1:154:U:H2'	51:1:155:A:C8	2.44	0.53
51:1:1103:A:H3'	51:1:1104:C:H5''	1.91	0.53
51:1:1161:C:H2'	51:1:1162:G:H8	1.74	0.53
51:1:1161:C:H2'	51:1:1162:G:C8	2.43	0.53
51:1:2106:U:H2'	51:1:2107:G:H4'	1.90	0.53
53:3:1088:G:H21	53:3:1167:A:N6	2.03	0.53
58:B1:352:ARG:HD2	59:B2:1268:GLN:HE21	1.68	0.53
12:L:78:ARG:C	12:L:80:GLY:H	2.17	0.53
13:M:29:SER:HB3	53:3:589:U:H5''	1.90	0.53
28:c:24:VAL:HG21	28:c:188:LEU:HD23	1.91	0.53
28:c:56:LYS:CE	51:1:2830:C:H5''	2.39	0.53
48:x:17:ARG:CG	51:1:380:G:H5'	2.36	0.53
51:1:455:C:H3'	51:1:456:C:H5''	1.91	0.53
51:1:940:G:H2'	51:1:941:A:C5'	2.39	0.53
53:3:410:G:H2'	53:3:429:U:C5	2.44	0.53
53:3:1014:A:H2	53:3:1219:A:H1'	1.73	0.53
53:3:1042:A:H2'	53:3:1043:G:O4'	2.09	0.53
59:B2:246:LEU:HB3	59:B2:269:ILE:HD13	1.91	0.53
60:W0:3:ARG:NH1	60:W0:55:GLU:OE2	2.40	0.53
11:K:5:GLU:HB2	11:K:90:MET:HB2	1.90	0.53
20:T:43:ALA:O	20:T:46:LYS:NZ	2.42	0.53
29:d:119:ILE:HB	29:d:187:VAL:HG12	1.91	0.53
38:n:49:GLU:HB3	51:1:2839:G:H4'	1.91	0.53
46:v:35:GLU:OE2	46:v:93:ARG:NH1	2.42	0.53
49:y:21:LEU:HA	49:y:25:GLN:HB3	1.91	0.53
51:1:1141:U:H4'	51:1:1142:A:O4'	2.09	0.53
51:1:2024:G:OP2	51:1:2034:U:H4'	2.09	0.53
53:3:3:A:H5'	53:3:613:C:H4'	1.91	0.53
53:3:1176:A:H2'	53:3:1177:G:C8	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:68:TYR:CA	58:B1:75:TYR:HE2	2.22	0.53
22:V:8:GLN:NE2	22:V:59:GLU:OE2	2.42	0.53
29:d:68:ALA:HA	51:1:1255:U:C5	2.44	0.53
30:e:65:LEU:HD22	52:2:42:C:C4	2.44	0.53
44:t:31:VAL:HG12	44:t:84:TYR:HA	1.91	0.53
58:B1:785:ASP:O	58:B1:789:LYS:HB2	2.08	0.53
58:B1:850:LYS:HB2	58:B1:857:LEU:HB2	1.91	0.53
10:J:76:ASN:HB3	10:J:81:GLN:HG2	1.90	0.52
11:K:2:ARG:HH12	11:K:91:ARG:HB2	1.72	0.52
22:V:11:VAL:HG13	22:V:20:ILE:HD11	1.90	0.52
26:Z:25:ALA:HA	26:Z:28:LEU:HB2	1.90	0.52
36:l:47:ARG:NH2	51:1:251:A:H4'	2.24	0.52
45:u:86:PHE:HE1	45:u:91:LYS:HG3	1.74	0.52
51:1:1066:U:H2'	51:1:1068:G:OP2	2.08	0.52
51:1:1273:U:H4'	51:1:1275:A:OP1	2.08	0.52
51:1:2760:C:O2'	51:1:2761:A:H5'	2.08	0.52
53:3:1391:U:H2'	53:3:1392:G:C8	2.44	0.52
58:B1:205:LEU:HG	58:B1:217:LEU:HB3	1.90	0.52
58:B1:975:ILE:HD11	58:B1:1003:LEU:HD11	1.91	0.52
30:e:154:THR:HG21	51:1:2314:A:H1'	1.90	0.52
39:o:10:ARG:HD2	51:1:2294:G:OP1	2.09	0.52
51:1:1345:C:H6	51:1:1345:C:H5'	1.74	0.52
53:3:1054:C:H4'	53:3:1056:U:OP2	2.10	0.52
58:B1:290:ILE:HG21	62:NG:93:ILE:O	2.09	0.52
66:0:388:LEU:HD23	66:0:391:VAL:HG11	1.91	0.52
13:M:42:GLU:HG2	13:M:100:ILE:HD13	1.91	0.52
51:1:817:C:O2'	51:1:839:U:H5''	2.10	0.52
51:1:917:A:H2	52:2:79:G:N3	2.07	0.52
51:1:2869:G:H2'	51:1:2870:C:O4'	2.09	0.52
1:A:62:LYS:HG3	24:X:20:LYS:HB3	1.91	0.52
13:M:75:GLN:HB2	13:M:127:TYR:HB2	1.90	0.52
15:O:67:ILE:HG23	19:S:95:LEU:HD23	1.91	0.52
40:p:84:SER:OG	40:p:86:LYS:NZ	2.42	0.52
51:1:2625:G:H2'	51:1:2626:C:O4'	2.09	0.52
51:1:2720:U:H6	51:1:2720:U:H5'	1.73	0.52
66:0:91:GLY:N	70:0:802:PO4:O1	2.40	0.52
51:1:1672:A:C2	51:1:2582:G:H5'	2.44	0.52
53:3:608:A:H2'	53:3:609:A:O4'	2.08	0.52
53:3:1270:G:H2'	53:3:1271:A:H8	1.75	0.52
58:B1:215:LYS:HA	58:B1:218:THR:HG22	1.92	0.52
11:K:36:ILE:HG22	11:K:64:VAL:HG13	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:i:69:VAL:O	33:i:71:LYS:NZ	2.43	0.52
51:1:1869:G:H3'	51:1:1870:C:H5'	1.92	0.52
53:3:134:G:H2'	53:3:135:C:O4'	2.08	0.52
53:3:1412:C:H2'	53:3:1413:A:C8	2.45	0.52
53:3:1436:U:H2'	53:3:1437:A:C8	2.43	0.52
66:0:53:MET:HE1	66:0:472:ARG:HG3	1.91	0.52
14:N:54:VAL:HG11	14:N:93:LEU:HD23	1.91	0.52
20:T:57:ARG:NH2	20:T:58:MET:SD	2.82	0.52
30:e:65:LEU:CD1	52:2:41:G:H2'	2.40	0.52
51:1:1637:A:H5'	51:1:1760:C:O2'	2.10	0.52
51:1:2114:A:C5	51:1:2115:G:H1'	2.45	0.52
53:3:235:C:H2'	53:3:236:A:C8	2.44	0.52
53:3:604:G:H2'	53:3:605:U:O4'	2.10	0.52
57:A2:140:ILE:HD12	57:A2:142:MET:HE3	1.92	0.52
58:B1:209:ASN:HA	58:B1:214:ARG:HH21	1.74	0.52
59:B2:714:VAL:HB	59:B2:787:PRO:HD2	1.92	0.52
59:B2:1070:HIS:NE2	59:B2:1114:GLU:OE1	2.36	0.52
12:L:91:ARG:NE	12:L:91:ARG:HA	2.25	0.52
34:j:118:MET:HA	34:j:121:LYS:HD3	1.91	0.52
51:1:118:A:OP2	51:1:119:A:H5''	2.10	0.52
51:1:1064:C:H2'	51:1:1065:U:C6	2.44	0.52
51:1:2628:C:H3'	51:1:2629:U:H5'	1.92	0.52
51:1:2800:A:C2	51:1:2895:G:H1'	2.45	0.52
51:1:2818:U:H2'	51:1:2819:G:H8	1.75	0.52
53:3:1353:G:O2'	53:3:1354:U:H5'	2.10	0.52
58:B1:144:TYR:CE1	58:B1:162:GLU:CD	2.88	0.52
9:I:53:GLN:HA	9:I:198:LEU:HD12	1.92	0.52
14:N:55:ASP:N	14:N:55:ASP:OD1	2.43	0.52
16:P:19:VAL:HG22	16:P:82:GLU:HB2	1.92	0.52
23:W:33:THR:OG1	23:W:34:GLU:N	2.43	0.52
39:o:51:ALA:HB3	39:o:78:VAL:HG12	1.92	0.52
51:1:519:U:H2'	51:1:520:G:C8	2.44	0.52
57:A1:100:LEU:HD21	57:A1:121:VAL:HG11	1.90	0.52
58:B1:770:LEU:CD1	59:B2:618:GLN:HG3	2.37	0.52
66:0:282:VAL:HA	66:0:286:LEU:HD12	1.91	0.52
17:Q:45:ASN:HB3	53:3:528:C:H41	1.75	0.52
27:b:140:VAL:HA	27:b:191:LEU:HA	1.91	0.52
32:g:84:ALA:HB2	32:g:148:ALA:HB1	1.90	0.52
51:1:154:U:H2'	51:1:155:A:H8	1.74	0.52
51:1:973:A:H5'	51:1:1188:U:H1'	1.92	0.52
51:1:1138:G:H2'	51:1:1139:G:O4'	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2650:U:H2'	51:1:2651:C:H6	1.74	0.52
53:3:210:C:H5'	53:3:211:G:N3	2.25	0.52
53:3:473:U:H2'	53:3:474:G:C8	2.45	0.52
59:B2:125:GLY:HA2	59:B2:499:SER:HB2	1.92	0.52
51:1:528:A:H2'	51:1:529:A:H5''	1.91	0.51
51:1:685:A:H5''	51:1:788:A:H62	1.74	0.51
51:1:857:G:H2'	51:1:858:G:O4'	2.10	0.51
53:3:123:U:OP1	53:3:312:C:H5'	2.10	0.51
53:3:1278:G:OP1	53:3:1279:G:H5'	2.10	0.51
58:B1:112:ALA:HA	58:B1:238:ILE:HA	1.91	0.51
58:B1:683:ILE:HD12	58:B1:754:ILE:HG21	1.93	0.51
25:Y:22:SER:HA	53:3:1458:G:O3'	2.11	0.51
41:q:54:ARG:NH2	51:1:1155:A:H4'	2.25	0.51
51:1:686:U:H3'	51:1:687:C:H5'	1.91	0.51
53:3:779:C:H2'	53:3:780:A:O4'	2.10	0.51
53:3:1042:A:H2'	53:3:1043:G:C1'	2.40	0.51
57:A1:16:ILE:HG23	57:A1:26:VAL:HG22	1.91	0.51
58:B1:390:LEU:N	58:B1:390:LEU:CD1	2.73	0.51
9:I:205:LYS:HE3	53:3:8:A:C5	2.45	0.51
48:x:7:THR:HG23	48:x:9:LYS:HG3	1.92	0.51
51:1:749:A:C2	51:1:1618:A:H2'	2.45	0.51
51:1:1447:C:H2'	51:1:1448:G:H8	1.75	0.51
53:3:1402:C:H2'	53:3:1403:C:O4'	2.10	0.51
53:3:1450:U:H1'	53:3:1454:G:N2	2.25	0.51
59:B2:524:ILE:HG21	59:B2:708:VAL:HG13	1.92	0.51
66:0:116:VAL:HG11	66:0:146:ARG:HD3	1.91	0.51
66:0:151:PHE:HE2	66:0:171:LEU:HG	1.75	0.51
11:K:38:ARG:NH1	11:K:40:GLU:OE1	2.43	0.51
29:d:58:LYS:NZ	29:d:62:GLN:OE1	2.43	0.51
29:d:63:LYS:HD3	51:1:2443:C:OP1	2.10	0.51
41:q:82:LEU:HD23	41:q:112:ALA:HB2	1.92	0.51
53:3:86:G:H4'	53:3:87:C:C5	2.44	0.51
53:3:1247:U:O2'	53:3:1248:A:H5'	2.10	0.51
53:3:1449:C:H2'	53:3:1450:U:O4'	2.10	0.51
53:3:1481:U:O2'	53:3:1482:G:H5'	2.09	0.51
8:H:13:ILE:HG13	8:H:14:VAL:HG23	1.91	0.51
23:W:41:SER:HB3	23:W:51:GLN:HE21	1.76	0.51
32:g:78:VAL:HG11	32:g:103:VAL:HG22	1.91	0.51
51:1:226:A:H2'	51:1:227:A:O4'	2.11	0.51
51:1:558:U:H2'	51:1:559:G:H8	1.76	0.51
51:1:1625:C:H2'	51:1:1626:A:O4'	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2165:C:H5''	51:1:2166:U:OP1	2.10	0.51
53:3:1411:C:H2'	53:3:1412:C:C6	2.45	0.51
59:B2:255:ILE:HB	59:B2:263:VAL:HB	1.93	0.51
66:0:97:ILE:HD11	66:0:443:PRO:HD2	1.92	0.51
66:0:105:VAL:HG22	66:0:337:ARG:HH11	1.75	0.51
66:0:342:VAL:HG12	66:0:378:ARG:HA	1.91	0.51
19:S:2:LYS:HG2	53:3:1048:G:H5''	1.92	0.51
27:b:106:PRO:HA	27:b:194:VAL:HA	1.92	0.51
31:f:40:VAL:O	31:f:54:ARG:NH2	2.43	0.51
36:l:108:ALA:HB3	36:l:125:LEU:HD11	1.92	0.51
39:o:21:LEU:HD11	51:1:2379:G:H4'	1.91	0.51
48:x:18:SER:HB2	51:1:2080:A:H5'	1.92	0.51
51:1:368:A:O2'	51:1:369:U:H5'	2.11	0.51
51:1:644:A:H2'	51:1:645:C:C4'	2.41	0.51
51:1:2432:A:H5'	64:6:76:A:O3'	2.09	0.51
53:3:1421:G:C5	53:3:1422:G:H1'	2.45	0.51
58:B1:99:ARG:HG3	58:B1:99:ARG:HH11	1.73	0.51
58:B1:201:LEU:HD12	58:B1:224:LEU:HD12	1.91	0.51
66:0:170:GLN:HE21	66:0:266:CYS:H	1.59	0.51
11:K:40:GLU:OE2	11:K:100:SER:OG	2.28	0.51
51:1:1068:G:O2'	51:1:1096:A:H4'	2.10	0.51
51:1:1669:A:O3'	51:1:2549:G:H5'	2.11	0.51
51:1:1906:G:H2'	51:1:1907:G:H5''	1.93	0.51
53:3:392:C:H2'	53:3:393:A:H8	1.75	0.51
53:3:701:U:C4'	53:3:703:G:H1'	2.41	0.51
55:8:13:DT:OP2	58:B1:791:ALA:CB	2.59	0.51
58:B1:99:ARG:HA	58:B1:248:ASP:HB2	1.92	0.51
4:D:8:SER:HA	51:1:1309:G:H5''	1.91	0.51
27:b:106:PRO:HD2	27:b:109:LEU:HD13	1.91	0.51
27:b:257:ARG:HH12	51:1:1799:G:H3'	1.75	0.51
29:d:145:ASP:HA	29:d:166:LYS:HB3	1.92	0.51
51:1:543:G:H3'	51:1:544:C:H5''	1.93	0.51
51:1:937:C:H2'	51:1:938:G:H8	1.74	0.51
53:3:184:G:H4'	53:3:224:U:O3'	2.11	0.51
53:3:757:U:H2'	53:3:758:C:O4'	2.10	0.51
23:W:70:THR:OG1	23:W:71:ASP:N	2.44	0.51
51:1:2104:C:H2'	51:1:2105:U:O4'	2.11	0.51
51:1:2586:U:H2'	51:1:2587:A:C8	2.46	0.51
53:3:406:G:O2'	53:3:407:U:H5'	2.11	0.51
53:3:1137:C:H4'	53:3:1138:G:C2	2.45	0.51
58:B1:375:GLU:HG2	59:B2:1245:ALA:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:437:PHE:HZ	58:B1:453:VAL:HG11	1.76	0.51
66:0:158:ILE:HG23	66:0:162:LEU:HD12	1.92	0.51
4:D:24:THR:O	4:D:28:ARG:NH1	2.44	0.51
9:I:73:ASN:OD1	9:I:76:LYS:NZ	2.44	0.51
9:I:82:LYS:O	9:I:88:ASN:ND2	2.36	0.51
16:P:121:ARG:HH22	53:3:1524:C:H5''	1.75	0.51
22:V:44:HIS:HB3	22:V:70:LYS:HG3	1.92	0.51
30:e:31:GLU:HB2	30:e:156:THR:HB	1.93	0.51
42:r:10:LYS:HE2	51:1:994:C:O2'	2.11	0.51
46:v:66:ASP:O	46:v:68:LYS:NZ	2.43	0.51
51:1:1645:G:H5''	51:1:1646:C:C5'	2.27	0.51
51:1:1907:G:H2'	51:1:1908:C:O4'	2.11	0.51
51:1:2743:U:C2'	51:1:2744:G:H5''	2.40	0.51
52:2:118:C:H2'	52:2:119:A:C4'	2.40	0.51
53:3:1138:G:H3'	53:3:1138:G:N3	2.25	0.51
58:B1:275:ARG:HH12	58:B1:278:ARG:NH1	2.09	0.51
20:T:13:GLU:O	20:T:83:ARG:NH2	2.42	0.50
33:i:91:LYS:HB2	33:i:94:LYS:HB2	1.92	0.50
37:m:17:ASN:ND2	37:m:97:GLN:OE1	2.36	0.50
51:1:878:A:H3'	51:1:879:G:H8	1.75	0.50
51:1:2186:G:H2'	51:1:2187:U:O4'	2.11	0.50
53:3:1206:G:H2'	53:3:1207:G:O4'	2.11	0.50
59:B2:93:SER:HA	59:B2:128:PRO:HA	1.93	0.50
59:B2:400:VAL:HG21	59:B2:452:ARG:HE	1.76	0.50
1:A:54:GLY:H	24:X:26:ASP:HA	1.76	0.50
7:G:103:TRP:HA	7:G:106:VAL:HG12	1.92	0.50
13:M:104:SER:O	53:3:642:A:H2	1.93	0.50
51:1:663:G:C3'	51:1:664:G:H5''	2.41	0.50
51:1:2881:U:H2'	51:1:2882:A:C8	2.46	0.50
53:3:407:U:H2'	53:3:408:A:C8	2.45	0.50
53:3:839:C:H2'	53:3:840:C:C6	2.46	0.50
66:0:158:ILE:HB	66:0:166:PRO:HG3	1.92	0.50
5:E:2:LYS:HG3	51:1:242:G:C8	2.46	0.50
9:I:104:MET:HG3	9:I:172:VAL:HG22	1.92	0.50
33:i:11:GLN:HB2	33:i:56:VAL:HG12	1.93	0.50
47:w:70:PRO:HD3	52:2:12:C:N4	2.26	0.50
53:3:35:G:H2'	53:3:36:C:C6	2.46	0.50
53:3:195:A:H2'	53:3:196:A:C8	2.47	0.50
59:B2:232:ILE:HG12	59:B2:237:LEU:HG	1.94	0.50
59:B2:400:VAL:HG11	59:B2:452:ARG:HD2	1.94	0.50
66:0:312:SER:OG	66:0:313:ASP:N	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:m:1:MET:HE1	63:5:63:G:O2'	2.11	0.50
51:1:859:G:HO2'	51:1:860:U:H6	1.58	0.50
51:1:1019:U:OP1	51:1:1035:U:O2'	2.29	0.50
51:1:1542:U:H2'	51:1:1543:G:O4'	2.10	0.50
51:1:2250:G:H21	51:1:2496:C:H5''	1.76	0.50
51:1:2266:A:H4'	51:1:2267:A:N3	2.26	0.50
51:1:2404:U:H2'	51:1:2405:G:O4'	2.10	0.50
53:3:91:U:H2'	53:3:92:U:H5''	1.93	0.50
53:3:458:U:H2'	53:3:459:A:H8	1.75	0.50
58:B1:395:LYS:NZ	58:B1:399:LYS:CD	2.74	0.50
58:B1:412:LEU:HD23	58:B1:416:ILE:HG13	1.92	0.50
66:0:94:ASP:HB3	66:0:465:HIS:HB2	1.93	0.50
14:N:27:ILE:HD12	14:N:34:LEU:HD22	1.93	0.50
27:b:59:GLN:HG2	27:b:84:PRO:HB2	1.93	0.50
33:i:8:VAL:HG11	33:i:26:ALA:HB1	1.93	0.50
33:i:14:ALA:HB1	33:i:45:THR:HG23	1.94	0.50
51:1:140:C:H2'	51:1:141:G:H4'	1.94	0.50
51:1:161:A:H3'	51:1:162:U:C5'	2.39	0.50
51:1:748:G:O2'	51:1:749:A:H5''	2.11	0.50
51:1:1159:U:H2'	51:1:1160:G:C8	2.46	0.50
51:1:2663:G:H8	51:1:2663:G:OP2	1.94	0.50
53:3:14:U:O2	53:3:17:U:H5	1.95	0.50
58:B1:749:LYS:HB3	58:B1:755:ILE:HD11	1.93	0.50
59:B2:974:ARG:HD2	59:B2:1014:LEU:HD21	1.92	0.50
65:a:12:ARG:HA	65:a:15:VAL:HB	1.92	0.50
66:0:139:ALA:N	66:0:263:LEU:O	2.43	0.50
4:D:10:LEU:HD23	51:1:770:G:H5''	1.94	0.50
33:i:92:PRO:HD2	51:1:1076:C:O2'	2.12	0.50
51:1:473:G:O2'	51:1:474:G:H5'	2.12	0.50
51:1:2041:U:H2'	51:1:2042:A:H8	1.77	0.50
51:1:2742:G:H1	51:1:2762:C:H42	1.60	0.50
53:3:267:C:O2	53:3:267:C:H2'	2.10	0.50
53:3:1441:A:H62	53:3:1461:G:H21	1.60	0.50
63:5:22:G:H2'	63:5:23:A:C8	2.47	0.50
63:5:23:A:H2'	63:5:24:G:C8	2.47	0.50
66:0:420:VAL:HG21	66:0:481:ALA:HB1	1.93	0.50
66:0:503:GLY:N	66:0:518:VAL:O	2.40	0.50
24:X:17:LYS:O	24:X:20:LYS:NZ	2.41	0.50
33:i:92:PRO:HB3	51:1:1077:A:H1'	1.92	0.50
51:1:1999:C:H5''	51:1:2723:C:O2'	2.12	0.50
51:1:2041:U:H2'	51:1:2042:A:C8	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:505:ASP:OD2	59:B2:812:PHE:HA	2.11	0.50
66:0:105:VAL:HG22	66:0:337:ARG:HD3	1.94	0.50
66:0:364:VAL:HG12	66:0:366:MET:H	1.77	0.50
67:h:6:5OH:N	67:h:6:5OH:CS	2.75	0.50
51:1:1536:C:H4'	51:1:1537:G:N2	2.27	0.50
58:B1:1371:ARG:HE	58:B1:1372:ARG:NH1	2.10	0.50
8:H:22:PHE:HE2	15:O:11:LYS:HD3	1.76	0.50
29:d:45:ALA:HB2	29:d:89:PRO:HD3	1.93	0.50
34:j:2:LYS:HA	51:1:995:C:N3	2.27	0.50
43:s:75:PHE:HE1	51:1:519:U:H1'	1.77	0.50
51:1:274:C:H2'	51:1:275:C:O4'	2.12	0.50
51:1:1434:A:H2'	51:1:1435:G:H8	1.77	0.50
51:1:1443:U:H2'	51:1:1444:G:H8	1.75	0.50
51:1:1472:C:H2'	51:1:1473:G:C8	2.47	0.50
53:3:1109:C:H2'	53:3:1110:A:O4'	2.12	0.50
57:A1:18:GLN:HA	57:A1:24:ALA:HA	1.94	0.50
62:NG:161:SER:HA	62:NG:170:PRO:HA	1.94	0.50
7:G:100:LEU:HB2	7:G:174:GLU:HG2	1.93	0.49
8:H:124:GLU:HG3	8:H:188:ALA:HB1	1.94	0.49
26:Z:32:ARG:HG3	26:Z:33:ARG:HG2	1.93	0.49
33:i:53:PRO:HD2	33:i:77:VAL:HB	1.94	0.49
51:1:355:U:H2'	51:1:356:G:C8	2.47	0.49
51:1:948:C:H2'	51:1:949:G:H8	1.77	0.49
51:1:2469:A:H2'	51:1:2470:G:O4'	2.12	0.49
53:3:38:G:H22	53:3:397:A:H5'	1.77	0.49
53:3:76:G:H2'	53:3:77:A:C5'	2.42	0.49
53:3:1386:G:H2'	53:3:1387:G:H8	1.77	0.49
25:Y:54:GLN:HE21	53:3:193:C:C1'	2.25	0.49
33:i:92:PRO:HB2	51:1:1077:A:C4'	2.42	0.49
46:v:45:ASP:N	46:v:45:ASP:OD1	2.44	0.49
51:1:864:G:H4'	52:2:101:A:H4'	1.94	0.49
51:1:948:C:H2'	51:1:949:G:C8	2.47	0.49
51:1:2811:G:H2'	51:1:2812:G:H8	1.77	0.49
53:3:89:U:H2'	53:3:90:C:O4'	2.12	0.49
53:3:599:C:H2'	53:3:600:A:C8	2.47	0.49
53:3:1013:G:N2	53:3:1015:G:H3'	2.27	0.49
54:4:44:G:OP1	59:B2:1073:LYS:NZ	2.37	0.49
58:B1:972:LYS:HD2	58:B1:1004:ALA:HA	1.93	0.49
59:B2:529:ARG:HH11	59:B2:572:ILE:HG22	1.77	0.49
65:a:166:ASP:OD2	65:a:172:HIS:ND1	2.45	0.49
10:J:37:VAL:HG11	10:J:113:VAL:HA	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:127:ARG:HB2	53:3:796:C:OP1	2.12	0.49
27:b:201:LEU:CD2	53:3:773:G:H5''	2.42	0.49
34:j:45:THR:HB	34:j:48:VAL:HG22	1.93	0.49
40:p:61:ARG:NH2	40:p:99:LEU:O	2.44	0.49
53:3:359:G:H2'	53:3:360:G:O4'	2.13	0.49
53:3:781:A:OP1	53:3:1523:G:H5'	2.12	0.49
58:B1:1179:PRO:HD2	58:B1:1184:ASP:HA	1.93	0.49
31:f:28:LYS:N	31:f:78:VAL:O	2.46	0.49
47:w:12:SER:HB3	51:1:2261:C:C6	2.47	0.49
51:1:341:C:H2'	51:1:342:A:C8	2.47	0.49
51:1:934:U:H2'	51:1:935:C:C6	2.47	0.49
51:1:2208:C:H2'	51:1:2209:G:C8	2.47	0.49
53:3:1023:U:H2'	53:3:1024:G:C8	2.48	0.49
58:B1:145:VAL:HG12	58:B1:184:ALA:HB1	1.94	0.49
9:I:50:TYR:CD2	53:3:508:U:H4'	2.48	0.49
11:K:62:MET:HB3	11:K:64:VAL:HG23	1.93	0.49
28:c:4:LEU:HD23	28:c:29:VAL:HG11	1.94	0.49
28:c:45:TYR:CZ	51:1:2637:U:H5'	2.47	0.49
51:1:1735:A:H2'	51:1:1736:U:O4'	2.11	0.49
57:A1:100:LEU:HB2	57:A1:144:ILE:HG23	1.95	0.49
12:L:110:ARG:NH1	12:L:125:ASP:OD2	2.46	0.49
21:U:4:ILE:HG12	21:U:21:VAL:HG22	1.94	0.49
31:f:48:THR:OG1	31:f:49:LEU:N	2.45	0.49
38:n:49:GLU:CB	51:1:2839:G:H4'	2.42	0.49
53:3:70:U:H4'	53:3:71:A:H8	1.78	0.49
53:3:952:U:H2'	53:3:953:G:H8	1.78	0.49
53:3:1316:G:C2'	53:3:1317:C:H5''	2.40	0.49
59:B2:411:ARG:NH2	59:B2:427:ASP:OD2	2.44	0.49
59:B2:533:LEU:HD13	59:B2:540:ARG:HH21	1.77	0.49
63:5:51:U:H2'	63:5:52:G:C8	2.48	0.49
15:O:65:TYR:HB3	19:S:95:LEU:HD22	1.95	0.49
21:U:70:ARG:NH2	53:3:451:A:OP2	2.45	0.49
29:d:125:SER:O	29:d:137:LYS:NZ	2.39	0.49
38:n:22:ARG:HG3	38:n:70:THR:HA	1.93	0.49
43:s:18:ARG:NH1	51:1:518:G:H4'	2.28	0.49
53:3:745:G:OP1	53:3:852:G:H5'	2.13	0.49
53:3:1391:U:H2'	53:3:1392:G:H8	1.77	0.49
53:3:1491:G:H2'	67:h:6:5OH:O	2.11	0.49
66:0:433:LEU:O	66:0:437:ARG:N	2.45	0.49
32:g:7:ASP:HA	32:g:15:LEU:HD23	1.94	0.49
51:1:26:G:H1'	51:1:515:A:H61	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1597:A:H5''	51:1:1598:A:H5'	1.94	0.49
51:1:2104:C:H42	51:1:2185:U:H3	1.60	0.49
51:1:2220:U:H2'	51:1:2221:G:C8	2.47	0.49
53:3:1128:C:O2'	53:3:1129:C:H5'	2.13	0.49
53:3:1492:A:H1'	54:4:5:U:O2'	2.13	0.49
58:B1:421:VAL:O	58:B1:436:ALA:HA	2.12	0.49
59:B2:9:LYS:HG2	59:B2:1171:ARG:HH12	1.77	0.49
59:B2:562:GLU:OE1	59:B2:662:SER:OG	2.28	0.49
7:G:53:LEU:HD22	7:G:219:THR:HG21	1.95	0.49
24:X:54:ARG:HG3	24:X:55:GLN:HG2	1.95	0.49
28:c:56:LYS:HZ1	51:1:2830:C:H5''	1.78	0.49
44:t:64:LYS:HE2	51:1:1601:G:OP1	2.13	0.49
50:z:40:THR:HG22	50:z:43:ILE:HG12	1.94	0.49
51:1:1029:A:H2'	51:1:1030:C:O4'	2.13	0.49
53:3:253:A:H2'	53:3:254:G:C8	2.47	0.49
53:3:632:U:H3'	53:3:633:G:H5'	1.95	0.49
58:B1:124:ILE:HG23	58:B1:128:LEU:HD12	1.94	0.49
59:B2:857:VAL:HG13	59:B2:919:ARG:HH21	1.78	0.49
62:NG:126:THR:CB	62:NG:175:PHE:CA	2.90	0.49
14:N:121:ARG:HD2	53:3:1348:U:H4'	1.95	0.49
17:Q:71:HIS:HB2	17:Q:73:LEU:HD23	1.95	0.49
38:n:32:GLU:HG2	38:n:115:LEU:HD12	1.94	0.49
41:q:3:VAL:HG12	41:q:5:ARG:H	1.78	0.49
51:1:1111:A:H2'	51:1:1111:A:N3	2.28	0.49
51:1:1417:C:C4'	51:1:1587:G:H21	2.26	0.49
51:1:2122:U:H2'	51:1:2123:G:H4'	1.95	0.49
51:1:2792:A:C3'	51:1:2793:C:H5''	2.43	0.49
58:B1:220:ARG:HG2	58:B1:220:ARG:NH1	2.26	0.49
59:B2:18:ARG:HE	59:B2:620:ASN:HA	1.77	0.49
64:6:37:A:H2'	64:6:38:A:O4'	2.13	0.49
64:6:44:A:H3'	64:6:45:G:H5''	1.95	0.49
21:U:56:ARG:HA	21:U:59:HIS:HB3	1.95	0.48
29:d:94:GLN:CD	51:1:660:C:H5''	2.38	0.48
43:s:4:ILE:HG22	43:s:106:VAL:HG13	1.93	0.48
51:1:2128:G:H1	51:1:2160:C:H42	1.58	0.48
53:3:802:A:H2'	53:3:803:G:O4'	2.13	0.48
53:3:916:U:H2'	53:3:917:G:C8	2.47	0.48
55:8:14:DC:H2'	55:8:15:DC:C6	2.48	0.48
59:B2:732:ILE:HD11	59:B2:769:PRO:HB3	1.95	0.48
66:0:12:ASN:HA	66:0:85:ASN:HB2	1.94	0.48
66:0:127:TRP:O	66:0:131:ASN:ND2	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:O:289:PRO:HB3	66:O:337:ARG:HH21	1.78	0.48
9:I:73:ASN:HA	9:I:76:LYS:HD2	1.95	0.48
15:O:86:ALA:HA	15:O:90:LEU:HD12	1.95	0.48
30:e:128:SER:HB2	30:e:154:THR:HG23	1.95	0.48
47:w:20:LYS:HE3	51:1:2355:G:O2'	2.13	0.48
51:1:616:A:H2'	51:1:617:G:O4'	2.12	0.48
51:1:686:U:H6	51:1:788:A:N1	2.12	0.48
51:1:1180:U:H5''	51:1:1181:U:H5	1.78	0.48
51:1:1335:C:H2'	51:1:1336:A:C8	2.48	0.48
51:1:1474:U:H2'	51:1:1475:G:H5'	1.96	0.48
51:1:2176:A:H5'	65:a:219:GLY:C	2.38	0.48
51:1:2364:C:H2'	51:1:2365:G:O4'	2.13	0.48
51:1:2583:G:H2'	51:1:2584:U:O4'	2.13	0.48
52:2:101:A:H2'	52:2:102:G:O4'	2.13	0.48
53:3:530:G:H3'	53:3:531:U:H5'	1.95	0.48
53:3:701:U:H4'	53:3:703:G:H1'	1.93	0.48
58:B1:102:MET:HG2	58:B1:246:PRO:HD3	1.94	0.48
59:B2:554:HIS:HD2	59:B2:558:VAL:HB	1.77	0.48
65:a:46:VAL:HG13	65:a:212:VAL:HG22	1.95	0.48
16:P:27:ASN:ND2	53:3:692:U:H5	2.11	0.48
30:e:36:ASN:HB3	30:e:152:ASP:HB3	1.95	0.48
40:p:1:SER:N	51:1:2875:C:H4'	2.27	0.48
46:v:14:LYS:HB2	52:2:98:G:N1	2.28	0.48
51:1:2898:U:H2'	51:1:2899:A:H8	1.78	0.48
52:2:28:C:H2'	52:2:29:A:C8	2.48	0.48
53:3:17:U:H2'	53:3:18:C:C6	2.48	0.48
53:3:59:A:N6	53:3:331:G:H1'	2.28	0.48
62:NG:126:THR:CB	62:NG:175:PHE:CB	2.91	0.48
41:q:111:LYS:HD2	42:r:48:LYS:HD3	1.95	0.48
51:1:1326:U:H2'	51:1:1327:A:C8	2.41	0.48
51:1:1447:C:H2'	51:1:1448:G:C8	2.48	0.48
51:1:1753:G:H22	51:1:1755:A:H3'	1.79	0.48
51:1:2221:G:O2'	51:1:2222:C:H5'	2.13	0.48
51:1:2522:U:H2'	51:1:2523:G:H5'	1.96	0.48
51:1:2565:A:O2'	51:1:2566:A:H5'	2.13	0.48
53:3:207:C:C2'	53:3:208:U:H5''	2.42	0.48
57:A1:182:ARG:O	57:A1:205:MET:HA	2.14	0.48
58:B1:550:VAL:O	58:B1:569:LEU:HA	2.13	0.48
64:6:68:C:H2'	64:6:69:C:C6	2.48	0.48
7:G:165:ALA:HB1	7:G:172:ILE:HD13	1.96	0.48
15:O:7:ARG:HA	15:O:75:ASP:HA	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:i:92:PRO:CG	51:1:1077:A:H1'	2.44	0.48
52:2:32:U:H2'	52:2:33:G:O4'	2.14	0.48
53:3:1305:G:N2	53:3:1331:G:H2'	2.28	0.48
58:B1:1027:VAL:HB	58:B1:1121:LEU:HB2	1.95	0.48
8:H:152:VAL:HG12	8:H:197:VAL:HG13	1.96	0.48
9:I:96:ARG:HH21	9:I:114:ARG:HH12	1.62	0.48
12:L:96:ASN:N	12:L:96:ASN:OD1	2.46	0.48
17:Q:33:CYS:H	17:Q:54:VAL:HG13	1.78	0.48
29:d:2:GLU:HB3	29:d:11:ALA:HB1	1.96	0.48
39:o:104:GLN:NE2	39:o:108:ASP:OD2	2.47	0.48
42:r:9:GLY:O	51:1:996:A:H1'	2.13	0.48
48:x:5:GLN:O	48:x:73:ARG:NH2	2.45	0.48
51:1:248:G:O5'	51:1:249:C:H5''	2.14	0.48
51:1:1357:C:H2'	51:1:1358:G:O4'	2.14	0.48
51:1:2165:C:H41	51:1:2171:A:H61	1.60	0.48
51:1:2366:A:H2'	51:1:2367:G:O4'	2.13	0.48
53:3:141:G:H2'	53:3:142:G:O4'	2.13	0.48
53:3:591:U:H2'	53:3:592:G:C8	2.48	0.48
58:B1:633:ALA:HB2	59:B2:808:ASN:N	2.19	0.48
59:B2:836:LEU:HD13	59:B2:1054:LEU:HD13	1.95	0.48
64:6:59:A:H2'	64:6:60:U:H5'	1.96	0.48
4:D:12:ARG:HD3	51:1:686:U:O4	2.13	0.48
21:U:14:ARG:NH1	53:3:618:C:H1'	2.21	0.48
28:c:79:LEU:HD12	51:1:2635:A:H4'	1.96	0.48
40:p:61:ARG:HH21	40:p:99:LEU:HB3	1.79	0.48
48:x:57:VAL:HG22	51:1:372:G:H2'	1.96	0.48
51:1:639:U:H2'	51:1:640:C:C6	2.48	0.48
51:1:2637:U:H2'	51:1:2638:G:O4'	2.13	0.48
51:1:2644:G:O2'	51:1:2645:G:H5'	2.13	0.48
53:3:508:U:H1'	53:3:509:A:N7	2.29	0.48
53:3:591:U:H2'	53:3:592:G:H8	1.79	0.48
53:3:681:A:H2'	53:3:682:G:C8	2.48	0.48
53:3:714:G:H2'	53:3:715:A:O4'	2.13	0.48
53:3:1220:G:H2'	53:3:1221:G:O4'	2.13	0.48
55:8:3:DC:H2''	55:8:4:DT:C7	2.42	0.48
66:0:468:ILE:O	66:0:472:ARG:N	2.47	0.48
14:N:91:GLU:HA	14:N:94:ARG:HB2	1.94	0.48
51:1:281:C:H2'	51:1:282:A:C8	2.49	0.48
51:1:572:A:H2'	51:1:572:A:N3	2.29	0.48
51:1:704:G:H1'	51:1:726:G:N2	2.28	0.48
53:3:5:U:H4'	53:3:6:G:C8	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:513:C:H2'	53:3:514:C:C6	2.49	0.48
53:3:631:C:H3'	53:3:632:U:H5'	1.95	0.48
53:3:1005:A:H2'	53:3:1006:G:C5'	2.44	0.48
58:B1:108:ALA:HB1	58:B1:279:LEU:HD22	1.96	0.48
58:B1:809:VAL:HG21	58:B1:909:ILE:HG12	1.95	0.48
12:L:77:ARG:HD3	12:L:86:VAL:HG21	1.94	0.48
18:R:99:GLN:HB3	53:3:949:A:OP1	2.13	0.48
29:d:98:LYS:HG3	51:1:607:U:P	2.53	0.48
51:1:1701:A:C2'	51:1:1702:G:H5'	2.43	0.48
51:1:2860:A:H2'	51:1:2861:U:H5'	1.95	0.48
53:3:994:A:C8	53:3:1216:A:H4'	2.49	0.48
59:B2:565:GLU:HA	59:B2:569:ILE:HG12	1.95	0.48
51:1:174:U:H2'	51:1:175:G:C8	2.49	0.48
51:1:225:C:H2'	51:1:226:A:O4'	2.14	0.48
51:1:327:G:O2'	51:1:328:U:H5'	2.14	0.48
51:1:435:C:H2'	51:1:436:C:H5'	1.95	0.48
51:1:845:A:N3	51:1:845:A:H3'	2.29	0.48
51:1:941:A:H2'	51:1:942:G:O4'	2.14	0.48
51:1:1819:A:H4'	51:1:1820:U:H5'	1.96	0.48
51:1:2504:U:H2'	51:1:2505:G:H5'	1.95	0.48
59:B2:363:LEU:HB3	59:B2:381:ALA:HB1	1.96	0.48
59:B2:1314:GLN:HB2	60:W0:28:ARG:HH12	1.78	0.48
63:5:50:U:H2'	63:5:51:U:C6	2.49	0.48
66:0:553:VAL:HG11	66:0:578:LEU:HD22	1.96	0.48
16:P:121:ARG:NH2	53:3:1524:C:OP1	2.46	0.47
16:P:126:ARG:HH21	53:3:796:C:H4'	1.79	0.47
23:W:20:ILE:HD12	23:W:53:GLN:HB2	1.96	0.47
28:c:13:ARG:NH2	28:c:21:SER:OG	2.47	0.47
33:i:55:PRO:HG2	33:i:71:LYS:HG3	1.96	0.47
36:l:16:GLY:HA2	51:1:662:G:H5''	1.96	0.47
39:o:29:HIS:HB3	39:o:36:TYR:HB2	1.96	0.47
46:v:7:GLU:HA	46:v:65:VAL:HG23	1.96	0.47
51:1:100:U:H4'	51:1:101:A:O4'	2.14	0.47
51:1:1343:G:H1'	51:1:1597:A:C4	2.49	0.47
51:1:2534:A:H2'	51:1:2535:G:O4'	2.14	0.47
51:1:2762:C:H2'	51:1:2763:G:H5'	1.95	0.47
51:1:2818:U:H2'	51:1:2819:G:C8	2.49	0.47
52:2:5:U:H2'	52:2:6:G:H8	1.79	0.47
53:3:392:C:H2'	53:3:393:A:C8	2.49	0.47
58:B1:103:GLY:H	58:B1:244:VAL:HG22	1.79	0.47
66:0:502:GLU:HA	66:0:519:VAL:HA	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:VAL:HG22	30:e:139:GLU:HA	1.96	0.47
9:I:131:ILE:HG21	53:3:620:C:O2	2.14	0.47
16:P:80:ASN:HA	16:P:104:PHE:HB3	1.96	0.47
22:V:56:ASP:N	22:V:56:ASP:OD1	2.47	0.47
24:X:14:LEU:HA	24:X:17:LYS:HD2	1.96	0.47
31:f:44:HIS:HA	31:f:49:LEU:HD23	1.96	0.47
51:1:1018:U:H2'	51:1:1019:U:O4'	2.13	0.47
53:3:1500:A:H5''	53:3:1508:A:H5'	1.94	0.47
58:B1:255:LEU:HD23	58:B1:261:ALA:HB2	1.95	0.47
58:B1:891:ASP:OD2	58:B1:1290:ARG:NH2	2.47	0.47
58:B1:1146:GLU:OE2	58:B1:1310:THR:HG22	2.14	0.47
58:B1:1150:PRO:HG3	58:B1:1214:PRO:HB2	1.96	0.47
59:B2:318:SER:OG	59:B2:320:ASP:OD1	2.31	0.47
9:I:1:ALA:HB2	53:3:499:A:H61	1.79	0.47
20:T:45:HIS:O	20:T:47:LYS:N	2.47	0.47
25:Y:20:ASN:O	25:Y:24:ARG:N	2.46	0.47
27:b:247:TRP:CD2	51:1:1805:A:H5''	2.49	0.47
27:b:255:LYS:NZ	51:1:1844:C:H4'	2.28	0.47
29:d:109:LEU:HD13	29:d:112:LEU:HD12	1.97	0.47
33:i:133:ARG:HB3	51:1:1077:A:O2'	2.14	0.47
51:1:1123:C:H2'	51:1:1124:G:C8	2.49	0.47
51:1:2184:A:H2'	51:1:2185:U:O4'	2.13	0.47
52:2:5:U:H2'	52:2:6:G:C8	2.49	0.47
53:3:939:G:N3	53:3:1375:A:H2	2.12	0.47
53:3:1427:C:O2	53:3:1427:C:H2'	2.12	0.47
53:3:1527:U:O5'	53:3:1527:U:H6	1.97	0.47
58:B1:395:LYS:NZ	58:B1:399:LYS:CE	2.78	0.47
58:B1:1221:LEU:HD22	58:B1:1306:LEU:HB2	1.96	0.47
27:b:233:GLY:HA3	51:1:2598:A:H5''	1.96	0.47
33:i:124:MET:HE3	33:i:124:MET:HB3	1.70	0.47
51:1:157:C:H2'	51:1:158:U:O4'	2.13	0.47
51:1:419:U:H2'	51:1:420:C:C6	2.49	0.47
51:1:2185:U:H2'	51:1:2186:G:C8	2.48	0.47
51:1:2553:G:C3'	51:1:2554:U:H5''	2.41	0.47
51:1:2852:G:H2'	51:1:2853:C:O4'	2.14	0.47
53:3:1211:U:H4'	53:3:1213:A:C4	2.49	0.47
55:8:14:DC:H2'	55:8:15:DC:H6	1.79	0.47
58:B1:115:TRP:O	58:B1:1333:THR:HG21	2.13	0.47
58:B1:190:LYS:HB2	58:B1:190:LYS:HE3	1.41	0.47
58:B1:201:LEU:HD11	58:B1:220:ARG:HG2	1.95	0.47
59:B2:1286:THR:O	59:B2:1290:MET:HB2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:NG:142:ALA:O	62:NG:143:ASP:CB	2.63	0.47
65:a:42:VAL:HB	65:a:175:ILE:HG22	1.96	0.47
14:N:4:GLN:HE22	53:3:1131:G:C5'	2.25	0.47
14:N:113:LYS:NZ	53:3:1367:C:C6	2.83	0.47
19:S:5:MET:SD	19:S:8:ARG:NH1	2.88	0.47
29:d:125:SER:OG	29:d:126:VAL:N	2.48	0.47
38:n:106:ASP:N	38:n:106:ASP:OD1	2.47	0.47
43:s:89:ALA:HB1	51:1:748:G:C8	2.49	0.47
49:y:31:GLN:HE21	49:y:36:GLN:HB2	1.80	0.47
51:1:118:A:H2'	51:1:120:U:O4	2.15	0.47
51:1:609:A:H2'	51:1:610:C:O4'	2.14	0.47
51:1:858:G:H5'	51:1:859:G:OP2	2.14	0.47
51:1:1182:G:H2'	51:1:1183:U:O4'	2.15	0.47
51:1:1533:C:C3'	51:1:1534:U:H5''	2.44	0.47
51:1:1932:A:H2'	51:1:1933:G:O4'	2.15	0.47
53:3:86:G:H4'	53:3:87:C:C6	2.50	0.47
53:3:110:C:H2'	53:3:111:G:O4'	2.13	0.47
66:0:557:ILE:HD13	66:0:576:ILE:HG12	1.96	0.47
9:I:80:ARG:NH1	53:3:613:C:OP2	2.47	0.47
46:v:21:ARG:NH2	52:2:76:G:O3'	2.47	0.47
48:x:22:ASN:HD22	51:1:200:U:H5'	1.79	0.47
51:1:41:C:C3'	51:1:42:A:H5''	2.44	0.47
51:1:282:A:H2'	51:1:283:G:C8	2.50	0.47
51:1:1018:U:H5''	51:1:1036:G:O2'	2.14	0.47
58:B1:29:MET:HG2	59:B2:1336:ASN:ND2	2.29	0.47
58:B1:120:LEU:HD22	58:B1:120:LEU:HA	1.77	0.47
59:B2:1311:GLY:O	60:W0:31:GLN:NE2	2.47	0.47
62:NG:161:SER:CA	62:NG:170:PRO:HA	2.44	0.47
8:H:17:TRP:O	8:H:53:ARG:NH2	2.47	0.47
18:R:102:LYS:HE2	53:3:952:U:O4	2.14	0.47
21:U:68:SER:OG	21:U:69:ASP:OD1	2.33	0.47
21:U:69:ASP:OD1	21:U:69:ASP:N	2.48	0.47
27:b:149:LYS:HG2	27:b:152:GLN:HE22	1.80	0.47
30:e:26:GLN:NE2	52:2:57:A:H4'	2.29	0.47
32:g:99:ILE:O	32:g:103:VAL:N	2.40	0.47
46:v:64:VAL:HA	46:v:69:GLU:HA	1.96	0.47
47:w:70:PRO:HB3	52:2:12:C:C5	2.50	0.47
51:1:395:U:H2'	51:1:396:G:C8	2.50	0.47
51:1:528:A:C2	51:1:2043:C:H4'	2.50	0.47
51:1:903:C:H2'	51:1:904:G:C8	2.49	0.47
51:1:1409:U:H2'	51:1:1410:G:C8	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1680:U:H2'	51:1:1681:G:O4'	2.15	0.47
51:1:1927:A:H2'	51:1:1928:A:C8	2.49	0.47
51:1:2146:C:H5''	51:1:2147:A:N7	2.30	0.47
51:1:2798:U:H4'	51:1:2799:A:C4	2.50	0.47
53:3:24:U:H2'	53:3:25:C:C6	2.50	0.47
53:3:110:C:H2'	53:3:111:G:C8	2.50	0.47
53:3:505:G:OP2	53:3:535:A:H5'	2.13	0.47
53:3:599:C:H2'	53:3:600:A:H8	1.80	0.47
53:3:946:A:H2'	53:3:947:G:C8	2.49	0.47
57:A2:102:LEU:HD12	57:A2:115:ILE:HG12	1.96	0.47
58:B1:198:CYS:HA	58:B1:221:ILE:CD1	2.45	0.47
58:B1:1036:ARG:HE	58:B1:1081:VAL:HG11	1.79	0.47
58:B1:1060:VAL:HG13	58:B1:1106:ILE:HG12	1.96	0.47
58:B1:1347:LEU:HG	58:B1:1357:ILE:HG23	1.96	0.47
58:B1:1361:THR:OG1	59:B2:1282:GLY:O	2.28	0.47
59:B2:689:ALA:HB2	59:B2:1233:LEU:HD23	1.97	0.47
63:5:26:A:N6	63:5:44:G:H1	2.13	0.47
66:0:176:GLU:O	66:0:179:PHE:N	2.47	0.47
10:J:18:ASN:OD1	10:J:33:THR:OG1	2.33	0.47
12:L:21:LEU:HD11	12:L:96:ASN:HD22	1.78	0.47
38:n:58:ASP:OD1	38:n:63:ARG:NH2	2.48	0.47
51:1:368:A:C2'	51:1:369:U:H5'	2.45	0.47
51:1:1409:U:H2'	51:1:1410:G:H8	1.80	0.47
51:1:1960:A:C2'	51:1:1961:C:H5''	2.44	0.47
51:1:2638:G:H1'	51:1:2778:A:N6	2.26	0.47
58:B1:526:VAL:HG12	58:B1:549:LYS:HB2	1.96	0.47
58:B1:1357:ILE:HD13	59:B2:1279:GLU:HG2	1.97	0.47
65:a:200:LYS:HD3	65:a:201:PRO:HD2	1.97	0.47
24:X:32:THR:HG1	24:X:34:SER:HG	1.62	0.47
35:k:66:LYS:HD2	51:1:1665:A:H5''	1.95	0.47
36:l:89:VAL:HA	36:l:121:THR:HB	1.97	0.47
39:o:67:ASN:HA	52:2:50:A:OP2	2.15	0.47
39:o:94:ARG:NH2	51:1:2293:G:H5''	2.30	0.47
42:r:78:ARG:NH1	51:1:990:A:H61	2.13	0.47
51:1:1387:A:H5'	51:1:1469:A:H1'	1.96	0.47
53:3:66:A:H5''	53:3:199:A:O2'	2.15	0.47
53:3:935:A:H2'	53:3:936:C:C6	2.50	0.47
53:3:987:G:H2'	53:3:988:G:H8	1.80	0.47
53:3:1223:C:H5	53:3:1224:U:H5	1.63	0.47
58:B1:128:LEU:HD21	58:B1:188:LEU:HB3	1.97	0.47
58:B1:968:ASN:HA	58:B1:1117:SER:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:1261:LEU:HD12	58:B1:1304:ARG:HH21	1.78	0.47
59:B2:400:VAL:HG22	59:B2:584:TYR:HB3	1.96	0.47
66:0:592:ALA:O	66:0:596:ALA:N	2.46	0.47
9:I:82:LYS:HE2	53:3:3:A:OP1	2.16	0.47
28:c:133:THR:HG22	28:c:134:HIS:H	1.80	0.47
41:q:105:PHE:HA	41:q:108:LEU:HD12	1.96	0.47
51:1:76:C:H2'	51:1:77:G:H8	1.80	0.47
51:1:552:U:H2'	51:1:553:G:H8	1.80	0.47
51:1:855:G:H3'	51:1:856:G:H5''	1.98	0.47
51:1:1175:A:H5'	51:1:1176:U:O4'	2.15	0.47
53:3:680:C:H2'	53:3:681:A:H8	1.80	0.47
57:A1:35:PHE:HA	57:A1:38:THR:HG22	1.97	0.47
58:B1:343:LEU:HD11	58:B1:1324:SER:HB3	1.97	0.47
58:B1:1219:ASP:O	58:B1:1223:LEU:HB2	2.15	0.47
59:B2:103:VAL:HG12	59:B2:117:ILE:HG22	1.97	0.47
59:B2:207:THR:OG1	59:B2:354:ASP:OD2	2.32	0.47
65:a:189:LEU:O	65:a:193:LEU:N	2.44	0.47
9:I:4:LEU:HD11	53:3:405:U:C6	2.50	0.46
15:O:42:LEU:HB3	15:O:71:LEU:HB2	1.96	0.46
29:d:155:GLU:HA	29:d:158:PHE:HB3	1.97	0.46
30:e:140:ILE:HG22	30:e:142:TYR:H	1.80	0.46
31:f:21:GLN:OE1	31:f:54:ARG:NH2	2.39	0.46
42:r:7:SER:OG	42:r:8:GLY:N	2.49	0.46
51:1:1906:G:C2'	51:1:1907:G:H5''	2.44	0.46
53:3:211:G:C2'	53:3:212:G:H5'	2.45	0.46
53:3:536:C:H2'	53:3:537:G:C8	2.49	0.46
58:B1:375:GLU:HB3	59:B2:1245:ALA:HB3	1.97	0.46
58:B1:833:GLU:N	58:B1:1242:ARG:HH12	2.12	0.46
63:5:8:U:H2'	63:5:13:C:N4	2.30	0.46
24:X:9:PHE:CE1	53:3:1318:A:H5'	2.50	0.46
39:o:13:ARG:HH21	39:o:17:LYS:HB2	1.80	0.46
50:z:17:PRO:HG3	51:1:969:G:OP1	2.14	0.46
51:1:311:A:H3'	51:1:312:G:C8	2.49	0.46
51:1:940:G:C3'	51:1:941:A:H5''	2.45	0.46
51:1:1017:G:H2'	51:1:1018:U:C6	2.50	0.46
51:1:1179:G:C4	51:1:1180:U:H1'	2.50	0.46
51:1:1300:G:H4'	51:1:1301:A:H5''	1.97	0.46
52:2:96:G:O2'	52:2:97:C:H5'	2.15	0.46
53:3:202:G:H2'	53:3:203:G:C8	2.50	0.46
53:3:479:U:H2'	53:3:480:U:H5'	1.96	0.46
53:3:1060:U:H2'	53:3:1061:G:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:772:TYR:HE2	59:B2:561:ILE:HG21	1.81	0.46
59:B2:28:LEU:HD21	59:B2:524:ILE:HG13	1.98	0.46
12:L:71:THR:O	12:L:90:VAL:HG22	2.16	0.46
14:N:4:GLN:HE22	53:3:1131:G:C4'	2.28	0.46
17:Q:68:GLY:O	53:3:521:G:H5'	2.15	0.46
17:Q:109:ARG:HG3	53:3:538:G:OP1	2.15	0.46
21:U:68:SER:OG	21:U:69:ASP:N	2.47	0.46
51:1:610:C:H2'	51:1:611:C:H6	1.80	0.46
51:1:1023:U:H2'	51:1:1024:G:H5'	1.97	0.46
51:1:2467:C:H2'	51:1:2468:A:O4'	2.15	0.46
53:3:390:U:H2'	53:3:391:G:C8	2.50	0.46
53:3:629:A:H2'	53:3:630:A:O4'	2.15	0.46
53:3:1210:C:OP1	66:0:584:HIS:CG	2.68	0.46
53:3:1329:A:O2'	53:3:1330:U:H5'	2.16	0.46
53:3:1369:C:H2'	53:3:1370:G:C8	2.49	0.46
58:B1:385:LEU:HD23	58:B1:390:LEU:HB2	1.98	0.46
59:B2:230:PHE:HB2	59:B2:333:ILE:HB	1.97	0.46
59:B2:735:LYS:HA	59:B2:748:ILE:HG22	1.97	0.46
65:a:69:THR:HA	65:a:176:GLY:HA2	1.97	0.46
66:0:624:PRO:HA	66:0:651:GLY:HA2	1.97	0.46
9:I:61:ARG:HH12	9:I:68:GLU:N	2.13	0.46
12:L:26:VAL:HG22	12:L:42:VAL:HG21	1.98	0.46
19:S:51:PRO:O	19:S:54:SER:OG	2.31	0.46
25:Y:9:ARG:NH1	53:3:107:G:O6	2.49	0.46
25:Y:73:ARG:NE	53:3:261:U:H5	2.12	0.46
27:b:46:GLY:HA3	51:1:773:U:H4'	1.97	0.46
27:b:140:VAL:HG23	27:b:161:VAL:HG13	1.96	0.46
33:i:129:GLU:HB2	33:i:139:VAL:HG21	1.98	0.46
39:o:30:ARG:HH21	39:o:97:PHE:HB3	1.80	0.46
51:1:562:U:O4'	51:1:2036:C:H5'	2.16	0.46
51:1:1557:C:H3'	51:1:1558:C:C5'	2.31	0.46
51:1:1717:A:H2'	51:1:1718:G:O4'	2.15	0.46
51:1:2126:A:C2'	51:1:2162:G:H21	2.29	0.46
53:3:82:G:C2'	53:3:83:C:H5'	2.45	0.46
53:3:1497:G:C2'	53:3:1498:U:H5'	2.46	0.46
58:B1:43:THR:HG22	58:B1:57:PHE:HE1	1.80	0.46
58:B1:111:THR:HG23	58:B1:300:GLN:NE2	2.24	0.46
58:B1:420:PRO:HA	58:B1:437:PHE:O	2.15	0.46
59:B2:800:MET:HB2	59:B2:800:MET:HE3	1.69	0.46
65:a:186:LYS:HA	65:a:189:LEU:HG	1.97	0.46
13:M:9:MET:HB2	13:M:32:LYS:HE2	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:70:GLY:O	14:N:74:GLN:N	2.41	0.46
14:N:128:LYS:HE3	64:6:34:C:OP2	2.16	0.46
27:b:48:ILE:HG22	51:1:779:U:P	2.55	0.46
27:b:200:MET:HE2	51:1:1820:U:C2	2.50	0.46
29:d:168:ASP:OD1	29:d:168:ASP:N	2.47	0.46
30:e:146:ASP:OD1	30:e:146:ASP:N	2.48	0.46
37:m:31:PHE:HB3	37:m:130:PHE:HE1	1.80	0.46
51:1:479:A:H4'	51:1:480:A:H5'	1.98	0.46
51:1:610:C:H2'	51:1:611:C:C6	2.50	0.46
51:1:1335:C:H2'	51:1:1336:A:H8	1.80	0.46
51:1:1709:U:H2'	51:1:1710:G:C8	2.50	0.46
51:1:1872:A:H2'	51:1:1873:G:O4'	2.15	0.46
51:1:2126:A:H5'	51:1:2127:G:O5'	2.16	0.46
51:1:2653:U:C3'	51:1:2654:A:H5''	2.38	0.46
51:1:2849:U:H4'	51:1:2868:A:C2	2.50	0.46
53:3:31:G:N2	53:3:47:C:H5''	2.31	0.46
53:3:177:G:O2'	53:3:1448:C:H4'	2.14	0.46
53:3:864:A:H2'	53:3:865:A:C8	2.50	0.46
58:B1:105:ILE:HD12	58:B1:242:LEU:CD2	2.44	0.46
58:B1:352:ARG:HB2	59:B2:1268:GLN:NE2	2.30	0.46
58:B1:847:ASP:N	58:B1:847:ASP:OD1	2.49	0.46
63:5:8:U:H2'	63:5:13:C:H41	1.80	0.46
1:A:53:THR:OG1	1:A:54:GLY:N	2.49	0.46
14:N:108:ARG:O	53:3:1347:G:H8	1.99	0.46
16:P:17:ASP:N	16:P:17:ASP:OD1	2.49	0.46
51:1:2644:G:C2'	51:1:2645:G:H5'	2.46	0.46
53:3:194:C:O2'	53:3:195:A:H5'	2.15	0.46
53:3:408:A:H2'	53:3:409:U:O4'	2.16	0.46
53:3:490:C:H2'	53:3:491:G:C8	2.50	0.46
53:3:1382:C:O2	53:3:1382:C:O4'	2.33	0.46
54:4:5:U:H2'	54:4:6:U:C6	2.50	0.46
58:B1:1167:LYS:NZ	58:B1:1170:LYS:HB2	2.30	0.46
66:0:20:ASP:HA	69:0:801:GDP:H5'	1.96	0.46
8:H:176:THR:HG22	8:H:179:ALA:H	1.81	0.46
21:U:5:ARG:HD2	53:3:376:G:H4'	1.97	0.46
32:g:103:VAL:O	32:g:107:GLY:N	2.49	0.46
41:q:92:LYS:NZ	51:1:995:C:O2'	2.44	0.46
51:1:1344:U:H3'	51:1:1345:C:H5'	1.96	0.46
51:1:1433:A:H2'	51:1:1434:A:O4'	2.16	0.46
51:1:1842:G:H2'	51:1:1843:C:O4'	2.16	0.46
53:3:51:A:H4'	53:3:52:C:H5''	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:A1:33:ARG:HE	57:A1:33:ARG:HB3	1.56	0.46
66:O:255:ARG:HD3	66:O:261:ILE:HB	1.97	0.46
12:L:87:PRO:HG3	12:L:148:LYS:HA	1.98	0.46
12:L:111:GLY:HA2	12:L:118:ARG:HD3	1.97	0.46
16:P:123:PRO:O	26:Z:34:ARG:N	2.40	0.46
17:Q:14:LYS:HE3	53:3:884:U:O2'	2.15	0.46
27:b:54:GLY:HA3	27:b:216:ARG:HG3	1.98	0.46
33:i:11:GLN:HG2	33:i:23:VAL:HG11	1.98	0.46
42:r:81:LYS:HD3	51:1:973:A:H5''	1.98	0.46
51:1:337:C:H2'	51:1:338:G:O4'	2.15	0.46
51:1:341:C:H2'	51:1:342:A:H8	1.80	0.46
51:1:621:A:H2'	51:1:622:G:O4'	2.15	0.46
51:1:1000:A:H2'	51:1:1001:A:C8	2.51	0.46
51:1:2670:A:H2'	51:1:2671:G:H8	1.81	0.46
51:1:2773:C:H2'	51:1:2774:C:C6	2.51	0.46
51:1:2898:U:H2'	51:1:2899:A:C8	2.51	0.46
53:3:70:U:H4'	53:3:71:A:C8	2.51	0.46
53:3:91:U:C2'	53:3:92:U:H5''	2.45	0.46
57:A1:29:GLU:HB3	57:A1:200:LYS:HG3	1.98	0.46
57:A2:294:ASN:HA	61:NA:464:ILE:N	2.28	0.46
62:NG:135:ARG:O	62:NG:178:VAL:HA	2.16	0.46
66:O:33:TYR:HE2	66:O:275:VAL:HB	1.81	0.46
1:A:63:ARG:HD2	53:3:1012:A:OP2	2.16	0.46
9:I:72:ARG:HG2	9:I:76:LYS:HE3	1.97	0.46
24:X:79:TYR:CZ	53:3:1226:C:H4'	2.51	0.46
27:b:200:MET:HE2	51:1:1820:U:N3	2.31	0.46
41:q:74:SER:OG	41:q:75:TYR:N	2.49	0.46
42:r:85:LYS:HA	51:1:814:C:OP1	2.16	0.46
47:w:38:GLY:CA	51:1:2330:G:H21	2.26	0.46
51:1:209:C:H4'	51:1:681:G:H4'	1.97	0.46
51:1:1015:U:H2'	51:1:1016:G:C8	2.51	0.46
51:1:1638:C:H5''	51:1:2710:C:O2'	2.16	0.46
51:1:2066:C:O2'	51:1:2067:G:H5'	2.16	0.46
51:1:2176:A:H5'	65:a:219:GLY:O	2.16	0.46
53:3:652:U:H2'	53:3:653:U:H5''	1.98	0.46
53:3:1414:U:H2'	53:3:1415:G:H8	1.81	0.46
60:W0:25:ARG:NH1	60:W0:61:ASN:OD1	2.49	0.46
63:5:70:G:H2'	63:5:71:G:C8	2.51	0.46
66:O:536:PHE:HD1	66:O:576:ILE:HG23	1.81	0.46
8:H:23:ALA:HB1	8:H:27:GLU:HG2	1.97	0.46
14:N:86:LEU:HD13	14:N:93:LEU:HD22	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:97:ARG:HG3	53:3:1308:U:OP2	2.16	0.46
34:j:80:HIS:CD2	51:1:2642:G:H5'	2.51	0.46
46:v:30:ILE:HG12	46:v:91:PHE:HB2	1.96	0.46
51:1:416:U:H3	51:1:2407:A:H61	1.63	0.46
51:1:878:A:H3'	51:1:879:G:C8	2.50	0.46
52:2:43:C:H2'	52:2:44:G:H5''	1.97	0.46
52:2:49:C:H2'	52:2:50:A:C8	2.49	0.46
53:3:312:C:H2'	53:3:313:A:C8	2.51	0.46
53:3:1268:G:H21	53:3:1327:C:H1'	1.80	0.46
55:8:20:DA:H4'	59:B2:143:ARG:NH1	2.31	0.46
57:A1:59:VAL:HG22	57:A1:144:ILE:HA	1.97	0.46
58:B1:109:SER:HB2	58:B1:296:LYS:HG2	1.98	0.46
66:0:515:TYR:HB3	66:0:584:HIS:CB	2.44	0.46
66:0:523:TYR:HD2	66:0:577:ARG:HH12	1.63	0.46
66:0:667:ALA:HB2	66:0:680:TYR:HE1	1.80	0.46
5:E:3:ILE:HD11	51:1:592:A:C2	2.51	0.45
24:X:36:ARG:HB3	53:3:1320:C:N4	2.30	0.45
27:b:141:HIS:ND1	27:b:192:GLY:O	2.37	0.45
38:n:64:ARG:HH11	51:1:2705:A:H2	1.62	0.45
44:t:2:ILE:HG13	44:t:5:GLU:HB3	1.98	0.45
51:1:863:A:H4'	52:2:100:G:N2	2.31	0.45
51:1:894:U:H2'	51:1:895:U:O4'	2.16	0.45
51:1:1758:U:C5	51:1:2696:U:H5'	2.51	0.45
51:1:1822:C:H2'	51:1:1823:G:H8	1.81	0.45
51:1:2211:A:H5'	51:1:2212:A:OP2	2.16	0.45
51:1:2573:C:H5''	51:1:2574:G:H5''	1.98	0.45
51:1:2649:C:H2'	51:1:2650:U:C6	2.51	0.45
51:1:2804:U:H2'	51:1:2805:C:C6	2.51	0.45
51:1:2811:G:H2'	51:1:2812:G:C8	2.51	0.45
52:2:66:A:N1	52:2:107:G:H2'	2.31	0.45
53:3:555:U:H2'	53:3:556:C:C6	2.52	0.45
53:3:1275:A:N1	53:3:1283:U:H5'	2.31	0.45
58:B1:209:ASN:HA	58:B1:214:ARG:NH2	2.30	0.45
58:B1:211:GLU:CG	58:B1:215:LYS:HE3	2.44	0.45
27:b:17:LYS:HE3	27:b:17:LYS:HB2	1.83	0.45
33:i:5:GLN:H	33:i:5:GLN:HG3	1.53	0.45
51:1:676:A:H62	51:1:802:A:H61	1.63	0.45
51:1:979:A:H2'	51:1:982:C:H42	1.81	0.45
51:1:1020:A:C1'	51:1:1021:A:OP2	2.60	0.45
51:1:1424:G:H2'	51:1:1425:G:O4'	2.17	0.45
51:1:2468:A:O2'	51:1:2469:A:H5'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2800:A:H3'	51:1:2801:G:C5'	2.45	0.45
53:3:253:A:H2'	53:3:254:G:H8	1.81	0.45
53:3:448:A:H3'	53:3:449:G:C8	2.51	0.45
53:3:1107:C:O2'	53:3:1191:A:H4'	2.16	0.45
53:3:1137:C:H5'	53:3:1138:G:H5'	1.97	0.45
53:3:1146:A:H2'	53:3:1147:C:H5'	1.97	0.45
53:3:1342:C:H2'	53:3:1343:G:C8	2.51	0.45
57:A2:64:VAL:HG11	57:A2:78:ILE:HG21	1.97	0.45
57:A2:80:GLU:HG3	59:B2:694:ARG:HH22	1.81	0.45
58:B1:202:ARG:HH11	58:B1:202:ARG:CG	2.14	0.45
58:B1:213:LYS:HA	58:B1:213:LYS:HE3	1.99	0.45
58:B1:842:ARG:HH22	58:B1:1250:ASP:HB2	1.80	0.45
59:B2:517:GLN:HB3	59:B2:760:ASN:H	1.79	0.45
66:0:131:ASN:OD1	66:0:137:ARG:NH2	2.50	0.45
9:I:173:ASP:HB3	9:I:178:GLU:H	1.82	0.45
15:O:6:ILE:HD12	15:O:102:LEU:HG	1.97	0.45
19:S:92:ILE:HD13	19:S:95:LEU:HD12	1.97	0.45
24:X:5:LYS:HG2	53:3:1313:U:P	2.56	0.45
25:Y:28:ARG:HD3	53:3:1438:G:OP1	2.16	0.45
25:Y:73:ARG:CZ	53:3:261:U:C5	2.98	0.45
30:e:12:VAL:HG13	30:e:27:VAL:HG11	1.98	0.45
39:o:24:THR:HB	39:o:42:PRO:HG3	1.97	0.45
39:o:27:VAL:HG12	39:o:93:ASP:HB3	1.98	0.45
43:s:33:LEU:O	43:s:37:THR:OG1	2.33	0.45
51:1:195:A:H3'	51:1:196:A:H4'	1.99	0.45
51:1:687:C:H2'	51:1:688:U:O4'	2.16	0.45
51:1:700:G:O2'	51:1:701:G:H5'	2.17	0.45
51:1:933:A:H5''	51:1:934:U:H5	1.81	0.45
51:1:999:U:O2'	51:1:1000:A:H5'	2.16	0.45
51:1:1112:G:O2'	51:1:1113:U:H5'	2.15	0.45
51:1:2146:C:H5''	51:1:2147:A:C8	2.51	0.45
51:1:2174:C:O2'	65:a:218:MET:HG2	2.17	0.45
51:1:2189:U:H2'	51:1:2190:G:C8	2.51	0.45
51:1:2385:C:H2'	51:1:2386:A:C8	2.51	0.45
53:3:405:U:C3'	53:3:406:G:H5'	2.40	0.45
53:3:1149:C:O2'	53:3:1150:A:H5'	2.17	0.45
58:B1:375:GLU:O	59:B2:1247:SER:HB3	2.16	0.45
58:B1:800:LEU:HD12	58:B1:800:LEU:HA	1.79	0.45
59:B2:1314:GLN:HA	60:W0:28:ARG:HH22	1.80	0.45
3:C:35:LEU:HD11	51:1:2286:G:N1	2.32	0.45
18:R:26:LYS:O	18:R:30:LYS:NZ	2.44	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:100:ARG:HH21	18:R:102:LYS:HD3	1.81	0.45
25:Y:2:ASN:N	53:3:332:G:OP2	2.50	0.45
50:z:40:THR:HG23	50:z:42:ALA:H	1.80	0.45
51:1:863:A:H2'	51:1:864:G:C8	2.51	0.45
51:1:1011:G:H1'	51:1:1013:C:O4'	2.16	0.45
51:1:2190:G:O2'	51:1:2191:A:H5'	2.16	0.45
51:1:2472:G:O6	51:1:2476:A:H4'	2.16	0.45
53:3:401:C:H2'	53:3:402:G:H8	1.81	0.45
66:0:305:THR:O	66:0:305:THR:OG1	2.34	0.45
11:K:49:TYR:HB3	23:W:73:HIS:CG	2.52	0.45
26:Z:66:ARG:HD2	53:3:1099:G:H4'	1.99	0.45
37:m:2:LEU:HD23	37:m:2:LEU:HA	1.85	0.45
51:1:677:A:O2'	51:1:2071:A:H5'	2.17	0.45
51:1:748:G:H2'	51:1:750:A:OP2	2.17	0.45
51:1:2843:G:O2'	51:1:2844:G:H5'	2.17	0.45
53:3:974:A:H5'	53:3:976:G:OP1	2.17	0.45
53:3:990:C:H2'	53:3:991:U:O4'	2.16	0.45
53:3:1005:A:C2'	53:3:1006:G:H5'	2.46	0.45
53:3:1202:U:H2'	53:3:1203:C:O4'	2.16	0.45
55:8:1:DC:H2''	55:8:2:DC:C6	2.51	0.45
55:8:13:DT:C6	58:B1:791:ALA:HA	2.51	0.45
58:B1:75:TYR:CD2	58:B1:75:TYR:O	2.70	0.45
58:B1:484:MET:CE	59:B2:1278:LEU:HD21	2.47	0.45
58:B1:926:PRO:HB2	58:B1:1241:TYR:HE1	1.82	0.45
63:5:6:G:H2'	63:5:7:A:C8	2.51	0.45
66:0:11:ARG:NH1	66:0:288:SER:OG	2.50	0.45
11:K:38:ARG:HB2	11:K:63:ASN:HB2	1.98	0.45
12:L:67:ASN:O	12:L:137:ARG:NH1	2.49	0.45
24:X:53:GLY:HA3	53:3:958:A:H61	1.81	0.45
38:n:21:PHE:HB3	38:n:47:VAL:HG21	1.99	0.45
40:p:27:VAL:HG13	40:p:42:PHE:HB3	1.98	0.45
50:z:27:GLY:HA3	50:z:37:ARG:HH21	1.81	0.45
51:1:2215:C:H2'	51:1:2216:G:H8	1.81	0.45
53:3:350:G:H2'	53:3:351:G:C8	2.52	0.45
53:3:423:G:H3'	53:3:423:G:N3	2.32	0.45
53:3:485:U:H5'	53:3:486:U:OP2	2.16	0.45
53:3:1005:A:H2'	53:3:1006:G:O4'	2.16	0.45
53:3:1306:A:C2	53:3:1332:A:H1'	2.51	0.45
57:A1:231:PHE:O	57:A2:218:ARG:NH1	2.49	0.45
58:B1:770:LEU:HD13	59:B2:618:GLN:CD	2.42	0.45
59:B2:893:THR:HB	59:B2:914:LYS:HA	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:107:GLY:CA	53:3:8:A:H1'	2.46	0.45
27:b:237:ARG:NH1	51:1:2590:A:O3'	2.49	0.45
38:n:39:PRO:HG3	51:1:1651:G:C5'	2.46	0.45
40:p:22:GLY:H	40:p:46:VAL:HG23	1.81	0.45
51:1:2332:C:H2'	51:1:2335:A:N3	2.31	0.45
52:2:97:C:H2'	52:2:98:G:C5'	2.46	0.45
53:3:315:A:H5''	53:3:317:U:OP2	2.17	0.45
53:3:820:U:H3'	53:3:821:G:C5'	2.47	0.45
58:B1:67:ASP:OD1	58:B1:67:ASP:O	2.35	0.45
58:B1:141:PHE:CE2	58:B1:296:LYS:CB	2.94	0.45
66:0:15:ILE:HG13	66:0:110:VAL:HB	1.99	0.45
5:E:34:LYS:HD2	51:1:2391:G:OP2	2.17	0.45
12:L:9:ARG:NH2	53:3:1346:A:C8	2.85	0.45
33:i:120:ASP:O	33:i:123:ALA:N	2.49	0.45
51:1:90:U:H2'	51:1:91:A:C8	2.51	0.45
51:1:503:A:H5''	51:1:505:A:OP1	2.17	0.45
51:1:634:C:H2'	51:1:635:C:C6	2.52	0.45
51:1:1528:A:H2'	51:1:1529:G:O4'	2.17	0.45
51:1:1725:U:H2'	51:1:1726:C:C6	2.51	0.45
51:1:1934:C:H4'	51:1:1974:C:O3'	2.17	0.45
57:A1:185:TYR:HA	57:A1:202:VAL:O	2.16	0.45
58:B1:33:TRP:HZ2	59:B2:1336:ASN:OD1	2.00	0.45
58:B1:213:LYS:HE3	58:B1:213:LYS:CA	2.47	0.45
58:B1:395:LYS:NZ	58:B1:399:LYS:HE2	2.32	0.45
63:5:33:U:H6	63:5:36:A:H8	1.65	0.45
63:5:69:G:H2'	63:5:70:G:C8	2.52	0.45
27:b:204:LEU:HD21	27:b:213:ARG:HH21	1.82	0.45
38:n:42:LYS:HG2	38:n:45:ARG:HH21	1.82	0.45
42:r:85:LYS:HE3	51:1:815:C:P	2.57	0.45
51:1:207:A:H2'	51:1:208:C:O4'	2.16	0.45
51:1:275:C:H2'	51:1:276:U:H4'	1.98	0.45
51:1:300:A:C5	51:1:334:C:H4'	2.52	0.45
51:1:519:U:H2'	51:1:520:G:H8	1.82	0.45
51:1:1045:C:C5'	51:1:1046:A:C8	2.94	0.45
51:1:1558:C:H6	51:1:1558:C:OP1	1.98	0.45
51:1:1697:G:H3'	51:1:1698:A:C5'	2.36	0.45
53:3:451:A:N6	53:3:480:U:H2'	2.32	0.45
53:3:556:C:H2'	53:3:557:G:O4'	2.17	0.45
53:3:819:A:H5'	53:3:820:U:H5	1.82	0.45
53:3:1261:A:H5''	53:3:1262:C:H5	1.82	0.45
59:B2:557:ARG:NH2	59:B2:607:SER:O	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:0:149:ALA:N	66:0:176:GLU:OE1	2.43	0.45
66:0:169:LEU:HG	66:0:263:LEU:HB3	1.99	0.45
6:F:29:ALA:O	31:f:169:ARG:NH1	2.44	0.45
28:c:103:ASP:OD1	28:c:103:ASP:N	2.49	0.45
30:e:70:ARG:HH12	30:e:71:LYS:HE3	1.82	0.45
31:f:120:ILE:HG22	31:f:134:GLY:HA3	1.99	0.45
51:1:322:A:H5'	51:1:340:A:C1'	2.46	0.45
51:1:1637:A:H4'	51:1:2711:A:O2'	2.16	0.45
51:1:2123:G:H2'	51:1:2124:G:C8	2.52	0.45
51:1:2177:C:H1'	65:a:172:HIS:NE2	2.32	0.45
51:1:2554:U:H2'	51:1:2555:U:C6	2.52	0.45
51:1:2646:C:H2'	51:1:2647:U:O4'	2.17	0.45
53:3:303:A:H2'	53:3:304:U:O4'	2.17	0.45
53:3:1449:C:O2'	53:3:1450:U:H5'	2.16	0.45
58:B1:506:VAL:HG23	58:B1:628:GLY:HA3	1.99	0.45
6:F:4:ARG:NH1	6:F:35:GLN:OE1	2.50	0.44
12:L:115:MET:HA	12:L:118:ARG:HB2	1.98	0.44
14:N:64:ILE:HG21	14:N:78:ILE:HG12	1.98	0.44
33:i:34:ILE:O	33:i:38:CYS:N	2.49	0.44
41:q:32:ARG:HB2	51:1:581:C:OP1	2.16	0.44
51:1:828:U:H2'	51:1:829:A:C8	2.51	0.44
51:1:942:G:H2'	51:1:943:A:O4'	2.16	0.44
51:1:2093:G:N7	51:1:2225:A:H2'	2.31	0.44
53:3:596:A:H5'	53:3:596:A:H8	1.82	0.44
53:3:1042:A:H2'	53:3:1043:G:H1'	1.99	0.44
53:3:1289:A:H2'	53:3:1290:G:H5'	1.99	0.44
58:B1:115:TRP:HB3	58:B1:1333:THR:CG2	2.46	0.44
59:B2:998:LEU:HG	59:B2:1011:LEU:HB3	1.99	0.44
59:B2:1246:ARG:HH11	59:B2:1266:GLY:HA2	1.82	0.44
66:0:514:GLN:HA	66:0:587:ASP:HB3	1.99	0.44
66:0:602:LYS:HD3	66:0:602:LYS:HA	1.82	0.44
9:I:24:VAL:H	53:3:409:U:H5''	1.82	0.44
9:I:141:VAL:HG23	9:I:180:THR:HG22	1.99	0.44
29:d:111:GLU:OE1	29:d:114:ARG:NH2	2.50	0.44
41:q:2:ARG:HH11	51:1:449:A:H4'	1.81	0.44
44:t:11:LEU:O	49:y:29:ARG:NH2	2.50	0.44
51:1:20:C:H2'	51:1:21:A:H8	1.81	0.44
51:1:311:A:H3'	51:1:312:G:H8	1.82	0.44
51:1:864:G:O2'	51:1:865:C:H5'	2.17	0.44
51:1:2157:G:H5''	51:1:2158:A:OP1	2.17	0.44
51:1:2206:C:H2'	51:1:2207:C:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:29:U:H5'	53:3:296:U:OP1	2.17	0.44
53:3:169:C:H2'	53:3:170:U:C5	2.52	0.44
53:3:513:C:H2'	53:3:514:C:H6	1.82	0.44
53:3:884:U:H4'	53:3:885:G:C5'	2.43	0.44
53:3:1222:G:O2'	53:3:1223:C:H5'	2.17	0.44
53:3:1268:G:H21	53:3:1327:C:C1'	2.29	0.44
55:8:16:DT:H2'	55:8:17:DC:C6	2.52	0.44
56:9:12:DC:H3'	58:B1:47:ARG:HH12	1.82	0.44
58:B1:76:LYS:NZ	58:B1:76:LYS:HB3	2.32	0.44
58:B1:141:PHE:HE2	58:B1:296:LYS:CB	2.23	0.44
58:B1:175:GLU:H	58:B1:175:GLU:HG3	1.66	0.44
58:B1:1158:GLU:HA	58:B1:1223:LEU:HD21	1.99	0.44
59:B2:1002:LEU:HD21	59:B2:1007:LYS:HB2	1.98	0.44
63:5:13:C:H42	63:5:46:G:N2	2.15	0.44
66:0:498:VAL:HG11	66:0:522:MET:H	1.82	0.44
15:O:64:GLN:NE2	53:3:1368:A:OP1	2.51	0.44
16:P:117:HIS:CD2	53:3:675:A:H1'	2.53	0.44
20:T:49:HIS:CD2	53:3:764:C:H5''	2.52	0.44
27:b:46:GLY:HA3	51:1:773:U:H5'	2.00	0.44
28:c:109:VAL:HG11	28:c:193:VAL:HB	1.99	0.44
51:1:133:U:H2'	51:1:134:G:C8	2.52	0.44
51:1:1102:C:H2'	51:1:1103:A:O4'	2.17	0.44
51:1:1822:C:H2'	51:1:1823:G:C8	2.53	0.44
51:1:2457:U:O2'	51:1:2458:G:H5'	2.18	0.44
51:1:2654:A:H8	51:1:2654:A:OP1	2.01	0.44
51:1:2670:A:H2'	51:1:2671:G:C8	2.53	0.44
53:3:495:A:H4'	53:3:496:A:H5'	1.99	0.44
53:3:1209:C:H2'	53:3:1210:C:C6	2.52	0.44
58:B1:388:ARG:HG2	58:B1:388:ARG:NH1	2.32	0.44
58:B1:472:LEU:CD1	59:B2:1294:LYS:HG2	2.47	0.44
58:B1:978:ARG:HD3	58:B1:999:TYR:H	1.82	0.44
58:B1:1227:HIS:HA	58:B1:1230:THR:HG22	1.99	0.44
58:B1:1357:ILE:HG22	58:B1:1359:ALA:H	1.83	0.44
59:B2:176:ILE:HD11	59:B2:428:VAL:HG21	1.98	0.44
63:5:49:C:H2'	63:5:50:U:C6	2.52	0.44
1:A:46:GLY:HA2	1:A:49:ARG:HG2	1.98	0.44
28:c:32:ASN:O	28:c:96:ILE:N	2.50	0.44
28:c:109:VAL:HG13	28:c:201:LEU:HD13	2.00	0.44
35:k:97:THR:OG1	35:k:98:ARG:N	2.51	0.44
37:m:34:LYS:HE3	37:m:131:VAL:HG11	1.98	0.44
38:n:35:LYS:NZ	38:n:100:CYS:SG	2.91	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:s:25:ARG:HE	43:s:74:ILE:HG23	1.82	0.44
44:t:30:ILE:HG23	44:t:85:VAL:HB	1.99	0.44
51:1:892:A:O2'	51:1:893:C:H5'	2.17	0.44
51:1:1363:C:O2'	51:1:1364:G:H5'	2.18	0.44
51:1:1595:C:H2'	51:1:1596:A:C8	2.52	0.44
51:1:2443:C:O2'	51:1:2444:G:H5'	2.17	0.44
57:A1:192:VAL:HG12	57:A1:193:GLU:H	1.83	0.44
58:B1:731:ARG:HB3	59:B2:1105:SER:HB2	1.99	0.44
65:a:46:VAL:HG22	65:a:212:VAL:HG13	1.99	0.44
65:a:65:LEU:HD13	65:a:188:ASN:HD21	1.83	0.44
65:a:173:THR:HG22	65:a:174:THR:H	1.82	0.44
66:0:491:ARG:HD2	66:0:570:PRO:HB2	1.99	0.44
1:A:58:ASP:HB2	24:X:20:LYS:HB2	1.99	0.44
7:G:58:LYS:O	7:G:61:SER:OG	2.32	0.44
8:H:135:ARG:HH22	54:4:14:U:H1'	1.83	0.44
28:c:114:LYS:HD2	51:1:2820:A:O2'	2.17	0.44
31:f:41:GLU:HA	31:f:54:ARG:HH21	1.81	0.44
40:p:15:ASP:N	40:p:15:ASP:OD1	2.48	0.44
51:1:367:G:O2'	51:1:368:A:H5'	2.18	0.44
51:1:716:A:C2	51:1:717:C:H1'	2.52	0.44
51:1:861:A:H2'	51:1:862:G:O4'	2.18	0.44
51:1:1064:C:C3'	51:1:1065:U:C5'	2.91	0.44
51:1:2189:U:H2'	51:1:2190:G:H8	1.83	0.44
51:1:2515:C:H2'	51:1:2516:A:H8	1.81	0.44
53:3:288:A:H2'	53:3:289:G:H4'	1.99	0.44
53:3:667:G:H2'	53:3:668:G:H8	1.83	0.44
53:3:993:G:N3	53:3:993:G:H2'	2.32	0.44
60:W0:58:LEU:HD12	60:W0:59:ILE:HG12	2.00	0.44
66:0:70:ALA:O	66:0:84:ILE:N	2.46	0.44
3:C:29:LYS:HE2	51:1:2286:G:H3'	1.99	0.44
7:G:160:LEU:HD11	7:G:175:ALA:HB2	1.98	0.44
10:J:131:ASN:ND2	53:3:18:C:H5''	2.33	0.44
24:X:43:MET:HE2	24:X:43:MET:HB2	1.92	0.44
27:b:58:LYS:HB3	51:1:1568:G:H4'	1.98	0.44
30:e:39:VAL:HG12	30:e:41:GLU:H	1.82	0.44
34:j:6:ALA:HB3	34:j:48:VAL:HG21	1.99	0.44
41:q:5:ARG:HG3	51:1:584:C:OP2	2.17	0.44
45:u:81:ARG:HD3	51:1:335:C:H5''	1.98	0.44
51:1:19:A:O2'	51:1:553:G:H4'	2.18	0.44
51:1:598:U:H2'	51:1:599:A:H8	1.83	0.44
51:1:1716:U:H2'	51:1:1717:A:H8	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1748:C:H2'	51:1:1749:A:C8	2.52	0.44
51:1:2326:C:H4'	51:1:2327:A:OP1	2.18	0.44
51:1:2798:U:H4'	51:1:2799:A:C5	2.53	0.44
53:3:163:C:H2'	53:3:164:G:O4'	2.17	0.44
53:3:357:G:OP1	53:3:367:U:H2'	2.17	0.44
53:3:819:A:H5'	53:3:820:U:C5	2.53	0.44
58:B1:375:GLU:HB3	59:B2:1245:ALA:CB	2.48	0.44
2:B:42:ILE:HG12	38:n:100:CYS:HA	1.99	0.44
4:D:8:SER:OG	51:1:686:U:O2	2.36	0.44
7:G:87:ASP:OD1	7:G:87:ASP:N	2.51	0.44
7:G:218:ALA:HA	7:G:221:ARG:HD3	2.00	0.44
14:N:91:GLU:O	14:N:95:SER:N	2.48	0.44
15:O:71:LEU:O	15:O:72:ARG:NH1	2.40	0.44
17:Q:93:ARG:NH1	53:3:911:U:OP2	2.51	0.44
27:b:42:ARG:HH12	51:1:779:U:H5''	1.82	0.44
35:k:8:LEU:HD23	35:k:82:ASN:HB3	2.00	0.44
45:u:17:ASP:HB3	45:u:20:LYS:HD2	2.00	0.44
51:1:41:C:C2'	51:1:42:A:H5''	2.46	0.44
51:1:1319:C:O2'	51:1:1320:C:H5'	2.18	0.44
51:1:1468:U:H2'	51:1:1522:A:N6	2.33	0.44
51:1:2070:A:O2'	51:1:2071:A:H5'	2.17	0.44
51:1:2358:A:H2'	51:1:2359:C:O4'	2.18	0.44
53:3:1270:G:H2'	53:3:1271:A:C8	2.53	0.44
57:A1:68:TYR:HE1	57:A1:79:LEU:HD13	1.82	0.44
58:B1:201:LEU:CD1	58:B1:224:LEU:HD12	2.46	0.44
58:B1:478:LEU:HD21	60:W0:47:THR:HG23	1.99	0.44
58:B1:515:ARG:NH2	58:B1:718:SER:O	2.48	0.44
58:B1:804:ALA:HB2	58:B1:1256:ILE:CD1	2.47	0.44
66:0:99:VAL:HG11	66:0:126:VAL:HG12	1.99	0.44
66:0:309:ARG:NH1	66:0:315:GLU:OE1	2.50	0.44
7:G:15:PHE:HA	7:G:42:LEU:HD11	1.99	0.44
7:G:110:ILE:O	7:G:114:LYS:N	2.51	0.44
14:N:114:LYS:HB2	14:N:117:LEU:HB2	1.99	0.44
28:c:56:LYS:NZ	51:1:2830:C:H5''	2.33	0.44
36:l:110:VAL:HB	36:l:127:VAL:HG13	1.99	0.44
41:q:23:TYR:HB2	41:q:28:SER:HB3	1.98	0.44
43:s:77:ASP:OD1	43:s:77:ASP:N	2.48	0.44
51:1:816:C:H2'	51:1:817:C:C6	2.53	0.44
51:1:1292:G:H2'	51:1:1293:C:C6	2.53	0.44
51:1:1440:U:H2'	51:1:1441:G:C8	2.53	0.44
51:1:1469:A:H2'	51:1:1470:A:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:2:75:G:H2'	52:2:76:G:O4'	2.18	0.44
53:3:16:A:O2'	53:3:17:U:H5'	2.18	0.44
59:B2:487:LEU:HD22	59:B2:487:LEU:HA	1.77	0.44
62:NG:161:SER:CB	62:NG:170:PRO:HA	2.48	0.44
66:0:360:PHE:HD1	66:0:360:PHE:HA	1.71	0.44
1:A:59:ARG:HD3	24:X:20:LYS:HE3	1.99	0.44
9:I:38:GLY:HA3	53:3:542:G:C5'	2.45	0.44
10:J:88:HIS:O	10:J:91:SER:OG	2.35	0.44
25:Y:25:SER:OG	53:3:1458:G:H5''	2.18	0.44
25:Y:34:VAL:HG11	25:Y:78:LEU:HD13	2.00	0.44
36:l:63:LYS:HE2	51:1:249:C:O2'	2.17	0.44
38:n:83:LEU:HG	38:n:86:ARG:HH21	1.83	0.44
51:1:48:G:O3'	51:1:51:G:H5'	2.17	0.44
53:3:410:G:C6	53:3:429:U:H1'	2.53	0.44
53:3:443:C:H2'	53:3:444:G:C8	2.53	0.44
53:3:1235:U:H2'	53:3:1236:A:O4'	2.18	0.44
54:4:4:U:H2'	54:4:5:U:C6	2.53	0.44
58:B1:111:THR:CG2	58:B1:300:GLN:HA	2.48	0.44
59:B2:24:VAL:HG11	59:B2:704:MET:HE1	1.99	0.44
59:B2:300:ASP:OD1	59:B2:313:ALA:N	2.51	0.44
59:B2:674:ASP:OD2	59:B2:1070:HIS:ND1	2.50	0.44
59:B2:811:ASN:ND2	59:B2:1098:LEU:O	2.51	0.44
65:a:9:ARG:HA	65:a:12:ARG:HB2	1.99	0.44
6:F:18:LYS:HE2	6:F:18:LYS:HB3	1.83	0.43
9:I:90:LEU:HD13	9:I:190:LEU:HD11	1.98	0.43
9:I:131:ILE:HD13	53:3:620:C:C2	2.52	0.43
10:J:75:LEU:HD13	10:J:119:VAL:HG13	2.00	0.43
12:L:91:ARG:HB3	12:L:92:PRO:HD2	1.99	0.43
22:V:18:LYS:HE2	53:3:255:G:H4'	1.99	0.43
23:W:11:ARG:HE	23:W:15:GLU:HB2	1.83	0.43
28:c:114:LYS:NZ	51:1:2723:C:OP1	2.52	0.43
36:l:28:GLY:H	36:l:31:GLY:HA2	1.82	0.43
40:p:52:ARG:HH21	51:1:2846:G:H5'	1.83	0.43
49:y:30:MET:SD	49:y:30:MET:N	2.91	0.43
51:1:196:A:N3	51:1:196:A:H2'	2.33	0.43
51:1:227:A:H1'	51:1:229:C:N4	2.34	0.43
51:1:596:U:H2'	51:1:597:G:H8	1.83	0.43
51:1:784:G:OP1	51:1:2588:G:H5''	2.18	0.43
51:1:941:A:O2'	51:1:1190:G:H4'	2.18	0.43
51:1:2039:U:H2'	51:1:2040:G:H8	1.83	0.43
53:3:212:G:H2'	53:3:213:G:O4'	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:961:U:H2'	53:3:962:C:O4'	2.18	0.43
57:A1:212:ASP:OD1	57:A1:212:ASP:N	2.48	0.43
58:B1:201:LEU:HD11	58:B1:220:ARG:NH1	2.32	0.43
58:B1:894:VAL:HG22	58:B1:1258:ARG:HH11	1.83	0.43
59:B2:11:ILE:HG22	59:B2:1172:LEU:HD11	1.99	0.43
59:B2:557:ARG:HB3	59:B2:587:LEU:HD13	2.00	0.43
59:B2:829:THR:HG23	59:B2:1059:ARG:HG2	2.00	0.43
66:0:537:ILE:HB	66:0:577:ARG:HG3	1.99	0.43
4:D:43:THR:HG23	4:D:44:VAL:H	1.83	0.43
10:J:146:MET:HE2	10:J:146:MET:HB3	1.90	0.43
22:V:15:LYS:CB	53:3:275:G:H5'	2.48	0.43
30:e:48:LEU:O	30:e:52:ALA:N	2.50	0.43
37:m:53:MET:HE1	37:m:103:TYR:HB3	1.99	0.43
39:o:26:LEU:HD13	39:o:39:VAL:HG22	2.00	0.43
42:r:102:SER:OG	42:r:103:ALA:N	2.51	0.43
47:w:33:ILE:HD11	47:w:78:ILE:HD11	2.00	0.43
48:x:36:ARG:HA	48:x:47:THR:HA	1.99	0.43
51:1:45:G:H5'	51:1:46:G:C5'	2.36	0.43
51:1:2888:C:H2'	51:1:2889:C:H6	1.82	0.43
53:3:1517:G:O2'	53:3:1518:A:H5'	2.19	0.43
58:B1:111:THR:HG21	58:B1:303:VAL:HB	2.00	0.43
58:B1:1033:GLY:HA3	58:B1:1081:VAL:O	2.18	0.43
59:B2:901:LEU:HD12	59:B2:901:LEU:HA	1.83	0.43
59:B2:1275:VAL:HG13	59:B2:1287:LEU:HD11	2.01	0.43
10:J:137:ARG:HH12	53:3:1078:U:H4'	1.83	0.43
22:V:24:ILE:HG23	22:V:41:THR:HB	1.99	0.43
24:X:4:LEU:HD23	24:X:9:PHE:HB2	2.01	0.43
33:i:72:THR:HB	33:i:115:ASP:HB2	2.01	0.43
37:m:74:THR:OG1	37:m:75:GLU:N	2.50	0.43
40:p:74:GLN:HB2	40:p:77:SER:HB3	2.00	0.43
51:1:121:G:H4'	51:1:149:A:H5'	2.00	0.43
51:1:532:A:H2'	51:1:532:A:N3	2.33	0.43
51:1:1156:A:H5'	51:1:1156:A:H8	1.82	0.43
51:1:2427:C:C5'	51:1:2429:G:H5'	2.47	0.43
59:B2:6:THR:OG1	59:B2:781:ASP:OD1	2.33	0.43
63:5:63:G:H2'	63:5:64:A:C8	2.53	0.43
66:0:75:MET:HE1	66:0:276:GLN:HB3	1.99	0.43
7:G:170:ILE:HA	7:G:173:LYS:HE2	1.99	0.43
8:H:110:LEU:HD22	8:H:145:ALA:HB2	1.99	0.43
12:L:65:LEU:O	12:L:69:ARG:HG3	2.18	0.43
28:c:53:GLY:HA3	28:c:77:ARG:HG2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:d:57:LYS:HB2	51:1:797:G:OP2	2.19	0.43
32:g:55:GLU:O	32:g:59:ALA:N	2.50	0.43
45:u:6:ARG:HB2	51:1:85:G:OP2	2.18	0.43
47:w:62:LYS:HE3	47:w:81:GLU:HG3	2.00	0.43
48:x:17:ARG:HD3	48:x:17:ARG:HA	1.80	0.43
51:1:285:G:O2'	51:1:286:U:H5'	2.18	0.43
51:1:1075:C:H3'	51:1:1076:C:C5'	2.40	0.43
51:1:1926:U:H2'	51:1:1927:A:H8	1.83	0.43
51:1:2250:G:N2	51:1:2496:C:H5''	2.33	0.43
51:1:2586:U:H2'	51:1:2587:A:H8	1.83	0.43
53:3:182:A:H2'	53:3:183:C:H5''	2.01	0.43
53:3:201:G:H21	53:3:469:C:H1'	1.83	0.43
53:3:1261:A:H5''	53:3:1262:C:C5	2.53	0.43
58:B1:161:THR:H	58:B1:164:GLN:HB2	1.82	0.43
58:B1:824:PRO:HD3	58:B1:835:LEU:HD12	2.00	0.43
66:0:617:MET:N	66:0:658:VAL:O	2.47	0.43
3:C:10:LEU:HD21	3:C:33:LEU:HD23	2.01	0.43
8:H:121:SER:HB2	8:H:125:ARG:HH12	1.82	0.43
9:I:115:GLN:HE22	53:3:406:G:H1'	1.84	0.43
16:P:24:ALA:HB2	16:P:29:THR:HG23	2.00	0.43
16:P:108:ASN:HB3	26:Z:6:ARG:HD3	1.99	0.43
19:S:70:HIS:HB3	53:3:974:A:H5'	2.00	0.43
19:S:74:ARG:NH2	53:3:1359:C:H3'	2.32	0.43
27:b:7:PRO:HA	27:b:13:ARG:HA	1.99	0.43
28:c:164:GLN:HE22	51:1:2822:G:H5''	1.83	0.43
35:k:2:ILE:HG13	35:k:62:VAL:HG11	1.99	0.43
51:1:566:U:O2'	51:1:567:U:H5'	2.18	0.43
51:1:752:A:O2'	51:1:1781:U:H5'	2.18	0.43
51:1:974:G:H1'	51:1:975:A:H8	1.77	0.43
51:1:1063:G:H5''	51:1:1064:C:C5	2.53	0.43
51:1:1117:C:H2'	51:1:1118:C:C6	2.54	0.43
51:1:1417:C:H2'	51:1:1418:G:O4'	2.19	0.43
51:1:1595:C:H2'	51:1:1596:A:H8	1.84	0.43
51:1:2122:U:H2'	51:1:2123:G:O4'	2.18	0.43
53:3:846:G:H2'	53:3:847:G:H8	1.83	0.43
58:B1:1079:LYS:HD3	58:B1:1098:GLN:HB3	1.99	0.43
5:E:40:LYS:HD3	51:1:2419:U:OP2	2.18	0.43
5:E:56:LEU:HD22	36:l:49:GLY:HA2	2.00	0.43
12:L:86:VAL:HG12	12:L:150:PHE:CZ	2.53	0.43
14:N:40:ARG:HD2	14:N:40:ARG:HA	1.78	0.43
25:Y:54:GLN:HE21	53:3:193:C:H1'	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:g:5:LEU:HD22	32:g:9:VAL:HG21	2.01	0.43
33:i:14:ALA:HB2	33:i:54:ILE:HG13	2.01	0.43
36:l:55:MET:HA	36:l:56:PRO:HD3	1.88	0.43
39:o:26:LEU:N	39:o:91:SER:O	2.48	0.43
41:q:30:VAL:HG13	51:1:580:U:O3'	2.19	0.43
44:t:34:VAL:HG21	44:t:43:ILE:HD11	1.99	0.43
51:1:1441:G:H4'	51:1:1628:G:C5'	2.49	0.43
51:1:1960:A:H2'	51:1:1961:C:C5'	2.47	0.43
51:1:2055:C:H5'	51:1:2056:G:O5'	2.18	0.43
51:1:2086:U:H2'	51:1:2087:G:C8	2.53	0.43
51:1:2303:G:O2'	51:1:2304:G:H5'	2.17	0.43
51:1:2529:G:H5''	51:1:2530:A:H5''	2.01	0.43
53:3:247:G:O2'	53:3:248:C:H5'	2.19	0.43
58:B1:40:LYS:HZ3	58:B1:40:LYS:HG2	1.74	0.43
58:B1:107:LEU:HA	58:B1:276:ASN:ND2	2.33	0.43
58:B1:128:LEU:CD2	58:B1:188:LEU:HB3	2.47	0.43
58:B1:1108:GLN:HG3	58:B1:1109:LEU:HD12	1.99	0.43
36:l:112:LEU:HD13	36:l:131:ALA:HA	2.00	0.43
39:o:15:ARG:CZ	52:2:8:C:H5''	2.49	0.43
51:1:1056:G:H21	51:1:1102:C:H5	1.65	0.43
51:1:1925:C:H2'	51:1:1926:U:O4'	2.18	0.43
53:3:556:C:O2'	53:3:557:G:H5'	2.19	0.43
53:3:650:G:O2'	53:3:651:C:H5'	2.17	0.43
53:3:839:C:H2'	53:3:840:C:H6	1.83	0.43
53:3:1352:C:H2'	53:3:1353:G:H8	1.83	0.43
58:B1:141:PHE:CD2	58:B1:297:ARG:HB2	2.54	0.43
58:B1:388:ARG:HG2	58:B1:388:ARG:HH11	1.84	0.43
58:B1:1024:THR:HG23	58:B1:1123:ARG:HA	2.00	0.43
65:a:47:ASN:HD22	65:a:170:ILE:HG13	1.84	0.43
66:0:491:ARG:O	66:0:613:LEU:N	2.45	0.43
66:0:505:HIS:N	66:0:516:GLY:O	2.43	0.43
7:G:123:GLY:HA3	7:G:127:LYS:HE2	2.00	0.43
10:J:111:ARG:O	10:J:115:GLU:N	2.51	0.43
19:S:58:ARG:HD2	53:3:980:C:H1'	2.01	0.43
20:T:17:ASP:OD1	20:T:17:ASP:N	2.51	0.43
44:t:7:LEU:HD22	44:t:46:ALA:HB2	1.99	0.43
51:1:20:C:H2'	51:1:21:A:C8	2.53	0.43
51:1:1091:G:O6	51:1:1099:G:O6	2.36	0.43
51:1:1808:A:H3'	51:1:1809:A:H8	1.82	0.43
51:1:2340:A:H2'	51:1:2341:G:H8	1.84	0.43
51:1:2461:A:H1'	51:1:2492:U:N3	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:52:C:H2'	53:3:53:A:C8	2.54	0.43
53:3:273:U:H2'	53:3:274:A:H5'	2.00	0.43
58:B1:242:LEU:C	58:B1:242:LEU:HD23	2.44	0.43
58:B1:434:ILE:HD11	59:B2:1274:GLU:HG3	2.00	0.43
58:B1:850:LYS:HB3	58:B1:855:ASP:HB2	2.00	0.43
65:a:216:THR:HG22	65:a:217:THR:H	1.83	0.43
66:0:70:ALA:N	66:0:84:ILE:O	2.48	0.43
66:0:520:ILE:HB	66:0:576:ILE:HD11	1.99	0.43
7:G:55:GLU:HB2	7:G:183:PHE:HZ	1.84	0.43
7:G:163:ILE:HD11	7:G:213:LEU:HD21	2.01	0.43
17:Q:86:VAL:HG22	17:Q:95:HIS:CE1	2.54	0.43
20:T:70:LYS:HE3	20:T:70:LYS:HB2	1.88	0.43
21:U:13:LYS:HE2	53:3:392:C:H5'	2.01	0.43
29:d:158:PHE:HA	29:d:169:VAL:HG21	2.00	0.43
37:m:64:TRP:NE1	51:1:873:C:H4'	2.33	0.43
37:m:109:PRO:HD2	37:m:112:LEU:HD11	2.00	0.43
50:z:10:ARG:NH1	51:1:1000:A:O2'	2.52	0.43
51:1:69:C:O2'	51:1:70:G:H5'	2.18	0.43
51:1:466:A:H2'	51:1:467:G:H5'	2.00	0.43
51:1:1343:G:N3	51:1:1343:G:H2'	2.34	0.43
51:1:2128:G:OP1	65:a:38:PHE:HB3	2.19	0.43
51:1:2724:U:H2'	51:1:2725:A:C8	2.54	0.43
53:3:605:U:O2'	53:3:606:G:H5'	2.19	0.43
53:3:865:A:H5'	53:3:1078:U:O4	2.18	0.43
55:8:2:DC:H6	55:8:2:DC:H2'	1.73	0.43
55:8:12:DG:OP1	58:B1:795:TYR:CE1	2.71	0.43
58:B1:45:ASN:HD22	58:B1:48:THR:H	1.65	0.43
58:B1:450:HIS:HA	58:B1:451:PRO:HD3	1.91	0.43
58:B1:568:SER:HB3	58:B1:570:LYS:NZ	2.34	0.43
58:B1:586:GLY:HA3	58:B1:612:LEU:HD11	2.01	0.43
58:B1:1026:PRO:HB2	58:B1:1028:ILE:HG23	2.00	0.43
4:D:21:ARG:NH2	51:1:684:G:OP1	2.52	0.43
8:H:113:LYS:HB2	8:H:184:ASN:HD22	1.84	0.43
8:H:172:VAL:HG23	53:3:1107:C:H5''	2.00	0.43
27:b:186:ASP:OD1	32:g:123:ARG:NH2	2.52	0.43
29:d:110:SER:O	29:d:114:ARG:NE	2.52	0.43
31:f:136:ASP:HB3	31:f:139:VAL:HG22	2.00	0.43
33:i:134:SER:HB2	51:1:1077:A:C2	2.54	0.43
51:1:1289:C:O2'	51:1:1330:C:H4'	2.19	0.43
51:1:1536:C:H4'	51:1:1537:G:C2	2.54	0.43
51:1:1786:A:H1'	51:1:1938:A:N6	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2484:G:O2'	51:1:2485:G:H5'	2.19	0.43
53:3:220:G:O2'	53:3:221:C:H5'	2.18	0.43
58:B1:58:CYS:SG	58:B1:60:ARG:HG2	2.59	0.43
58:B1:201:LEU:CB	58:B1:221:ILE:HD13	2.47	0.43
58:B1:609:TYR:HD2	58:B1:610:ARG:NH1	2.17	0.43
58:B1:797:THR:HG22	58:B1:924:GLY:HA3	2.01	0.43
58:B1:950:ILE:HB	58:B1:1018:ALA:HB3	2.01	0.43
59:B2:616:ILE:HG13	59:B2:652:TYR:HB2	2.01	0.43
62:NG:135:ARG:O	62:NG:178:VAL:CA	2.67	0.43
64:6:69:C:H2'	64:6:70:G:C5'	2.39	0.43
65:a:51:ASP:HB3	65:a:54:LYS:HB3	2.01	0.43
66:0:245:GLU:HA	66:0:248:ILE:HD12	2.01	0.43
3:C:20:TYR:OH	51:1:2348:U:H5'	2.19	0.42
5:E:4:LYS:O	36:l:48:ARG:NH1	2.43	0.42
9:I:23:GLY:HA3	53:3:409:U:OP1	2.19	0.42
10:J:73:VAL:HG23	10:J:75:LEU:HG	2.00	0.42
12:L:86:VAL:HG12	12:L:150:PHE:CE2	2.53	0.42
51:1:919:U:H2'	51:1:920:A:O4'	2.19	0.42
51:1:1278:C:H2'	51:1:1279:G:C8	2.54	0.42
51:1:1539:U:H2'	51:1:1540:G:H8	1.84	0.42
51:1:1557:C:C5	51:1:1558:C:H2'	2.54	0.42
51:1:2170:A:C4	51:1:2171:A:H8	2.37	0.42
58:B1:903:LEU:HD12	58:B1:903:LEU:HA	1.77	0.42
66:0:69:THR:OG1	66:0:367:HIS:NE2	2.34	0.42
10:J:12:GLU:HA	10:J:38:VAL:HG12	2.00	0.42
10:J:137:ARG:NH1	53:3:1078:U:H4'	2.34	0.42
16:P:34:THR:HA	16:P:40:ALA:HA	2.00	0.42
18:R:6:ILE:HG13	18:R:7:ASN:H	1.84	0.42
19:S:81:ILE:HG21	53:3:1202:U:C2	2.55	0.42
21:U:20:VAL:HG12	21:U:35:ARG:HA	2.01	0.42
30:e:84:ILE:HG21	51:1:2312:U:C4'	2.48	0.42
31:f:70:LEU:HD11	51:1:2758:A:N1	2.34	0.42
33:i:27:LEU:HD11	33:i:34:ILE:HD13	2.00	0.42
41:q:24:TYR:CE1	51:1:17:G:H4'	2.54	0.42
51:1:792:A:H3'	51:1:793:A:H5'	2.00	0.42
51:1:1132:U:H2'	51:1:1133:A:C8	2.54	0.42
51:1:1645:G:C5'	51:1:1646:C:H5'	2.31	0.42
51:1:1923:U:H2'	51:1:1924:C:C6	2.54	0.42
53:3:613:C:H2'	53:3:614:C:C6	2.53	0.42
53:3:1211:U:H4'	53:3:1213:A:N3	2.34	0.42
53:3:1517:G:C2'	53:3:1518:A:H5'	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:8:3:DC:N1	55:8:4:DT:H72	2.34	0.42
58:B1:62:PHE:N	58:B1:62:PHE:CD1	2.86	0.42
58:B1:137:ARG:HA	58:B1:142:GLU:HG2	2.02	0.42
58:B1:139:LEU:HD23	58:B1:139:LEU:HA	1.89	0.42
58:B1:515:ARG:HH12	58:B1:724:MET:HG2	1.84	0.42
66:0:170:GLN:NE2	66:0:266:CYS:H	2.18	0.42
4:D:25:LYS:HE2	4:D:25:LYS:HB2	1.89	0.42
14:N:17:ARG:HH12	53:3:1129:C:H5'	1.84	0.42
18:R:47:LEU:HD22	18:R:51:GLN:HE21	1.83	0.42
35:k:22:ILE:HD12	51:1:1952:A:C2	2.55	0.42
36:l:19:LEU:HD23	51:1:587:C:O2	2.18	0.42
51:1:186:G:O2'	51:1:187:G:H5'	2.19	0.42
51:1:467:G:O2'	51:1:468:G:H5'	2.20	0.42
51:1:1726:C:H2'	51:1:1727:C:H6	1.82	0.42
58:B1:24:LEU:HD21	58:B1:116:PHE:CE2	2.54	0.42
58:B1:1046:ILE:HG22	58:B1:1061:VAL:HA	2.00	0.42
59:B2:125:GLY:H	59:B2:495:ALA:HB1	1.84	0.42
59:B2:1157:GLN:HG3	59:B2:1159:VAL:HG13	2.00	0.42
59:B2:1313:HIS:CD2	60:W0:31:GLN:HE22	2.37	0.42
62:NG:130:PRO:HA	62:NG:148:VAL:O	2.19	0.42
63:5:25:C:H2'	63:5:26:A:H8	1.84	0.42
7:G:134:LEU:O	7:G:137:THR:OG1	2.38	0.42
12:L:115:MET:HB3	53:3:1240:U:OP2	2.20	0.42
15:O:47:GLU:HG3	53:3:1254:A:OP1	2.19	0.42
16:P:121:ARG:HA	16:P:122:PRO:HD3	1.82	0.42
17:Q:109:ARG:CZ	53:3:537:G:H5''	2.50	0.42
18:R:96:VAL:HG22	53:3:1308:U:OP1	2.20	0.42
18:R:107:THR:HG21	53:3:1306:A:N3	2.33	0.42
20:T:80:LEU:HD12	20:T:80:LEU:HA	1.90	0.42
34:j:60:ASP:HA	34:j:93:ILE:HD11	1.99	0.42
37:m:19:GLY:O	37:m:38:ARG:NH1	2.44	0.42
37:m:57:VAL:HB	37:m:60:GLN:HB3	2.01	0.42
50:z:13:ILE:H	50:z:13:ILE:HG13	1.70	0.42
51:1:526:A:N6	51:1:2626:C:H4'	2.35	0.42
51:1:1047:G:H2'	51:1:1110:G:N2	2.34	0.42
51:1:1278:C:H2'	51:1:1279:G:H8	1.84	0.42
51:1:1837:C:H2'	51:1:1899:A:N6	2.32	0.42
51:1:2314:A:H2'	51:1:2315:G:C8	2.54	0.42
51:1:2332:C:H2'	51:1:2335:A:C2	2.55	0.42
51:1:2425:A:H4'	51:1:2426:A:C5'	2.49	0.42
51:1:2881:U:H2'	51:1:2882:A:H8	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:794:A:H4'	53:3:1521:C:O2'	2.19	0.42
53:3:1062:U:H2'	53:3:1063:C:C6	2.54	0.42
53:3:1065:U:P	53:3:1190:G:H22	2.42	0.42
53:3:1479:C:H2'	53:3:1480:A:C8	2.51	0.42
54:4:43:G:H5'	59:B2:688:GLN:HE22	1.84	0.42
57:A1:78:ILE:HA	57:A1:81:ILE:HG22	2.00	0.42
58:B1:362:ARG:HB2	58:B1:364:HIS:HD2	1.83	0.42
59:B2:444:ASP:OD1	59:B2:444:ASP:N	2.51	0.42
59:B2:699:LEU:HG	59:B2:799:ASN:HD22	1.85	0.42
2:B:37:HIS:ND1	2:B:38:LEU:O	2.41	0.42
13:M:31:LEU:HD22	53:3:643:C:H5''	2.01	0.42
14:N:122:ARG:HG3	53:3:1343:G:O2'	2.18	0.42
18:R:111:PRO:HB2	18:R:113:LYS:HG3	2.02	0.42
21:U:21:VAL:HG12	21:U:33:ILE:HB	2.01	0.42
28:c:148:GLN:HB2	28:c:152:PRO:HG3	2.01	0.42
33:i:67:THR:HG22	33:i:68:PHE:H	1.85	0.42
36:l:78:ARG:CZ	51:1:626:A:H2'	2.49	0.42
51:1:2323:G:O2'	51:1:2324:U:H5'	2.19	0.42
51:1:2720:U:H5'	51:1:2720:U:C6	2.53	0.42
55:8:15:DC:H5'	59:B2:1269:ARG:HD3	2.00	0.42
58:B1:96:LYS:NZ	59:B2:1298:VAL:HG11	2.34	0.42
58:B1:244:VAL:HA	58:B1:269:TYR:OH	2.19	0.42
59:B2:469:VAL:HA	59:B2:472:GLU:HG2	2.02	0.42
8:H:15:LYS:HD2	8:H:15:LYS:HA	1.81	0.42
9:I:40:HIS:HB3	9:I:43:ARG:HH21	1.85	0.42
27:b:200:MET:HG3	51:1:1820:U:C2	2.54	0.42
28:c:118:PHE:HE1	51:1:2048:G:H21	1.66	0.42
36:l:90:VAL:N	36:l:121:THR:O	2.52	0.42
37:m:1:MET:SD	37:m:1:MET:N	2.88	0.42
37:m:112:LEU:HA	37:m:115:GLU:HB3	2.00	0.42
40:p:2:ASN:ND2	51:1:2876:G:H4'	2.32	0.42
41:q:92:LYS:HZ2	51:1:995:C:HO2'	1.64	0.42
51:1:123:G:H5''	51:1:1375:U:O2'	2.20	0.42
51:1:1545:A:H2'	51:1:1546:G:O4'	2.19	0.42
51:1:1916:A:N1	53:3:1409:C:H5'	2.34	0.42
51:1:1922:G:H2'	51:1:1923:U:O4'	2.19	0.42
51:1:2039:U:H2'	51:1:2040:G:C8	2.55	0.42
51:1:2138:G:C2'	51:1:2139:U:H5'	2.49	0.42
51:1:2743:U:H2'	51:1:2744:G:C4'	2.48	0.42
51:1:2788:C:H2'	51:1:2789:C:C6	2.53	0.42
53:3:505:G:O5'	53:3:505:G:H8	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:879:C:H2'	53:3:880:C:C6	2.54	0.42
53:3:1163:A:H2'	53:3:1164:G:C8	2.55	0.42
53:3:1330:U:H2'	53:3:1331:G:O4'	2.19	0.42
58:B1:848:VAL:HB	58:B1:858:VAL:HG22	2.02	0.42
59:B2:646:SER:OG	59:B2:647:ARG:N	2.52	0.42
63:5:4:C:H2'	63:5:5:G:C8	2.55	0.42
64:6:17(A):U:O2'	64:6:18:G:H5''	2.19	0.42
66:0:34:THR:OG1	66:0:71:PHE:O	2.37	0.42
13:M:91:LEU:HD23	13:M:91:LEU:HA	1.86	0.42
15:O:100:ILE:HB	62:NG:170:PRO:O	2.19	0.42
28:c:123:LYS:HE2	38:n:1:MET:HE1	2.01	0.42
32:g:11:ASN:ND2	51:1:2095:A:O5'	2.53	0.42
32:g:118:PRO:HD2	32:g:130:VAL:HG13	2.01	0.42
48:x:22:ASN:HD22	48:x:22:ASN:HA	1.65	0.42
51:1:234:U:O2'	51:1:235:U:H5'	2.19	0.42
51:1:288:U:H2'	51:1:289:G:H8	1.83	0.42
51:1:744:U:H4'	51:1:1658:C:H4'	2.02	0.42
51:1:970:U:H2'	51:1:971:G:C8	2.55	0.42
51:1:1071:G:H5''	51:1:1072:C:H5	1.84	0.42
51:1:1201:U:H2'	51:1:1202:G:C8	2.54	0.42
51:1:1649:G:H2'	51:1:1650:A:H8	1.84	0.42
51:1:2240:U:H2'	51:1:2241:A:H8	1.85	0.42
53:3:97:G:H2'	53:3:98:A:O4'	2.20	0.42
53:3:216:U:H2'	53:3:217:C:C6	2.55	0.42
58:B1:102:MET:HG2	58:B1:246:PRO:CG	2.49	0.42
59:B2:998:LEU:HD21	59:B2:1015:ALA:HB2	2.02	0.42
66:0:148:GLY:N	66:0:176:GLU:OE1	2.52	0.42
66:0:487:GLN:HB3	66:0:488:VAL:H	1.70	0.42
66:0:665:GLY:O	66:0:668:THR:OG1	2.37	0.42
3:C:35:LEU:HD13	3:C:37:LYS:HE2	2.01	0.42
14:N:17:ARG:HH12	53:3:1129:C:H4'	1.85	0.42
18:R:16:ILE:O	18:R:19:THR:OG1	2.33	0.42
20:T:47:LYS:O	20:T:49:HIS:ND1	2.53	0.42
28:c:12:THR:OG1	28:c:13:ARG:N	2.51	0.42
33:i:131:THR:HG22	33:i:135:MET:CE	2.50	0.42
34:j:104:ALA:CB	51:1:1139:G:H5'	2.50	0.42
46:v:42:LEU:HD12	46:v:47:VAL:HG11	2.02	0.42
51:1:239:C:H2'	51:1:240:C:O4'	2.20	0.42
51:1:436:C:H2'	51:1:437:U:C6	2.55	0.42
51:1:627:A:H8	51:1:627:A:OP1	2.03	0.42
51:1:1120:G:H2'	51:1:1121:C:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1258:U:H2'	51:1:1259:G:H8	1.85	0.42
51:1:2233:U:H2'	51:1:2234:G:C8	2.54	0.42
51:1:2432:A:H1'	64:6:75:C:O4'	2.20	0.42
51:1:2736:A:H2'	51:1:2737:G:H8	1.85	0.42
53:3:34:C:H2'	53:3:35:G:C8	2.54	0.42
53:3:66:A:H5'	53:3:173:U:C4	2.55	0.42
53:3:521:G:O2'	53:3:522:C:H5'	2.19	0.42
53:3:1306:A:H2'	53:3:1307:U:O4'	2.20	0.42
59:B2:538:LEU:HD13	59:B2:543:ALA:HB2	2.00	0.42
66:0:505:HIS:CE1	66:0:595:LEU:HB3	2.55	0.42
1:A:37:CYS:H	1:A:40:CYS:HB3	1.85	0.42
5:E:15:LYS:HB2	5:E:64:ALA:HB1	2.02	0.42
5:E:54:LEU:HD12	5:E:54:LEU:HA	1.90	0.42
14:N:95:SER:OG	14:N:96:GLU:N	2.53	0.42
15:O:25:ILE:HD12	15:O:25:ILE:HA	1.95	0.42
21:U:79:ASN:N	21:U:79:ASN:OD1	2.53	0.42
22:V:30:HIS:HD2	22:V:33:TYR:H	1.66	0.42
27:b:258:SER:O	27:b:258:SER:OG	2.34	0.42
34:j:27:ARG:HD2	51:1:1143:A:N6	2.34	0.42
36:l:51:GLU:OE1	36:l:60:ARG:NH1	2.52	0.42
38:n:64:ARG:NH2	51:1:2852:G:H5'	2.34	0.42
41:q:73:ILE:HD11	41:q:77:LYS:HB3	2.01	0.42
43:s:97:LEU:HD23	43:s:97:LEU:HA	1.91	0.42
51:1:198:C:O5'	51:1:198:C:H6	2.03	0.42
51:1:1068:G:H21	51:1:1096:A:H5'	1.85	0.42
51:1:1318:U:H2'	51:1:1319:C:H6	1.83	0.42
51:1:1449:G:O2'	51:1:1450:G:H5'	2.20	0.42
51:1:2533:U:H2'	51:1:2534:A:O4'	2.19	0.42
51:1:2534:A:H2'	51:1:2535:G:H5''	2.02	0.42
51:1:2685:G:H2'	51:1:2686:G:H8	1.84	0.42
51:1:2802:G:H2'	51:1:2803:G:O4'	2.20	0.42
51:1:2834:G:H2'	51:1:2879:A:H61	1.84	0.42
53:3:146:G:O2'	53:3:147:G:H5'	2.20	0.42
53:3:749:A:H2'	53:3:750:C:O4'	2.20	0.42
53:3:1428:A:OP2	53:3:1428:A:O4'	2.37	0.42
57:A1:51:MET:HA	57:A1:52:PRO:HD3	1.93	0.42
58:B1:385:LEU:CD2	58:B1:390:LEU:HB2	2.50	0.42
58:B1:390:LEU:N	58:B1:390:LEU:HD13	2.35	0.42
58:B1:434:ILE:HD11	59:B2:1274:GLU:CG	2.49	0.42
58:B1:930:LEU:HA	58:B1:1244:GLN:HG3	2.02	0.42
59:B2:50:GLU:HG2	59:B2:73:TYR:HE1	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:B2:524:ILE:HD12	59:B2:712:SER:HB2	2.02	0.42
66:0:210:ASP:OD1	66:0:210:ASP:N	2.51	0.42
7:G:66:ILE:HB	7:G:88:GLN:HG3	2.02	0.42
9:I:184:LYS:HB3	9:I:184:LYS:HE3	1.77	0.42
28:c:35:THR:OG1	28:c:49:GLN:O	2.36	0.42
41:q:84:LYS:HB3	41:q:115:ALA:HB1	2.02	0.42
42:r:80:ARG:N	51:1:565:C:OP2	2.51	0.42
43:s:28:LYS:O	43:s:32:ALA:N	2.50	0.42
47:w:14:ALA:HB1	51:1:2271:G:OP1	2.20	0.42
48:x:60:LYS:NZ	51:1:372:G:O4'	2.49	0.42
50:z:10:ARG:HB2	50:z:53:MET:CB	2.50	0.42
51:1:2689:U:O2	51:1:2713:U:H5''	2.19	0.42
51:1:2704:C:H2'	51:1:2705:A:O4'	2.20	0.42
53:3:768:A:H2'	53:3:769:G:O4'	2.20	0.42
53:3:1037:C:H2'	53:3:1038:C:C6	2.54	0.42
53:3:1341:U:O2'	53:3:1342:C:H5'	2.20	0.42
53:3:1494:G:H8	53:3:1494:G:OP2	2.03	0.42
58:B1:144:TYR:N	58:B1:144:TYR:CD1	2.88	0.42
58:B1:394:ILE:O	58:B1:394:ILE:HG13	2.19	0.42
58:B1:1272:SER:OG	58:B1:1273:ASP:N	2.53	0.42
7:G:70:GLY:HA3	7:G:163:ILE:HB	2.02	0.41
8:H:156:LEU:H	8:H:156:LEU:HG	1.67	0.41
11:K:49:TYR:OH	23:W:62:ARG:O	2.30	0.41
16:P:118:ASN:HB2	53:3:718:A:H5'	2.02	0.41
17:Q:88:ASP:HB3	53:3:523:A:H61	1.84	0.41
18:R:7:ASN:HD21	18:R:18:LEU:HD13	1.84	0.41
21:U:6:LEU:HD11	21:U:70:ARG:HD2	2.01	0.41
22:V:70:LYS:HD3	53:3:254:G:H5''	2.02	0.41
27:b:110:LYS:N	27:b:113:ASP:OD2	2.51	0.41
28:c:173:GLN:NE2	51:1:2771:C:O2'	2.50	0.41
30:e:133:GLU:HG3	30:e:135:ILE:H	1.85	0.41
31:f:28:LYS:HE2	31:f:28:LYS:HB2	1.92	0.41
34:j:44:TYR:O	41:q:63:ARG:NE	2.53	0.41
47:w:18:GLY:N	47:w:35:ARG:O	2.52	0.41
47:w:58:LYS:HE2	51:1:2366:A:H4'	2.01	0.41
51:1:353:C:H2'	51:1:354:A:H8	1.85	0.41
51:1:1017:G:C6	51:1:1018:U:O4	2.73	0.41
51:1:1275:A:N6	51:1:1296:G:H4'	2.35	0.41
51:1:1472:C:H2'	51:1:1473:G:H8	1.85	0.41
51:1:1882:U:H2'	51:1:1883:U:C6	2.54	0.41
52:2:78:A:H2'	52:2:79:G:O4'	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:1289:ASN:O	58:B1:1293:GLU:HB2	2.20	0.41
65:a:200:LYS:HB2	65:a:200:LYS:HE2	1.87	0.41
67:h:2:DPP:NG	67:h:3:SER:N	2.65	0.41
8:H:19:SER:OG	19:S:91:GLU:O	2.30	0.41
15:O:102:LEU:HD13	62:NG:172:GLU:H	1.85	0.41
16:P:52:ARG:NH1	53:3:689:C:OP2	2.51	0.41
18:R:106:ARG:HB3	53:3:947:G:OP1	2.20	0.41
25:Y:55:PRO:HA	53:3:194:C:H5'	2.02	0.41
27:b:167:ASP:OD2	53:3:682:G:H5'	2.19	0.41
27:b:253:GLY:HA2	51:1:1797:G:H5'	2.01	0.41
29:d:130:LYS:HA	51:1:321:U:OP2	2.19	0.41
36:l:95:LEU:HD22	36:l:100:ILE:HD11	2.01	0.41
51:1:479:A:H1'	51:1:481:G:H5''	2.02	0.41
51:1:524:G:H5'	51:1:539:G:N2	2.35	0.41
51:1:974:G:N3	51:1:974:G:H2'	2.35	0.41
51:1:1069:A:H2	51:1:1096:A:OP1	2.02	0.41
51:1:1494:A:H2'	51:1:1495:A:O4'	2.20	0.41
51:1:2480:C:OP2	51:1:2537:U:H4'	2.20	0.41
51:1:2547:A:H2'	51:1:2548:U:C6	2.55	0.41
51:1:2692:G:H1'	51:1:2847:U:H1'	2.02	0.41
51:1:2773:C:H2'	51:1:2774:C:H6	1.86	0.41
53:3:114:U:O2'	53:3:115:G:H5'	2.20	0.41
53:3:834:U:H2'	53:3:835:U:C6	2.55	0.41
53:3:1049:U:H4'	53:3:1050:G:H5''	2.02	0.41
53:3:1223:C:C5	53:3:1224:U:H5	2.38	0.41
58:B1:243:PRO:HG2	59:B2:1332:SER:C	2.44	0.41
59:B2:22:LEU:HD22	59:B2:603:ILE:HG21	2.02	0.41
6:F:1:MET:HE2	6:F:1:MET:HB2	1.89	0.41
11:K:9:MET:HE3	11:K:86:ARG:HB3	2.03	0.41
23:W:11:ARG:NH2	53:3:845:A:H4'	2.36	0.41
27:b:143:VAL:HB	27:b:153:LEU:HD22	2.01	0.41
28:c:149:ASN:HB2	51:1:2574:G:O2'	2.20	0.41
31:f:71:LEU:HD23	31:f:71:LEU:HA	1.84	0.41
32:g:43:ASN:O	32:g:47:PHE:N	2.54	0.41
33:i:123:ALA:CB	51:1:1081:U:H4'	2.33	0.41
36:l:2:ARG:NH1	36:l:2:ARG:O	2.45	0.41
36:l:59:ARG:HD2	51:1:250:G:H4'	2.03	0.41
41:q:90:ASP:OD2	51:1:996:A:H4'	2.19	0.41
49:y:41:HIS:CD2	51:1:96:C:H4'	2.55	0.41
51:1:214:G:H1'	51:1:217:A:H5'	2.02	0.41
51:1:278:A:H2'	51:1:278:A:N3	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:596:U:H2'	51:1:597:G:C8	2.55	0.41
51:1:1062:G:O2'	51:1:1063:G:C4'	2.69	0.41
51:1:1872:A:H2'	51:1:1873:G:H5'	2.02	0.41
53:3:675:A:H2'	53:3:676:A:O4'	2.19	0.41
53:3:947:G:H4'	53:3:1332:A:H2	1.86	0.41
53:3:1129:C:H42	53:3:1143:G:H1	1.66	0.41
53:3:1311:A:H2'	53:3:1312:G:O4'	2.20	0.41
53:3:1499:A:O2'	53:3:1520:C:H5'	2.19	0.41
57:A1:205:MET:HE1	57:A1:217:ILE:HG13	2.02	0.41
58:B1:144:TYR:CE1	58:B1:162:GLU:OE1	2.73	0.41
58:B1:559:ALA:HB3	58:B1:562:GLU:HB3	2.01	0.41
59:B2:22:LEU:HB3	59:B2:655:VAL:HG11	2.01	0.41
62:NG:175:PHE:O	62:NG:178:VAL:O	2.38	0.41
63:5:17:C:H6	63:5:17:C:H2'	1.69	0.41
13:M:12:ARG:HD2	13:M:26:MET:HE2	2.02	0.41
16:P:38:GLY:HA2	53:3:708:C:O4'	2.19	0.41
22:V:57:VAL:HG13	22:V:78:VAL:HB	2.03	0.41
34:j:108:MET:HB3	51:1:1006:C:O2'	2.20	0.41
51:1:181:A:H2'	51:1:182:A:C8	2.55	0.41
51:1:1916:A:H2'	51:1:1917:U:O4'	2.20	0.41
51:1:2472:G:H2'	51:1:2475:C:H42	1.84	0.41
53:3:47:C:H4'	53:3:48:C:O5'	2.20	0.41
53:3:226:G:O2'	53:3:227:G:H5'	2.21	0.41
53:3:938:A:H1'	53:3:1376:U:O2'	2.21	0.41
53:3:1479:C:C4	53:3:1480:A:N7	2.89	0.41
57:A1:76:GLU:HB3	57:A1:80:GLU:HB3	2.01	0.41
58:B1:71:LEU:HB2	58:B1:90:VAL:HG11	2.03	0.41
58:B1:647:PRO:HG3	58:B1:697:MET:HB3	2.01	0.41
59:B2:478:ARG:HD2	59:B2:492:MET:HA	2.02	0.41
8:H:5:HIS:HA	8:H:6:PRO:HD3	1.94	0.41
8:H:162:ALA:HB2	53:3:1056:U:C5'	2.48	0.41
9:I:32:LYS:HA	9:I:32:LYS:HD3	1.67	0.41
9:I:66:VAL:HB	9:I:71:PHE:HD2	1.84	0.41
17:Q:29:LYS:HD2	17:Q:29:LYS:HA	1.79	0.41
23:W:11:ARG:NH1	53:3:845:A:H5'	2.35	0.41
25:Y:56:ILE:HD13	25:Y:59:ARG:HH22	1.84	0.41
27:b:55:GLY:HA2	51:1:692:C:OP1	2.21	0.41
28:c:130:GLN:HE22	51:1:2578:G:H21	1.69	0.41
32:g:116:ARG:HA	32:g:116:ARG:HD3	1.82	0.41
35:k:17:ARG:NH1	53:3:1471:U:OP1	2.53	0.41
41:q:23:TYR:CE1	51:1:533:G:H5'	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:t:23:ALA:HB1	44:t:29:THR:HB	2.02	0.41
51:1:373:U:H2'	51:1:374:A:H8	1.85	0.41
51:1:2259:U:H2'	51:1:2260:C:H6	1.85	0.41
51:1:2427:C:H5''	51:1:2429:G:H5'	2.02	0.41
51:1:2701:U:H3'	51:1:2702:G:H5''	2.02	0.41
53:3:627:G:H2'	53:3:628:G:O4'	2.21	0.41
53:3:817:C:H4'	53:3:818:G:H5''	2.03	0.41
59:B2:902:LEU:HD11	59:B2:908:GLU:HB2	2.02	0.41
66:0:438:LEU:HD11	66:0:472:ARG:HD3	2.03	0.41
66:0:513:GLY:O	66:0:584:HIS:CD2	2.74	0.41
5:E:27:ASN:O	5:E:35:LYS:NZ	2.47	0.41
9:I:50:TYR:HD2	53:3:509:A:H5''	1.84	0.41
18:R:7:ASN:O	18:R:9:PRO:HD3	2.20	0.41
18:R:13:HIS:CE1	53:3:1296:C:H5'	2.55	0.41
38:n:49:GLU:O	38:n:53:THR:OG1	2.32	0.41
38:n:92:GLY:HA3	51:1:2880:C:H1'	2.03	0.41
51:1:690:G:H2'	51:1:691:C:O4'	2.19	0.41
51:1:799:G:H5''	51:1:800:A:H2'	2.02	0.41
51:1:910:A:N1	51:1:2277:G:H1'	2.36	0.41
51:1:1917:U:O2'	51:1:1918:A:H5'	2.20	0.41
51:1:2361:G:O2'	51:1:2362:C:H5'	2.20	0.41
51:1:2385:C:H2'	51:1:2386:A:H8	1.86	0.41
51:1:2528:U:H2'	51:1:2530:A:O5'	2.20	0.41
51:1:2564:A:OP1	51:1:2648:G:H4'	2.21	0.41
51:1:2646:C:O5'	51:1:2646:C:H6	2.03	0.41
51:1:2698:U:H2'	51:1:2699:C:C6	2.55	0.41
51:1:2799:A:C2'	51:1:2800:A:H5'	2.43	0.41
53:3:215:C:H2'	53:3:216:U:C6	2.56	0.41
58:B1:59:ALA:HB1	58:B1:90:VAL:HG23	2.01	0.41
58:B1:513:MET:HG3	58:B1:544:LEU:HD11	2.01	0.41
58:B1:576:ARG:HD3	58:B1:593:ASN:HA	2.03	0.41
58:B1:820:ILE:HG12	58:B1:884:SER:HB2	2.01	0.41
59:B2:687:ARG:HH11	59:B2:687:ARG:HD3	1.75	0.41
66:0:504:LYS:HE2	66:0:504:LYS:HB2	1.82	0.41
1:A:1:MET:HE2	1:A:1:MET:HB3	1.74	0.41
15:O:61:ALA:HB2	53:3:1061:G:H5''	2.03	0.41
15:O:92:LEU:HB3	15:O:93:ALA:H	1.69	0.41
22:V:9:GLY:H	22:V:24:ILE:HD13	1.86	0.41
27:b:209:ALA:HA	27:b:212:TRP:CE2	2.55	0.41
28:c:16:THR:OG1	28:c:18:ASP:OD1	2.35	0.41
28:c:133:THR:HG21	51:1:1676:A:H1'	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:i:133:ARG:HD2	33:i:133:ARG:HA	1.82	0.41
36:l:57:LEU:HD12	36:l:57:LEU:HA	1.93	0.41
41:q:4:LYS:HB3	41:q:4:LYS:HE2	1.92	0.41
42:r:85:LYS:HE3	51:1:815:C:OP2	2.20	0.41
44:t:38:ALA:O	44:t:81:LYS:NZ	2.39	0.41
47:w:47:VAL:HG21	47:w:76:ILE:HG22	2.02	0.41
49:y:19:LEU:HA	49:y:23:ARG:HH21	1.86	0.41
51:1:671:C:H2'	51:1:672:C:C6	2.56	0.41
51:1:1636:U:H2'	51:1:1637:A:C8	2.55	0.41
51:1:1748:C:H2'	51:1:1749:A:H8	1.84	0.41
51:1:2096:C:H2'	51:1:2097:A:C8	2.55	0.41
53:3:842:U:H2'	53:3:844:G:H5'	2.02	0.41
57:A2:28:LEU:HB2	57:A2:201:LEU:HB3	2.02	0.41
58:B1:144:TYR:OH	58:B1:162:GLU:OE1	2.34	0.41
58:B1:1350:ASN:HA	58:B1:1353:VAL:HG12	2.02	0.41
59:B2:27:LEU:O	59:B2:528:ARG:NH1	2.43	0.41
59:B2:886:LYS:HE2	59:B2:918:LEU:HD13	2.03	0.41
64:6:53:G:H1'	65:a:55:SER:OG	2.21	0.41
9:I:80:ARG:HG3	53:3:613:C:OP1	2.21	0.41
9:I:205:LYS:NZ	53:3:26:A:H2	2.19	0.41
12:L:83:THR:O	12:L:83:THR:HG22	2.21	0.41
14:N:18:VAL:HG22	14:N:64:ILE:HG23	2.02	0.41
17:Q:101:LEU:O	17:Q:103:CYS:N	2.54	0.41
31:f:148:ARG:HA	31:f:161:VAL:HB	2.03	0.41
32:g:2:GLN:HE21	32:g:20:ASN:HB2	1.85	0.41
33:i:94:LYS:NZ	51:1:1076:C:H4'	2.36	0.41
33:i:100:ILE:HB	33:i:139:VAL:HG12	2.02	0.41
51:1:1091:G:H2'	51:1:1092:C:C6	2.56	0.41
53:3:78:A:H61	53:3:91:U:H3	1.69	0.41
53:3:1201:A:H4'	53:3:1202:U:C5'	2.49	0.41
53:3:1230:C:O2'	53:3:1231:G:H5'	2.20	0.41
53:3:1255:G:H2'	53:3:1279:G:H1	1.85	0.41
58:B1:839:VAL:HG12	58:B1:864:LEU:HD12	2.02	0.41
58:B1:1050:THR:HG23	58:B1:1057:SER:HB3	2.03	0.41
59:B2:746:ALA:O	59:B2:974:ARG:NH2	2.45	0.41
1:A:1:MET:HB2	52:2:43:C:OP1	2.20	0.41
1:A:64:PHE:HA	53:3:1011:C:H5'	2.03	0.41
2:B:7:PRO:HD2	51:1:1263:U:O2'	2.21	0.41
9:I:145:ARG:HH22	9:I:147:LYS:HD2	1.86	0.41
11:K:44:ARG:HA	11:K:58:HIS:HA	2.03	0.41
17:Q:114:SER:N	53:3:502:A:OP1	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:86:ALA:HB1	19:S:91:GLU:HB2	2.03	0.41
25:Y:66:ILE:HG23	25:Y:70:LYS:HD3	2.01	0.41
30:e:65:LEU:HD11	52:2:41:G:H2'	2.02	0.41
33:i:135:MET:SD	51:1:1063:G:H1'	2.60	0.41
36:l:99:ASN:ND2	51:1:621:A:OP2	2.54	0.41
44:t:8:LEU:O	49:y:29:ARG:NH1	2.53	0.41
47:w:19:VAL:HG13	47:w:34:VAL:HG22	2.03	0.41
51:1:610:C:O5'	51:1:610:C:H6	2.03	0.41
51:1:732:C:H2'	51:1:733:G:O4'	2.21	0.41
51:1:1137:G:H2'	51:1:1138:G:H8	1.85	0.41
51:1:1341:G:H5''	51:1:1397:U:O2	2.21	0.41
51:1:1429:G:H2'	51:1:1430:G:H8	1.85	0.41
51:1:2700:A:H2'	51:1:2701:U:C6	2.56	0.41
51:1:2739:U:O2'	51:1:2740:A:H5'	2.21	0.41
53:3:20:U:H2'	53:3:21:G:O4'	2.20	0.41
53:3:55:A:C4	66:0:329:PHE:HB3	2.56	0.41
53:3:244:U:O4	53:3:906:A:H1'	2.20	0.41
53:3:987:G:H2'	53:3:988:G:C8	2.55	0.41
53:3:1448:C:H2'	53:3:1449:C:C6	2.56	0.41
55:8:14:DC:C2	55:8:15:DC:C5	3.09	0.41
58:B1:239:LEU:N	58:B1:239:LEU:HD23	2.36	0.41
58:B1:245:LEU:CG	58:B1:246:PRO:HD2	2.47	0.41
58:B1:279:LEU:HD13	58:B1:299:LEU:HD13	2.02	0.41
58:B1:616:PRO:HA	58:B1:619:ILE:HG22	2.02	0.41
58:B1:1177:ILE:HD12	58:B1:1186:TYR:HE2	1.85	0.41
59:B2:310:ILE:HG21	59:B2:325:LEU:HB3	2.03	0.41
59:B2:590:PRO:HB2	59:B2:655:VAL:HG21	2.01	0.41
59:B2:657:THR:HG21	59:B2:1188:ASP:HB2	2.03	0.41
66:0:145:ASP:CG	69:0:801:GDP:HN21	2.29	0.41
66:0:162:LEU:HD23	66:0:162:LEU:HA	1.94	0.41
66:0:200:VAL:HG23	66:0:201:THR:HG23	2.02	0.41
66:0:521:ASP:HB2	66:0:579:HIS:HD2	1.86	0.41
15:O:15:HIS:HD2	53:3:1152:A:H5'	1.86	0.41
27:b:179:GLU:HB2	27:b:270:ARG:HB3	2.02	0.41
28:c:47:ALA:HA	28:c:84:LEU:HG	2.04	0.41
29:d:131:THR:HG23	51:1:321:U:H5''	2.03	0.41
29:d:163:ASN:HD21	51:1:322:A:C2'	2.32	0.41
32:g:14:SER:O	32:g:14:SER:OG	2.36	0.41
34:j:132:HIS:ND1	51:1:7:G:H5'	2.36	0.41
37:m:88:ASN:OD1	37:m:88:ASN:N	2.52	0.41
41:q:24:TYR:HE1	51:1:17:G:H4'	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:4:U:H2'	51:1:5:A:C8	2.56	0.41
51:1:399:U:OP1	51:1:2090:A:H5''	2.21	0.41
51:1:535:G:H2'	51:1:536:G:O4'	2.20	0.41
51:1:1944:U:O2'	51:1:1945:G:H5''	2.21	0.41
51:1:2360:G:H2'	51:1:2361:G:O4'	2.21	0.41
53:3:26:A:H61	53:3:558:G:H1'	1.86	0.41
53:3:346:G:H3'	53:3:346:G:N3	2.36	0.41
53:3:619:U:H3'	53:3:619:U:H6	1.86	0.41
55:8:2:DC:C6	55:8:2:DC:H5'	2.56	0.41
57:A1:48:LEU:HA	57:A1:48:LEU:HD12	1.78	0.41
58:B1:233:LYS:HA	58:B1:234:PRO:HD3	1.89	0.41
58:B1:777:HIS:CD2	59:B2:550:VAL:HG13	2.56	0.41
58:B1:1263:LYS:NZ	58:B1:1315:ALA:O	2.49	0.41
59:B2:854:ILE:HG21	59:B2:917:SER:CB	2.39	0.41
27:b:129:LEU:HD12	27:b:133:ASN:HB2	2.03	0.40
28:c:29:VAL:HB	28:c:98:VAL:HG22	2.02	0.40
31:f:159:LYS:NZ	51:1:2657:A:O2'	2.53	0.40
43:s:42:LYS:CB	51:1:2010:G:H5''	2.47	0.40
49:y:32:ALA:HB2	49:y:37:LEU:HD23	2.03	0.40
51:1:284:U:H2'	51:1:285:G:C8	2.55	0.40
51:1:1130:U:O2'	51:1:1131:G:OP1	2.35	0.40
51:1:2004:G:H2'	51:1:2005:A:O4'	2.21	0.40
51:1:2548:U:C4	51:1:2549:G:N7	2.88	0.40
53:3:471:U:H2'	53:3:472:U:C6	2.56	0.40
53:3:546:A:H4'	53:3:548:G:O3'	2.20	0.40
53:3:623:C:H2'	53:3:624:C:C6	2.56	0.40
53:3:1097:C:H2'	53:3:1098:C:C6	2.56	0.40
57:A2:42:ALA:HB1	57:A2:224:LEU:HD11	2.03	0.40
58:B1:68:TYR:CB	58:B1:75:TYR:HE2	2.34	0.40
66:0:352:SER:OG	66:0:396:THR:O	2.33	0.40
1:A:27:THR:OG1	30:e:58:ALA:O	2.37	0.40
12:L:65:LEU:HA	12:L:68:VAL:HG12	2.03	0.40
19:S:50:LEU:HD23	19:S:50:LEU:HA	1.85	0.40
19:S:97:LYS:HB3	19:S:97:LYS:HE2	1.86	0.40
27:b:144:GLU:OE1	27:b:150:GLY:N	2.55	0.40
27:b:211:ARG:HG3	51:1:764:A:N3	2.36	0.40
42:r:16:GLU:HG2	42:r:101:ILE:HG12	2.04	0.40
45:u:48:VAL:HA	45:u:49:PRO:HD3	1.96	0.40
51:1:94:A:H2'	51:1:95:A:O4'	2.21	0.40
51:1:179:C:O2'	51:1:180:G:H5'	2.21	0.40
51:1:227:A:H1'	51:1:229:C:H41	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:272:A:H2'	51:1:273:G:H8	1.86	0.40
51:1:631:A:H1'	51:1:2415:G:O2'	2.21	0.40
51:1:917:A:C2	52:2:79:G:N3	2.88	0.40
51:1:1380:G:C8	51:1:1380:G:O5'	2.74	0.40
51:1:1508:A:H2'	51:1:1509:A:O4'	2.21	0.40
51:1:1757:A:O5'	51:1:1757:A:H8	2.04	0.40
51:1:2441:U:H2'	51:1:2442:C:H6	1.87	0.40
53:3:401:C:H2'	53:3:402:G:C8	2.56	0.40
53:3:812:G:OP1	53:3:903:G:H1'	2.21	0.40
53:3:876:C:H2'	53:3:877:G:H8	1.86	0.40
57:A2:104:LYS:O	57:A2:139:SER:OG	2.36	0.40
58:B1:1361:THR:N	59:B2:1282:GLY:O	2.53	0.40
59:B2:861:ALA:HB1	59:B2:882:ILE:HD13	2.01	0.40
66:0:176:GLU:O	66:0:178:HIS:N	2.54	0.40
66:0:197:ASP:C	66:0:199:GLY:H	2.29	0.40
66:0:230:SER:HB2	66:0:233:LEU:HB3	2.03	0.40
4:D:19:ARG:NH2	51:1:124:G:C5	2.89	0.40
12:L:78:ARG:HA	12:L:78:ARG:HD3	1.81	0.40
20:T:11:VAL:HG23	20:T:26:VAL:HG11	2.04	0.40
21:U:4:ILE:HD12	21:U:67:ILE:HG13	2.03	0.40
33:i:73:PRO:HA	33:i:74:PRO:HD3	1.94	0.40
36:l:62:PRO:HG3	51:1:2393:U:H5''	2.04	0.40
48:x:9:LYS:HZ2	48:x:9:LYS:HG2	1.75	0.40
51:1:118:A:N3	51:1:178:G:H1'	2.36	0.40
51:1:123:G:H4'	51:1:1376:C:O5'	2.21	0.40
51:1:606:U:H4'	51:1:658:U:HO2'	1.86	0.40
51:1:935:C:H2'	51:1:936:A:H8	1.87	0.40
51:1:1507:C:H2'	51:1:1508:A:O4'	2.21	0.40
51:1:1747:U:H2'	51:1:1748:C:C6	2.56	0.40
51:1:1808:A:H3'	51:1:1809:A:C8	2.56	0.40
51:1:1913:A:O2'	67:h:4:SER:HA	2.22	0.40
53:3:78:A:H8	53:3:78:A:O5'	2.05	0.40
53:3:1100:C:C2	53:3:1102:A:H5'	2.57	0.40
58:B1:111:THR:HG23	58:B1:300:GLN:HA	2.03	0.40
58:B1:390:LEU:HD13	58:B1:390:LEU:H	1.86	0.40
58:B1:472:LEU:HD11	59:B2:1294:LYS:HG2	2.03	0.40
58:B1:515:ARG:HG2	58:B1:516:ASP:H	1.85	0.40
59:B2:741:MET:HE3	59:B2:974:ARG:HH12	1.85	0.40
59:B2:870:ILE:HB	59:B2:944:ARG:HD3	2.02	0.40
59:B2:912:ASP:HB3	59:B2:913:VAL:H	1.72	0.40
63:5:17:C:H2'	63:5:18:G:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:5:37:A:H3'	63:5:38:A:C8	2.56	0.40
65:a:167:LYS:HE2	65:a:167:LYS:HB2	1.76	0.40
7:G:203:ASP:OD1	7:G:203:ASP:N	2.54	0.40
10:J:24:VAL:HG12	10:J:25:LYS:H	1.87	0.40
12:L:3:ARG:HB3	12:L:4:ARG:HH11	1.87	0.40
17:Q:40:THR:HG21	67:h:6:5OH:OS	2.21	0.40
18:R:97:ARG:NH1	53:3:1308:U:H5	2.19	0.40
19:S:63:CYS:SG	19:S:64:ARG:N	2.94	0.40
24:X:79:TYR:CE1	53:3:1226:C:H4'	2.57	0.40
27:b:68:ARG:O	27:b:188:ARG:NH2	2.55	0.40
44:t:1:MET:HE2	51:1:136:G:H21	1.85	0.40
46:v:80:HIS:H	46:v:86:LEU:HA	1.86	0.40
51:1:1461:C:O5'	51:1:1461:C:H6	2.05	0.40
51:1:2011:U:H2'	51:1:2012:G:O4'	2.22	0.40
51:1:2853:C:H2'	51:1:2854:G:H8	1.86	0.40
53:3:216:U:O3'	53:3:464:U:H4'	2.21	0.40
53:3:404:G:H2'	53:3:405:U:C6	2.55	0.40
53:3:702:A:H2'	53:3:702:A:N3	2.37	0.40
58:B1:109:SER:CB	58:B1:296:LYS:HG2	2.51	0.40
58:B1:182:ALA:HB1	58:B1:238:ILE:CG2	2.52	0.40
58:B1:820:ILE:HD11	58:B1:822:MET:HE2	2.02	0.40
59:B2:805:MET:HB2	59:B2:805:MET:HE3	1.86	0.40
65:a:6:LYS:HA	65:a:9:ARG:HG2	2.03	0.40
7:G:155:GLY:HA3	61:NA:219:GLU:CB	2.50	0.40
14:N:104:THR:HG22	14:N:106:ASP:H	1.86	0.40
17:Q:58:ASN:OD1	17:Q:58:ASN:N	2.52	0.40
23:W:47:ARG:H	23:W:47:ARG:HG2	1.60	0.40
26:Z:7:GLU:HG3	26:Z:15:LEU:HB2	2.02	0.40
29:d:148:ILE:HB	29:d:169:VAL:HG12	2.04	0.40
32:g:8:LYS:HG3	32:g:14:SER:HA	2.04	0.40
36:l:63:LYS:HE3	51:1:2394:C:H5''	2.03	0.40
46:v:26:PHE:HE2	46:v:89:ILE:HG13	1.87	0.40
51:1:859:G:O2'	51:1:860:U:H6	2.04	0.40
51:1:987:C:H2'	51:1:988:A:O4'	2.21	0.40
51:1:2701:U:H3'	51:1:2702:G:C5'	2.51	0.40
51:1:2722:G:H8	51:1:2722:G:O5'	2.05	0.40
53:3:26:A:N6	53:3:558:G:H1'	2.36	0.40
58:B1:349:TYR:HA	59:B2:1246:ARG:O	2.22	0.40
59:B2:159:SER:HB2	59:B2:442:VAL:HG11	2.04	0.40
66:0:68:THR:HG22	66:0:69:THR:H	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	64/70 (91%)	54 (84%)	10 (16%)	0	100	100
2	B	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
3	C	48/55 (87%)	46 (96%)	2 (4%)	0	100	100
4	D	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
5	E	62/65 (95%)	56 (90%)	5 (8%)	1 (2%)	7	37
6	F	36/38 (95%)	33 (92%)	3 (8%)	0	100	100
7	G	216/241 (90%)	186 (86%)	29 (13%)	1 (0%)	24	63
8	H	204/233 (88%)	184 (90%)	19 (9%)	1 (0%)	24	63
9	I	203/206 (98%)	178 (88%)	24 (12%)	1 (0%)	24	63
10	J	155/167 (93%)	131 (84%)	22 (14%)	2 (1%)	9	41
11	K	98/135 (73%)	83 (85%)	14 (14%)	1 (1%)	12	47
12	L	149/179 (83%)	129 (87%)	18 (12%)	2 (1%)	9	41
13	M	127/130 (98%)	120 (94%)	7 (6%)	0	100	100
14	N	125/130 (96%)	95 (76%)	25 (20%)	5 (4%)	2	18
15	O	96/103 (93%)	77 (80%)	18 (19%)	1 (1%)	12	47
16	P	114/129 (88%)	90 (79%)	22 (19%)	2 (2%)	6	33
17	Q	121/124 (98%)	97 (80%)	18 (15%)	6 (5%)	1	16
18	R	112/118 (95%)	99 (88%)	12 (11%)	1 (1%)	14	49
19	S	98/101 (97%)	80 (82%)	15 (15%)	3 (3%)	3	22
20	T	86/89 (97%)	77 (90%)	8 (9%)	1 (1%)	10	43
21	U	80/82 (98%)	69 (86%)	10 (12%)	1 (1%)	9	41
22	V	78/84 (93%)	67 (86%)	10 (13%)	1 (1%)	9	41
23	W	63/75 (84%)	59 (94%)	4 (6%)	0	100	100
24	X	77/92 (84%)	69 (90%)	8 (10%)	0	100	100
25	Y	83/87 (95%)	80 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	Z	63/71 (89%)	45 (71%)	18 (29%)	0	100	100
27	b	269/273 (98%)	233 (87%)	31 (12%)	5 (2%)	6	32
28	c	207/209 (99%)	181 (87%)	25 (12%)	1 (0%)	24	63
29	d	199/201 (99%)	186 (94%)	13 (6%)	0	100	100
30	e	175/179 (98%)	155 (89%)	18 (10%)	2 (1%)	11	45
31	f	174/177 (98%)	152 (87%)	19 (11%)	3 (2%)	7	35
32	g	147/149 (99%)	133 (90%)	13 (9%)	1 (1%)	18	55
33	i	139/142 (98%)	116 (84%)	22 (16%)	1 (1%)	18	55
34	j	140/142 (99%)	128 (91%)	11 (8%)	1 (1%)	18	55
35	k	120/123 (98%)	99 (82%)	19 (16%)	2 (2%)	7	35
36	l	141/144 (98%)	121 (86%)	20 (14%)	0	100	100
37	m	134/136 (98%)	126 (94%)	8 (6%)	0	100	100
38	n	118/127 (93%)	101 (86%)	17 (14%)	0	100	100
39	o	114/117 (97%)	103 (90%)	10 (9%)	1 (1%)	14	49
40	p	112/115 (97%)	102 (91%)	10 (9%)	0	100	100
41	q	115/118 (98%)	111 (96%)	3 (3%)	1 (1%)	14	49
42	r	101/103 (98%)	86 (85%)	14 (14%)	1 (1%)	12	47
43	s	108/110 (98%)	99 (92%)	9 (8%)	0	100	100
44	t	91/100 (91%)	78 (86%)	13 (14%)	0	100	100
45	u	100/104 (96%)	81 (81%)	18 (18%)	1 (1%)	12	47
46	v	92/94 (98%)	86 (94%)	6 (6%)	0	100	100
47	w	73/85 (86%)	68 (93%)	5 (7%)	0	100	100
48	x	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
49	y	61/63 (97%)	57 (93%)	3 (5%)	1 (2%)	7	37
50	z	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
57	A1	295/329 (90%)	276 (94%)	19 (6%)	0	100	100
57	A2	282/329 (86%)	271 (96%)	11 (4%)	0	100	100
58	B1	1329/1407 (94%)	1205 (91%)	119 (9%)	5 (0%)	30	67
59	B2	1338/1342 (100%)	1206 (90%)	128 (10%)	4 (0%)	36	71
60	W0	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
61	NA	490/495 (99%)	482 (98%)	8 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
62	NG	150/181 (83%)	135 (90%)	11 (7%)	4 (3%)	4	25
65	a	130/234 (56%)	112 (86%)	18 (14%)	0	100	100
66	0	695/716 (97%)	621 (89%)	71 (10%)	3 (0%)	30	67
67	h	2/6 (33%)	1 (50%)	1 (50%)	0	100	100
All	All	10508/11185 (94%)	9407 (90%)	1034 (10%)	67 (1%)	23	58

All (67) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	E	31	ILE
9	I	29	THR
14	N	57	VAL
14	N	90	ASP
14	N	91	GLU
17	Q	87	LYS
20	T	46	LYS
30	e	175	PRO
31	f	45	ALA
32	g	136	SER
35	k	92	GLU
42	r	54	VAL
49	y	24	GLU
58	B1	121	PRO
10	J	75	LEU
11	K	56	LYS
17	Q	3	VAL
17	Q	24	GLU
17	Q	102	ASP
19	S	60	ARG
21	U	45	GLU
27	b	46	GLY
28	c	197	THR
33	i	121	ILE
59	B2	43	PRO
59	B2	918	LEU
62	NG	102	PRO
66	0	176	GLU
66	0	177	GLU
12	L	6	ILE
17	Q	101	LEU
17	Q	108	ASP

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Mol	Chain	Res	Type
19	S	61	ASN
27	b	205	GLY
39	o	34	HIS
41	q	5	ARG
58	B1	904	ALA
59	B2	888	THR
62	NG	124	PRO
7	G	20	ARG
14	N	23	GLY
16	P	89	GLY
22	V	50	ASN
31	f	44	HIS
58	B1	43	THR
58	B1	193	ASP
14	N	102	PHE
27	b	255	LYS
30	e	174	PHE
31	f	174	LYS
35	k	93	GLN
45	u	6	ARG
58	B1	1325	PHE
66	0	198	GLN
16	P	88	PRO
18	R	7	ASN
19	S	35	ALA
62	NG	129	GLU
34	j	110	PRO
27	b	232	GLY
8	H	12	GLY
12	L	79	VAL
27	b	240	GLY
59	B2	1317	PRO
62	NG	122	PRO
10	J	97	PRO
15	O	57	VAL

5.3.2 Protein sidechains ⓘ

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	59/62 (95%)	56 (95%)	3 (5%)	21	43
2	B	47/48 (98%)	44 (94%)	3 (6%)	16	38
3	C	45/49 (92%)	45 (100%)	0	100	100
4	D	38/38 (100%)	37 (97%)	1 (3%)	40	60
5	E	51/52 (98%)	51 (100%)	0	100	100
6	F	34/34 (100%)	34 (100%)	0	100	100
7	G	180/199 (90%)	175 (97%)	5 (3%)	38	59
8	H	169/190 (89%)	165 (98%)	4 (2%)	43	63
9	I	172/173 (99%)	169 (98%)	3 (2%)	53	67
10	J	118/126 (94%)	115 (98%)	3 (2%)	42	62
11	K	87/116 (75%)	83 (95%)	4 (5%)	24	46
12	L	124/147 (84%)	122 (98%)	2 (2%)	55	69
13	M	104/105 (99%)	104 (100%)	0	100	100
14	N	105/107 (98%)	102 (97%)	3 (3%)	37	58
15	O	86/90 (96%)	80 (93%)	6 (7%)	14	36
16	P	89/99 (90%)	88 (99%)	1 (1%)	65	74
17	Q	103/104 (99%)	98 (95%)	5 (5%)	22	44
18	R	92/96 (96%)	91 (99%)	1 (1%)	65	74
19	S	83/84 (99%)	82 (99%)	1 (1%)	63	73
20	T	76/77 (99%)	75 (99%)	1 (1%)	61	72
21	U	65/65 (100%)	64 (98%)	1 (2%)	57	70
22	V	74/78 (95%)	73 (99%)	1 (1%)	59	71
23	W	56/65 (86%)	54 (96%)	2 (4%)	31	52
24	X	70/79 (89%)	69 (99%)	1 (1%)	59	71
25	Y	65/66 (98%)	65 (100%)	0	100	100
26	Z	55/61 (90%)	52 (94%)	3 (6%)	19	42
27	b	216/218 (99%)	212 (98%)	4 (2%)	50	66
28	c	164/164 (100%)	162 (99%)	2 (1%)	63	73
29	d	165/165 (100%)	163 (99%)	2 (1%)	63	73
30	e	148/150 (99%)	147 (99%)	1 (1%)	76	79
31	f	137/138 (99%)	137 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	g	114/114 (100%)	112 (98%)	2 (2%)	51	67
33	i	109/110 (99%)	95 (87%)	14 (13%)	4	17
34	j	116/116 (100%)	115 (99%)	1 (1%)	70	76
35	k	103/104 (99%)	100 (97%)	3 (3%)	37	58
36	l	102/103 (99%)	100 (98%)	2 (2%)	48	65
37	m	109/109 (100%)	109 (100%)	0	100	100
38	n	100/103 (97%)	99 (99%)	1 (1%)	68	76
39	o	86/87 (99%)	86 (100%)	0	100	100
40	p	99/100 (99%)	97 (98%)	2 (2%)	48	65
41	q	89/90 (99%)	86 (97%)	3 (3%)	32	54
42	r	84/84 (100%)	81 (96%)	3 (4%)	31	52
43	s	93/93 (100%)	93 (100%)	0	100	100
44	t	80/84 (95%)	79 (99%)	1 (1%)	61	72
45	u	82/85 (96%)	81 (99%)	1 (1%)	63	73
46	v	78/78 (100%)	77 (99%)	1 (1%)	61	72
47	w	57/63 (90%)	56 (98%)	1 (2%)	51	67
48	x	67/68 (98%)	67 (100%)	0	100	100
49	y	55/55 (100%)	55 (100%)	0	100	100
50	z	48/49 (98%)	46 (96%)	2 (4%)	26	48
57	A1	185/286 (65%)	174 (94%)	11 (6%)	18	40
57	A2	186/286 (65%)	185 (100%)	1 (0%)	81	81
58	B1	1110/1168 (95%)	1021 (92%)	89 (8%)	11	32
59	B2	1150/1157 (99%)	1119 (97%)	31 (3%)	39	59
60	W0	70/75 (93%)	69 (99%)	1 (1%)	59	71
65	a	110/181 (61%)	110 (100%)	0	100	100
66	0	574/588 (98%)	546 (95%)	28 (5%)	22	44
67	h	2/2 (100%)	2 (100%)	0	100	100
All	All	8135/8683 (94%)	7874 (97%)	261 (3%)	35	55

All (261) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	LEU

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Mol	Chain	Res	Type
1	A	35	ASP
1	A	57	VAL
2	B	2	VAL
2	B	21	LEU
2	B	24	VAL
4	D	43	THR
7	G	17	HIS
7	G	20	ARG
7	G	46	VAL
7	G	48	MET
7	G	160	LEU
8	H	62	SER
8	H	63	ILE
8	H	156	LEU
8	H	172	VAL
9	I	32	LYS
9	I	33	ILE
9	I	170	LEU
10	J	120	HIS
10	J	121	ASN
10	J	123	LEU
11	K	47	LEU
11	K	53	LYS
11	K	92	THR
11	K	93	LYS
12	L	29	LEU
12	L	134	VAL
14	N	20	ILE
14	N	21	LYS
14	N	24	ASN
15	O	83	THR
15	O	84	VAL
15	O	87	LEU
15	O	89	ARG
15	O	99	GLN
15	O	102	LEU
16	P	15	VAL
17	Q	20	VAL
17	Q	42	LYS
17	Q	43	LYS
17	Q	45	ASN
17	Q	97	VAL

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Mol	Chain	Res	Type
18	R	82	LEU
19	S	78	LEU
20	T	55	LEU
21	U	19	VAL
22	V	40	THR
23	W	28	LEU
23	W	47	ARG
24	X	38	THR
26	Z	24	LYS
26	Z	35	GLU
26	Z	40	PRO
27	b	12	ARG
27	b	18	VAL
27	b	171	VAL
27	b	194	VAL
28	c	79	LEU
28	c	98	VAL
29	d	79	ARG
29	d	80	SER
30	e	108	PRO
32	g	5	LEU
32	g	143	ILE
33	i	2	LYS
33	i	3	LYS
33	i	5	GLN
33	i	18	ASN
33	i	23	VAL
33	i	27	LEU
33	i	29	GLN
33	i	67	THR
33	i	72	THR
33	i	117	THR
33	i	124	MET
33	i	131	THR
33	i	134	SER
33	i	135	MET
34	j	10	THR
35	k	61	VAL
35	k	85	VAL
35	k	86	LEU
36	l	85	VAL
36	l	127	VAL

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Mol	Chain	Res	Type
38	n	50	PRO
40	p	32	VAL
40	p	109	ILE
41	q	82	LEU
41	q	84	LYS
41	q	86	SER
42	r	48	LYS
42	r	49	ILE
42	r	51	VAL
44	t	67	VAL
45	u	27	VAL
46	v	70	ILE
47	w	19	VAL
50	z	10	ARG
50	z	15	ARG
57	A1	9	LEU
57	A1	12	ARG
57	A1	13	LEU
57	A1	18	GLN
57	A1	19	VAL
57	A1	22	THR
57	A1	27	THR
57	A1	28	LEU
57	A1	33	ARG
57	A1	46	ILE
57	A1	48	LEU
57	A2	74	VAL
58	B1	24	LEU
58	B1	40	LYS
58	B1	42	GLU
58	B1	44	ILE
58	B1	47	ARG
58	B1	49	PHE
58	B1	50	LYS
58	B1	60	ARG
58	B1	66	LYS
58	B1	69	GLU
58	B1	71	LEU
58	B1	74	LYS
58	B1	76	LYS
58	B1	78	LEU
58	B1	80	HIS

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Mol	Chain	Res	Type
58	B1	81	ARG
58	B1	87	LYS
58	B1	91	GLU
58	B1	93	THR
58	B1	94	GLN
58	B1	95	THR
58	B1	96	LYS
58	B1	99	ARG
58	B1	100	GLU
58	B1	114	ILE
58	B1	117	LEU
58	B1	120	LEU
58	B1	126	LEU
58	B1	132	LEU
58	B1	135	ILE
58	B1	142	GLU
58	B1	144	TYR
58	B1	145	VAL
58	B1	146	VAL
58	B1	147	ILE
58	B1	152	THR
58	B1	154	LEU
58	B1	157	GLN
58	B1	159	ILE
58	B1	172	PHE
58	B1	174	ASP
58	B1	175	GLU
58	B1	180	MET
58	B1	190	LYS
58	B1	193	ASP
58	B1	196	GLN
58	B1	210	SER
58	B1	212	THR
58	B1	216	LYS
58	B1	222	LYS
58	B1	223	LEU
58	B1	227	PHE
58	B1	233	LYS
58	B1	237	MET
58	B1	238	ILE
58	B1	239	LEU
58	B1	240	THR

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Mol	Chain	Res	Type
58	B1	244	VAL
58	B1	255	LEU
58	B1	256	ASP
58	B1	259	ARG
58	B1	317	THR
58	B1	322	ARG
58	B1	324	LEU
58	B1	363	LEU
58	B1	385	LEU
58	B1	386	GLU
58	B1	387	LEU
58	B1	390	LEU
58	B1	393	THR
58	B1	394	ILE
58	B1	395	LYS
58	B1	416	ILE
58	B1	417	ARG
58	B1	425	ARG
58	B1	506	VAL
58	B1	514	THR
58	B1	800	LEU
58	B1	807	LEU
58	B1	839	VAL
58	B1	901	ARG
58	B1	903	LEU
58	B1	1172	LYS
58	B1	1181	ASP
58	B1	1233	ILE
58	B1	1327	GLU
58	B1	1328	THR
58	B1	1331	VAL
58	B1	1332	LEU
59	B2	4	SER
59	B2	44	GLU
59	B2	49	LEU
59	B2	56	VAL
59	B2	146	VAL
59	B2	483	ASP
59	B2	487	LEU
59	B2	516	ASP
59	B2	538	LEU
59	B2	540	ARG

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Mol	Chain	Res	Type
59	B2	545	PHE
59	B2	546	GLU
59	B2	615	VAL
59	B2	857	VAL
59	B2	859	GLU
59	B2	887	VAL
59	B2	890	LYS
59	B2	893	THR
59	B2	894	GLN
59	B2	895	LEU
59	B2	900	LYS
59	B2	901	LEU
59	B2	902	LEU
59	B2	903	ARG
59	B2	905	ILE
59	B2	912	ASP
59	B2	918	LEU
59	B2	920	VAL
59	B2	922	ASN
59	B2	1076	ILE
59	B2	1151	LEU
60	W0	63	ILE
66	0	31	LEU
66	0	97	ILE
66	0	214	LEU
66	0	360	PHE
66	0	415	VAL
66	0	418	ILE
66	0	483	VAL
66	0	485	LYS
66	0	488	VAL
66	0	507	LYS
66	0	512	ARG
66	0	519	VAL
66	0	522	MET
66	0	525	LEU
66	0	526	GLU
66	0	551	PRO
66	0	584	HIS
66	0	626	GLU
66	0	627	ASN
66	0	628	THR

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Mol	Chain	Res	Type
66	0	630	ASP
66	0	636	SER
66	0	638	ARG
66	0	642	LEU
66	0	643	LYS
66	0	646	GLU
66	0	648	GLU
66	0	649	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (151) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	HIS
2	B	5	ASN
4	D	26	ASN
7	G	17	HIS
7	G	57	ASN
7	G	93	HIS
7	G	176	ASN
8	H	138	GLN
8	H	139	ASN
9	I	53	GLN
9	I	58	GLN
9	I	84	ASN
10	J	81	GLN
10	J	88	HIS
10	J	131	ASN
10	J	145	ASN
10	J	147	ASN
12	L	121	ASN
12	L	147	ASN
13	M	66	GLN
14	N	4	GLN
14	N	24	ASN
14	N	30	ASN
15	O	15	HIS
15	O	35	GLN
16	P	27	ASN
16	P	37	GLN
16	P	39	ASN
16	P	63	GLN
16	P	100	ASN

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Mol	Chain	Res	Type
17	Q	45	ASN
17	Q	76	HIS
17	Q	95	HIS
17	Q	111	GLN
18	R	13	HIS
19	S	48	GLN
20	T	27	GLN
21	U	26	ASN
21	U	63	GLN
23	W	51	GLN
25	Y	54	GLN
25	Y	67	HIS
25	Y	69	ASN
25	Y	74	HIS
26	Z	63	ASN
27	b	24	HIS
27	b	52	HIS
27	b	57	HIS
27	b	114	GLN
27	b	152	GLN
28	c	42	ASN
28	c	49	GLN
28	c	58	ASN
28	c	136	ASN
28	c	164	GLN
29	d	94	GLN
29	d	97	ASN
29	d	163	ASN
30	e	26	GLN
31	f	63	GLN
31	f	87	GLN
31	f	103	ASN
31	f	110	HIS
31	f	142	GLN
32	g	11	ASN
32	g	73	ASN
32	g	135	HIS
33	i	110	GLN
34	j	40	HIS
34	j	135	GLN
35	k	3	GLN
35	k	9	ASN

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Mol	Chain	Res	Type
36	l	99	ASN
37	m	3	GLN
37	m	17	ASN
37	m	97	GLN
38	n	9	GLN
38	n	73	ASN
38	n	81	ASN
39	o	61	GLN
39	o	98	GLN
40	p	55	HIS
40	p	74	GLN
41	q	70	GLN
42	r	11	GLN
43	s	57	ASN
44	t	15	HIS
44	t	48	GLN
44	t	59	ASN
45	u	68	ASN
46	v	49	ASN
46	v	78	GLN
47	w	8	ASN
47	w	53	HIS
48	x	22	ASN
48	x	35	HIS
49	y	20	ASN
49	y	25	GLN
49	y	31	GLN
50	z	8	GLN
57	A1	66	HIS
57	A1	84	ASN
57	A1	117	HIS
57	A1	128	HIS
57	A1	227	GLN
57	A2	23	HIS
57	A2	227	GLN
58	B1	45	ASN
58	B1	196	GLN
58	B1	364	HIS
58	B1	424	ASN
58	B1	450	HIS
58	B1	469	HIS
58	B1	805	GLN

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Mol	Chain	Res	Type
58	B1	817	HIS
58	B1	865	HIS
58	B1	1195	GLN
58	B1	1238	GLN
58	B1	1259	GLN
59	B2	69	GLN
59	B2	314	ASN
59	B2	330	HIS
59	B2	343	HIS
59	B2	518	ASN
59	B2	554	HIS
59	B2	580	GLN
59	B2	688	GLN
59	B2	762	ASN
59	B2	808	ASN
59	B2	965	GLN
59	B2	1237	HIS
59	B2	1268	GLN
59	B2	1313	HIS
60	W0	7	GLN
60	W0	31	GLN
60	W0	62	GLN
65	a	24	ASN
65	a	47	ASN
66	0	44	HIS
66	0	85	ASN
66	0	157	GLN
66	0	272	ASN
66	0	296	ASN
66	0	344	ASN
66	0	365	GLN
66	0	428	GLN
66	0	487	GLN
66	0	505	HIS
66	0	517	HIS
66	0	530	ASN
66	0	579	HIS

5.3.3 RNA ⓘ

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	1	2902/2904 (99%)	420 (14%)	10 (0%)
52	2	119/120 (99%)	12 (10%)	1 (0%)
53	3	1538/1542 (99%)	181 (11%)	6 (0%)
54	4	28/44 (63%)	13 (46%)	3 (10%)
63	5	75/76 (98%)	38 (50%)	7 (9%)
64	6	76/77 (98%)	18 (23%)	0
All	All	4738/4763 (99%)	682 (14%)	27 (0%)

All (682) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
51	1	10	A
51	1	12	U
51	1	35	G
51	1	42	A
51	1	46	G
51	1	51	G
51	1	63	A
51	1	71	A
51	1	74	A
51	1	75	G
51	1	98	G
51	1	102	U
51	1	103	A
51	1	119	A
51	1	120	U
51	1	139	U
51	1	140	C
51	1	141	G
51	1	142	A
51	1	149	A
51	1	162	U
51	1	163	C
51	1	181	A
51	1	196	A
51	1	215	G
51	1	216	A
51	1	219	A
51	1	221	A
51	1	222	A
51	1	228	C

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Mol	Chain	Res	Type
51	1	229	C
51	1	232	G
51	1	233	A
51	1	248	G
51	1	255	A
51	1	266	G
51	1	276	U
51	1	278	A
51	1	281	C
51	1	285	G
51	1	294	A
51	1	311	A
51	1	323	C
51	1	324	A
51	1	329	G
51	1	330	A
51	1	346	A
51	1	353	C
51	1	361	G
51	1	362	A
51	1	371	A
51	1	372	G
51	1	386	G
51	1	387	U
51	1	404	A
51	1	405	U
51	1	411	G
51	1	412	A
51	1	424	G
51	1	451	U
51	1	455	C
51	1	456	C
51	1	481	G
51	1	491	G
51	1	504	A
51	1	508	A
51	1	528	A
51	1	531	C
51	1	532	A
51	1	533	G
51	1	544	C
51	1	545	U

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Mol	Chain	Res	Type
51	1	563	A
51	1	572	A
51	1	573	U
51	1	586	A
51	1	588	U
51	1	603	A
51	1	614	A
51	1	627	A
51	1	637	A
51	1	646	U
51	1	654	A
51	1	655	A
51	1	664	G
51	1	686	U
51	1	687	C
51	1	695	G
51	1	717	C
51	1	730	A
51	1	740	C
51	1	747	C
51	1	748	G
51	1	749	A
51	1	760	G
51	1	764	A
51	1	774	G
51	1	776	G
51	1	782	A
51	1	784	G
51	1	785	G
51	1	803	U
51	1	805	G
51	1	812	C
51	1	819	A
51	1	827	U
51	1	828	U
51	1	830	G
51	1	845	A
51	1	846	U
51	1	856	G
51	1	858	G
51	1	860	U
51	1	869	G

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Mol	Chain	Res	Type
51	1	871	U
51	1	872	U
51	1	877	A
51	1	878	A
51	1	885	C
51	1	887	U
51	1	896	A
51	1	897	C
51	1	907	G
51	1	910	A
51	1	914	G
51	1	915	C
51	1	932	U
51	1	934	U
51	1	941	A
51	1	946	C
51	1	961	C
51	1	974	G
51	1	975	A
51	1	983	A
51	1	985	C
51	1	995	C
51	1	1012	U
51	1	1013	C
51	1	1021	A
51	1	1022	G
51	1	1023	U
51	1	1026	G
51	1	1033	U
51	1	1034	G
51	1	1045	C
51	1	1046	A
51	1	1047	G
51	1	1053	C
51	1	1055	G
51	1	1057	A
51	1	1058	U
51	1	1059	G
51	1	1062	G
51	1	1064	C
51	1	1065	U
51	1	1066	U

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Mol	Chain	Res	Type
51	1	1069	A
51	1	1070	A
51	1	1071	G
51	1	1072	C
51	1	1073	A
51	1	1076	C
51	1	1078	U
51	1	1080	A
51	1	1081	U
51	1	1082	U
51	1	1083	U
51	1	1084	A
51	1	1085	A
51	1	1086	A
51	1	1087	G
51	1	1088	A
51	1	1092	C
51	1	1104	C
51	1	1105	U
51	1	1106	G
51	1	1111	A
51	1	1131	G
51	1	1132	U
51	1	1133	A
51	1	1135	C
51	1	1143	A
51	1	1157	G
51	1	1172	C
51	1	1173	U
51	1	1175	A
51	1	1177	G
51	1	1179	G
51	1	1180	U
51	1	1211	C
51	1	1212	G
51	1	1221	C
51	1	1248	G
51	1	1249	U
51	1	1253	A
51	1	1256	G
51	1	1271	G
51	1	1272	A

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Mol	Chain	Res	Type
51	1	1273	U
51	1	1275	A
51	1	1289	C
51	1	1300	G
51	1	1301	A
51	1	1341	G
51	1	1345	C
51	1	1352	U
51	1	1365	A
51	1	1378	A
51	1	1379	U
51	1	1383	A
51	1	1398	C
51	1	1416	G
51	1	1419	A
51	1	1420	A
51	1	1427	A
51	1	1428	C
51	1	1458	U
51	1	1478	G
51	1	1482	G
51	1	1490	A
51	1	1491	G
51	1	1493	C
51	1	1504	A
51	1	1515	A
51	1	1524	G
51	1	1533	C
51	1	1534	U
51	1	1535	A
51	1	1536	C
51	1	1537	G
51	1	1555	G
51	1	1558	C
51	1	1559	U
51	1	1560	G
51	1	1569	A
51	1	1578	U
51	1	1584	U
51	1	1608	A
51	1	1611	C
51	1	1616	A

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Mol	Chain	Res	Type
51	1	1618	A
51	1	1647	U
51	1	1648	U
51	1	1654	A
51	1	1674	G
51	1	1682	G
51	1	1698	A
51	1	1715	G
51	1	1729	U
51	1	1730	C
51	1	1732	C
51	1	1733	G
51	1	1738	G
51	1	1758	U
51	1	1764	C
51	1	1773	A
51	1	1780	A
51	1	1785	A
51	1	1791	A
51	1	1800	C
51	1	1801	A
51	1	1808	A
51	1	1816	C
51	1	1820	U
51	1	1821	A
51	1	1829	A
51	1	1839	G
51	1	1857	G
51	1	1869	G
51	1	1870	C
51	1	1871	A
51	1	1901	A
51	1	1906	G
51	1	1907	G
51	1	1912	A
51	1	1913	A
51	1	1914	C
51	1	1925	C
51	1	1929	G
51	1	1930	G
51	1	1937	A
51	1	1938	A

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Mol	Chain	Res	Type
51	1	1944	U
51	1	1955	U
51	1	1961	C
51	1	1963	U
51	1	1967	C
51	1	1970	A
51	1	1971	U
51	1	1972	G
51	1	1991	U
51	1	1992	G
51	1	1993	U
51	1	1996	C
51	1	1997	C
51	1	2022	U
51	1	2023	C
51	1	2030	A
51	1	2031	A
51	1	2043	C
51	1	2055	C
51	1	2056	G
51	1	2060	A
51	1	2061	G
51	1	2062	A
51	1	2069	G
51	1	2072	C
51	1	2077	A
51	1	2092	U
51	1	2095	A
51	1	2096	C
51	1	2100	G
51	1	2106	U
51	1	2111	U
51	1	2112	G
51	1	2114	A
51	1	2118	U
51	1	2119	A
51	1	2120	G
51	1	2122	U
51	1	2125	G
51	1	2128	G
51	1	2132	U
51	1	2133	G

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Mol	Chain	Res	Type
51	1	2134	A
51	1	2138	G
51	1	2141	G
51	1	2145	C
51	1	2153	C
51	1	2158	A
51	1	2162	G
51	1	2166	U
51	1	2172	U
51	1	2173	A
51	1	2178	C
51	1	2182	U
51	1	2184	A
51	1	2192	U
51	1	2198	A
51	1	2203	U
51	1	2204	G
51	1	2211	A
51	1	2225	A
51	1	2239	G
51	1	2278	A
51	1	2283	C
51	1	2287	A
51	1	2297	A
51	1	2305	U
51	1	2309	A
51	1	2325	G
51	1	2327	A
51	1	2333	A
51	1	2337	G
51	1	2350	C
51	1	2385	C
51	1	2402	U
51	1	2406	A
51	1	2423	U
51	1	2425	A
51	1	2426	A
51	1	2427	C
51	1	2428	G
51	1	2429	G
51	1	2430	A
51	1	2435	A

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Mol	Chain	Res	Type
51	1	2441	U
51	1	2447	G
51	1	2448	A
51	1	2469	A
51	1	2474	U
51	1	2476	A
51	1	2480	C
51	1	2491	U
51	1	2502	G
51	1	2505	G
51	1	2518	A
51	1	2529	G
51	1	2535	G
51	1	2547	A
51	1	2554	U
51	1	2566	A
51	1	2567	G
51	1	2572	A
51	1	2602	A
51	1	2603	G
51	1	2609	U
51	1	2613	U
51	1	2615	U
51	1	2636	C
51	1	2646	C
51	1	2654	A
51	1	2689	U
51	1	2690	U
51	1	2714	G
51	1	2716	C
51	1	2720	U
51	1	2724	U
51	1	2733	A
51	1	2744	G
51	1	2748	A
51	1	2757	A
51	1	2758	A
51	1	2764	A
51	1	2765	A
51	1	2778	A
51	1	2779	U
51	1	2791	G

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Mol	Chain	Res	Type
51	1	2793	C
51	1	2798	U
51	1	2800	A
51	1	2801	G
51	1	2820	A
51	1	2821	A
51	1	2867	G
51	1	2868	A
51	1	2872	A
51	1	2880	C
51	1	2884	U
51	1	2893	A
52	2	2	G
52	2	4	C
52	2	13	G
52	2	35	C
52	2	53	A
52	2	56	G
52	2	67	G
52	2	88	C
52	2	89	U
52	2	90	C
52	2	108	A
52	2	109	A
53	3	6	G
53	3	9	G
53	3	22	G
53	3	32	A
53	3	39	G
53	3	44	A
53	3	48	C
53	3	50	A
53	3	51	A
53	3	54	C
53	3	71	A
53	3	78	A
53	3	84	U
53	3	85	U
53	3	87	C
53	3	92	U
53	3	94	G
53	3	100	G

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Mol	Chain	Res	Type
53	3	101	A
53	3	110	C
53	3	121	U
53	3	130	A
53	3	144	G
53	3	173	U
53	3	183	C
53	3	197	A
53	3	208	U
53	3	210	C
53	3	211	G
53	3	247	G
53	3	251	G
53	3	253	A
53	3	266	G
53	3	267	C
53	3	280	C
53	3	281	G
53	3	289	G
53	3	328	C
53	3	352	C
53	3	354	G
53	3	367	U
53	3	369	G
53	3	372	C
53	3	397	A
53	3	413	G
53	3	414	A
53	3	419	C
53	3	422	C
53	3	423	G
53	3	429	U
53	3	467	U
53	3	468	A
53	3	474	G
53	3	479	U
53	3	480	U
53	3	485	U
53	3	486	U
53	3	495	A
53	3	496	A
53	3	497	G

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Mol	Chain	Res	Type
53	3	509	A
53	3	531	U
53	3	532	A
53	3	547	A
53	3	559	A
53	3	561	U
53	3	566	G
53	3	572	A
53	3	573	A
53	3	575	G
53	3	576	C
53	3	577	G
53	3	596	A
53	3	633	G
53	3	653	U
53	3	665	A
53	3	671	G
53	3	686	U
53	3	687	A
53	3	688	G
53	3	703	G
53	3	724	G
53	3	731	G
53	3	733	G
53	3	755	G
53	3	777	A
53	3	793	U
53	3	794	A
53	3	814	A
53	3	817	C
53	3	818	G
53	3	819	A
53	3	821	G
53	3	842	U
53	3	843	U
53	3	844	G
53	3	846	G
53	3	887	G
53	3	902	G
53	3	934	C
53	3	935	A
53	3	938	A

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Mol	Chain	Res	Type
53	3	943	U
53	3	960	U
53	3	963	G
53	3	966	G
53	3	969	A
53	3	975	A
53	3	976	G
53	3	977	A
53	3	992	U
53	3	993	G
53	3	994	A
53	3	1004	A
53	3	1012	A
53	3	1026	G
53	3	1029	U
53	3	1031	C
53	3	1032	G
53	3	1033	G
53	3	1053	G
53	3	1054	C
53	3	1055	A
53	3	1086	U
53	3	1094	G
53	3	1096	C
53	3	1101	A
53	3	1130	A
53	3	1133	G
53	3	1136	C
53	3	1137	C
53	3	1138	G
53	3	1139	G
53	3	1146	A
53	3	1159	U
53	3	1168	U
53	3	1182	G
53	3	1184	G
53	3	1196	A
53	3	1212	U
53	3	1225	A
53	3	1238	A
53	3	1241	G
53	3	1275	A

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Mol	Chain	Res	Type
53	3	1278	G
53	3	1280	A
53	3	1282	C
53	3	1286	U
53	3	1287	A
53	3	1290	G
53	3	1299	A
53	3	1300	G
53	3	1301	U
53	3	1302	C
53	3	1305	G
53	3	1317	C
53	3	1320	C
53	3	1363	A
53	3	1378	C
53	3	1381	U
53	3	1394	A
53	3	1395	C
53	3	1398	A
53	3	1419	G
53	3	1422	G
53	3	1428	A
53	3	1431	A
53	3	1446	A
53	3	1448	C
53	3	1452	C
53	3	1453	G
53	3	1492	A
53	3	1497	G
53	3	1499	A
53	3	1503	A
53	3	1505	G
53	3	1506	U
53	3	1508	A
53	3	1517	G
53	3	1529	G
53	3	1530	G
54	4	4	U
54	4	8	U
54	4	9	U
54	4	10	C
54	4	12	U

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Mol	Chain	Res	Type
54	4	13	U
54	4	14	U
54	4	15	U
54	4	16	U
54	4	17	U
54	4	18	U
54	4	19	U
54	4	20	U
63	5	2	C
63	5	7	A
63	5	8	U
63	5	9	A
63	5	11	C
63	5	13	C
63	5	15	G
63	5	17	C
63	5	18	G
63	5	19	G
63	5	20	U
63	5	21	A
63	5	26	A
63	5	32	U
63	5	33	U
63	5	35	A
63	5	36	A
63	5	38	A
63	5	39	U
63	5	43	C
63	5	44	G
63	5	46	G
63	5	47	U
63	5	48	C
63	5	49	C
63	5	52	G
63	5	53	G
63	5	55	U
63	5	56	C
63	5	57	G
63	5	58	A
63	5	59	U
63	5	60	U
63	5	61	C

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Mol	Chain	Res	Type
63	5	66	U
63	5	73	A
63	5	74	C
63	5	76	A
64	6	5	G
64	6	7	G
64	6	9	G
64	6	10	G
64	6	14	A
64	6	18	G
64	6	19	G
64	6	21	A
64	6	22	G
64	6	27	U
64	6	43	A
64	6	44	A
64	6	45	G
64	6	47	U
64	6	48	C
64	6	49	G
64	6	59	A
64	6	70	G

All (27) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
51	1	227	A
51	1	490	C
51	1	784	G
51	1	859	G
51	1	1020	A
51	1	1130	U
51	1	2296	U
51	1	2326	C
51	1	2756	U
51	1	2873	A
52	2	88	C
53	3	70	U
53	3	413	G
53	3	1012	A
53	3	1054	C
53	3	1301	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
53	3	1395	C
54	4	13	U
54	4	18	U
54	4	19	U
63	5	7	A
63	5	35	A
63	5	48	C
63	5	57	G
63	5	60	U
63	5	73	A
63	5	75	C

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

4 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	$\# Z > 2$
67	UAL	h	5	67	6,8,9	2.36	2 (33%)	4,9,11	1.89	1 (25%)
67	DPP	h	2	67	4,5,6	0.50	0	1,5,7	0.07	0
67	KBE	h	1	67	8,8,9	0.58	0	6,8,10	1.18	0
67	5OH	h	6	67	7,12,13	0.72	0	4,16,18	1.33	1 (25%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
67	UAL	h	5	67	-	0/3/7/9	-
67	DPP	h	2	67	-	0/2/4/6	-
67	KBE	h	1	67	-	0/7/7/8	-
67	5OH	h	6	67	-	0/2/18/20	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
67	h	5	UAL	C1-N1	-4.95	1.32	1.40
67	h	5	UAL	C-CA	-2.82	1.40	1.45

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
67	h	5	UAL	O-C-CA	-3.31	121.25	125.39
67	h	6	5OH	CR-CB-CA	-2.40	110.06	112.61

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
67	h	5	UAL	1	0
67	h	2	DPP	1	0
67	h	6	5OH	4	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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	$\# Z > 2$
70	PO4	0	802	-	4,4,4	1.15	0	6,6,6	0.73	0
69	GDP	0	801	-	29,30,30	1.13	4 (13%)	45,47,47	1.76	6 (13%)

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
69	GDP	0	801	-	-	0/16/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
69	0	801	GDP	C5-C4	2.84	1.46	1.38
69	0	801	GDP	C6-N1	-2.47	1.34	1.38
69	0	801	GDP	C5-N7	-2.25	1.34	1.39
69	0	801	GDP	C4-N9	-2.18	1.32	1.38

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
69	0	801	GDP	C5-C4-N3	-5.58	119.52	128.39
69	0	801	GDP	C2-N3-C4	4.88	120.71	112.30
69	0	801	GDP	N9-C4-N3	3.93	133.80	125.95
69	0	801	GDP	C6-C5-N7	3.51	136.69	130.29
69	0	801	GDP	C4-C5-N7	-2.55	106.63	110.67
69	0	801	GDP	O6-C6-C5	-2.35	120.33	126.53

There are no chirality outliers.

There are no torsion outliers.

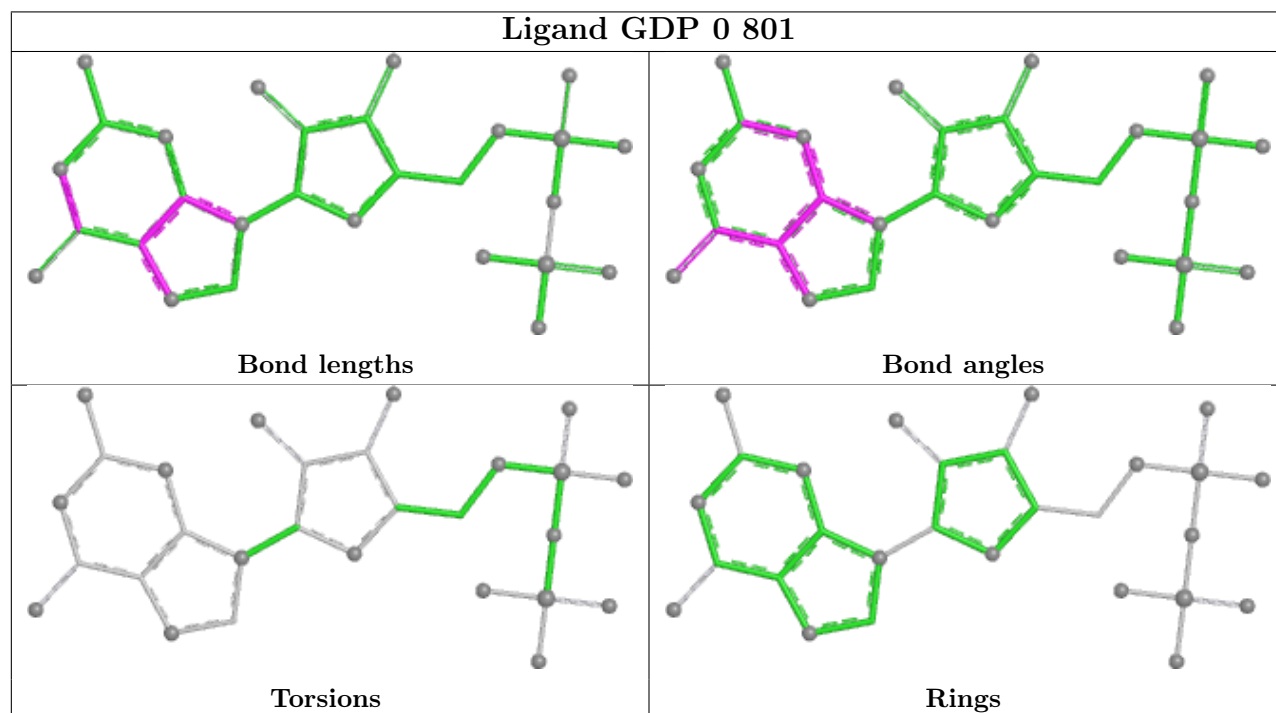
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
70	0	802	PO4	1	0
69	0	801	GDP	2	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.

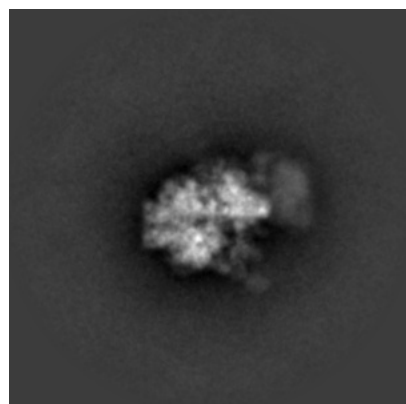
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38942. These allow visual inspection of the internal detail of the map and identification of artifacts.

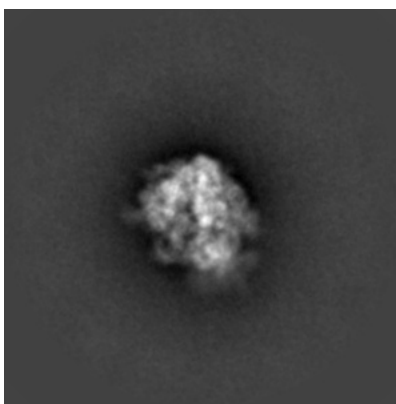
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

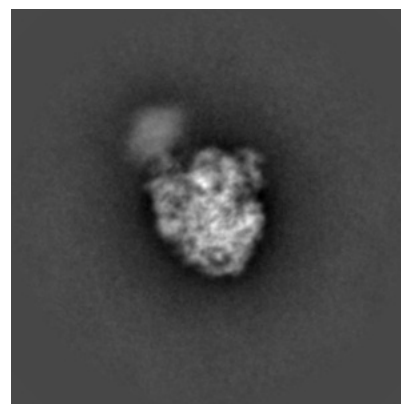
6.1.1 Primary map



X

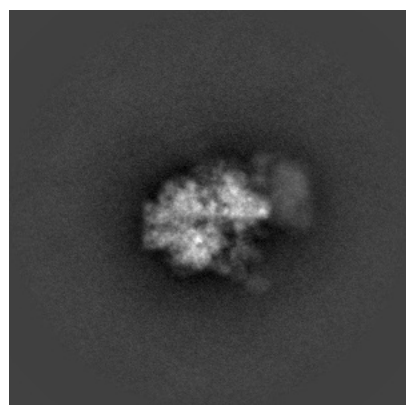


Y

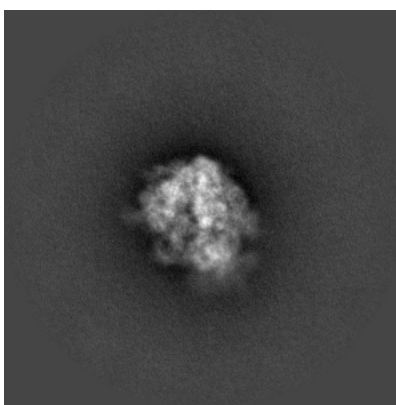


Z

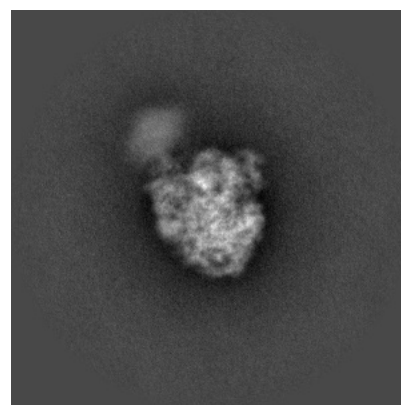
6.1.2 Raw map



X



Y

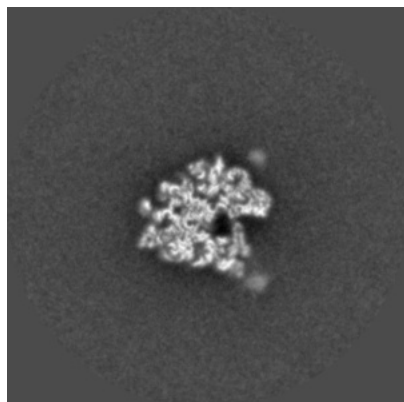


Z

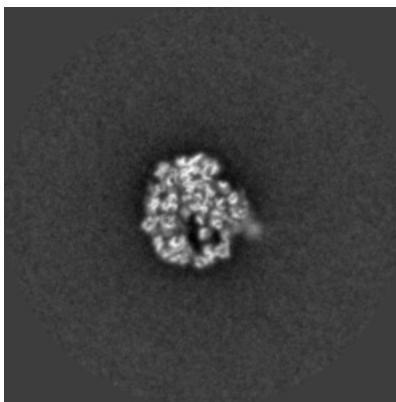
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

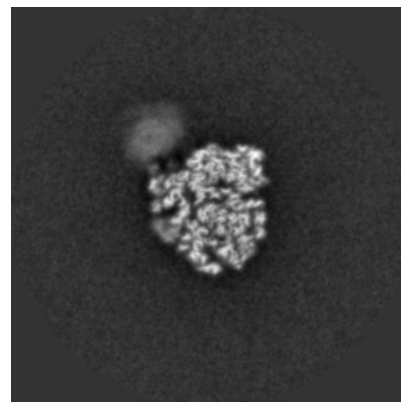
6.2.1 Primary map



X Index: 240

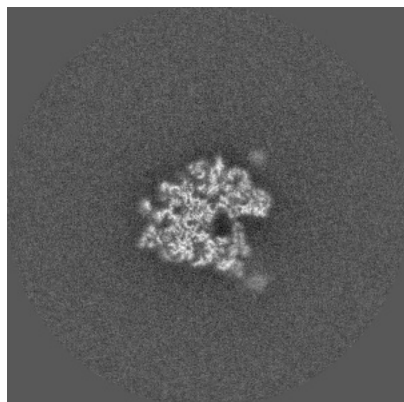


Y Index: 240

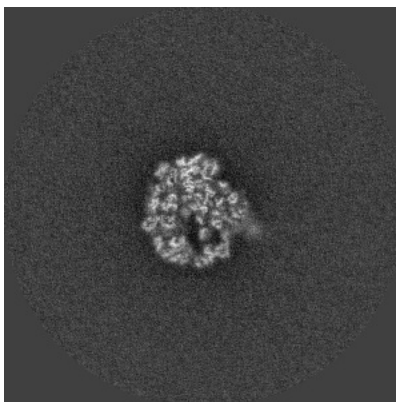


Z Index: 240

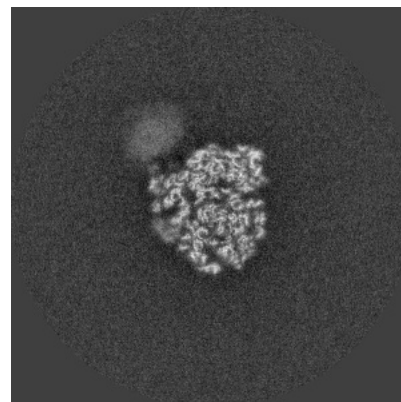
6.2.2 Raw map



X Index: 240



Y Index: 240

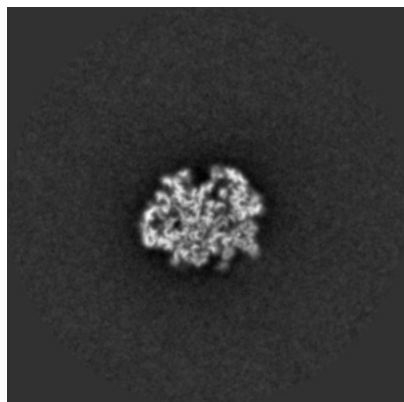


Z Index: 240

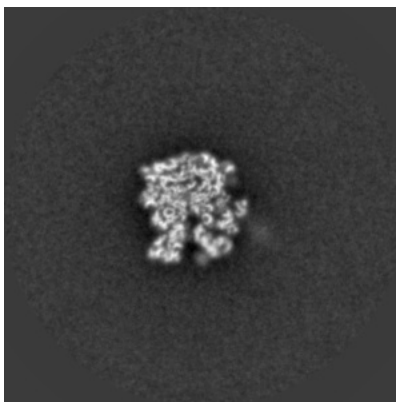
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

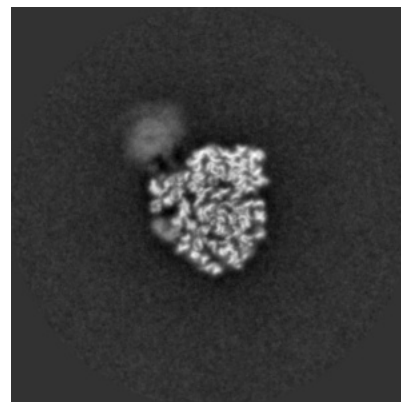
6.3.1 Primary map



X Index: 264

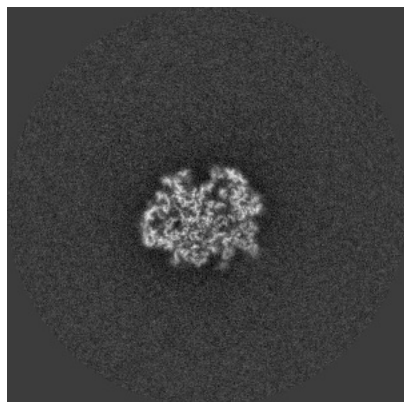


Y Index: 223

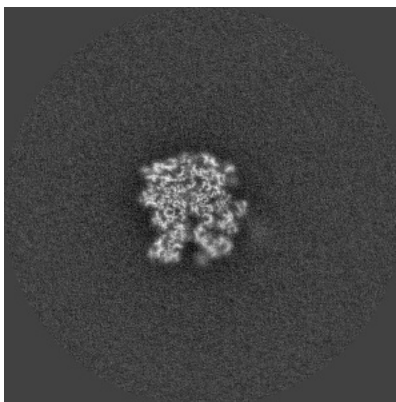


Z Index: 238

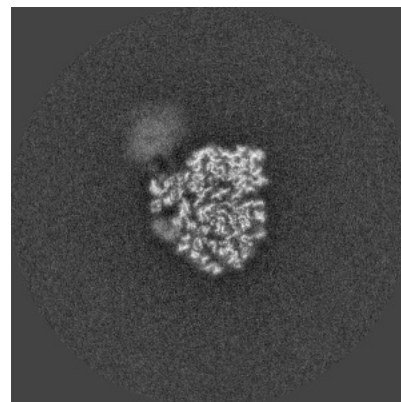
6.3.2 Raw map



X Index: 264



Y Index: 222



Z Index: 238

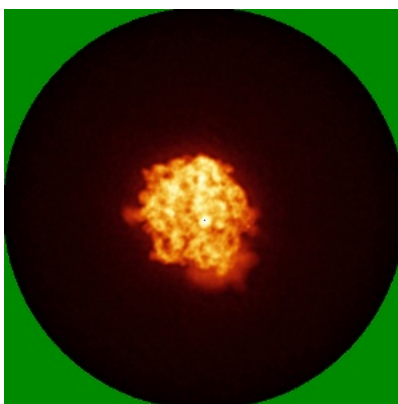
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

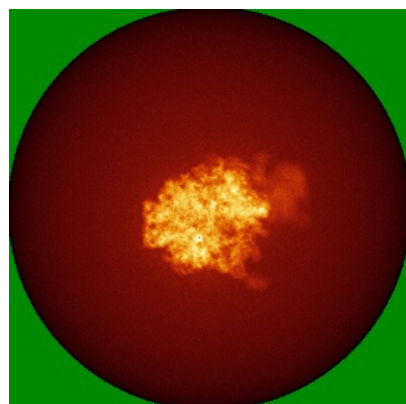


Y

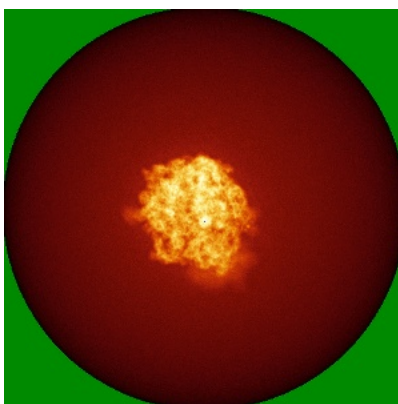


Z

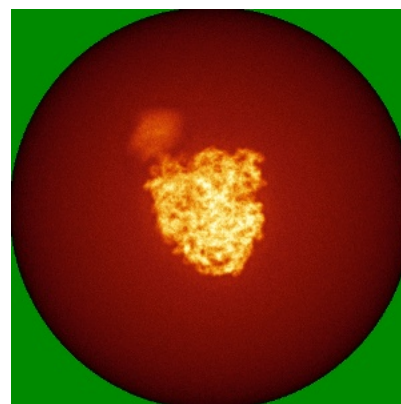
6.4.2 Raw map



X



Y

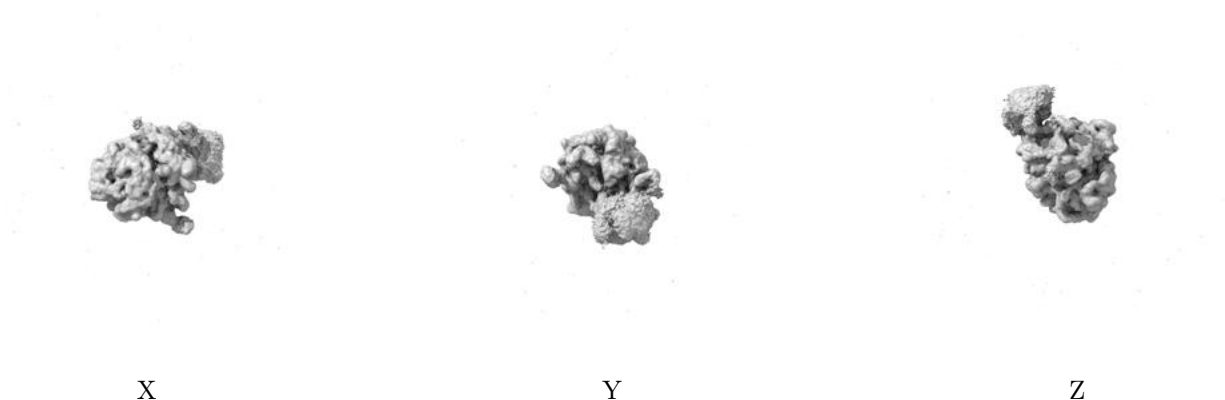


Z

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

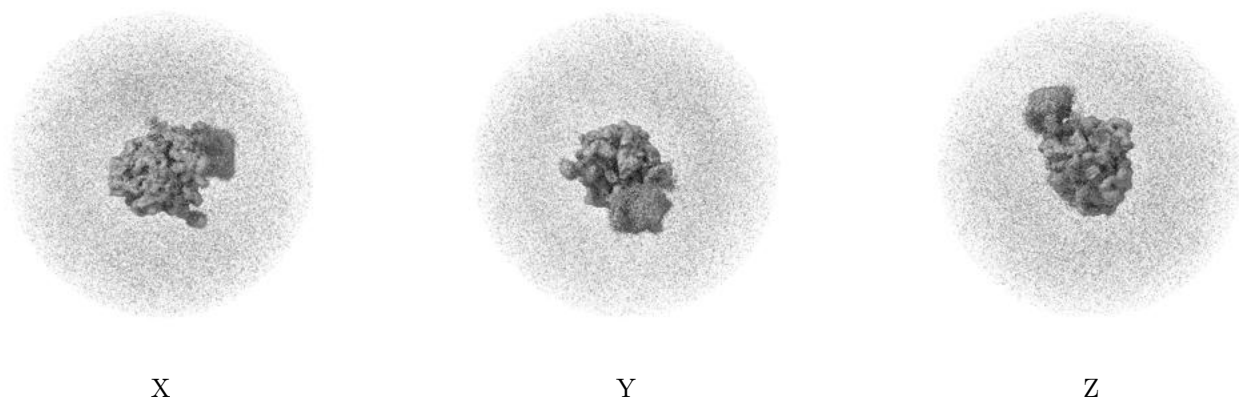
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0075. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

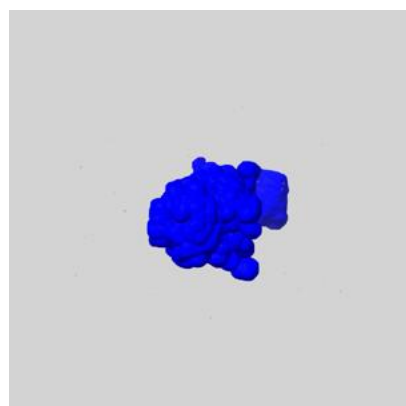
6.6 Mask visualisation [i](#)

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

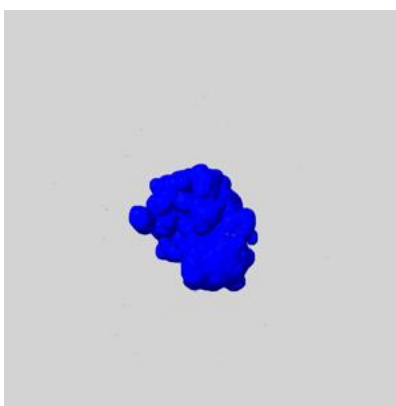
A mask typically either:

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

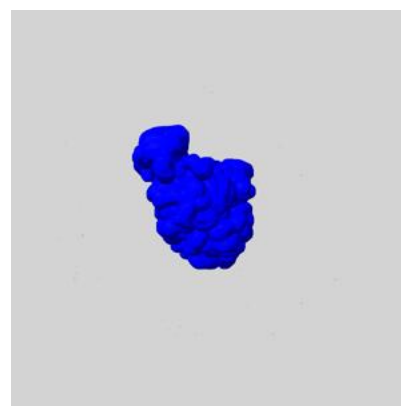
6.6.1 emd_38942_msk_1.map [i](#)



X



Y

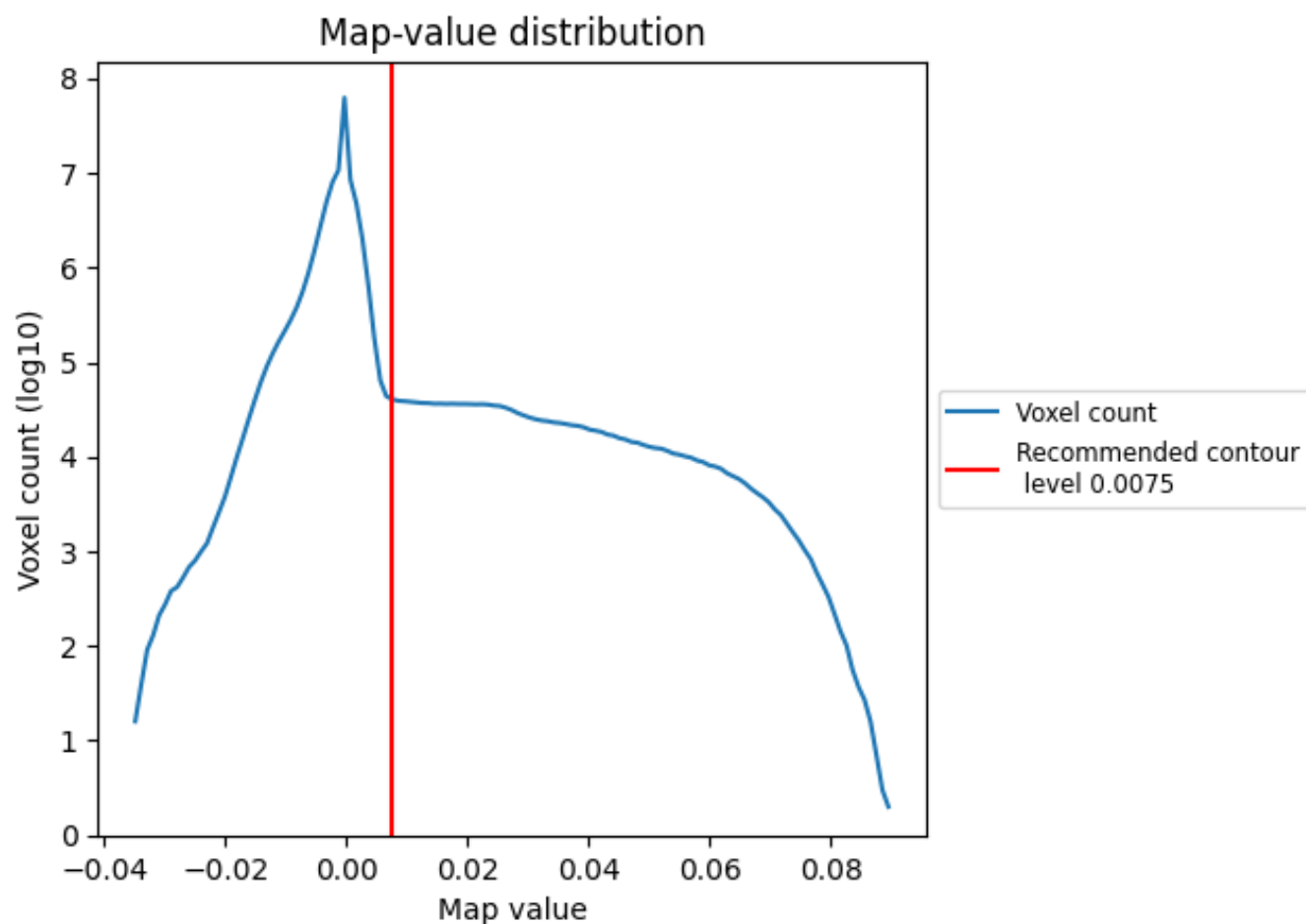


Z

7 Map analysis [i](#)

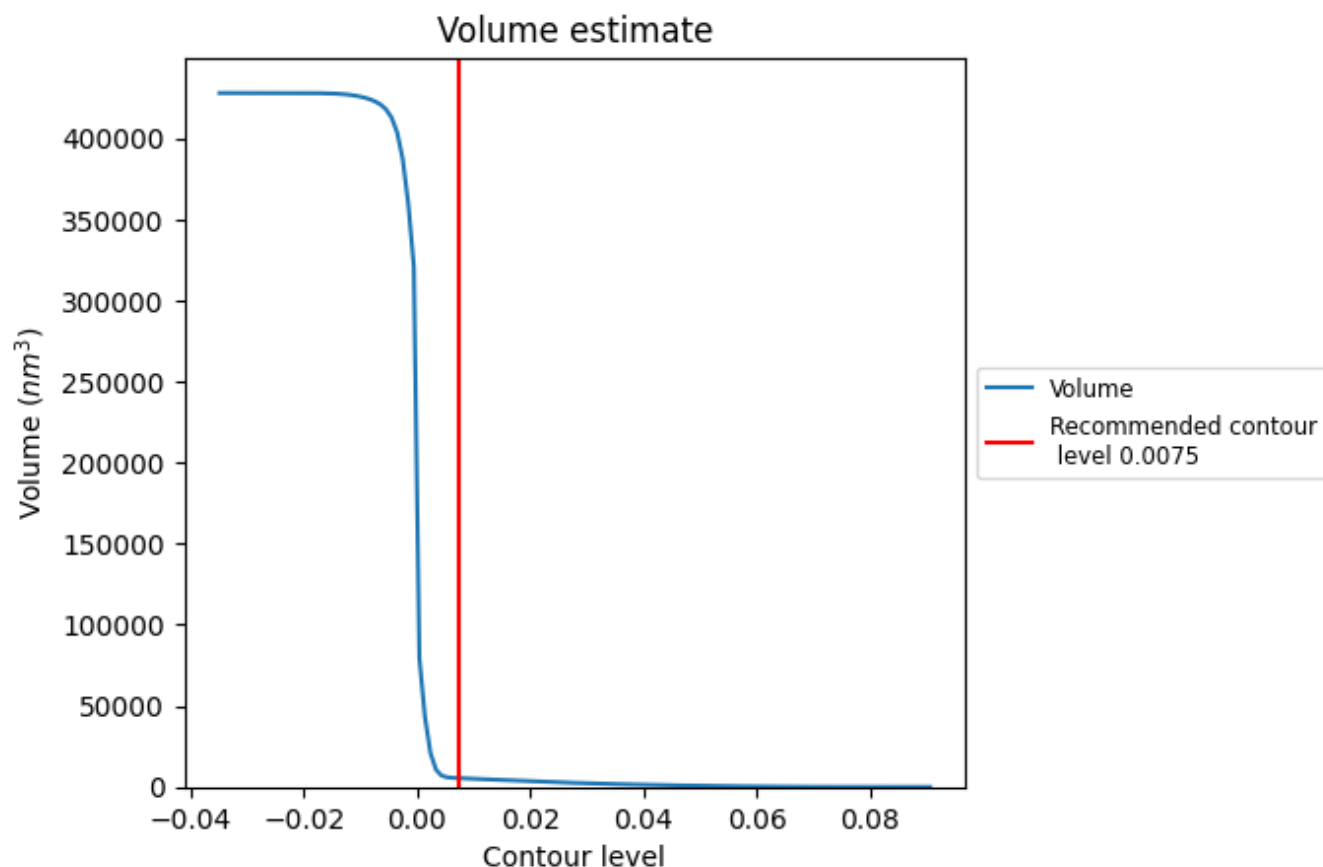
This section contains the results of statistical analysis of the map.

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.

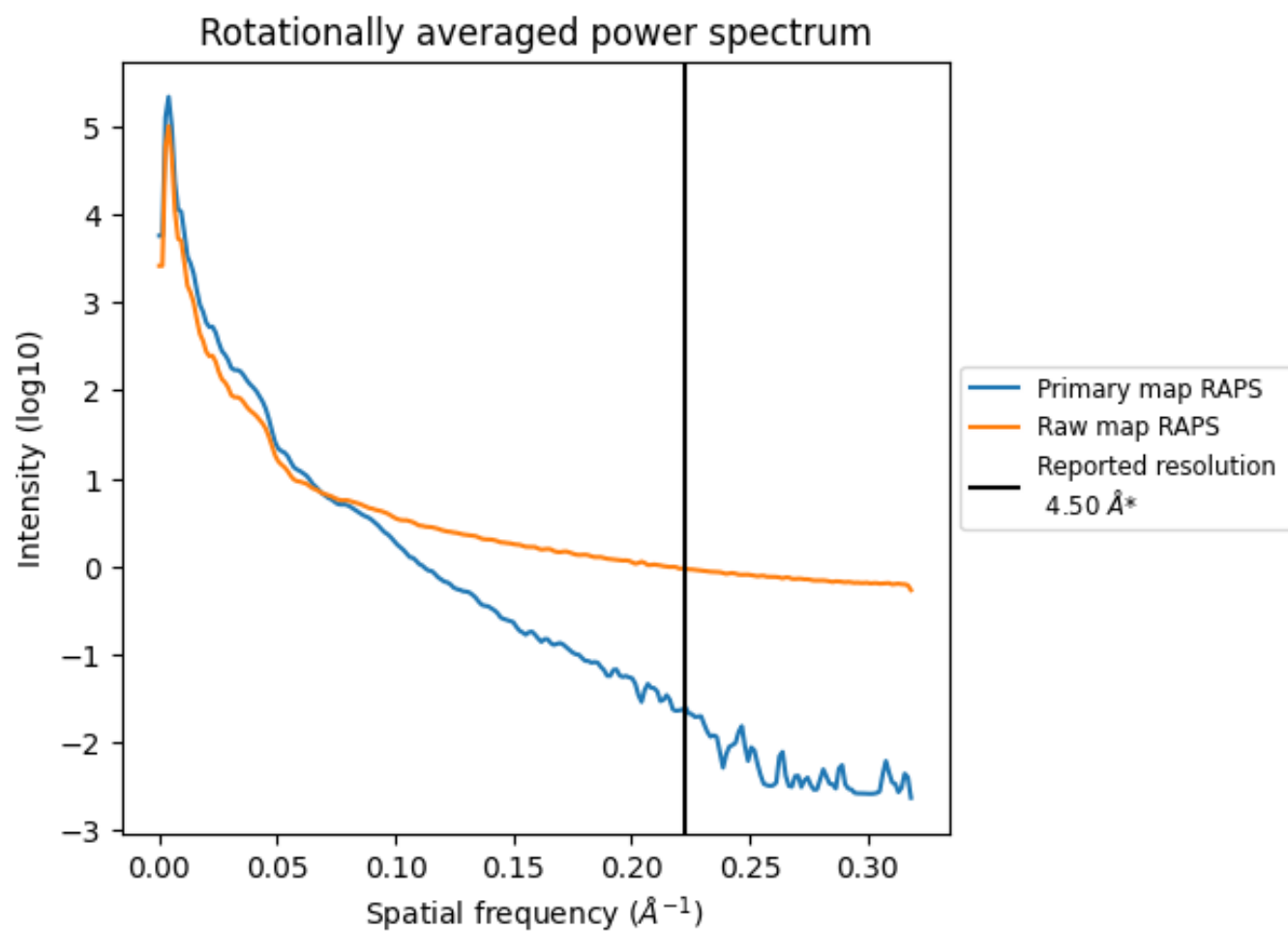
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5419 nm^3 ; this corresponds to an approximate mass of 4895 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 ⓘ

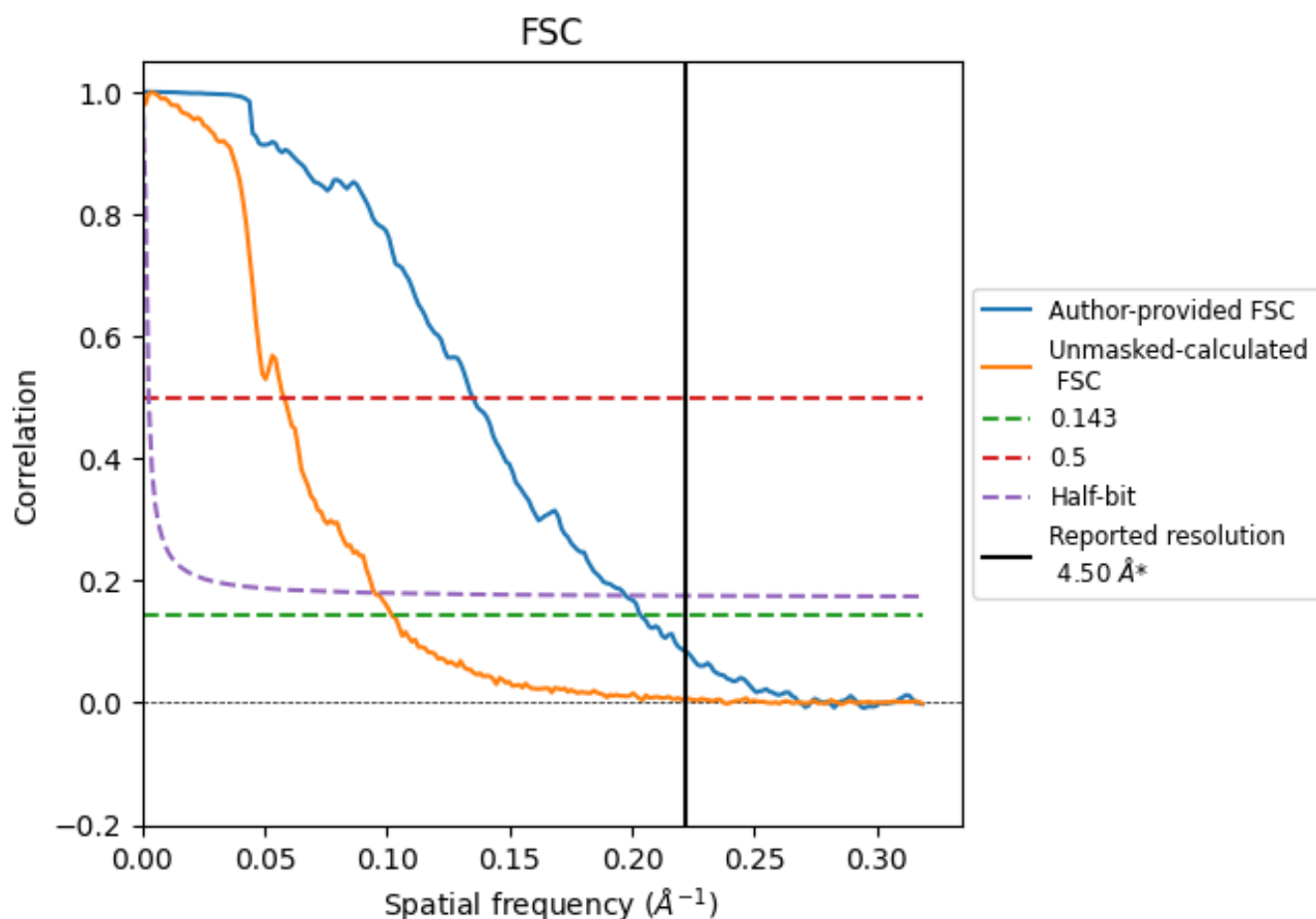


*Reported resolution corresponds to spatial frequency of 0.222 Å⁻¹

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 0.222 Å⁻¹

8.2 Resolution estimates [i](#)

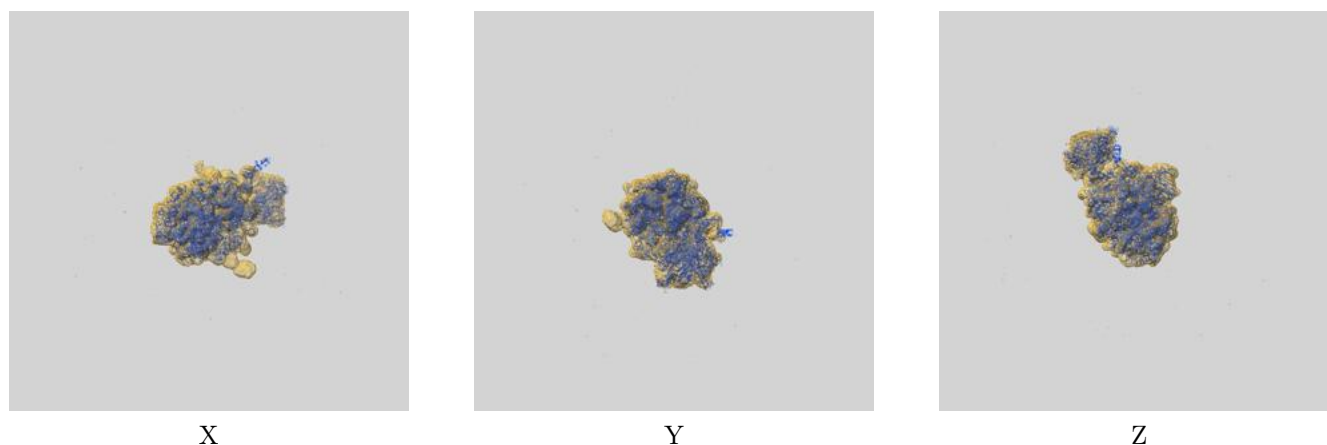
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.50	-	-
Author-provided FSC curve	4.91	7.41	5.07
Unmasked-calculated*	9.81	17.30	10.52

*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 9.81 differs from the reported value 4.5 by more than 10 %

9 Map-model fit [i](#)

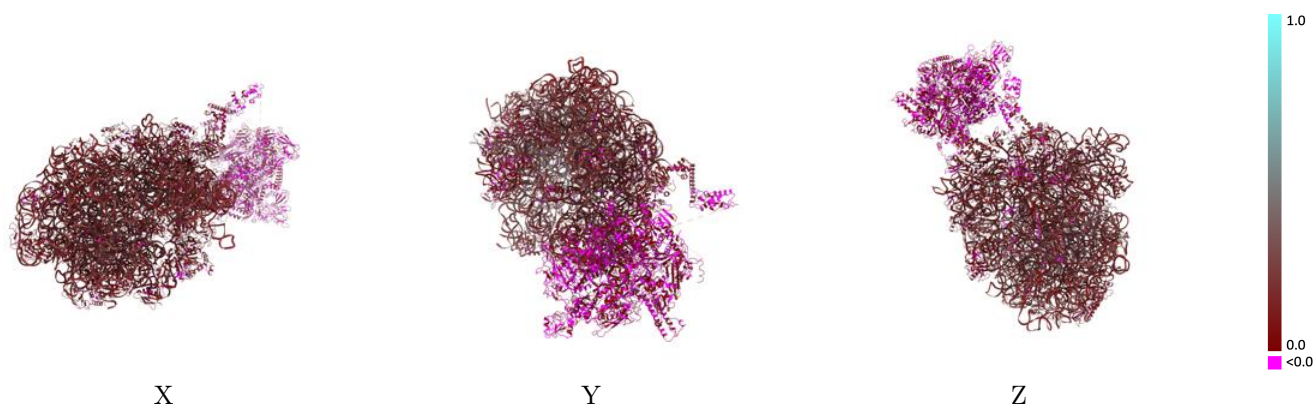
This section contains information regarding the fit between EMDB map EMD-38942 and PDB model 8Y5M. Per-residue inclusion information can be found in section 3 on page 18.

9.1 Map-model overlay [i](#)



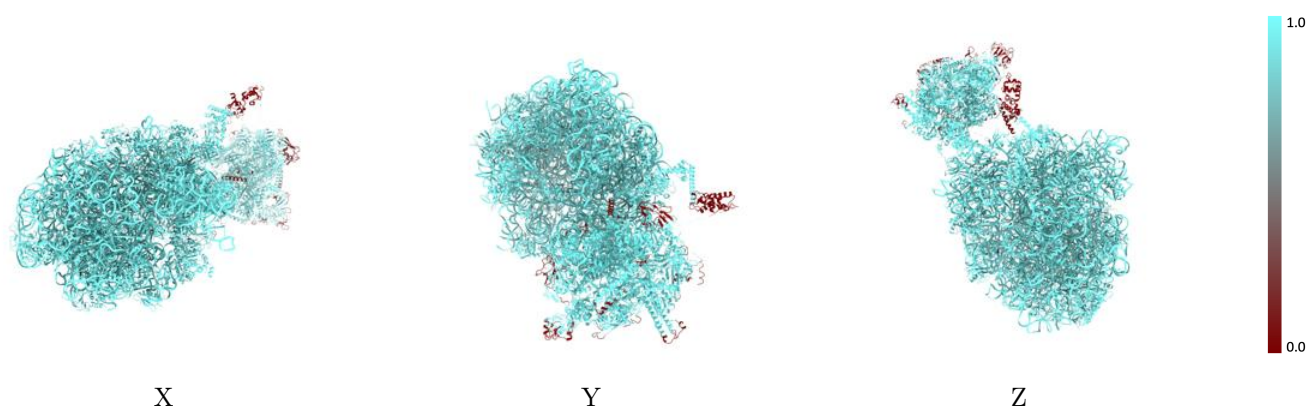
The images above show the 3D surface view of the map at the recommended contour level 0.0075 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



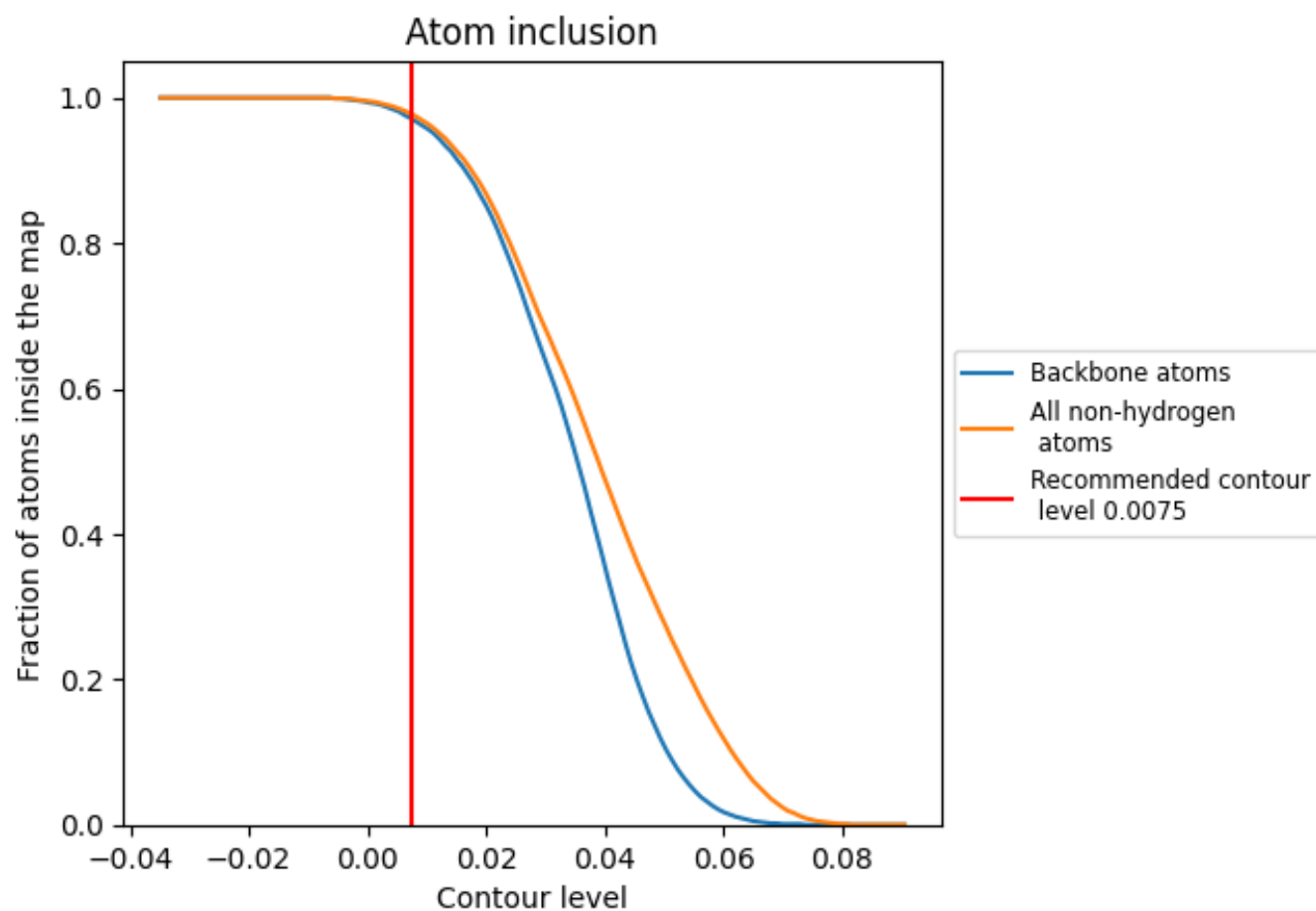
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0075).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 98% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.0075) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9770	 0.1550
0	 0.9680	 0.1420
1	 1.0000	 0.2040
2	 1.0000	 0.1720
3	 1.0000	 0.1910
4	 0.9750	 0.0940
5	 0.9950	 0.1250
6	 0.9950	 0.1820
8	 1.0000	 0.0050
9	 1.0000	 0.0520
A	 0.9260	 0.0890
A1	 0.6540	 0.0140
A2	 0.8070	 0.0190
B	 0.9980	 0.1500
B1	 0.9130	 0.0230
B2	 0.9190	 0.0300
C	 0.9880	 0.1570
D	 0.9750	 0.1320
E	 1.0000	 0.1560
F	 1.0000	 0.0960
G	 0.9920	 0.1230
H	 0.9890	 0.1510
I	 0.9990	 0.1330
J	 0.9930	 0.1430
K	 0.9840	 0.1350
L	 0.9780	 0.1450
M	 0.9740	 0.1270
N	 0.9990	 0.1190
NA	 0.8830	 0.1380
NG	 0.9660	 0.0530
O	 0.9960	 0.1270
P	 0.9960	 0.1510
Q	 0.9570	 0.1600
R	 0.9910	 0.1590
S	 0.9990	 0.1480



Continued on next page...

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Chain	Atom inclusion	Q-score
T	 0.9930	 0.1370
U	 0.9970	 0.1330
V	 0.9910	 0.1450
W	 1.0000	 0.1240
W0	 0.5980	 -0.0110
X	 1.0000	 0.1500
Y	 0.9890	 0.1540
Z	 0.9790	 0.1320
a	 0.9950	 0.0760
b	 0.9920	 0.1670
c	 0.9940	 0.1590
d	 0.9950	 0.1600
e	 0.9800	 0.1280
f	 0.9920	 0.1440
g	 0.9090	 0.1210
h	 1.0000	 0.1620
i	 0.9800	 0.0990
j	 0.9960	 0.1460
k	 0.9810	 0.2100
l	 0.9970	 0.1540
m	 0.9920	 0.1580
n	 0.9980	 0.1480
o	 1.0000	 0.1230
p	 0.9930	 0.1850
q	 0.9990	 0.1340
r	 0.9990	 0.1460
s	 0.9920	 0.1640
t	 0.9900	 0.1180
u	 0.9950	 0.1290
v	 0.9960	 0.1260
w	 1.0000	 0.1280
x	 0.9970	 0.1560
y	 0.9960	 0.1260
z	 0.9950	 0.1560